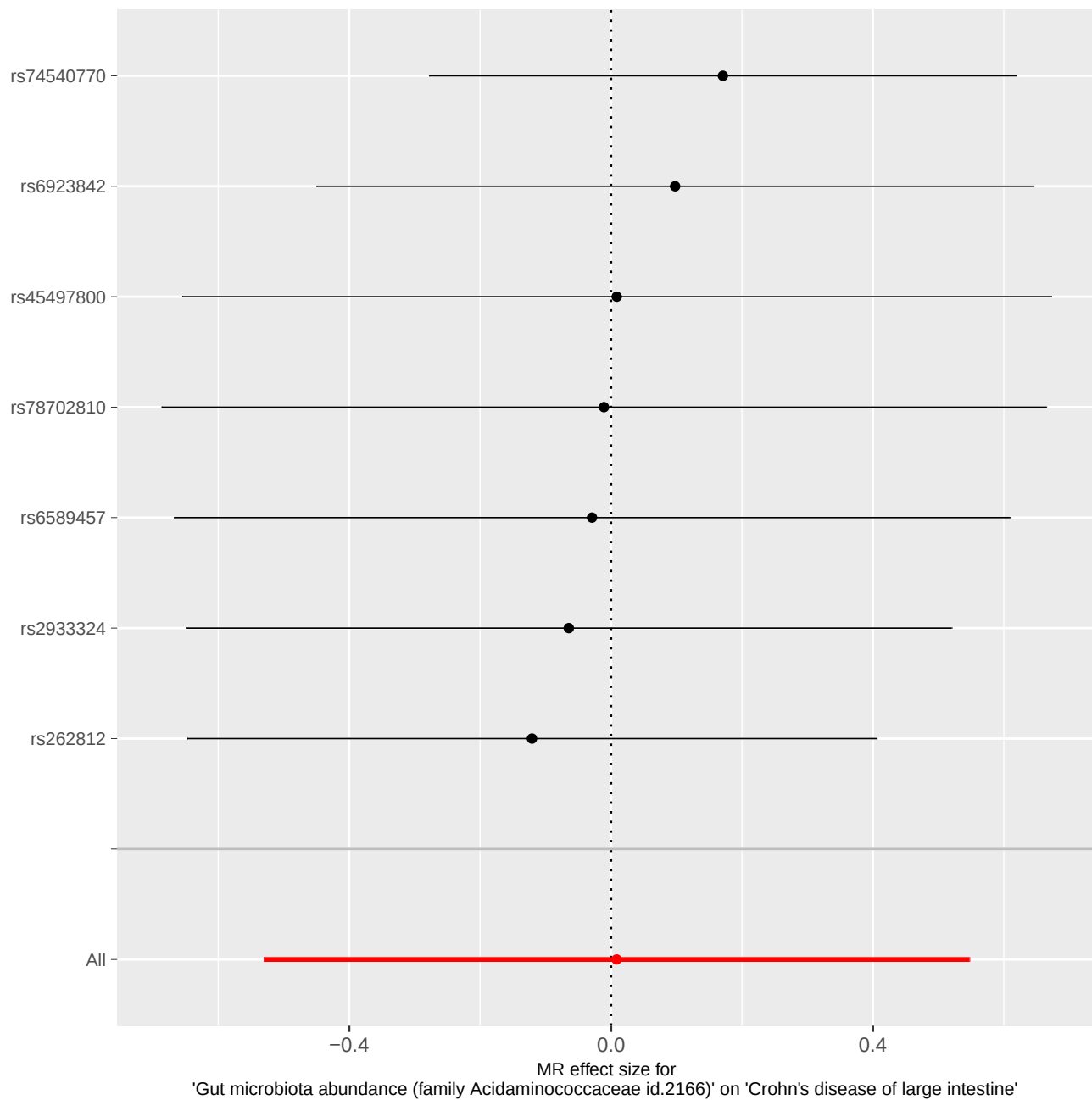
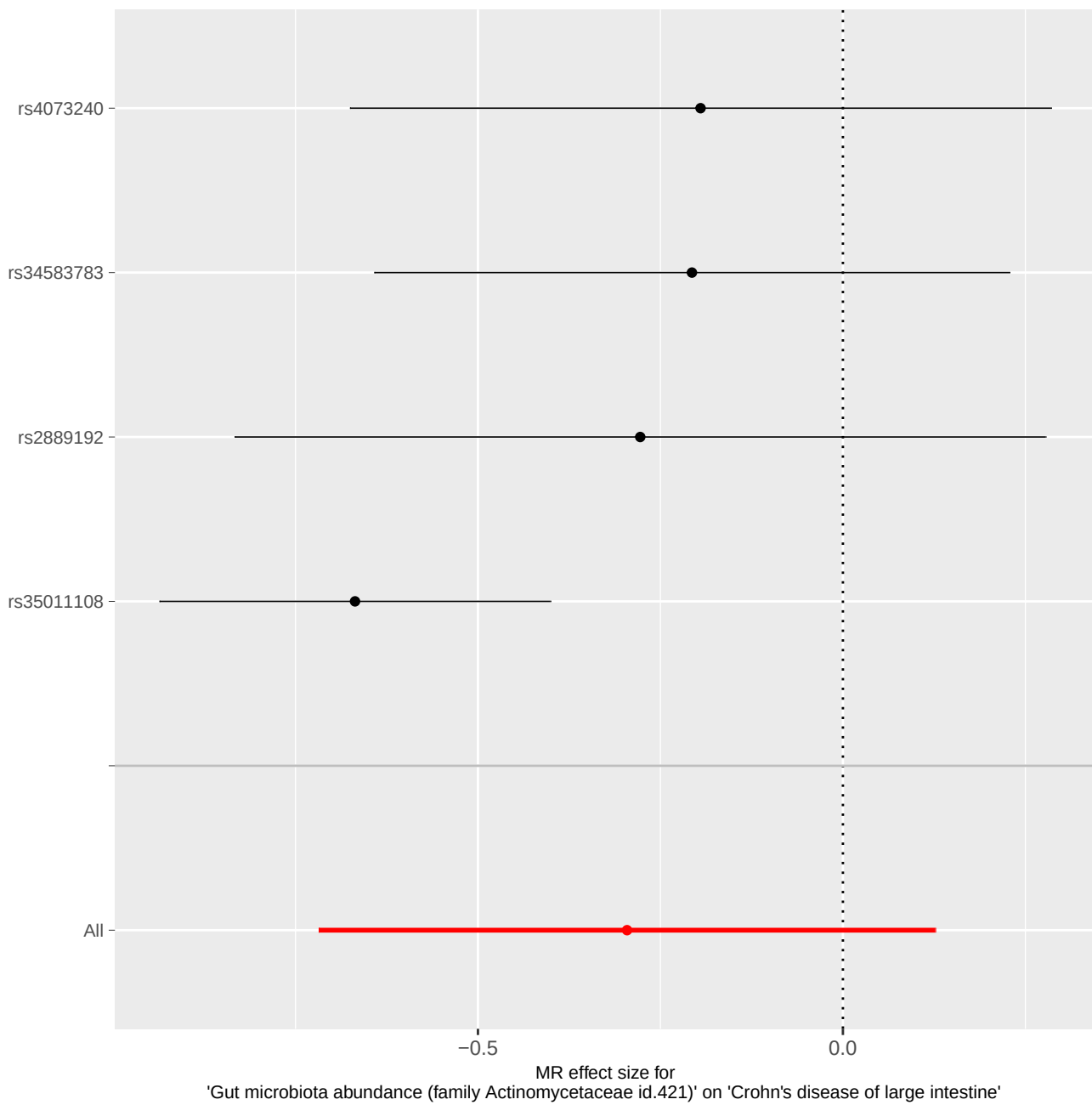
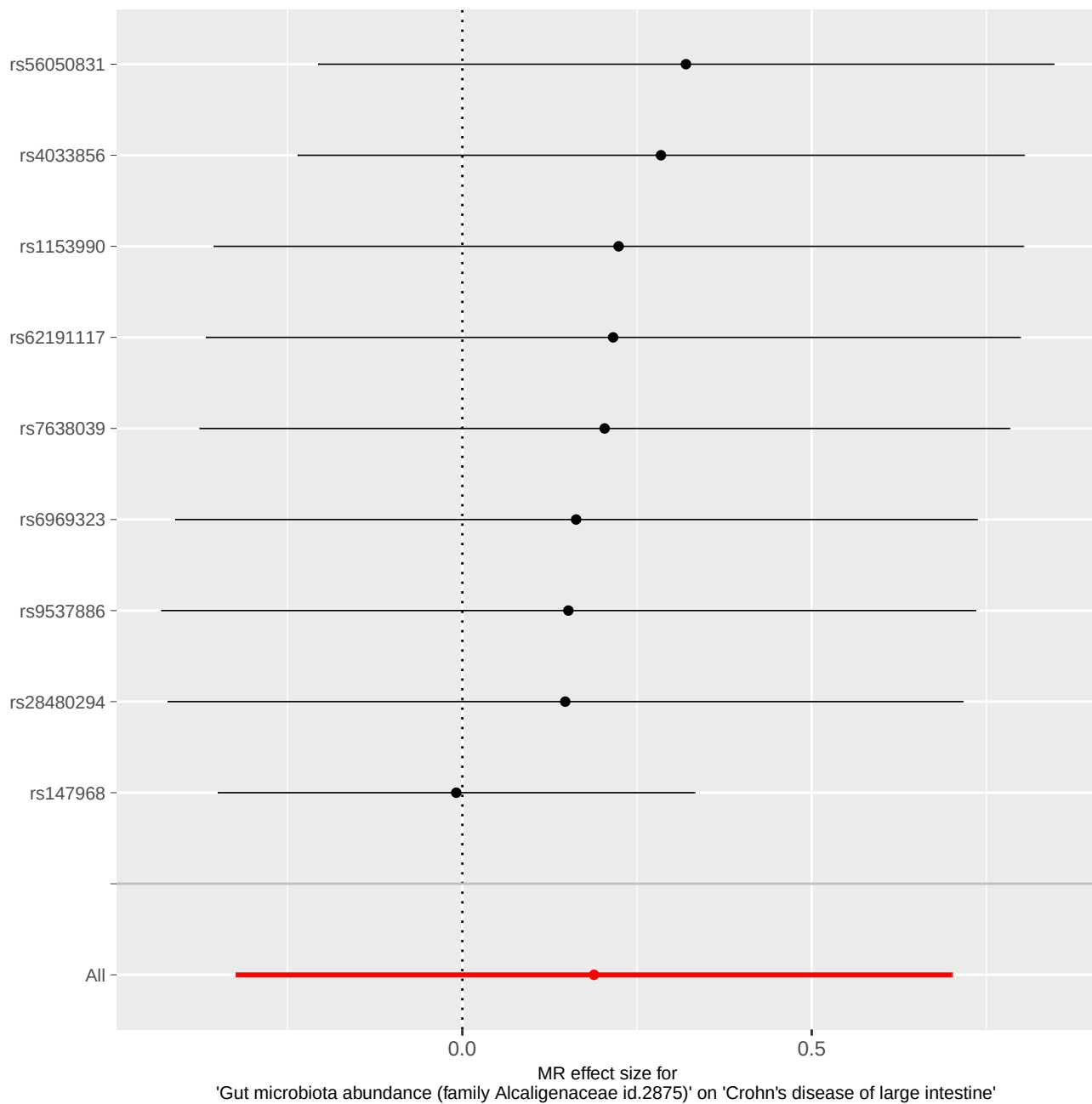


Batch 1 : Gut microbiota abundance (family Acidaminococcaceae id.2166) on Crohn's disease of large intestine

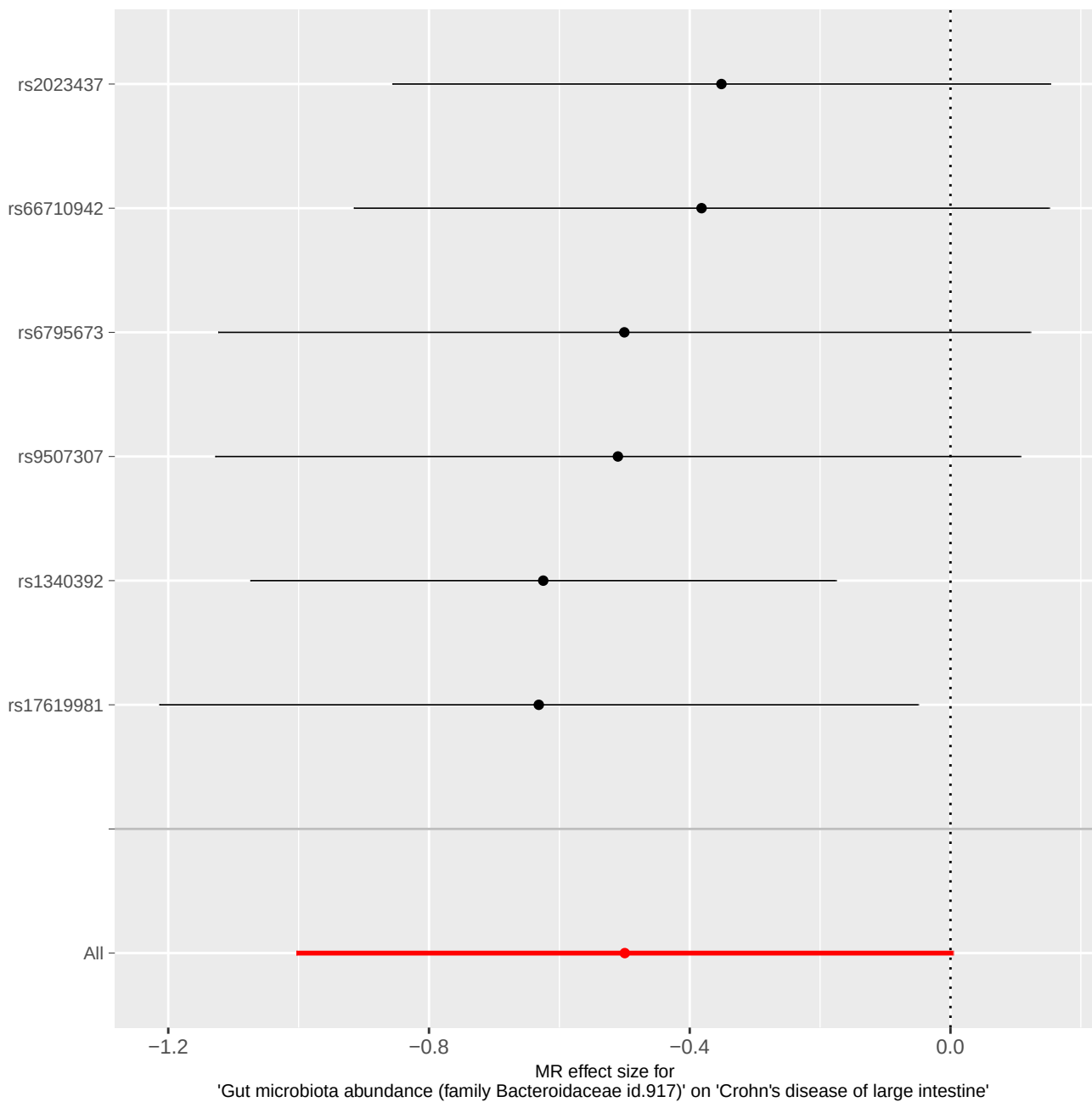


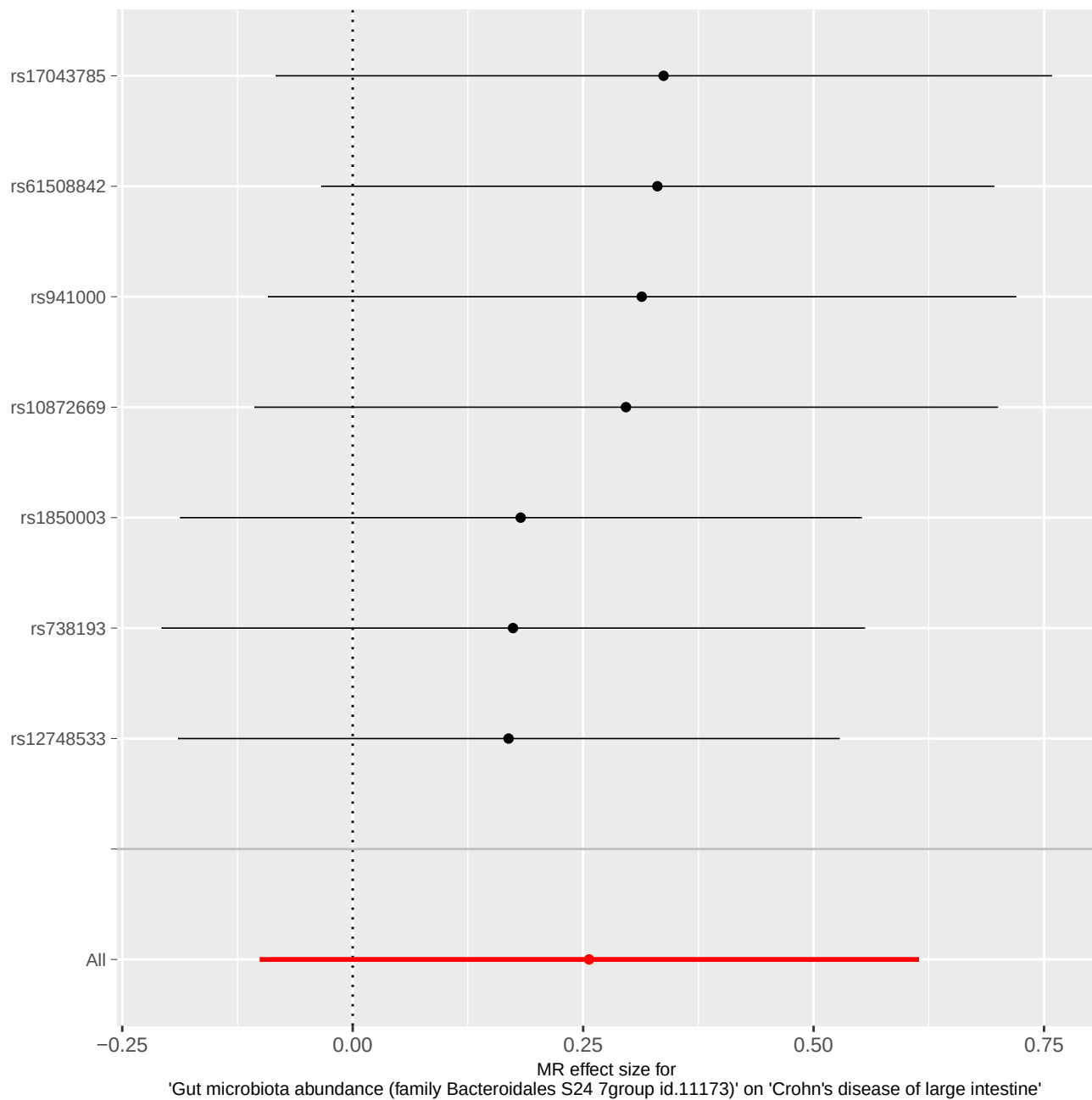
Batch 2 : Gut microbiota abundance (family Actinomycetaceae id.421) on Crohn's disease of large intestine

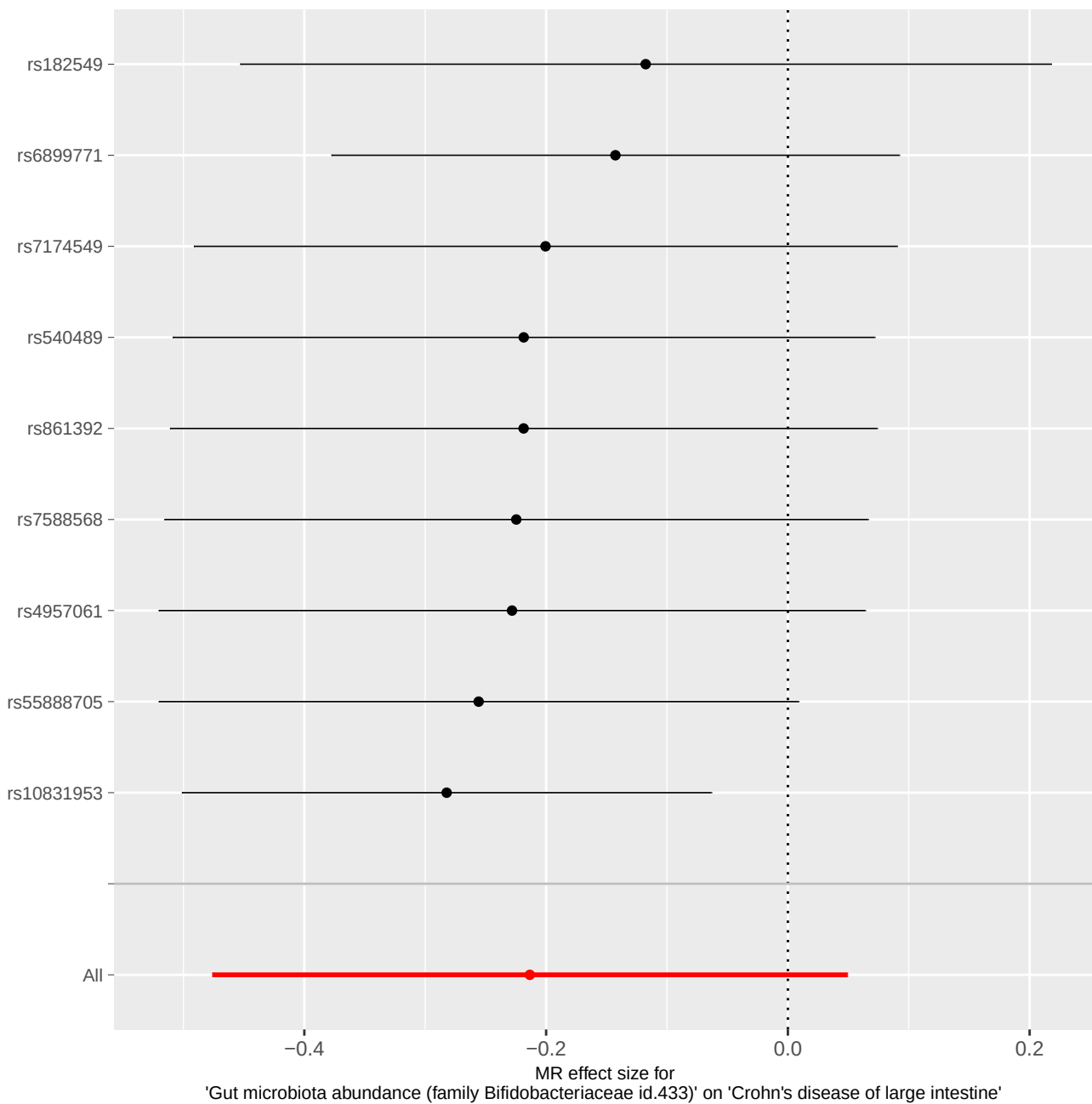




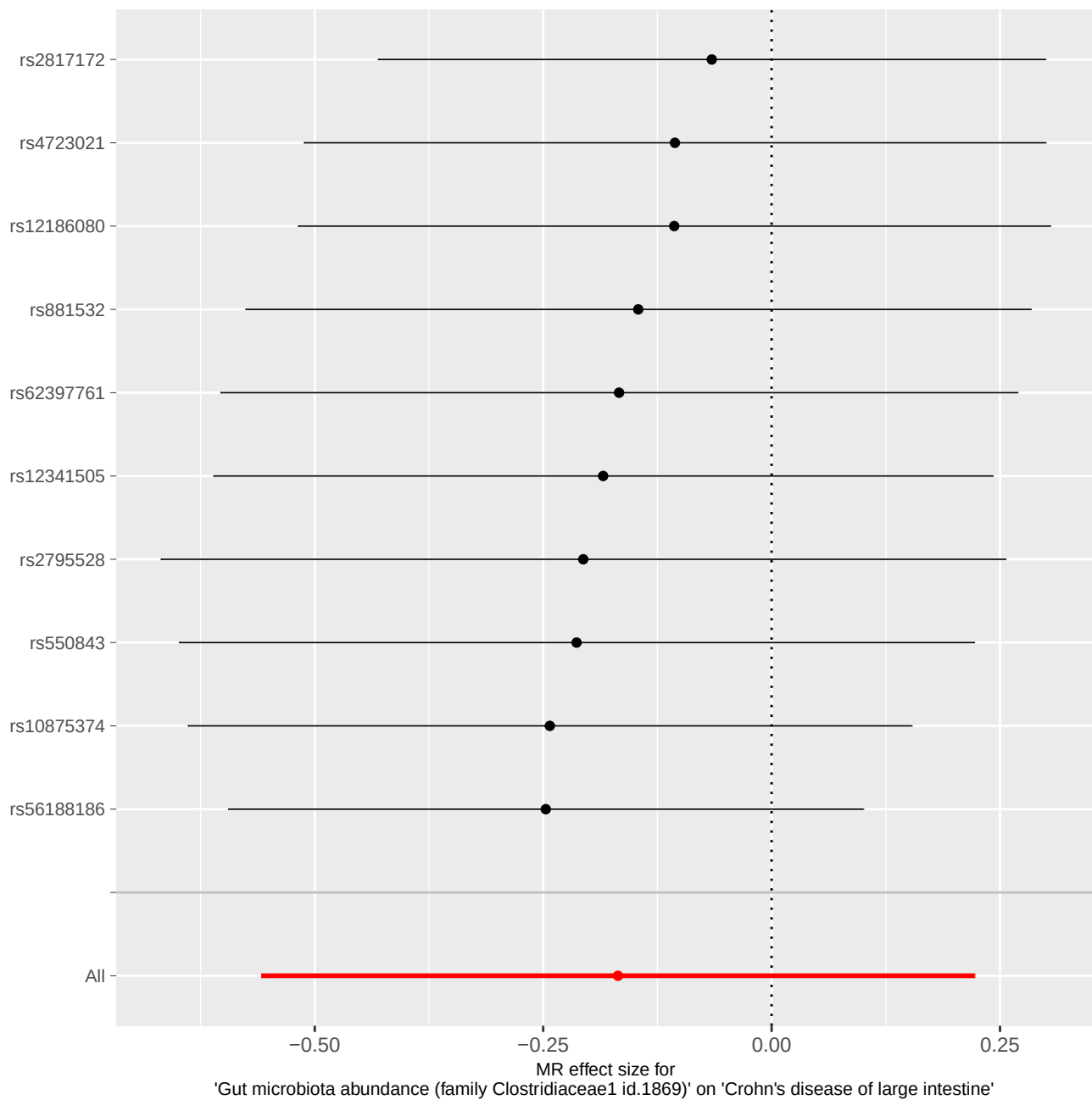
Batch 4 : Gut microbiota abundance (family Bacteroidaceae id.917) on Crohn's disease of large intestine



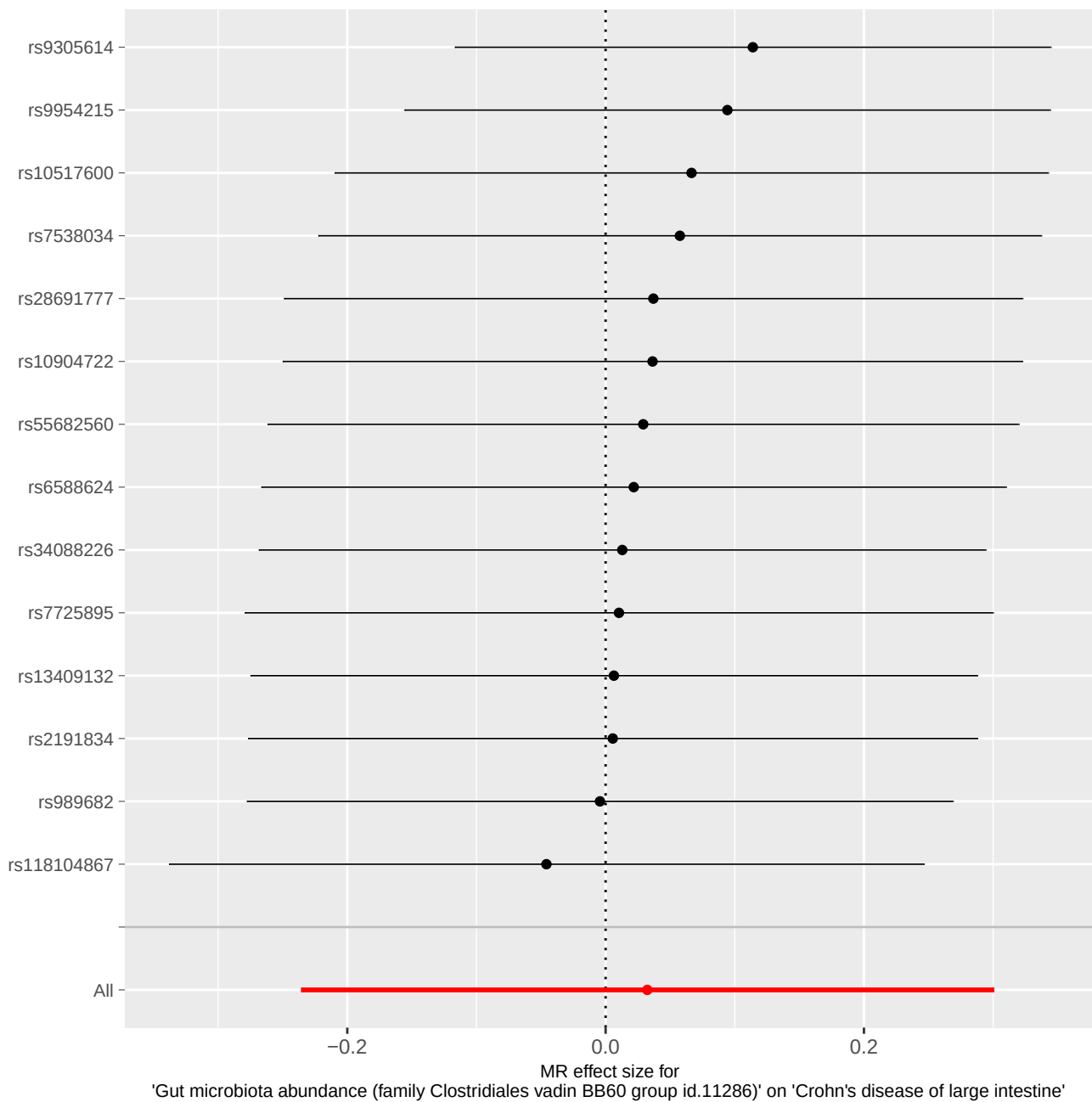




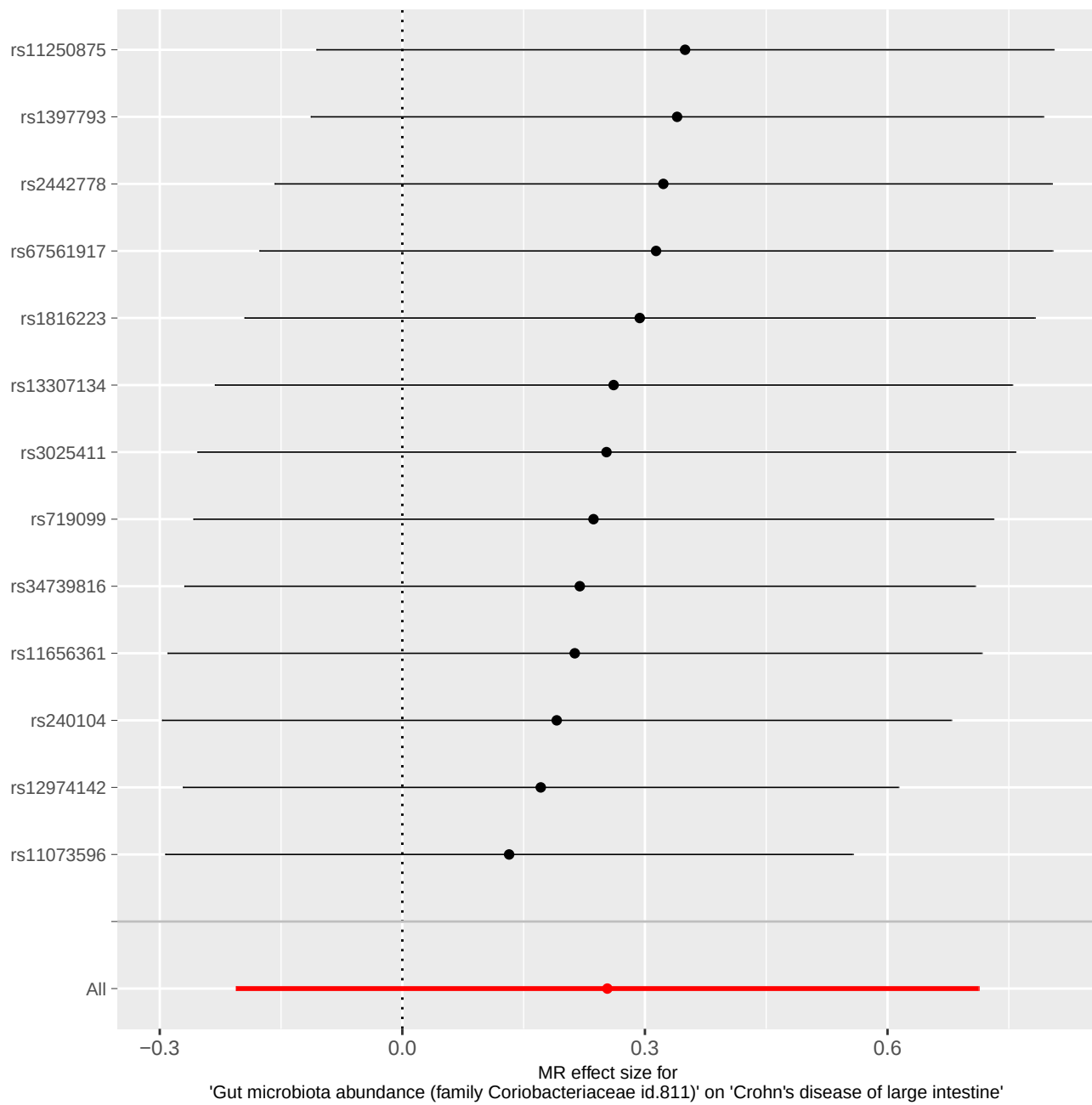
Batch 8 : Gut microbiota abundance (family Clostridiaceae1 id.1869) on Crohn's disease of large intestine

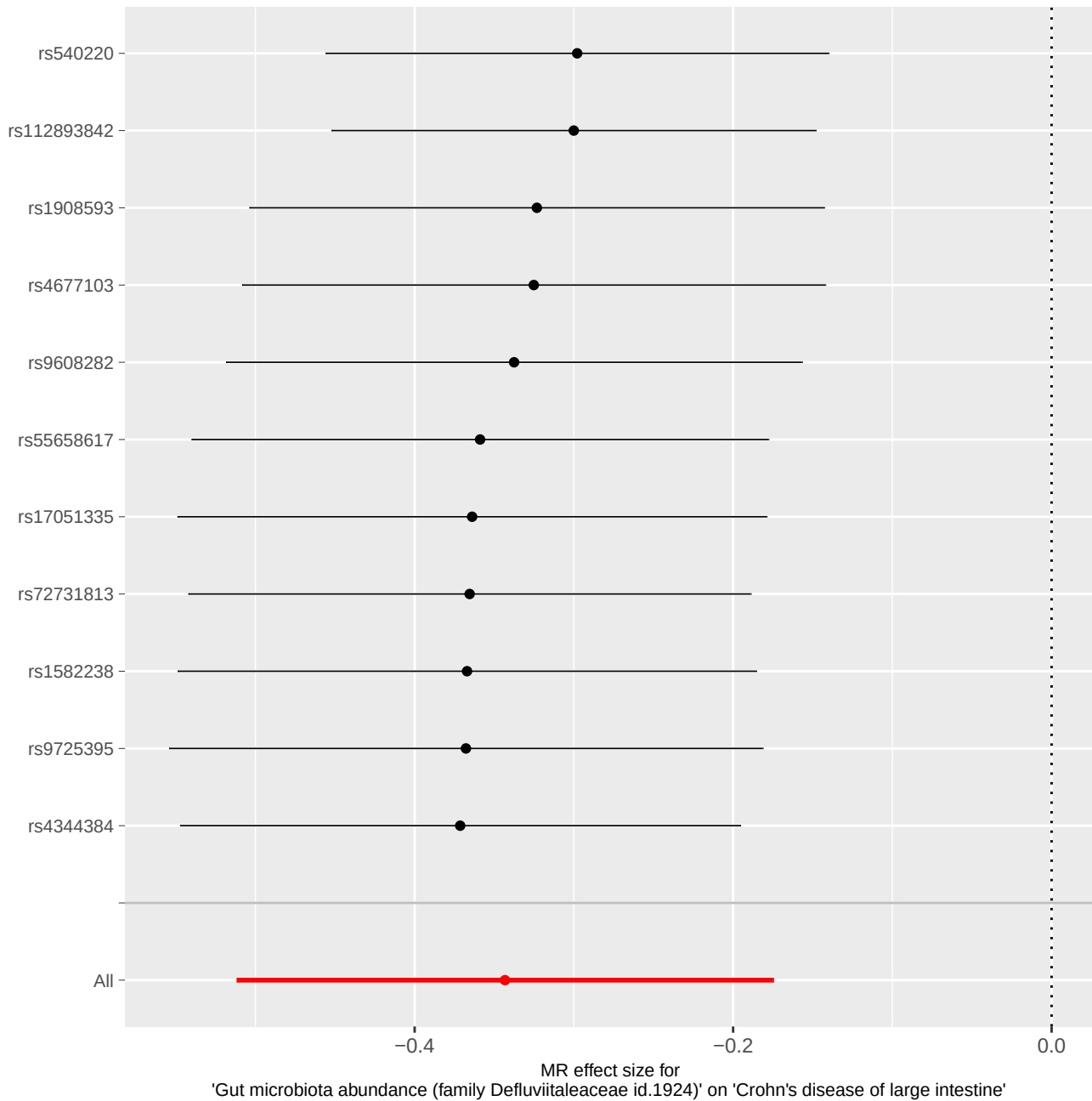


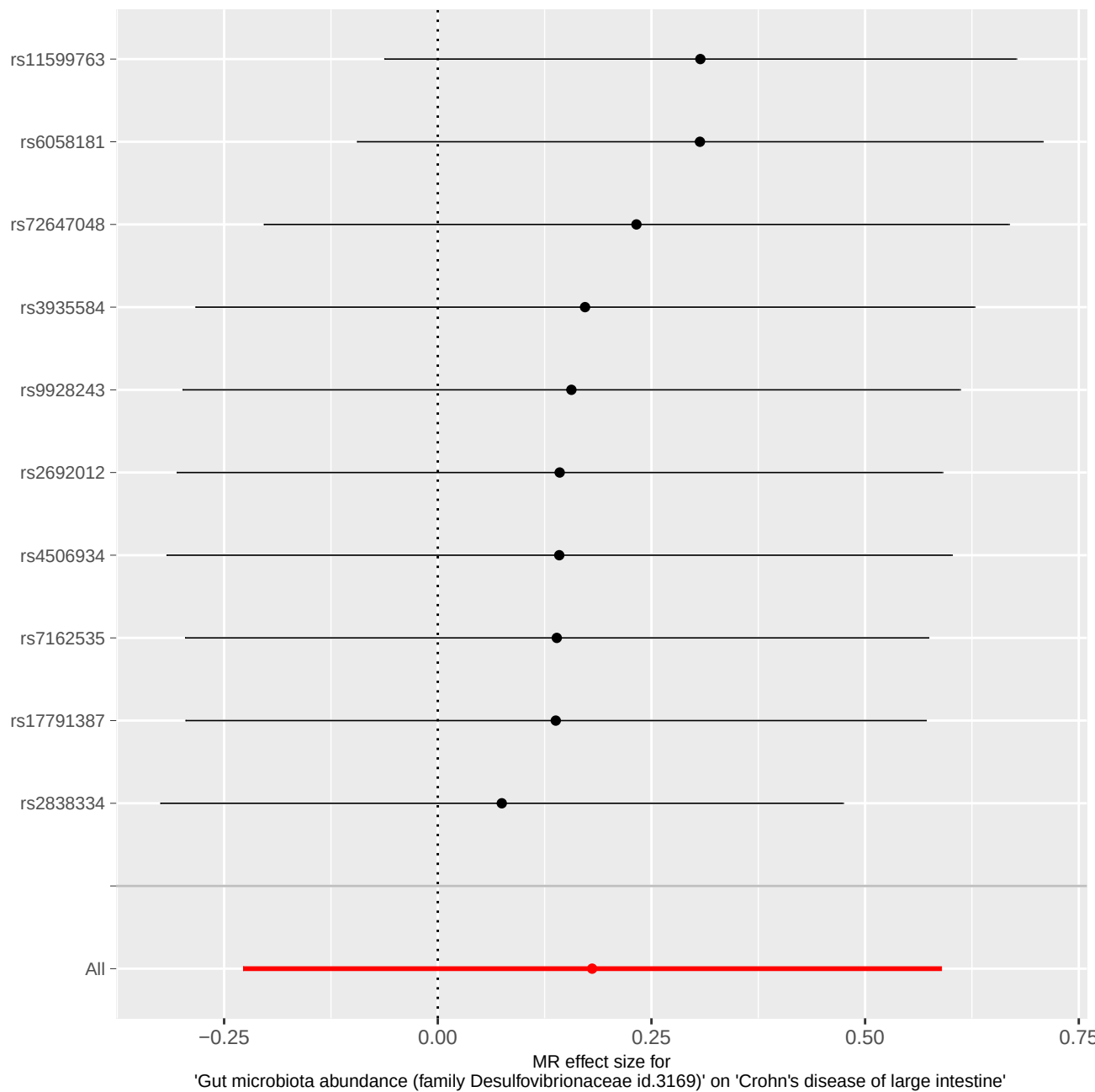
Batch 9 : Gut microbiota abundance (family Clostridiales vadin BB60 group id.11286) on Crohn's disease of large intestine



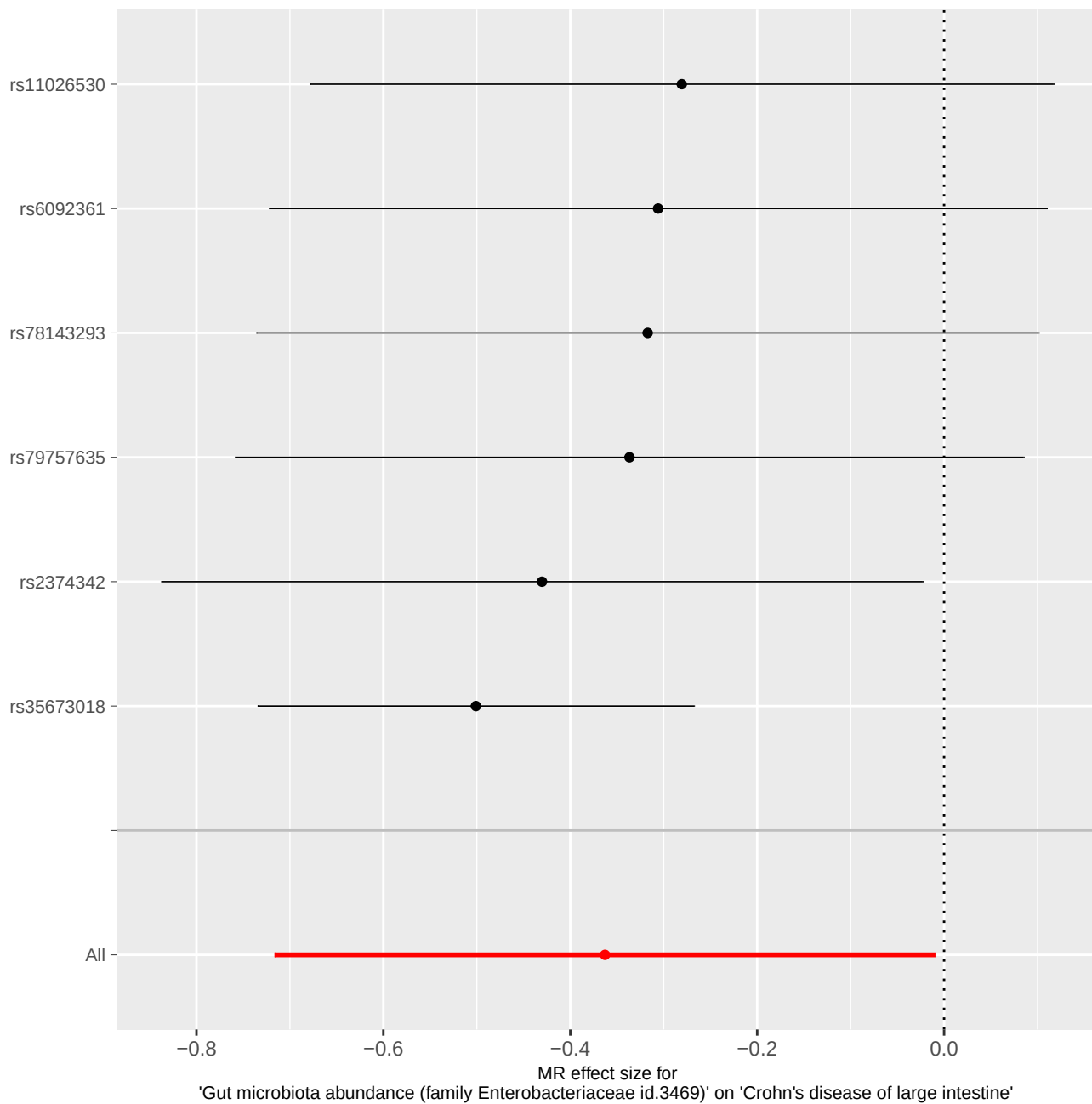
Batch 10 : Gut microbiota abundance (family Coriobacteriaceae id.811) on Crohn's disease of large intestine

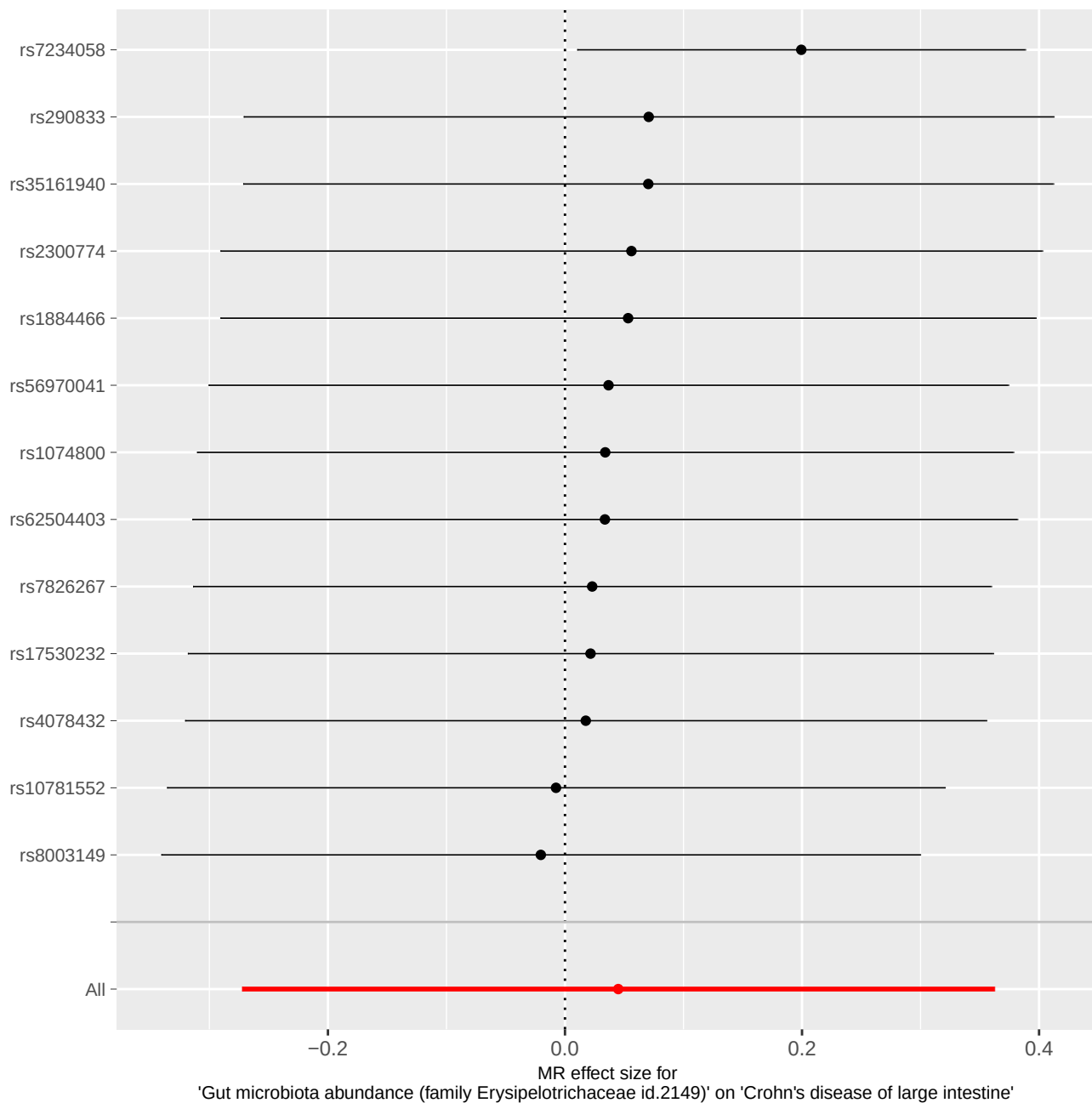




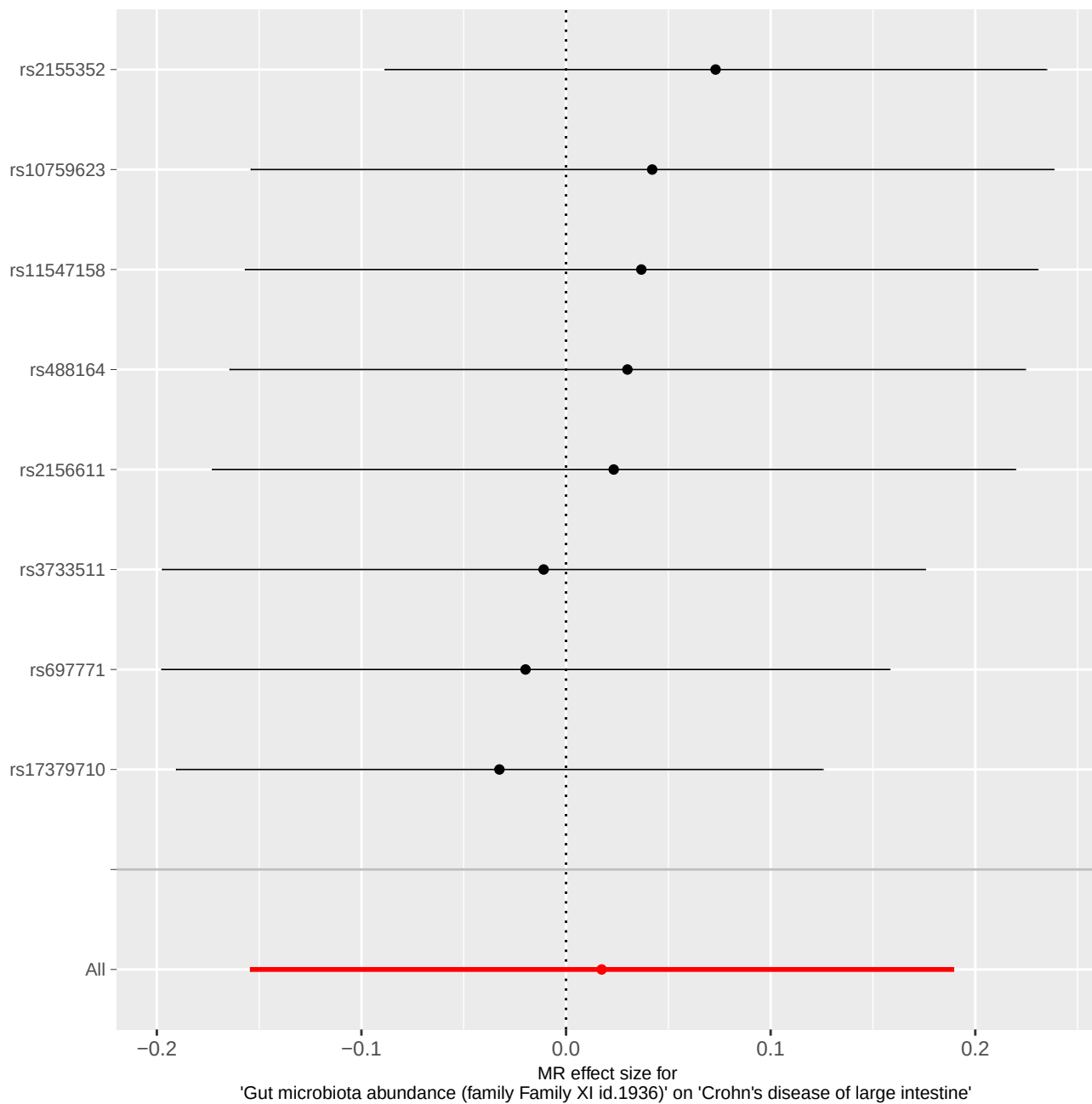


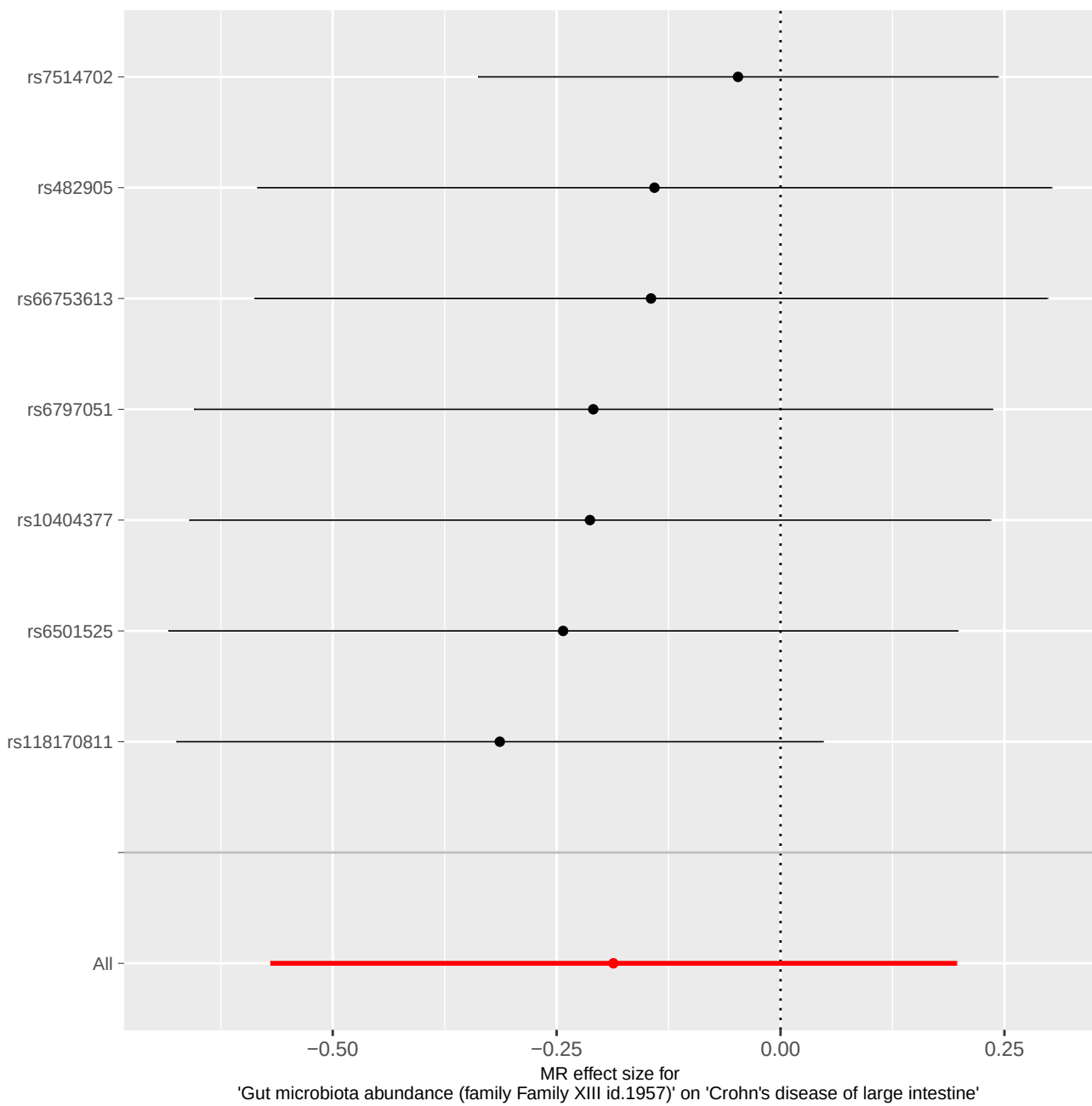
Batch 13 : Gut microbiota abundance (family Enterobacteriaceae id.3469) on Crohn's disease of large intestine



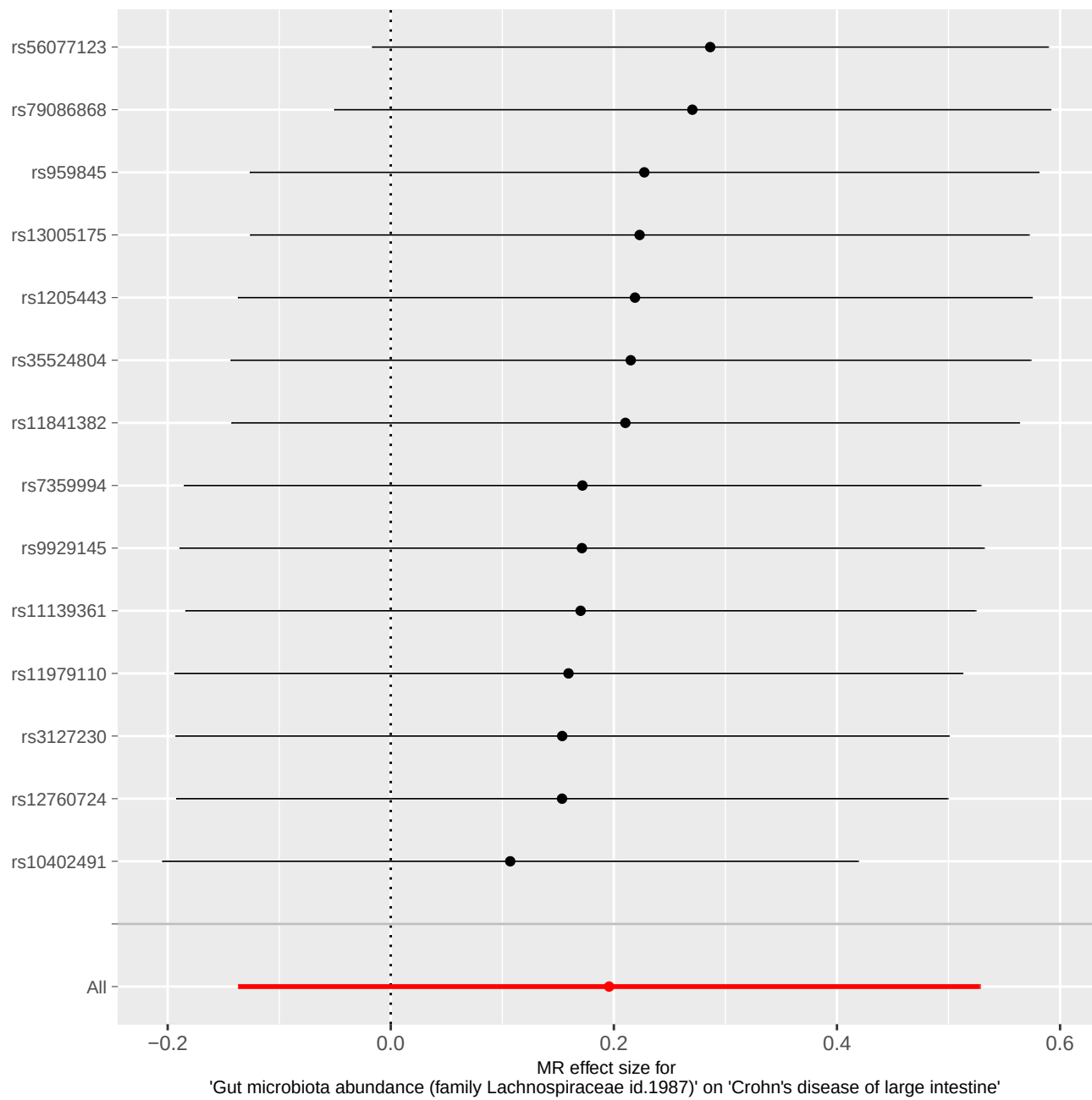


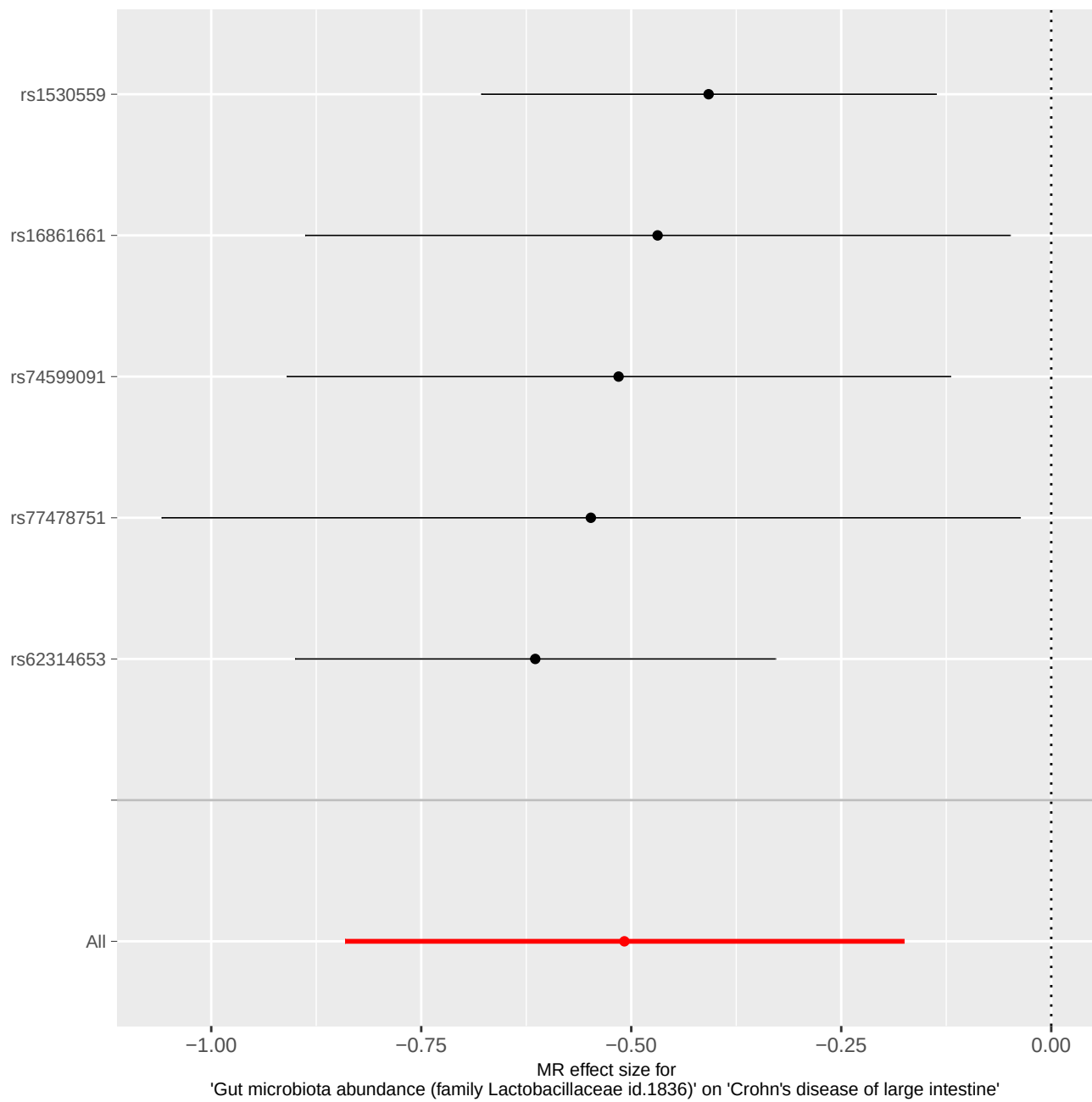
Batch 15 : Gut microbiota abundance (family Family XI id.1936) on Crohn's disease of large intestine

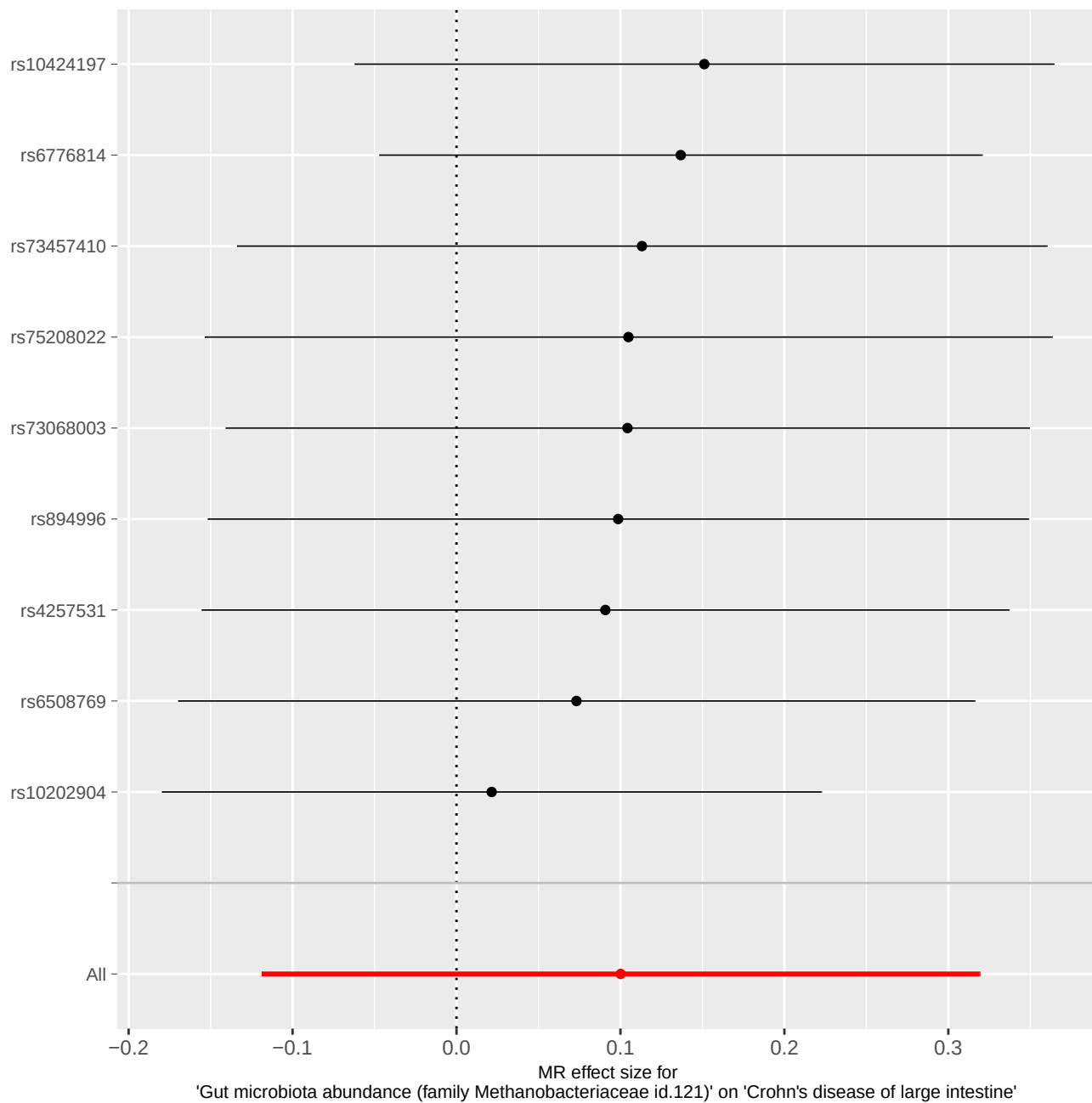


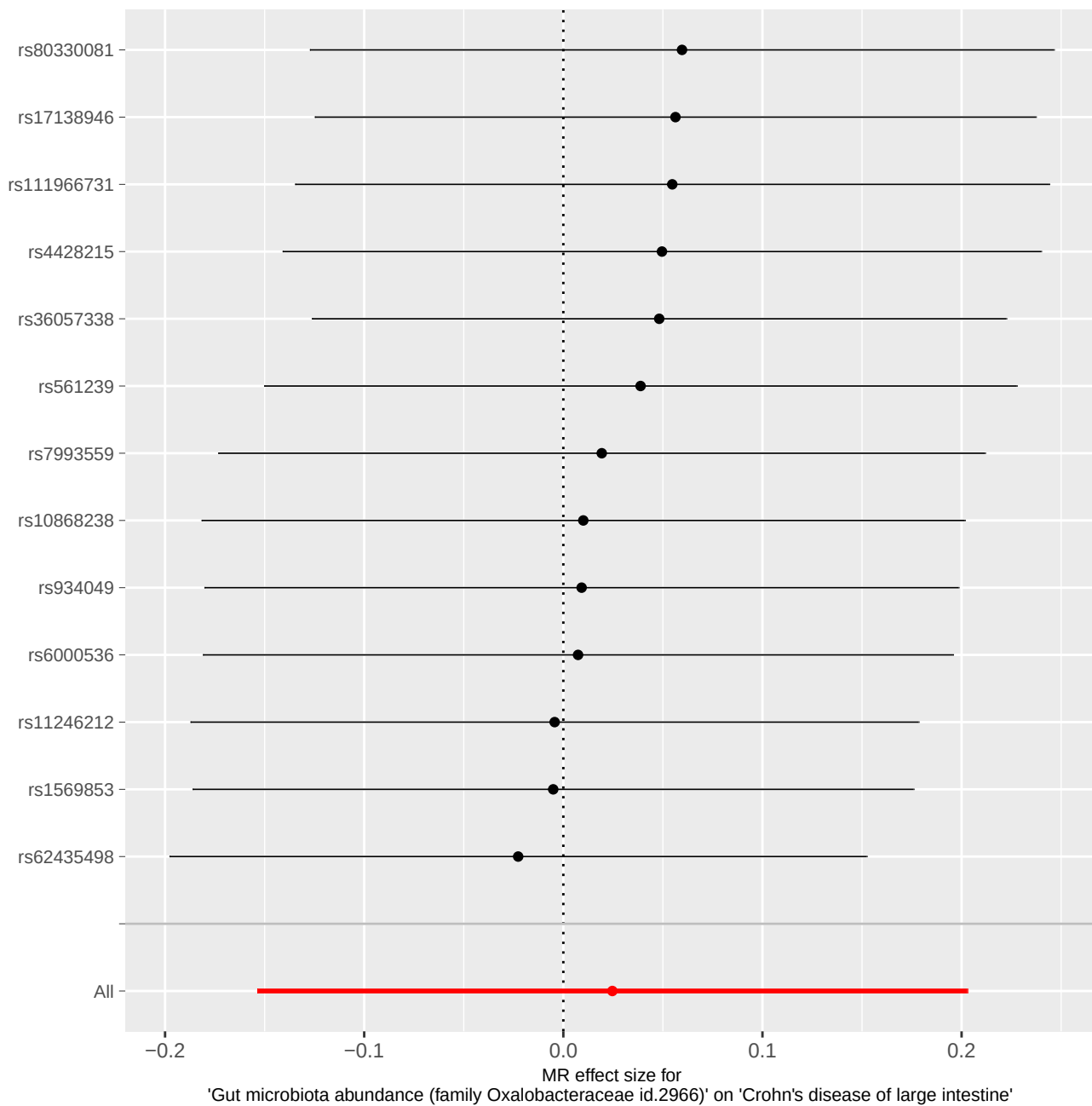


Batch 17 : Gut microbiota abundance (family Lachnospiraceae id.1987) on Crohn's disease of large intestine

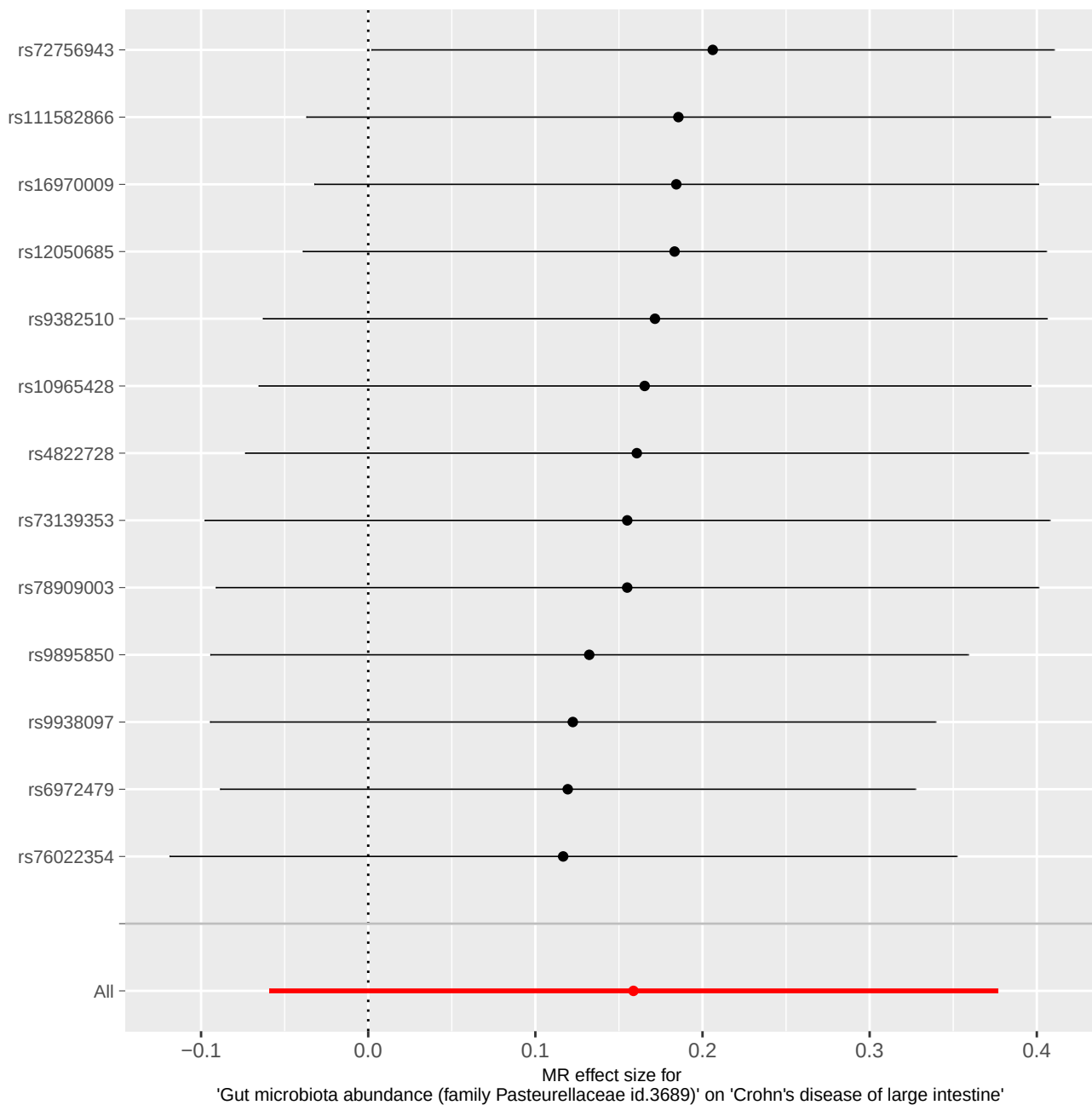




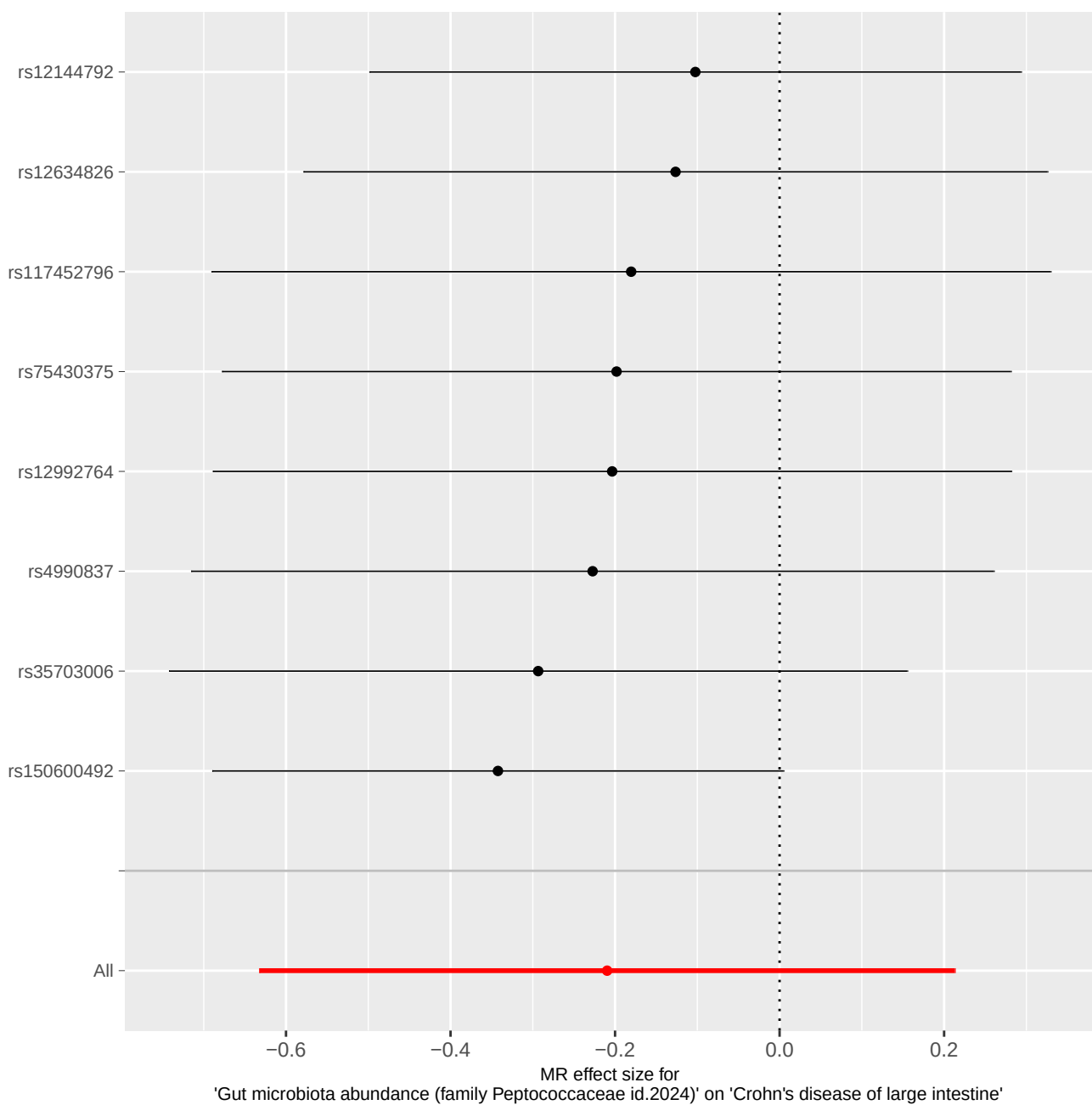


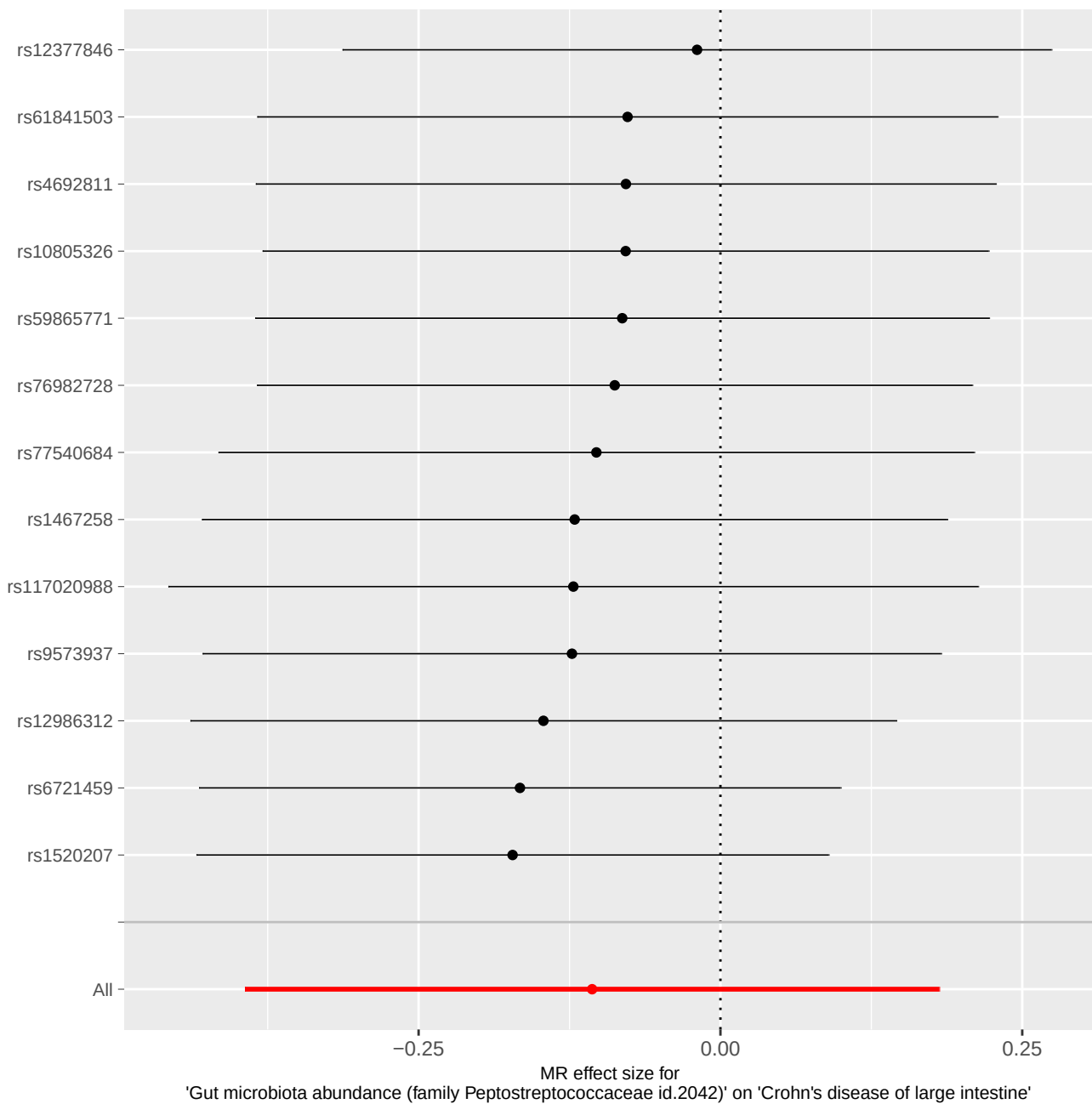


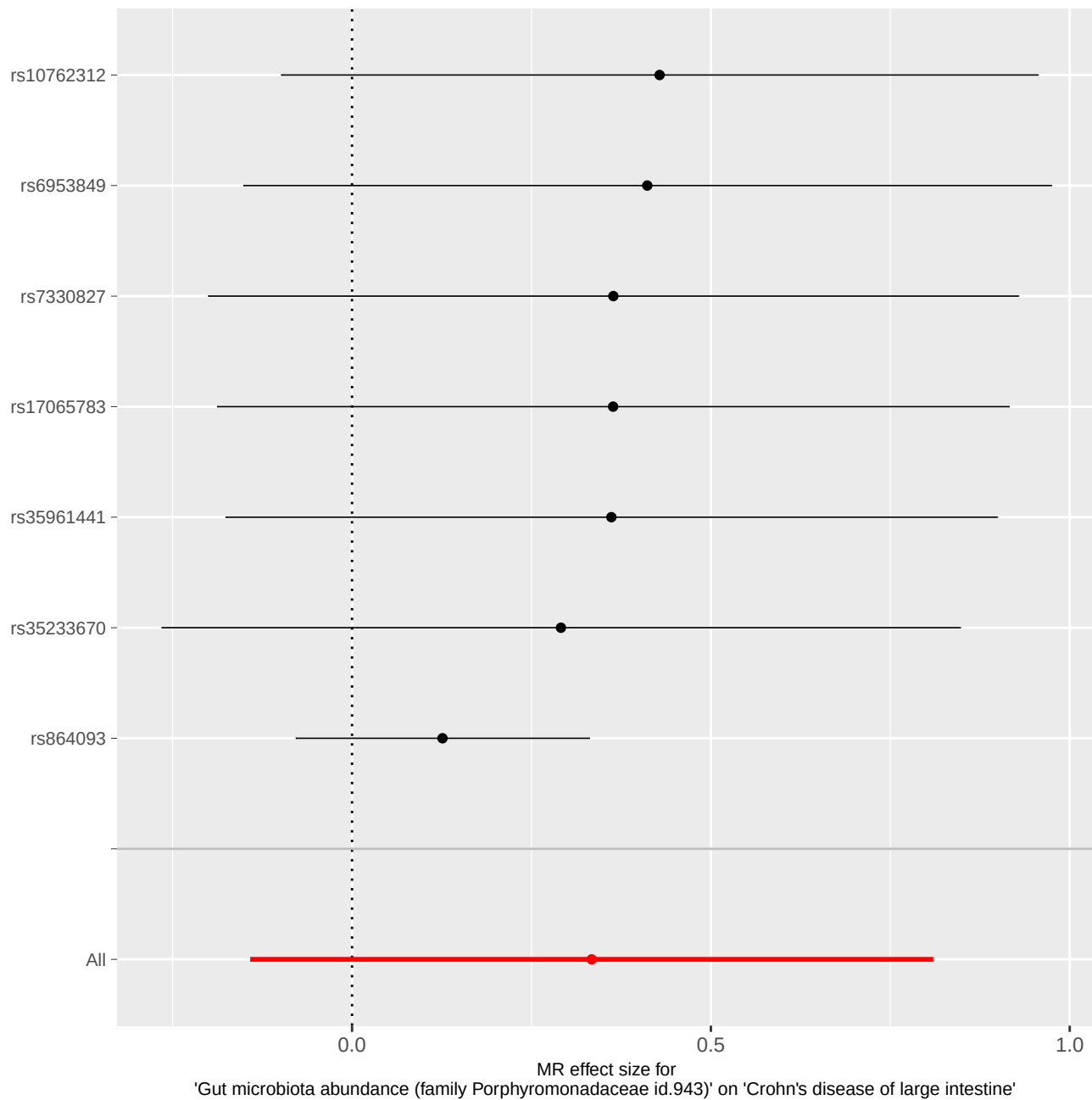
Batch 21 : Gut microbiota abundance (family Pasteurellaceae id.3689) on Crohn's disease of large intestine



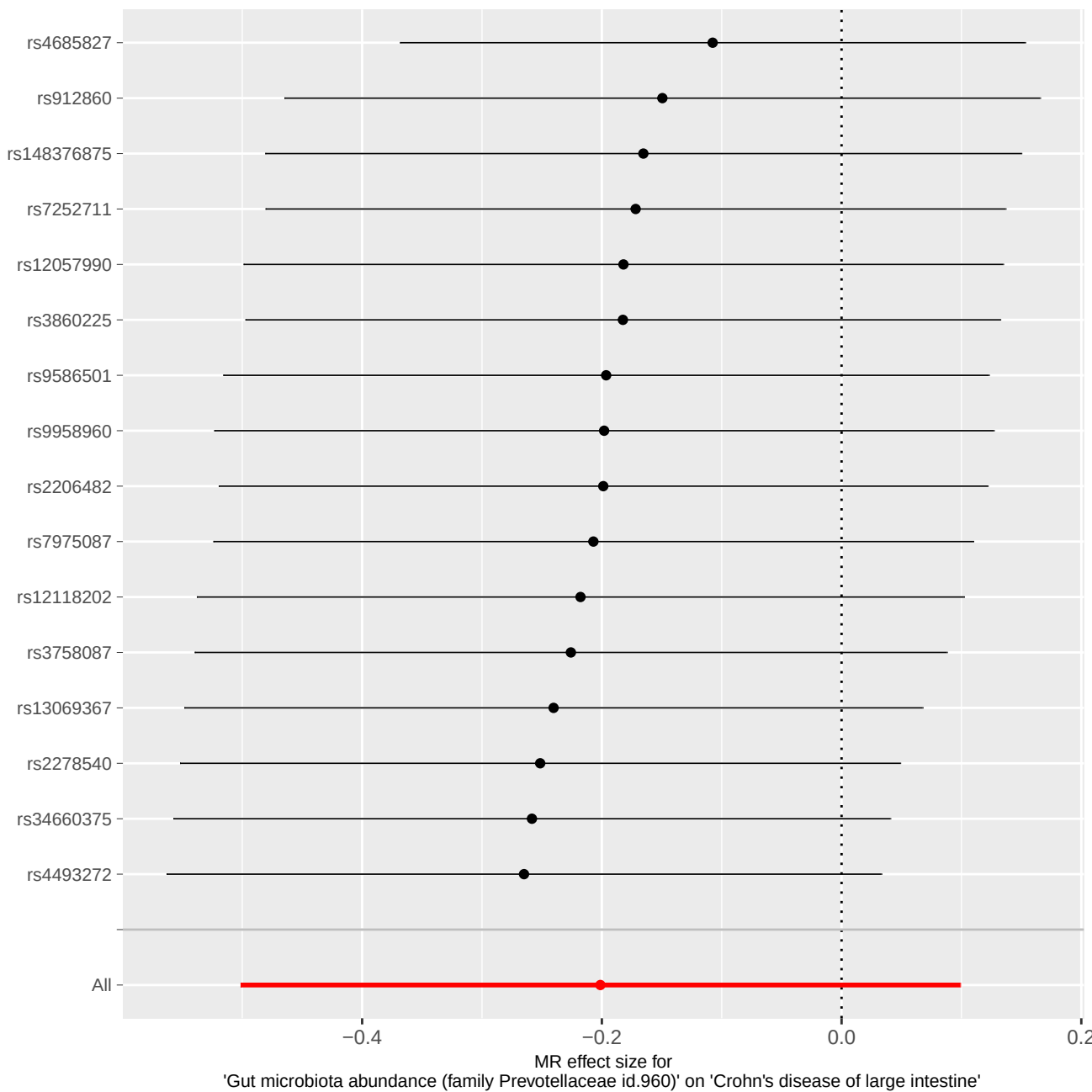
Batch 22 : Gut microbiota abundance (family Peptococcaceae id.2024) on Crohn's disease of large intestine

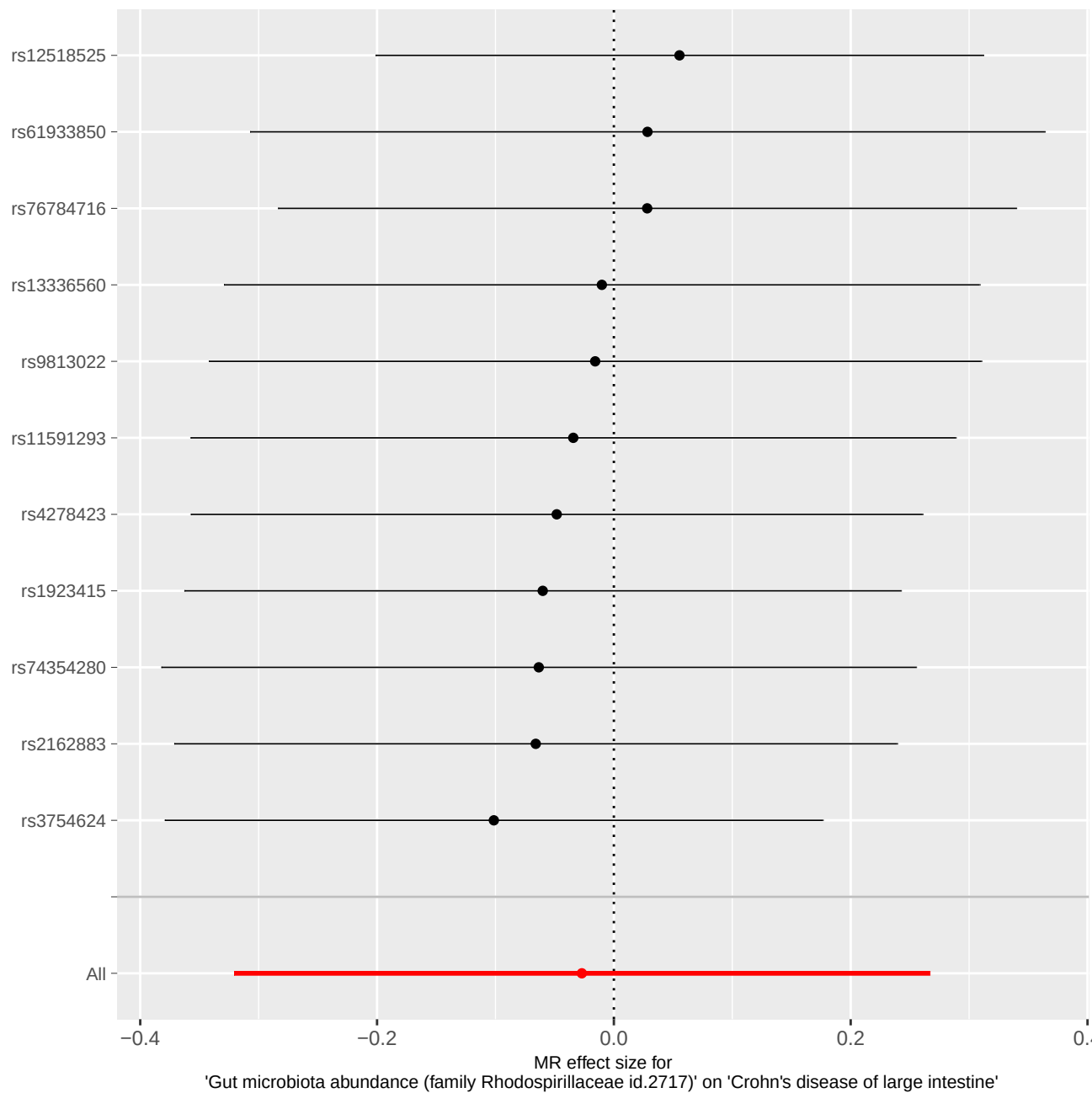




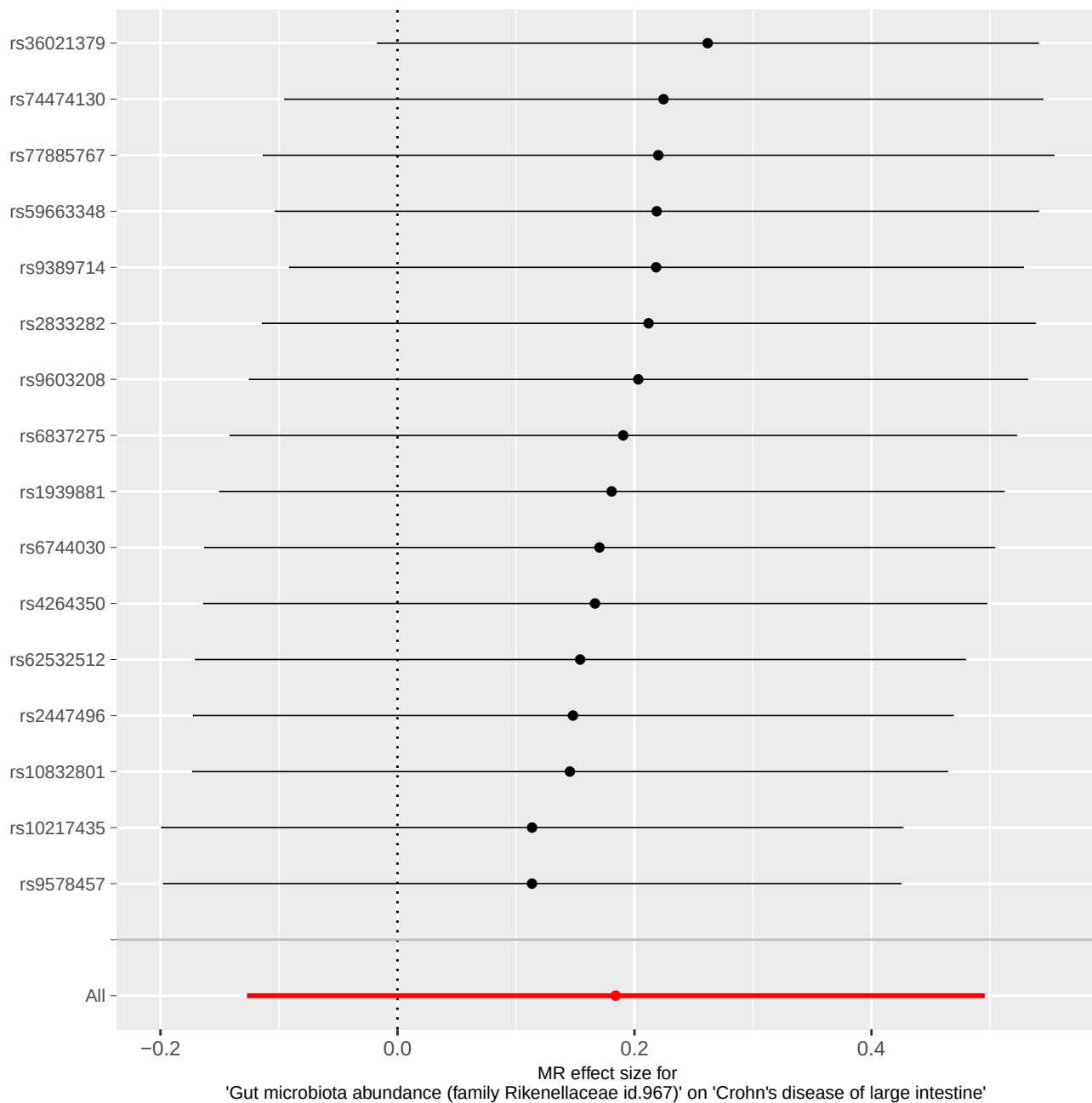


Batch 25 : Gut microbiota abundance (family Prevotellaceae id.960) on Crohn's disease of large intestine

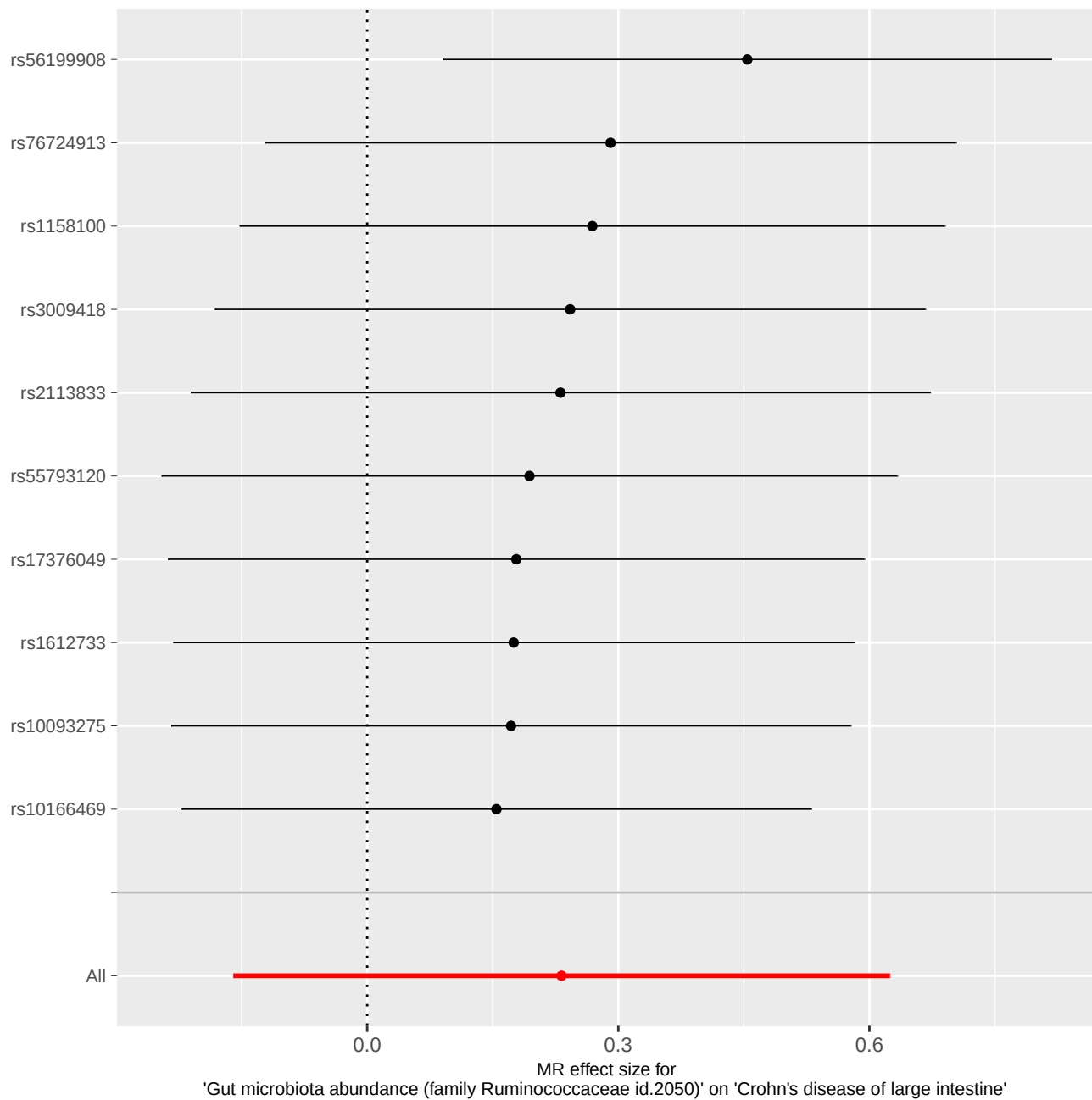




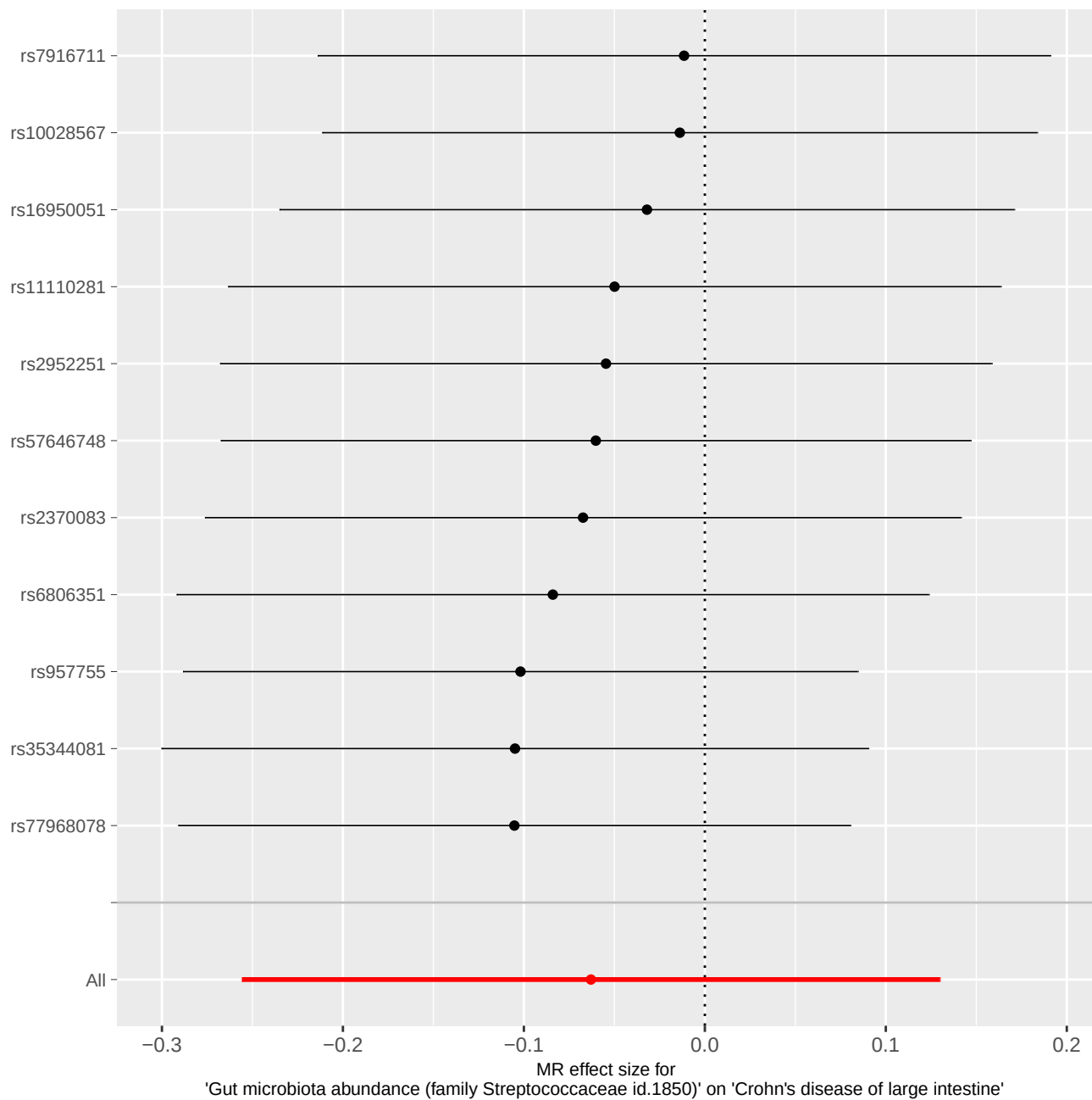
Batch 27 : Gut microbiota abundance (family Rikenellaceae id.967) on Crohn's disease of large intestine



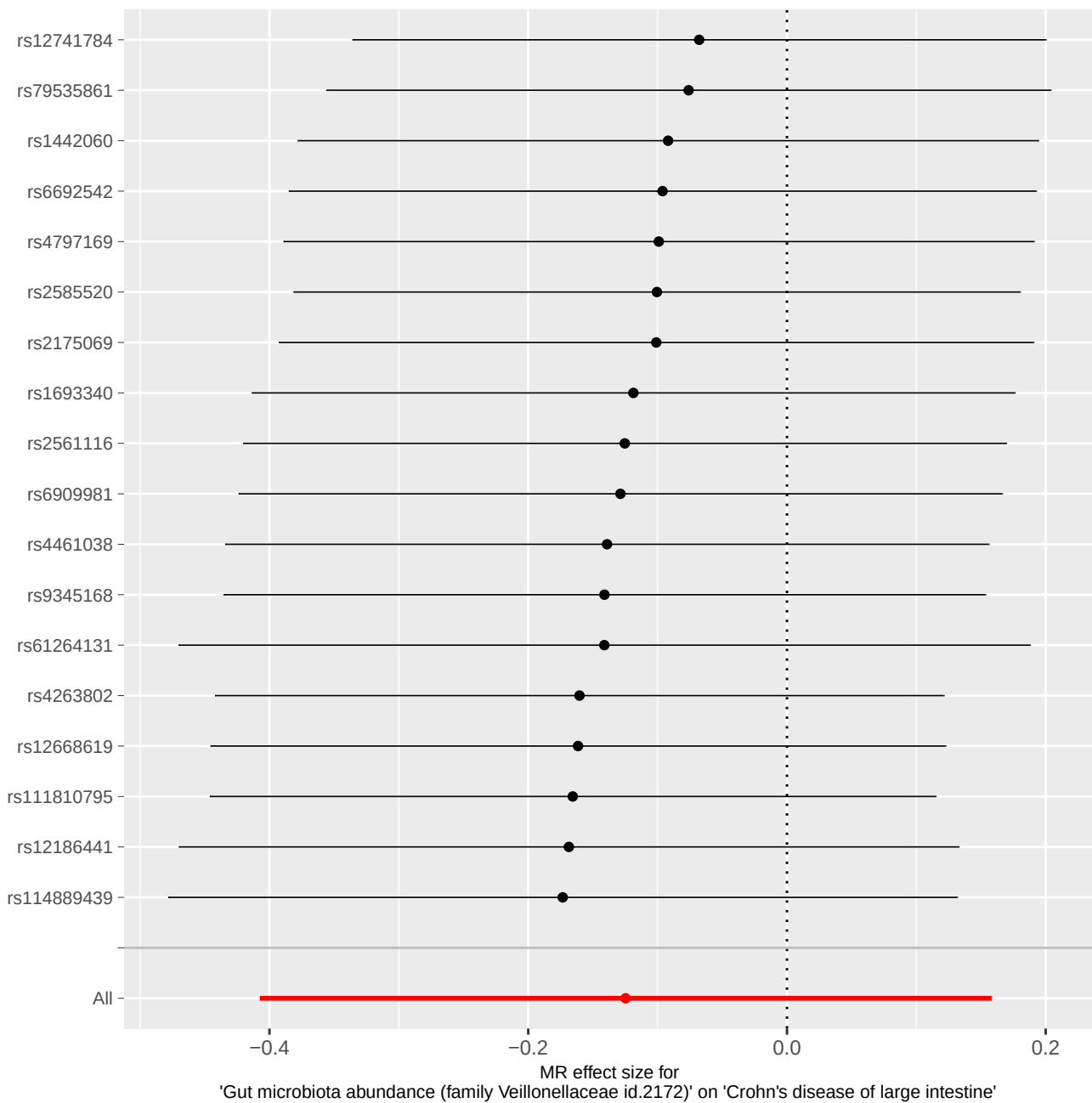
Batch 28 : Gut microbiota abundance (family Ruminococcaceae id.2050) on Crohn's disease of large intestine



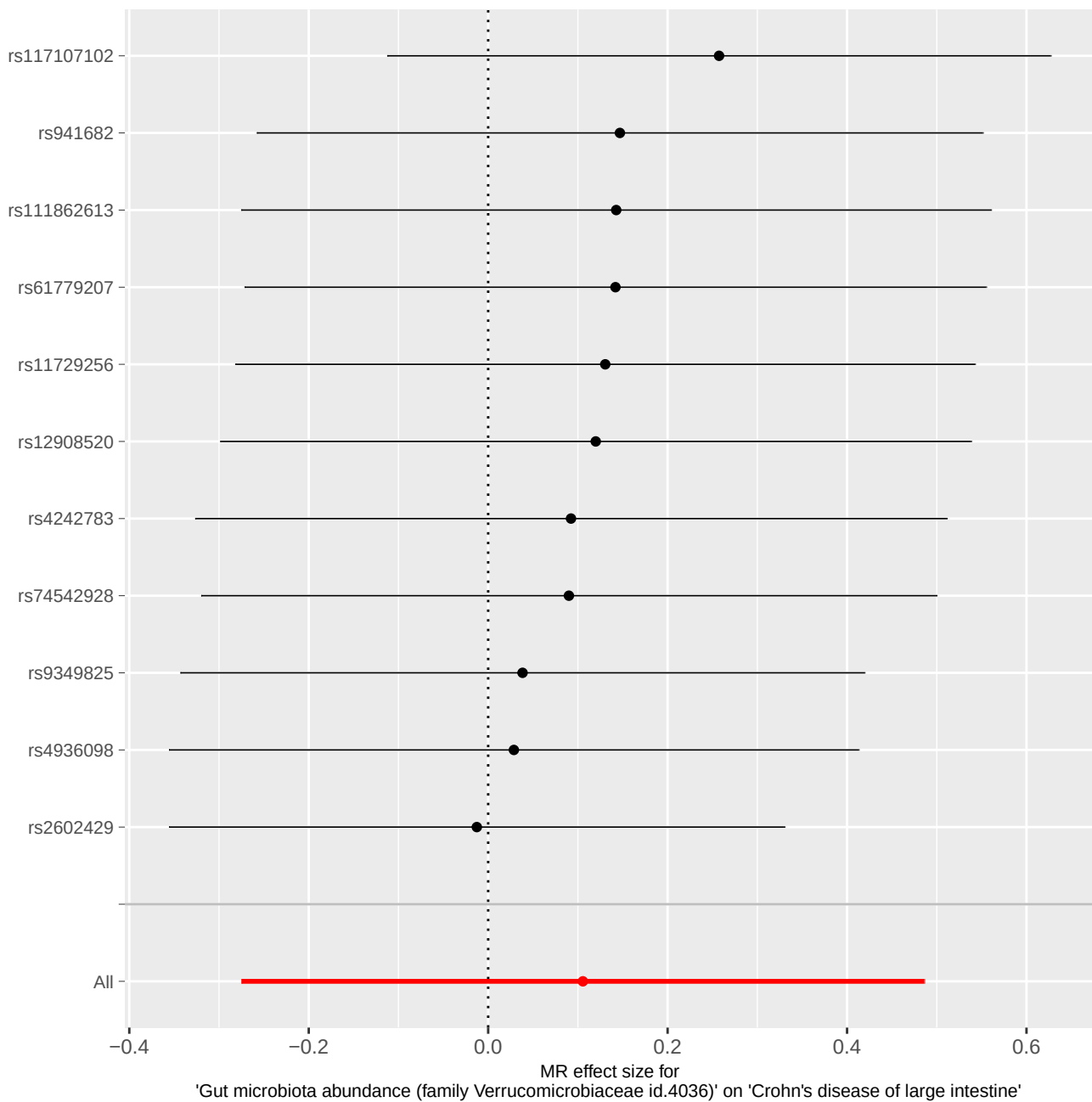
Batch 29 : Gut microbiota abundance (family Streptococcaceae id.1850) on Crohn's disease of large intestine



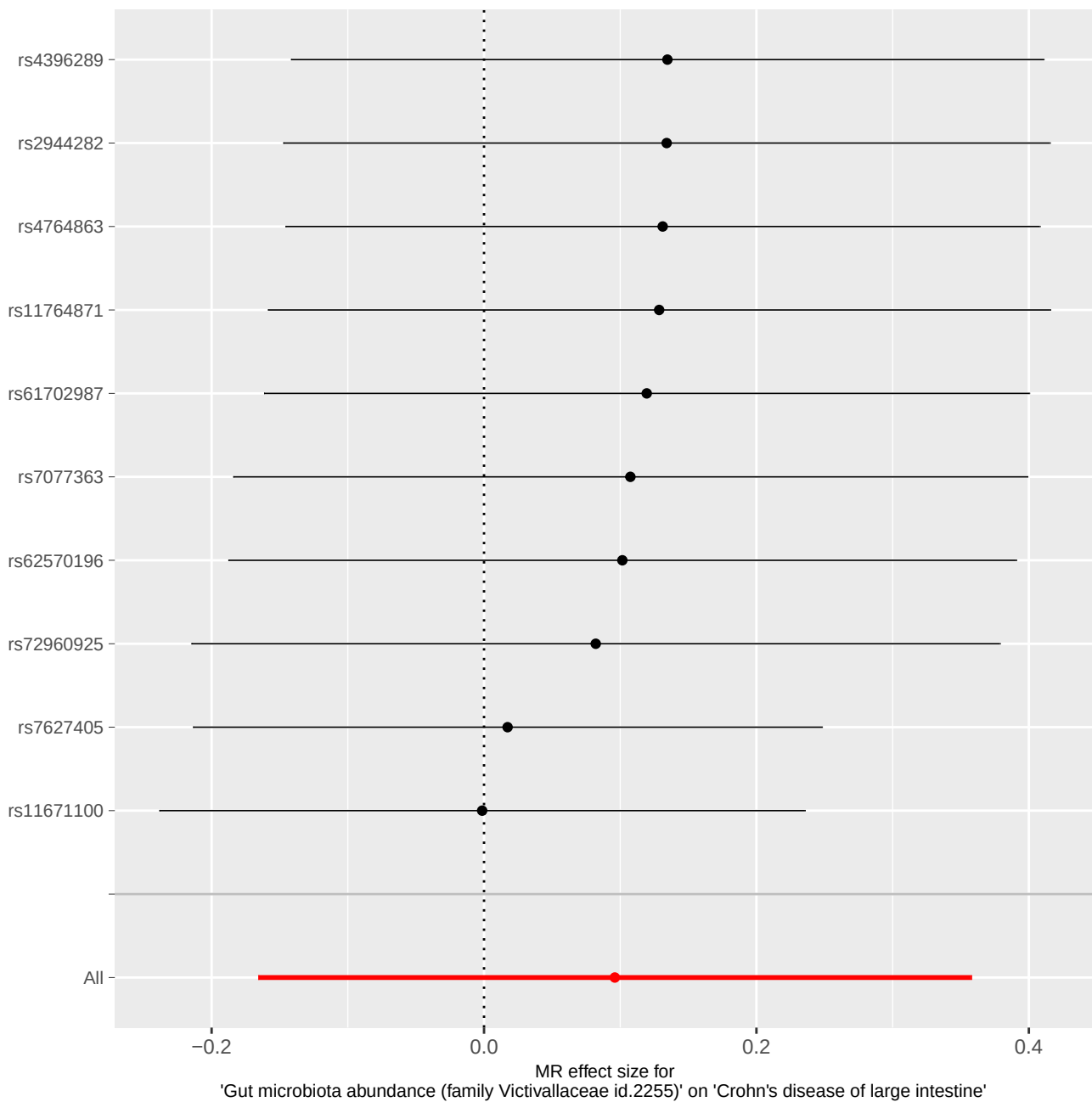
Batch 30 : Gut microbiota abundance (family Veillonellaceae id.2172) on Crohn's disease of large intestine



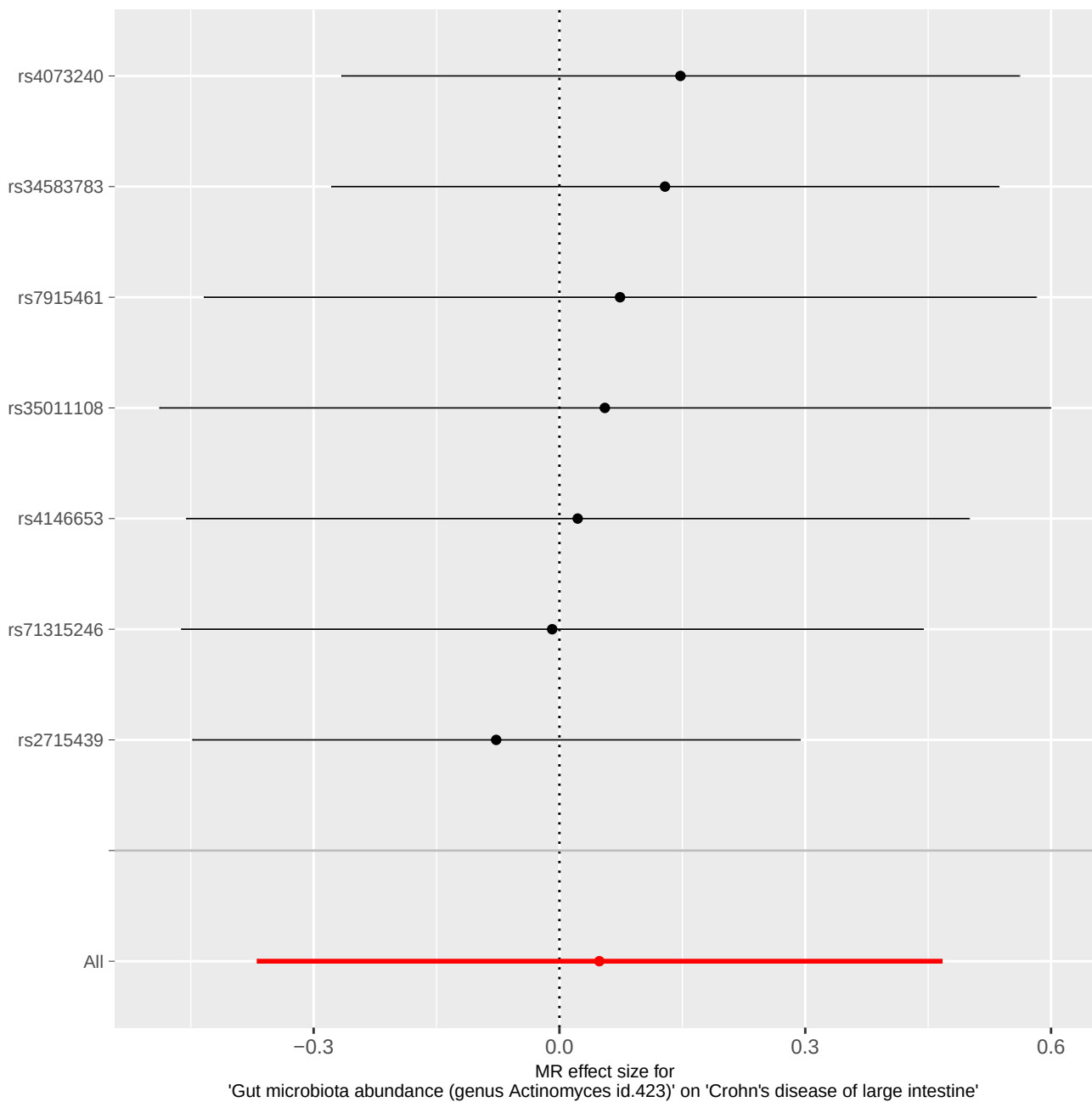
Batch 31 : Gut microbiota abundance (family Verrucomicrobiaceae id.4036) on Crohn's disease of large intestine

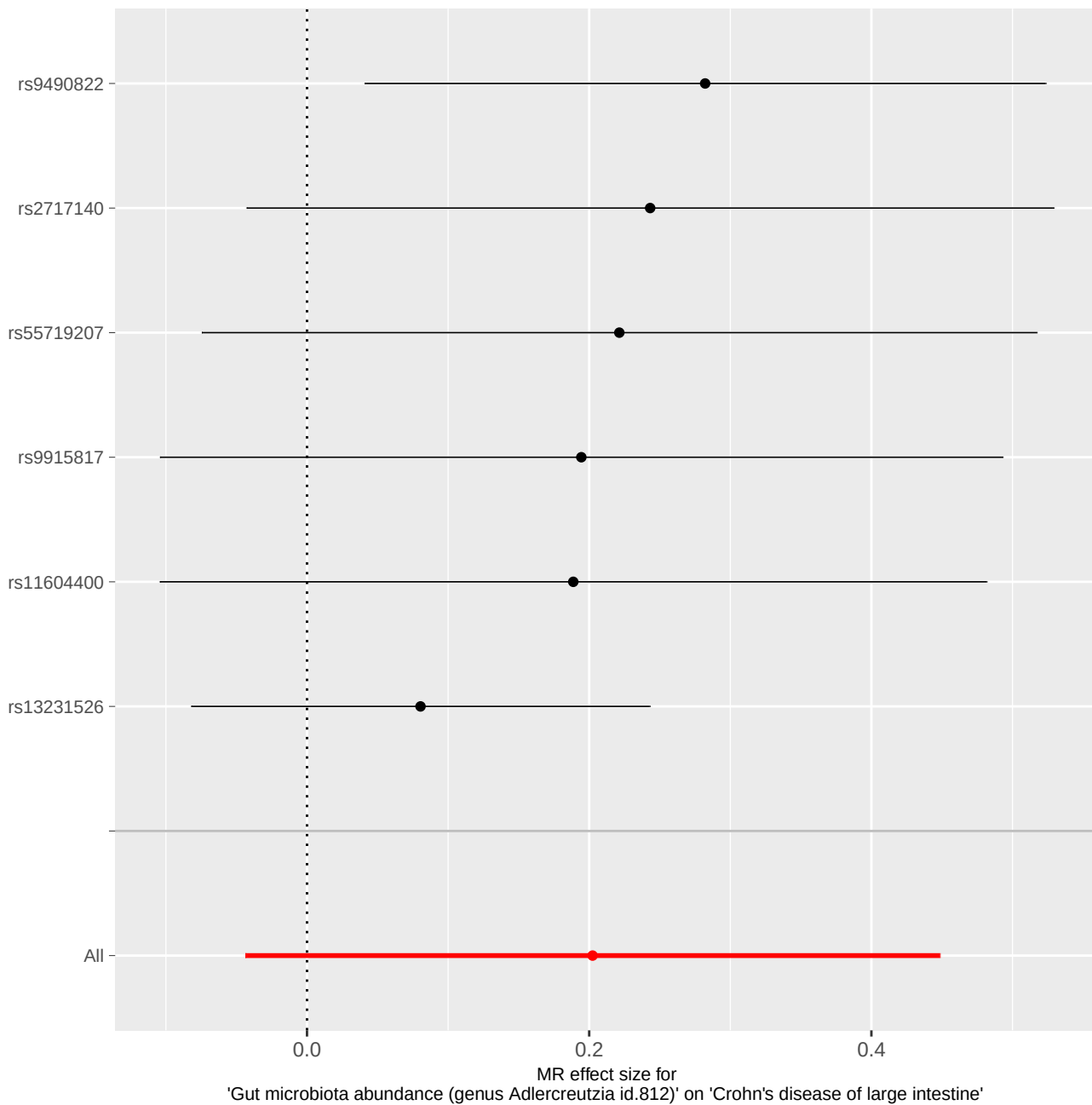


Batch 32 : Gut microbiota abundance (family Victivallaceae id.2255) on Crohn's disease of large intestine

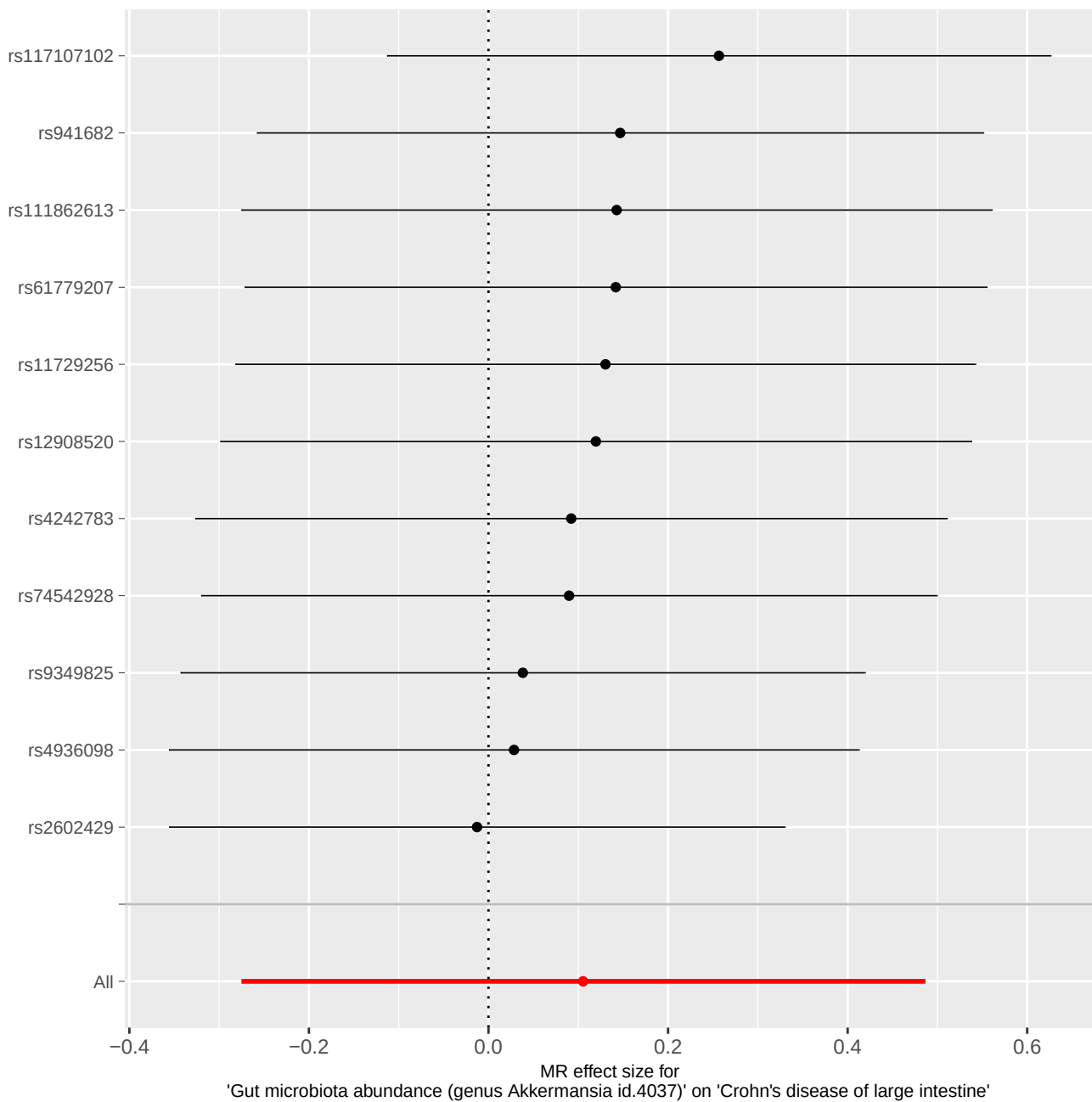


Batch 33 : Gut microbiota abundance (genus Actinomyces id.423) on Crohn's disease of large intestine

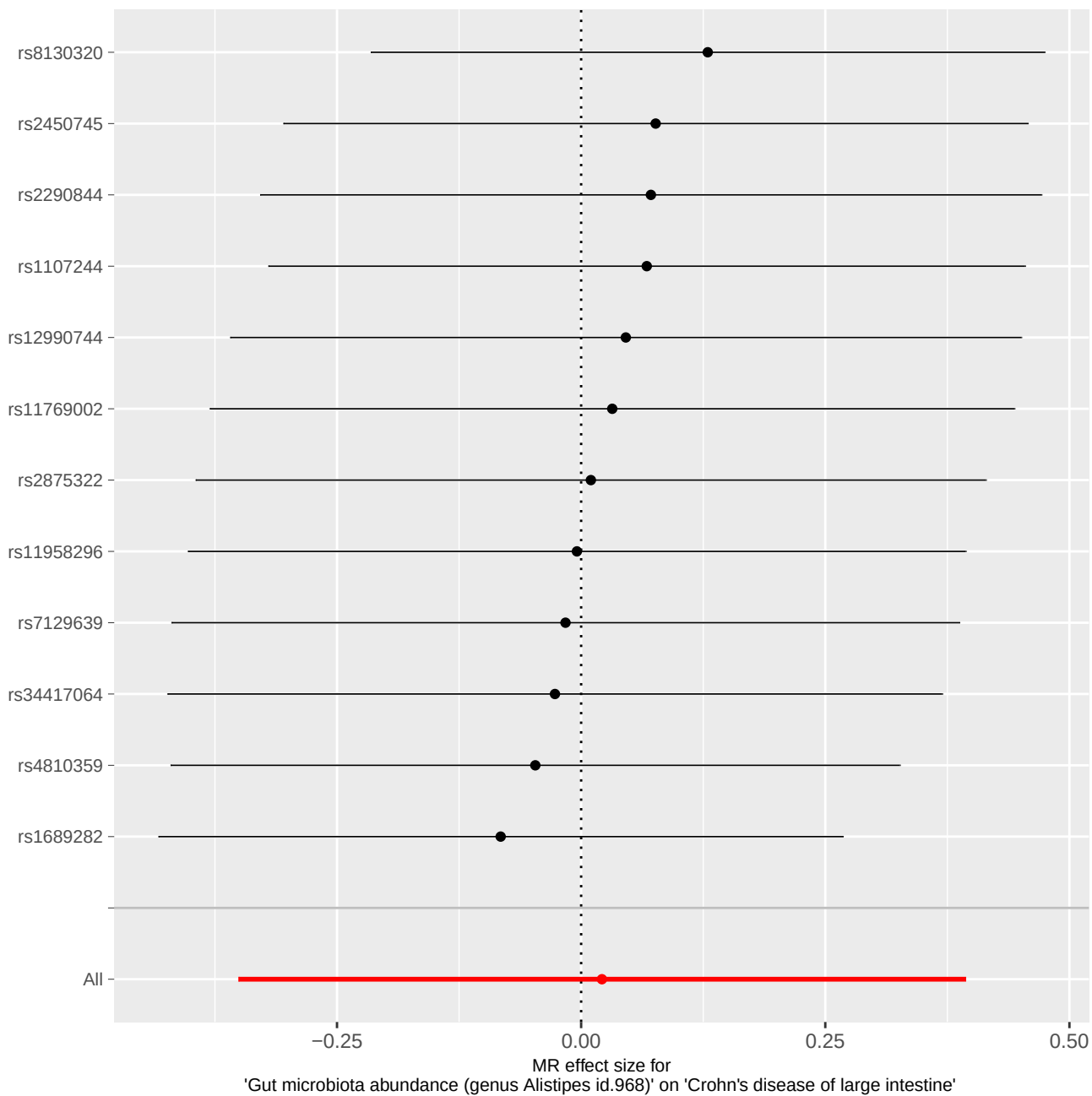




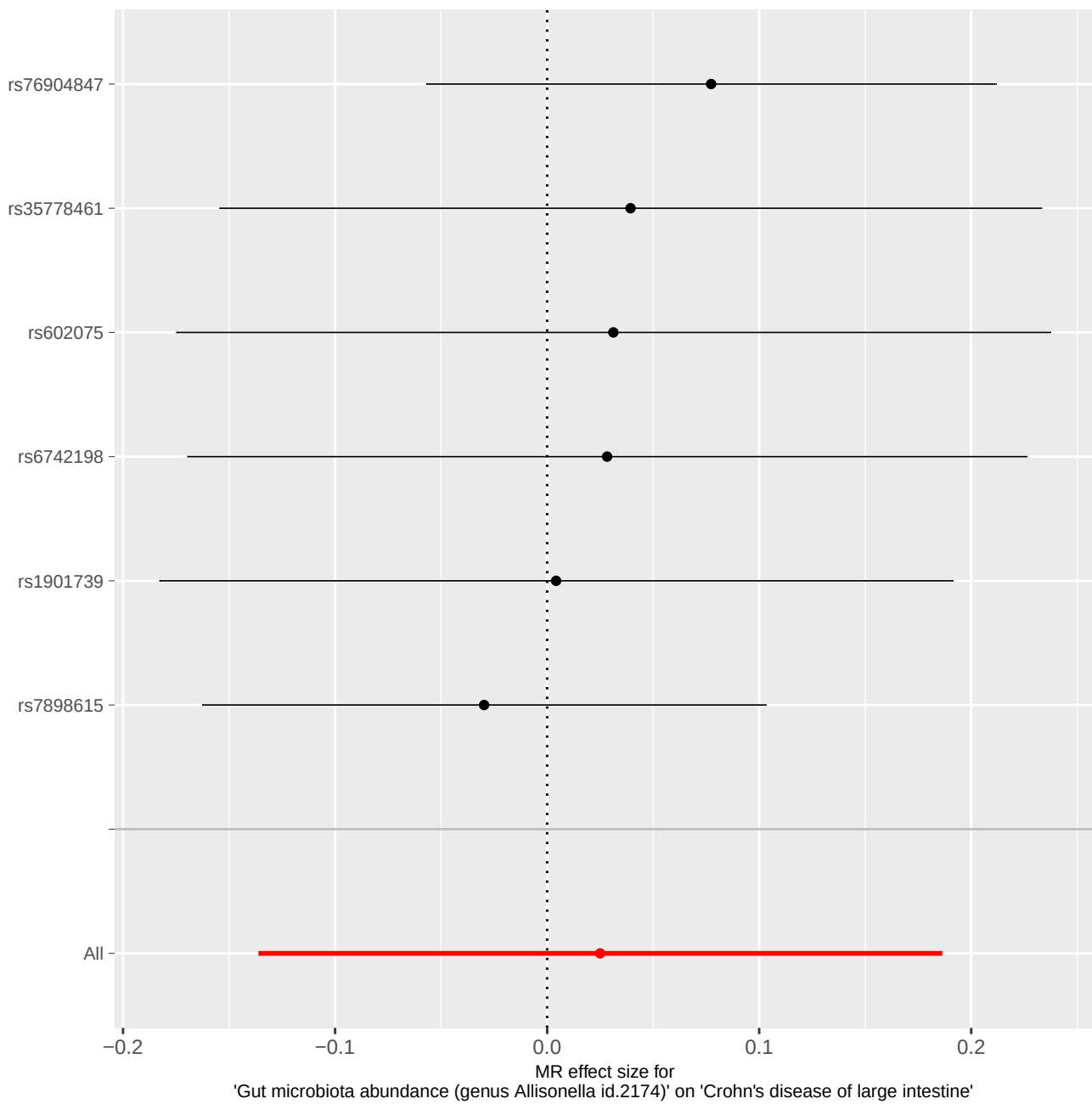
Batch 35 : Gut microbiota abundance (genus Akkermansia id.4037) on Crohn's disease of large intestine

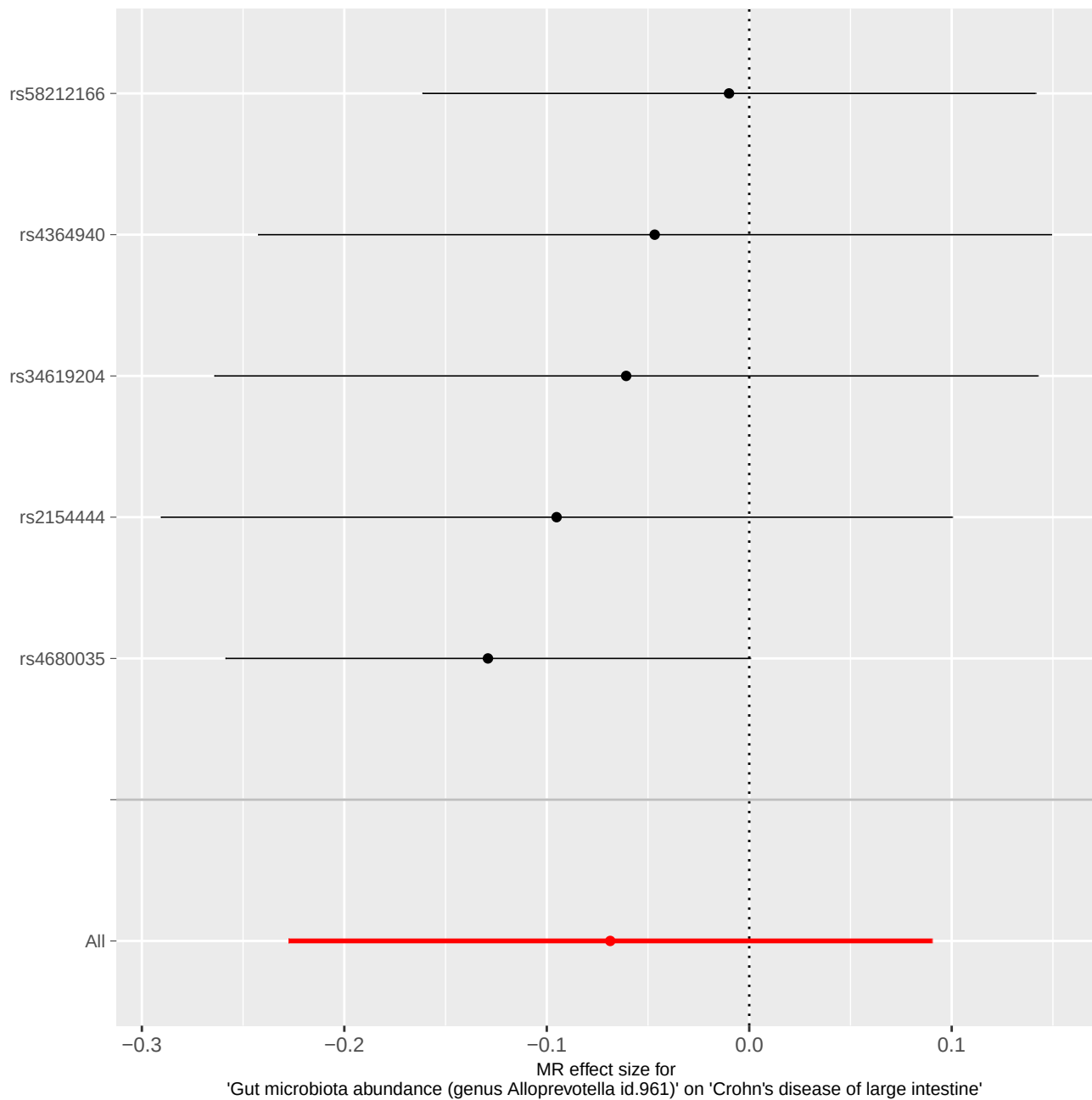


Batch 36 : Gut microbiota abundance (genus Alistipes id.968) on Crohn's disease of large intestine

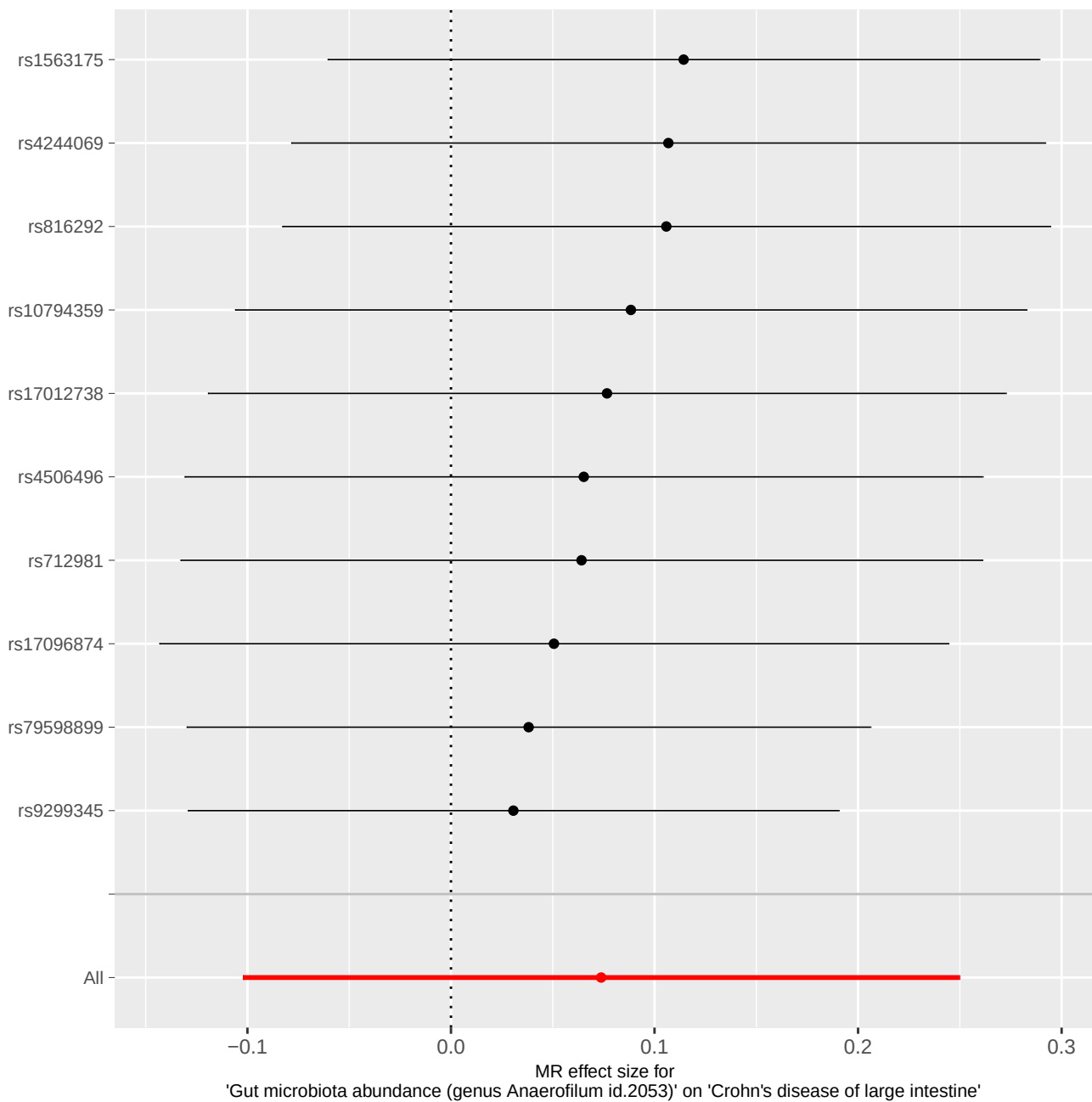


Batch 37 : Gut microbiota abundance (genus Allisonella id.2174) on Crohn's disease of large intestine

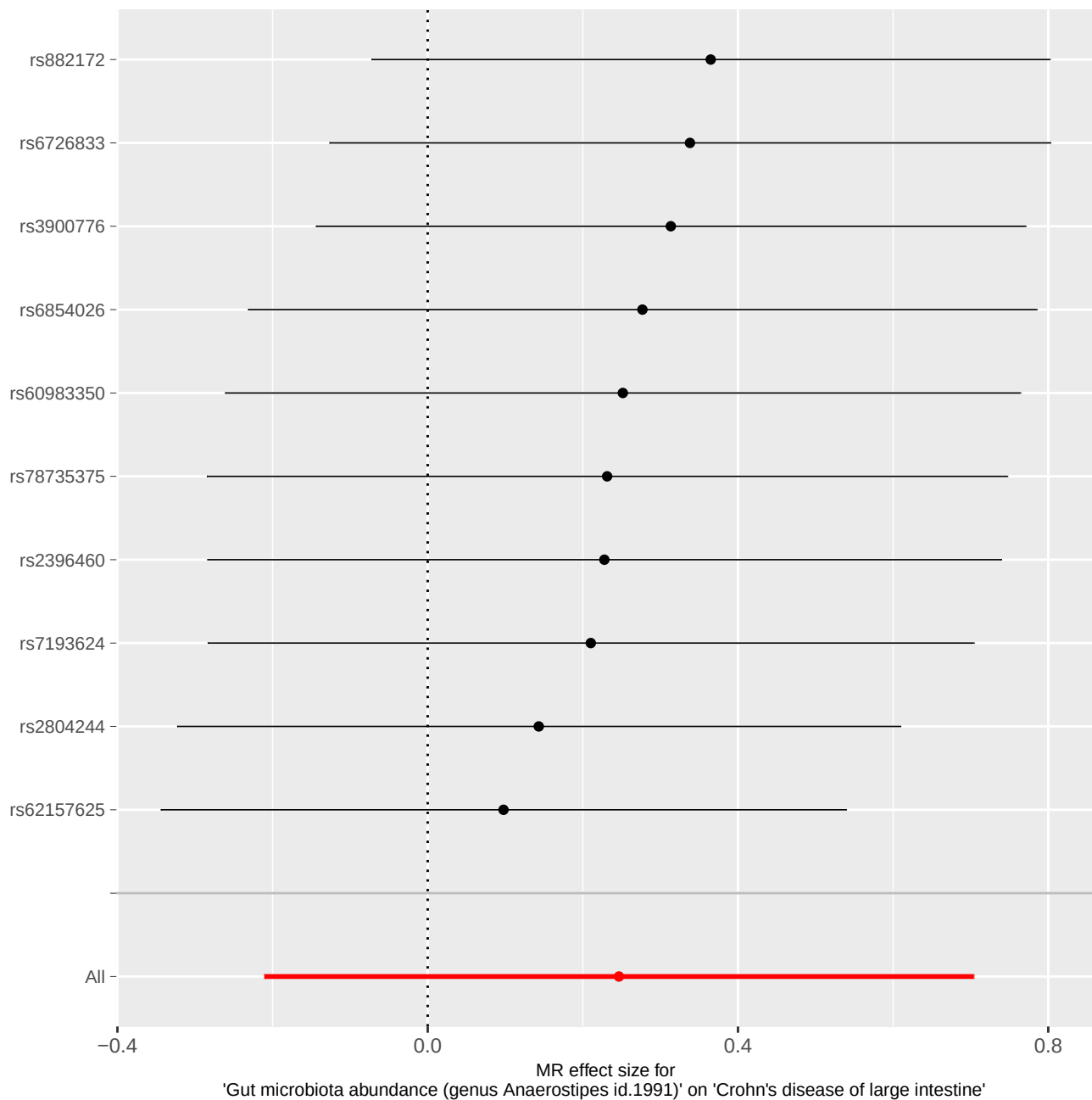




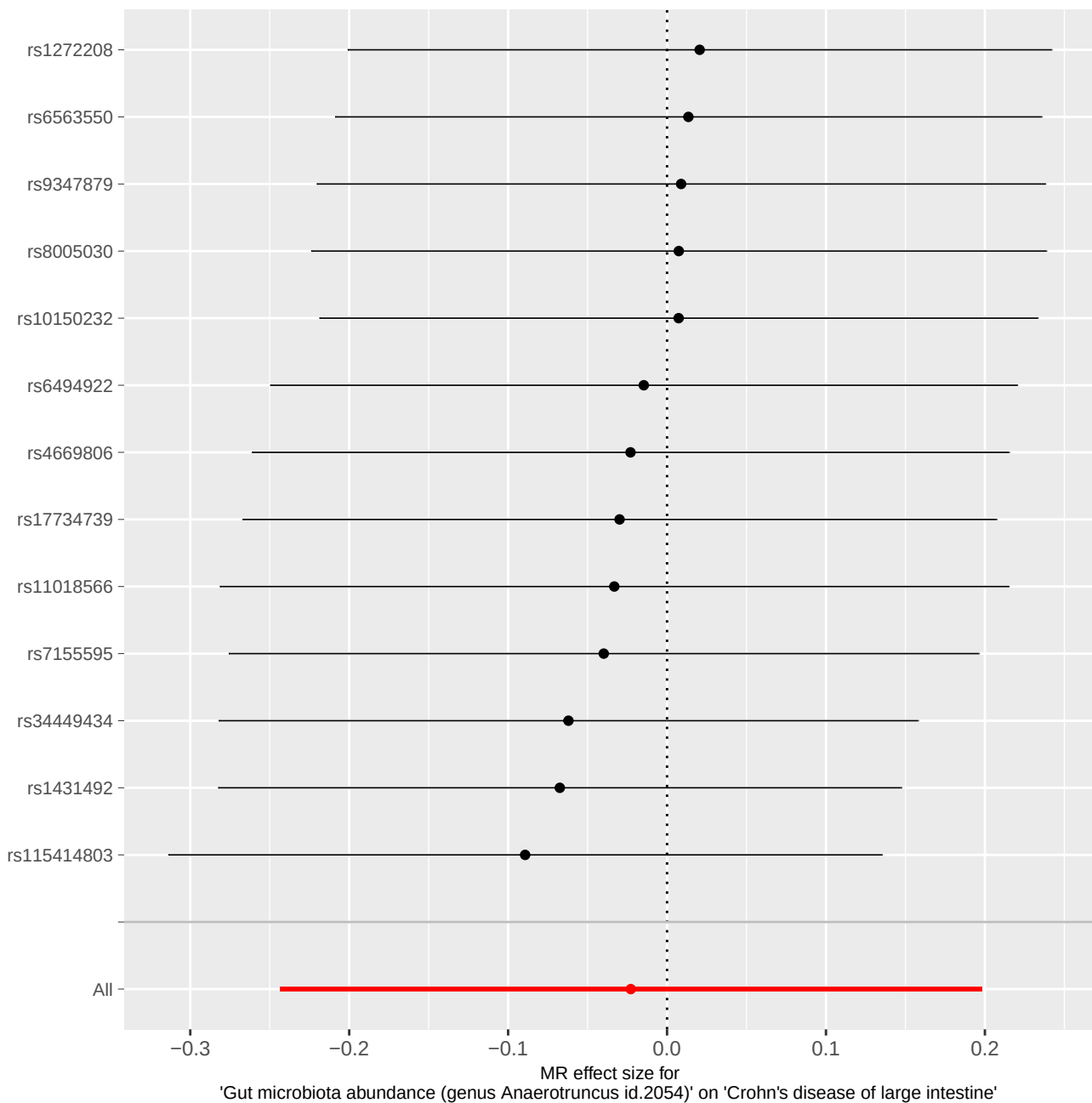
Batch 39 : Gut microbiota abundance (genus Anaerofilum id.2053) on Crohn's disease of large intestine

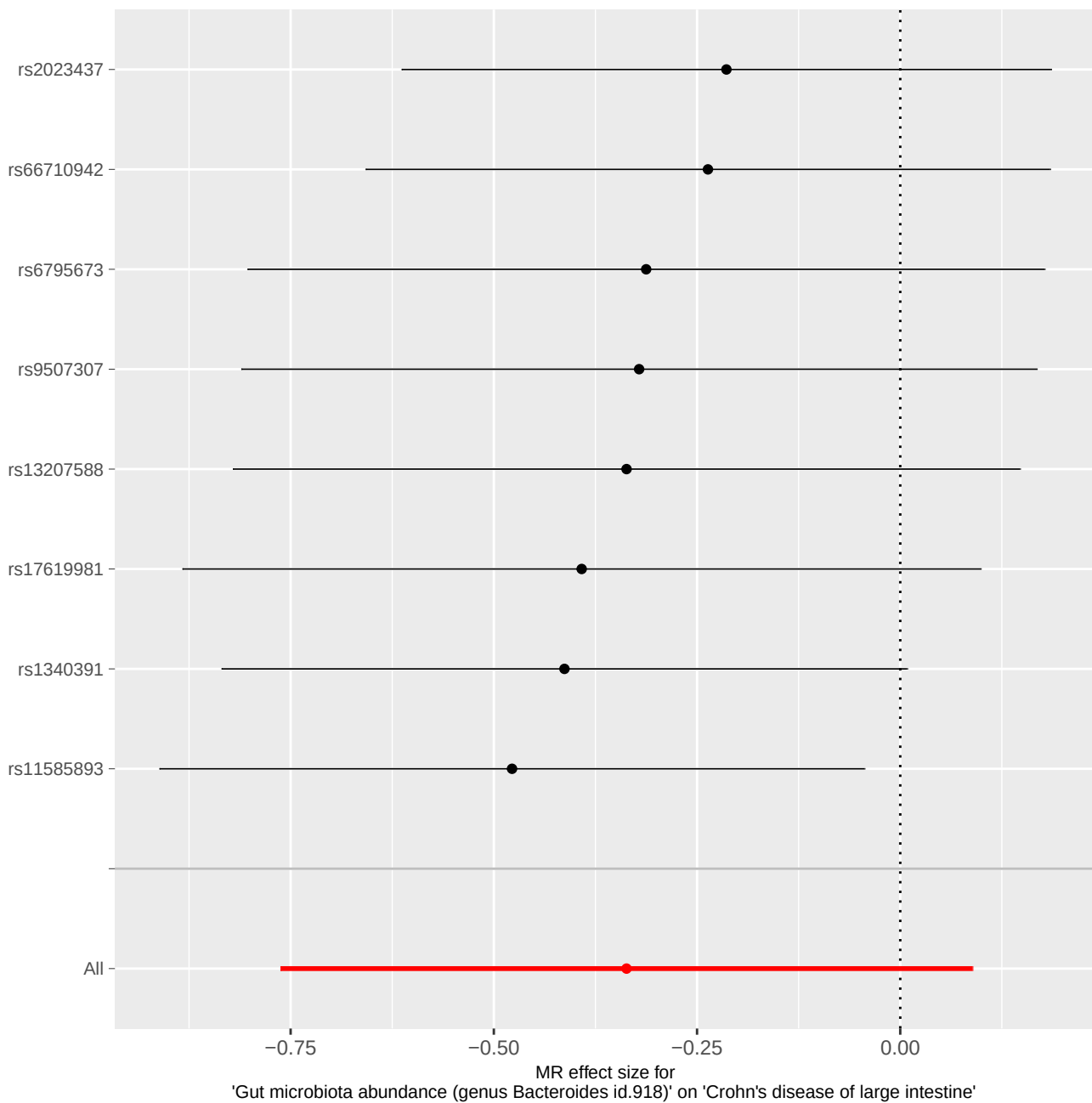


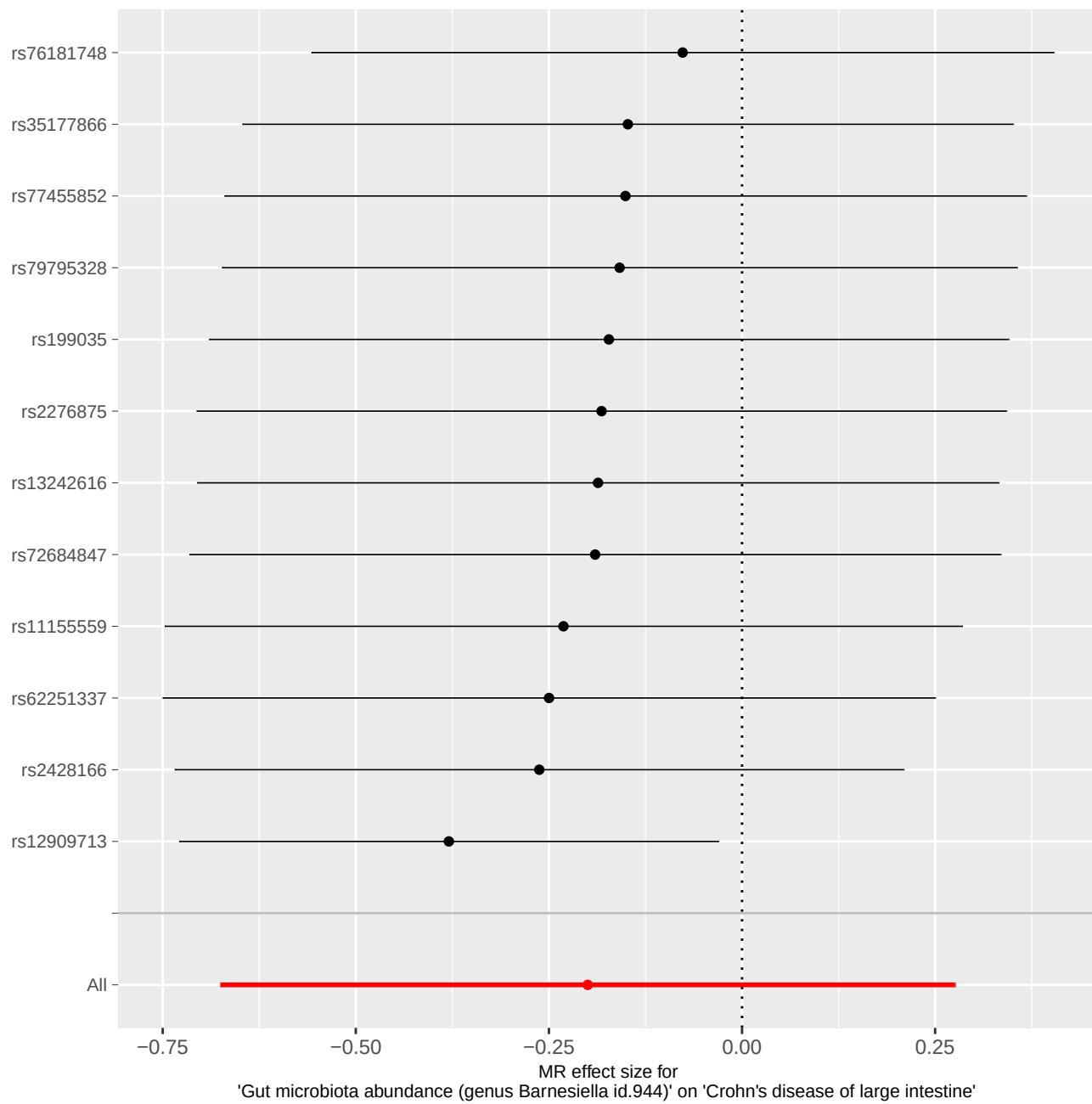
Batch 40 : Gut microbiota abundance (genus Anaerostipes id.1991) on Crohn's disease of large intestine



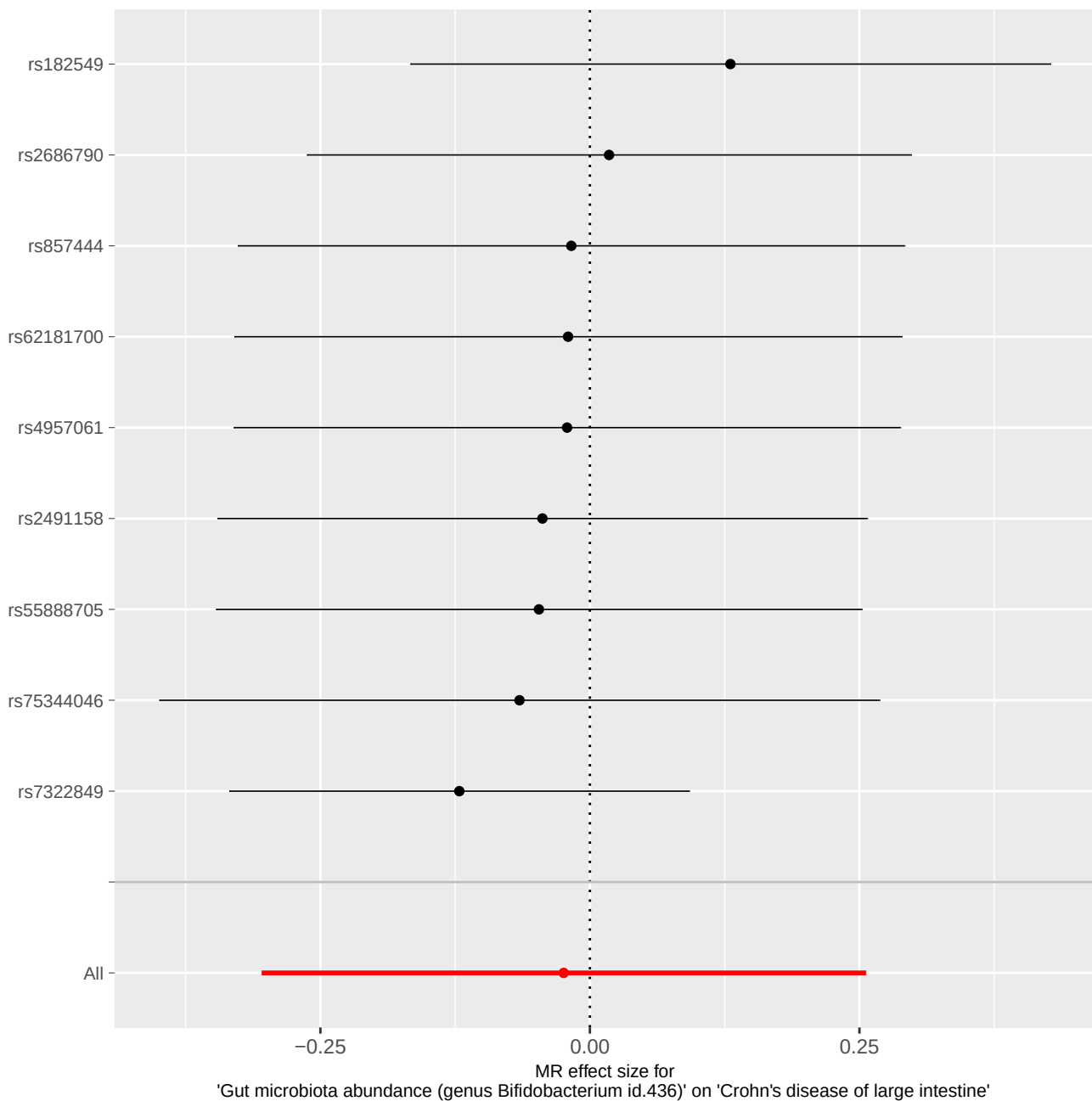
Batch 41 : Gut microbiota abundance (genus Anaerotruncus id.2054) on Crohn's disease of large intestine



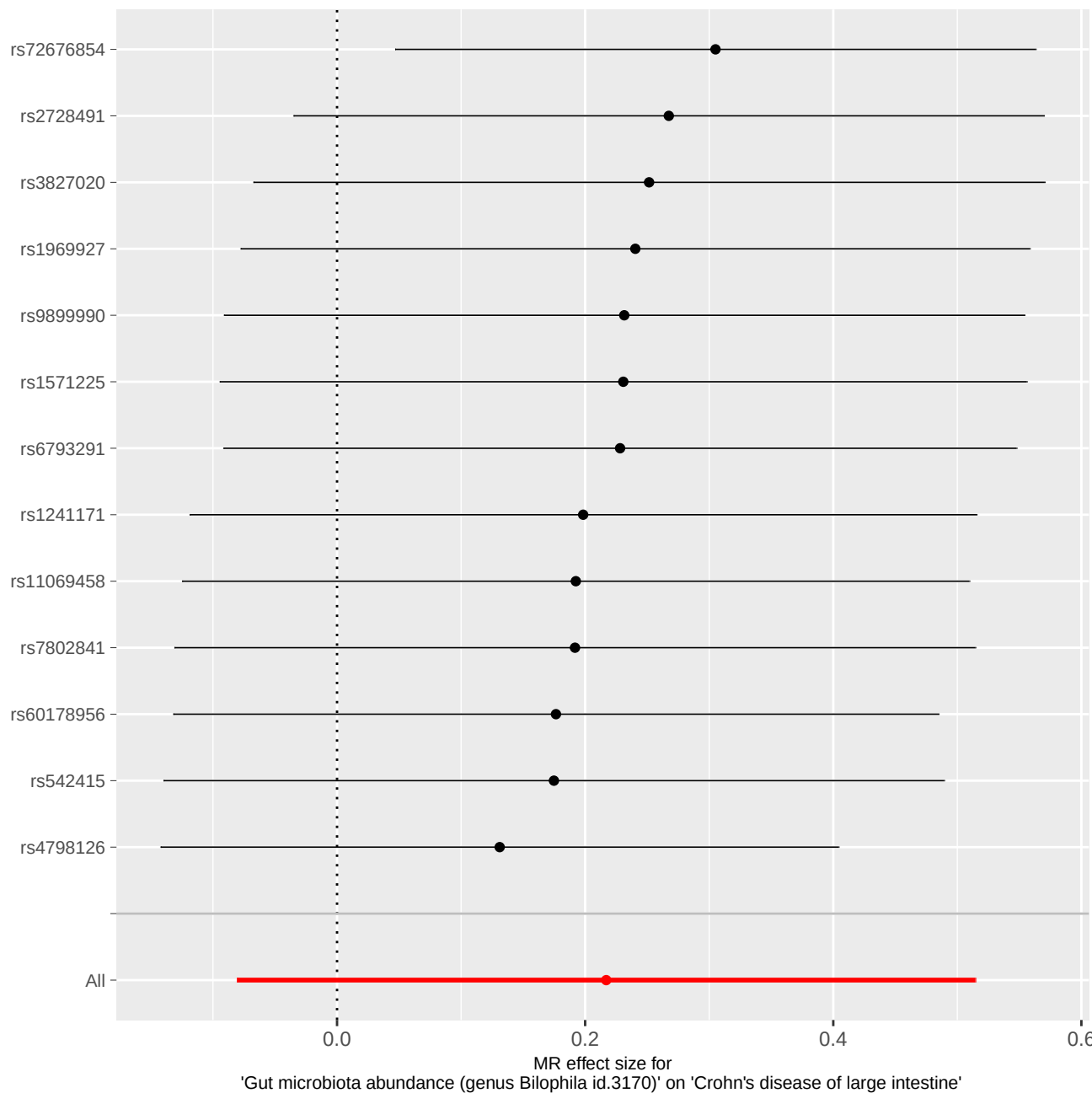


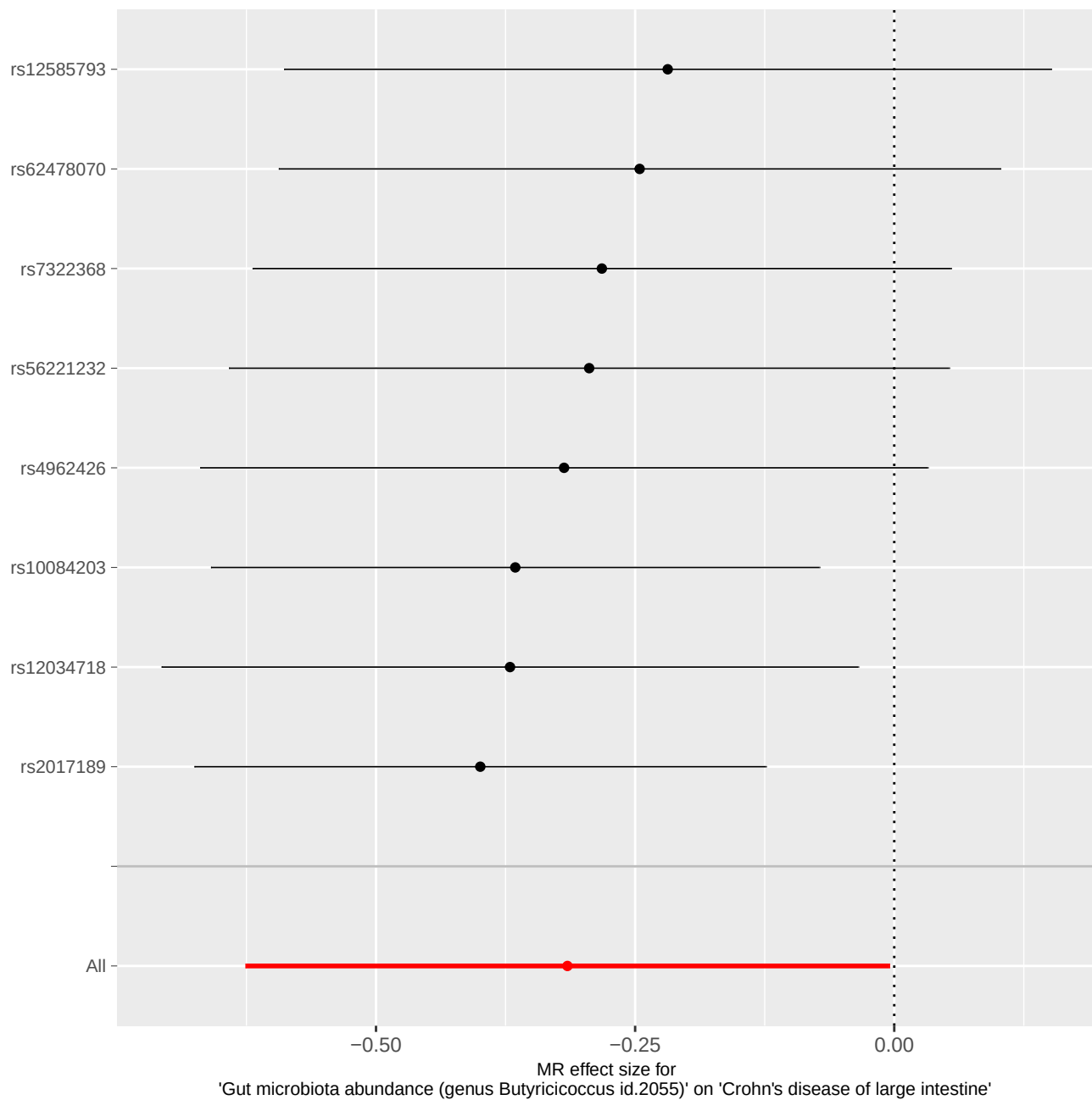


Batch 44 : Gut microbiota abundance (genus Bifidobacterium id.436) on Crohn's disease of large intestine

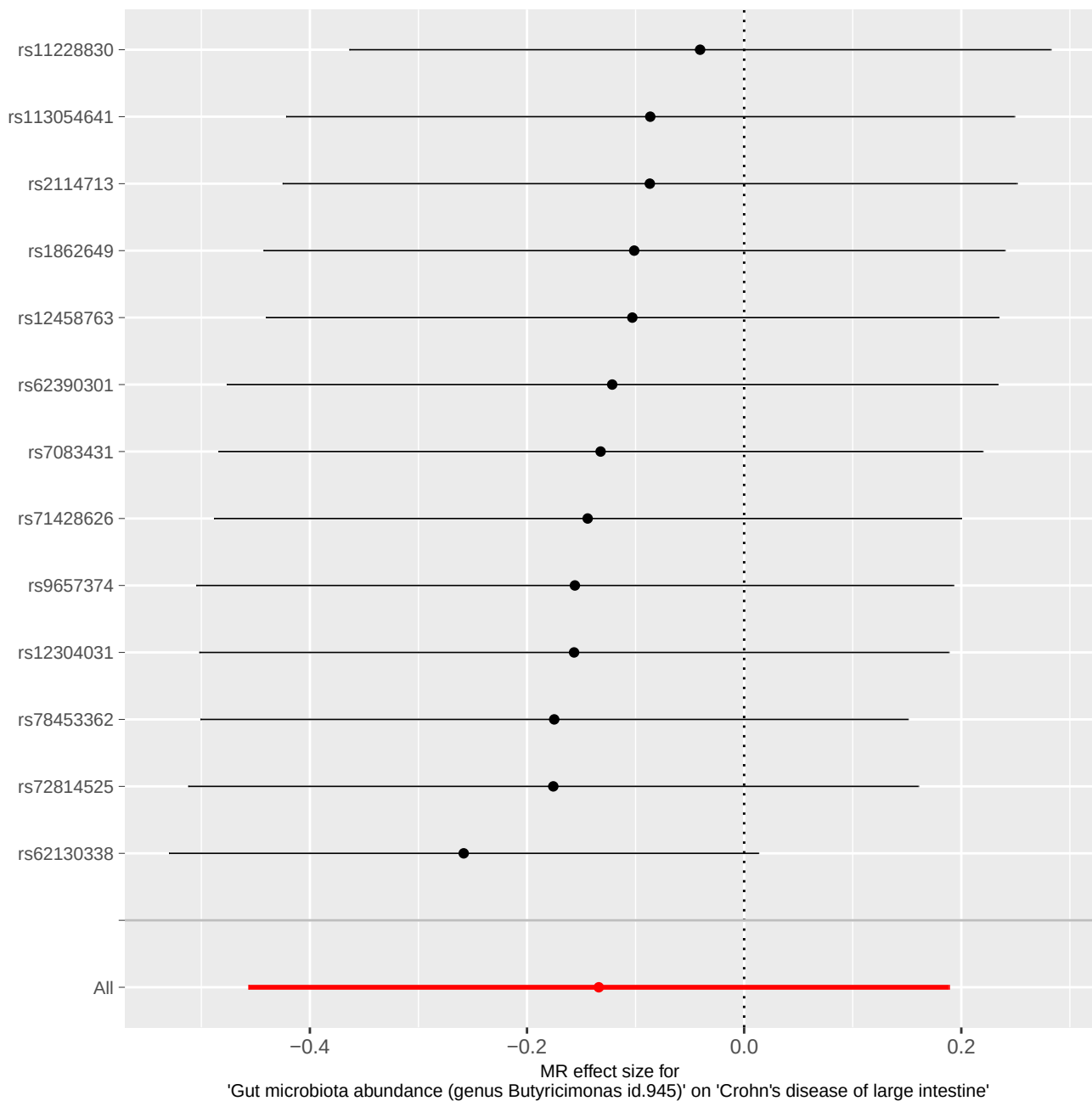


Batch 45 : Gut microbiota abundance (genus Bilophila id.3170) on Crohn's disease of large intestine

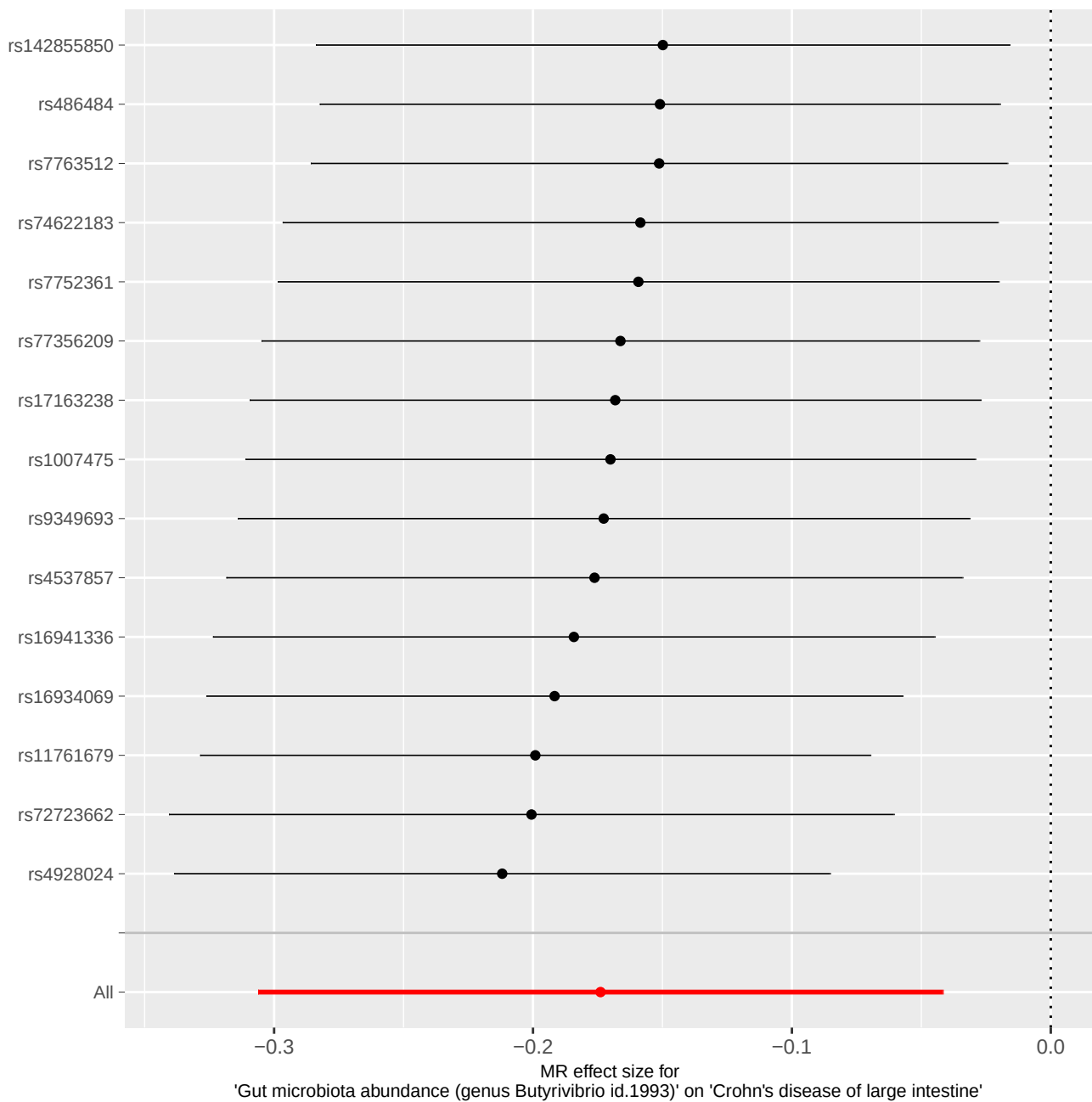


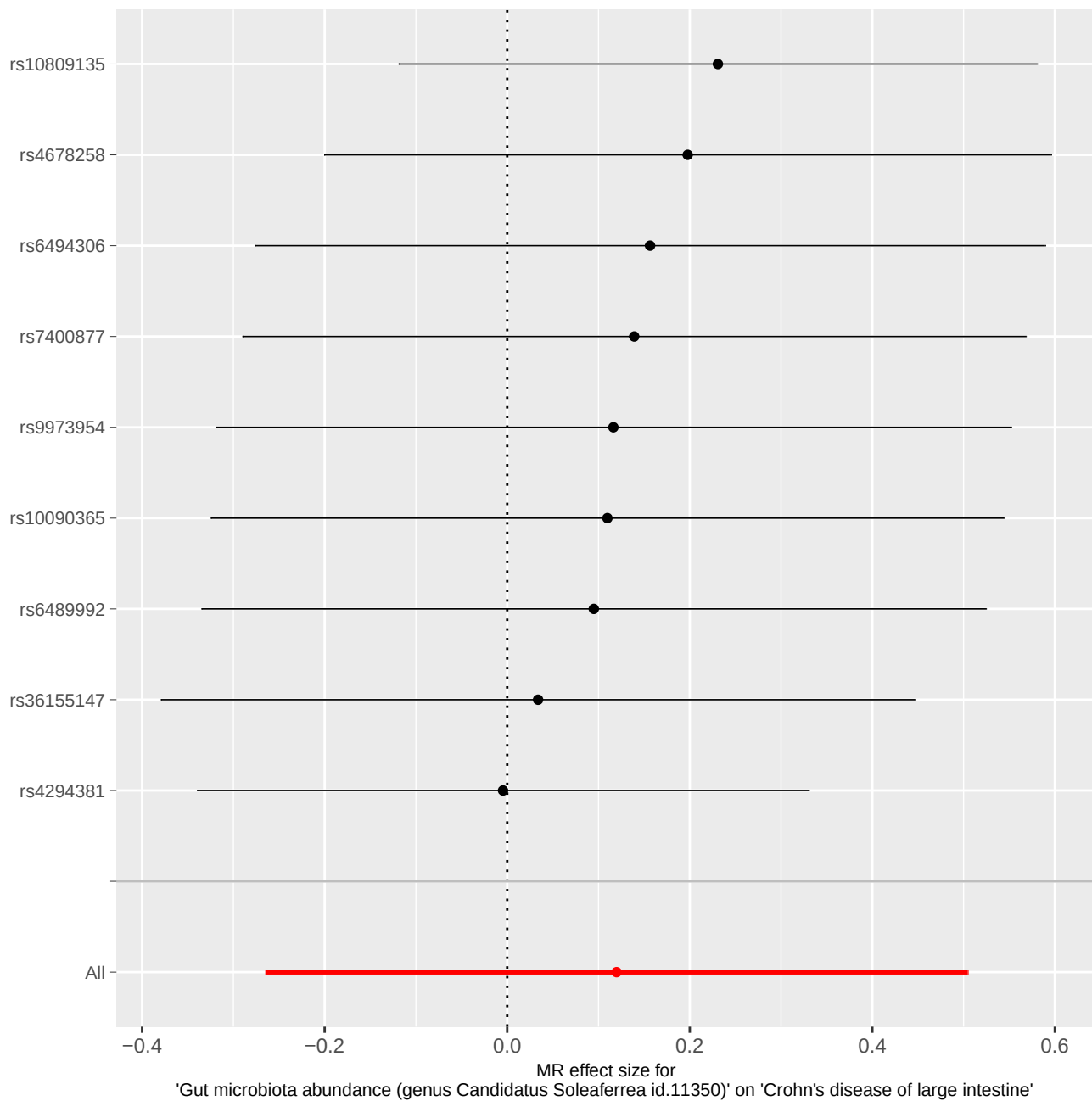


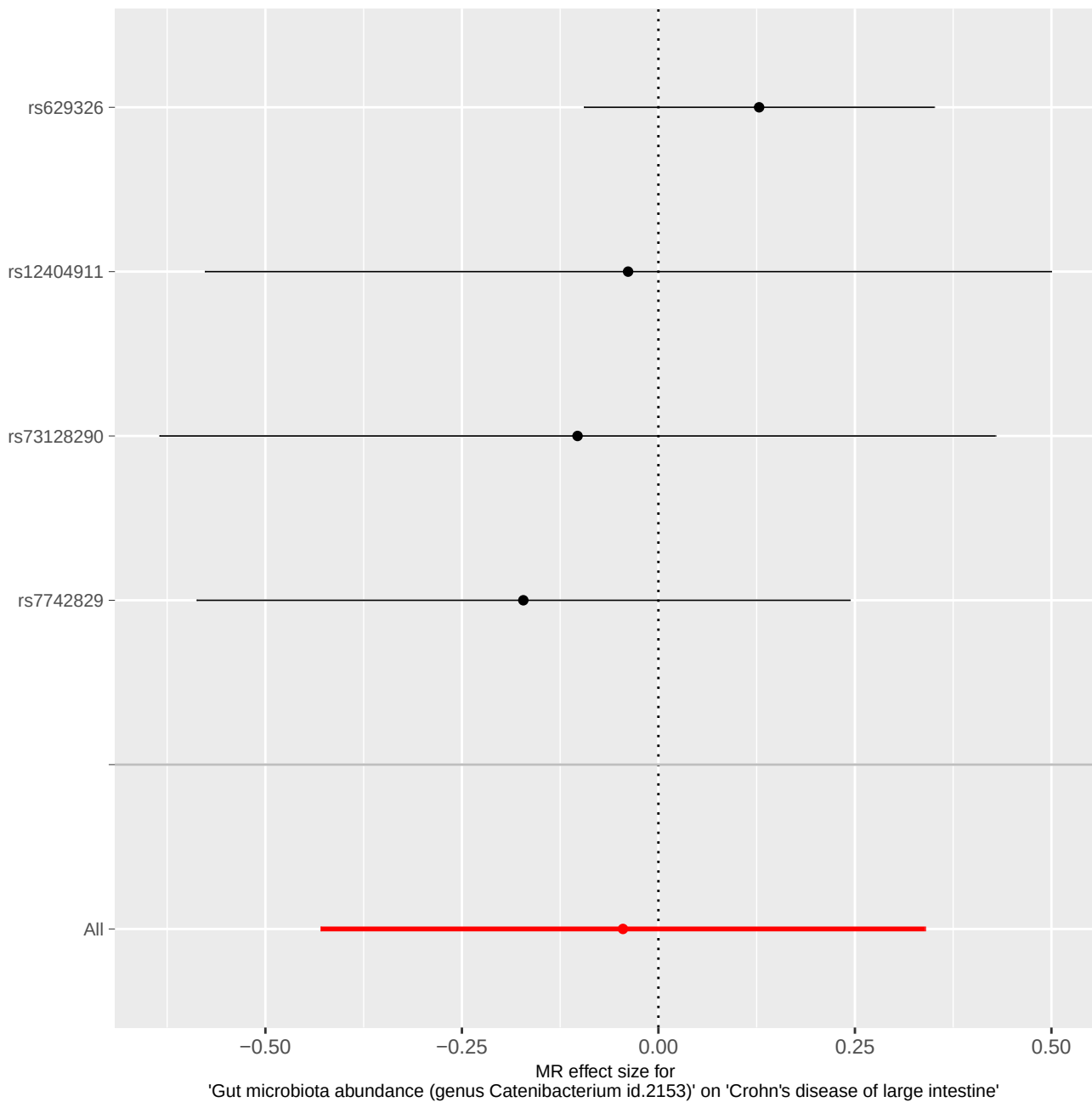
Batch 48 : Gut microbiota abundance (genus Butyricimonas id.945) on Crohn's disease of large intestine

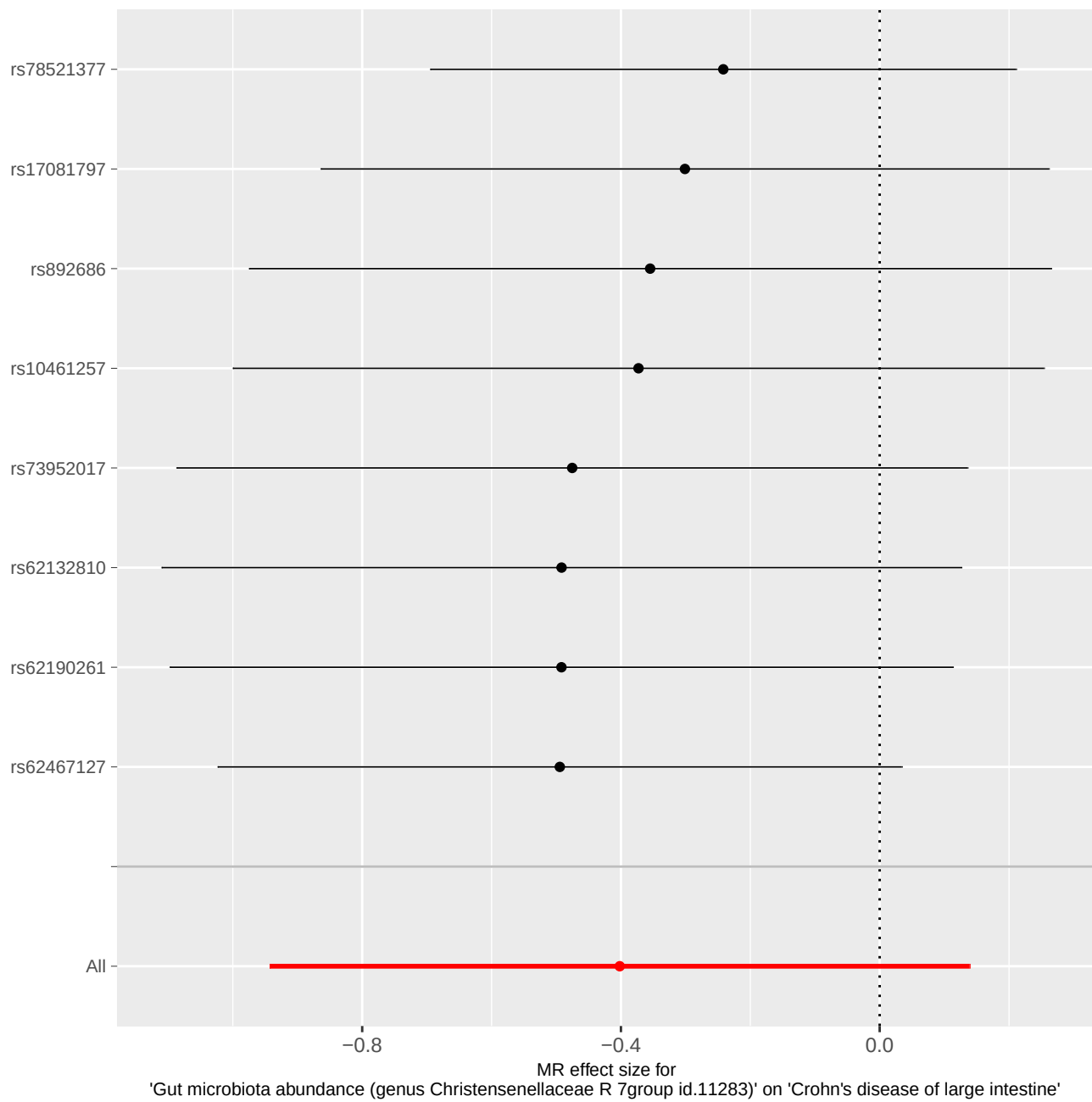


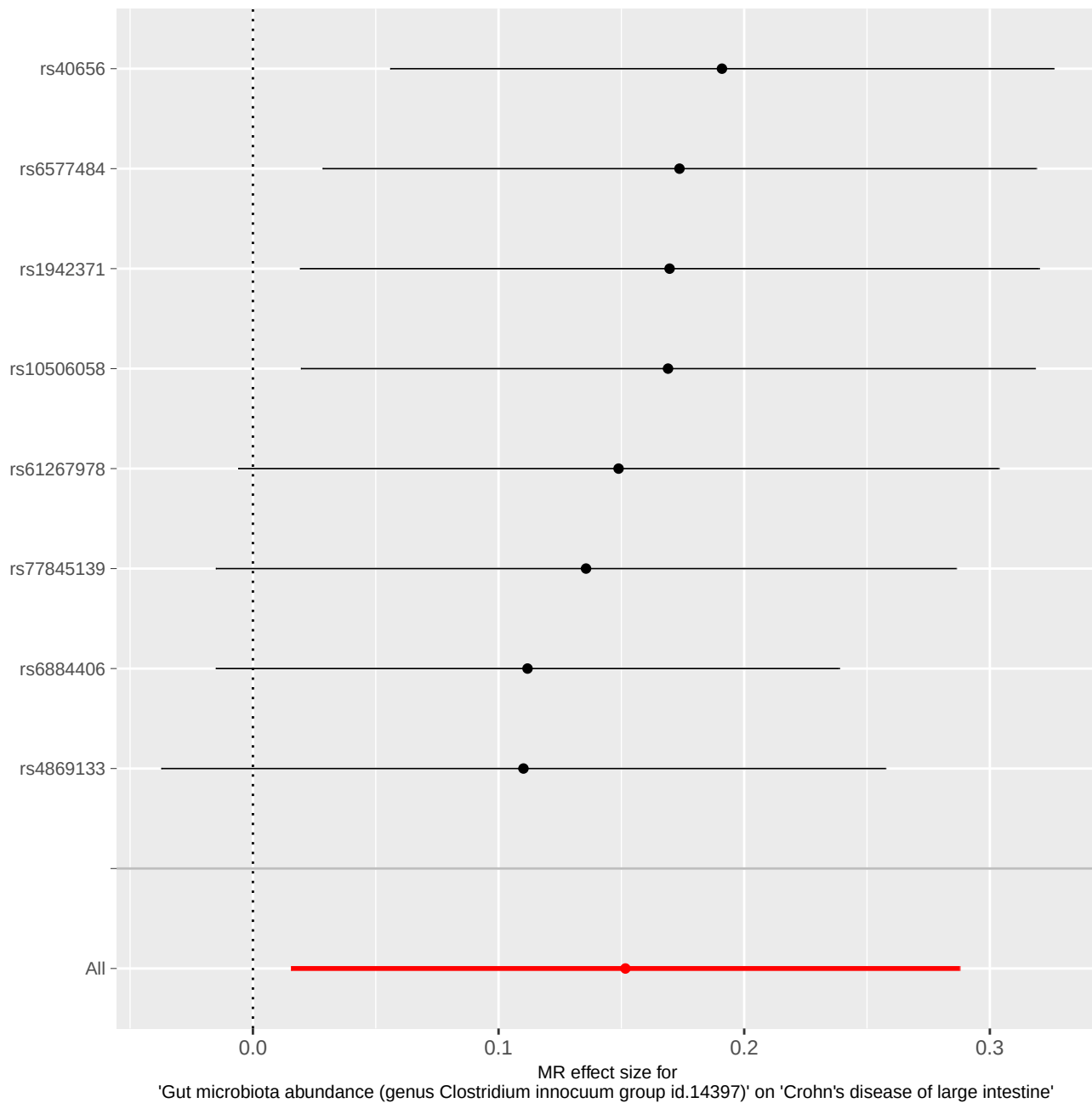
Batch 49 : Gut microbiota abundance (genus Butyrivibrio id.1993) on Crohn's disease of large intestine

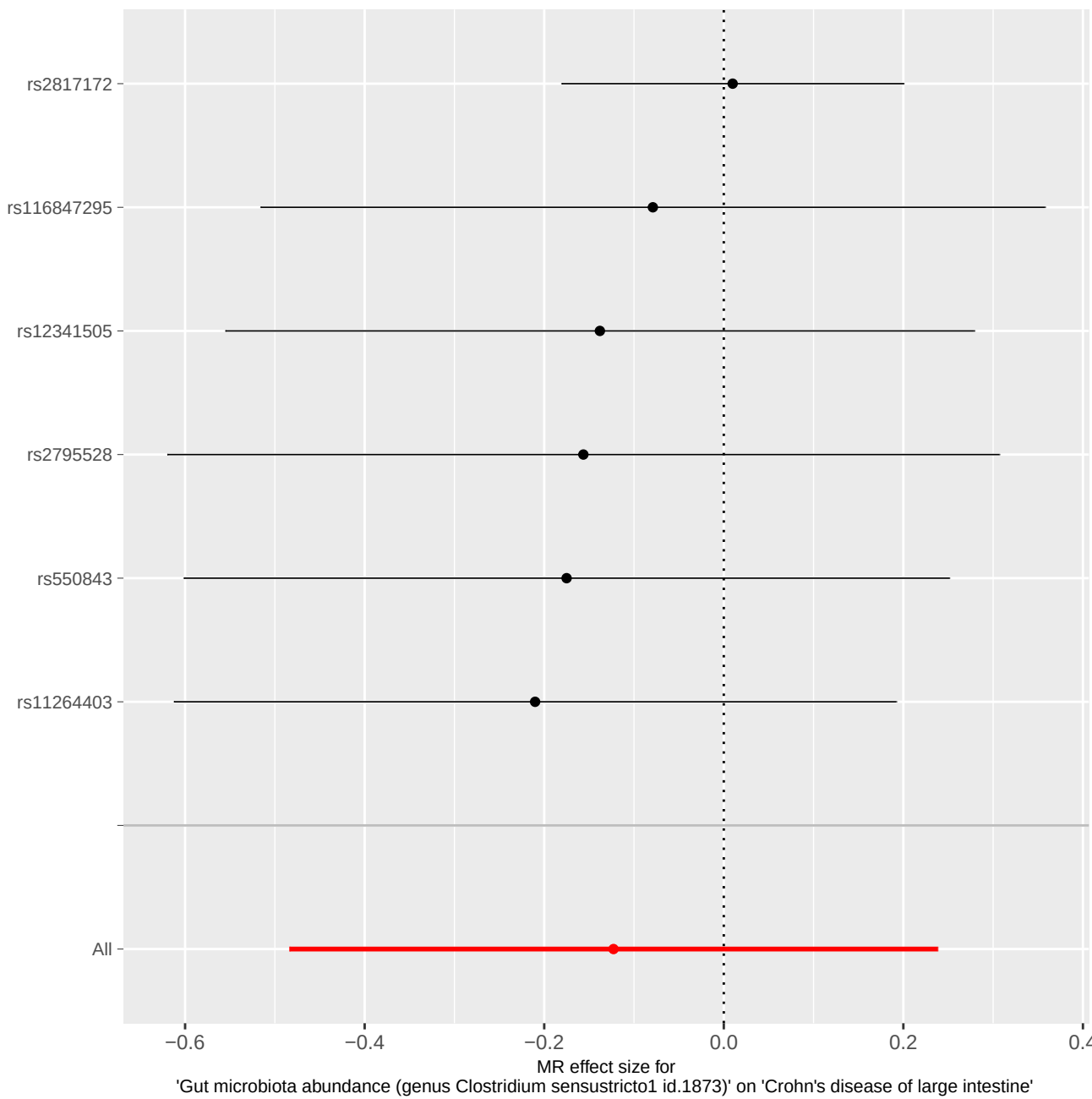




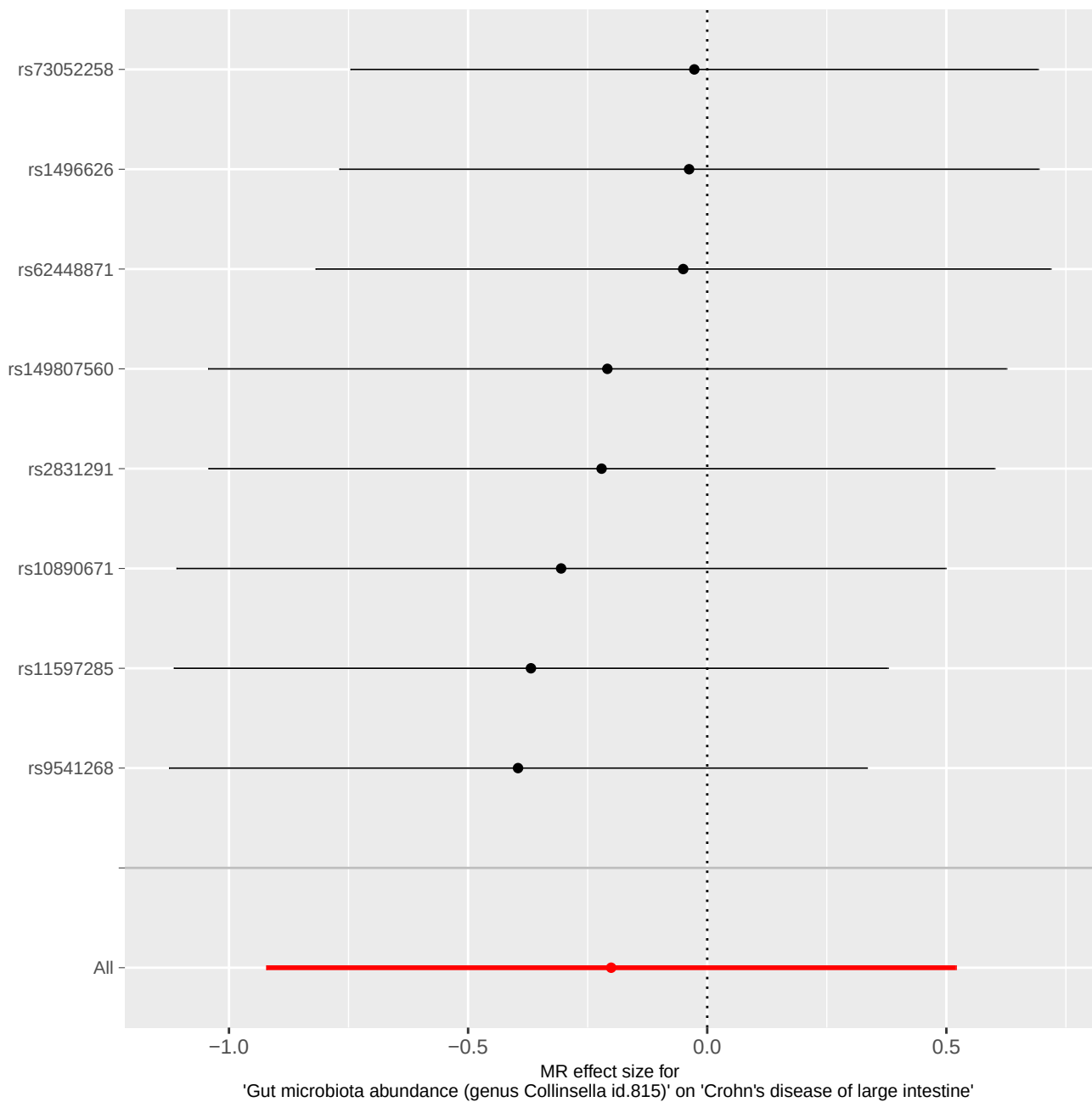


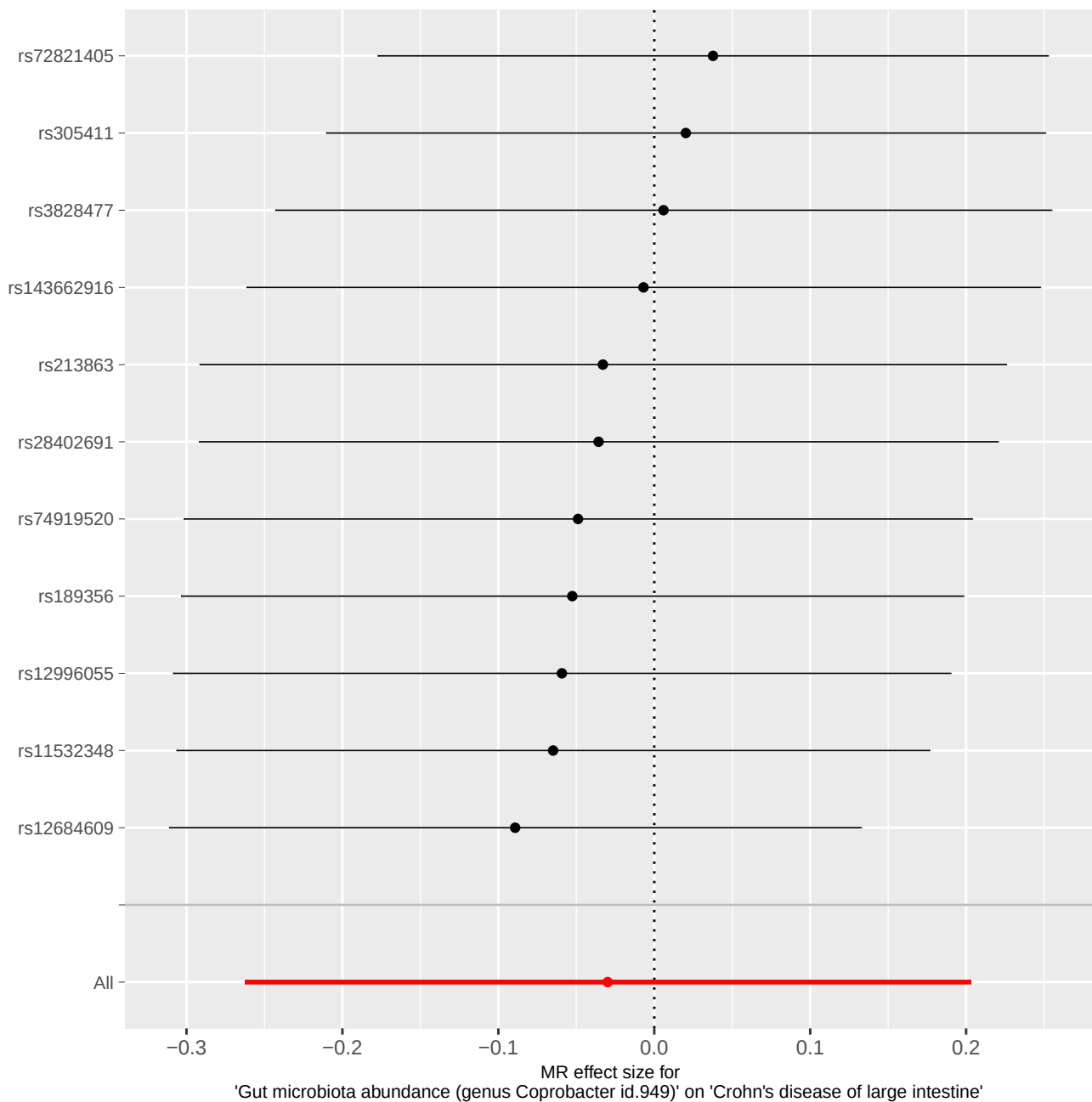




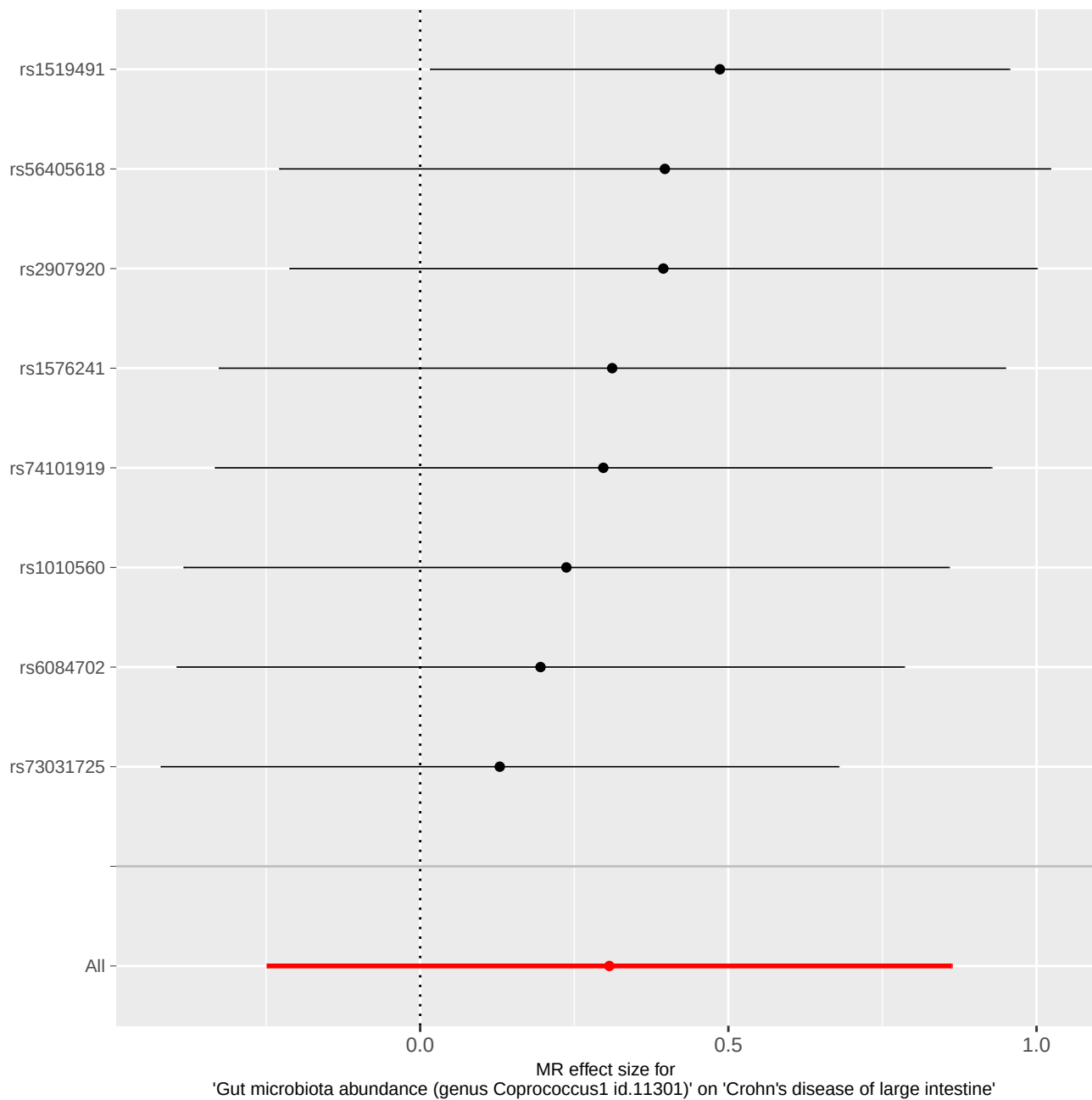


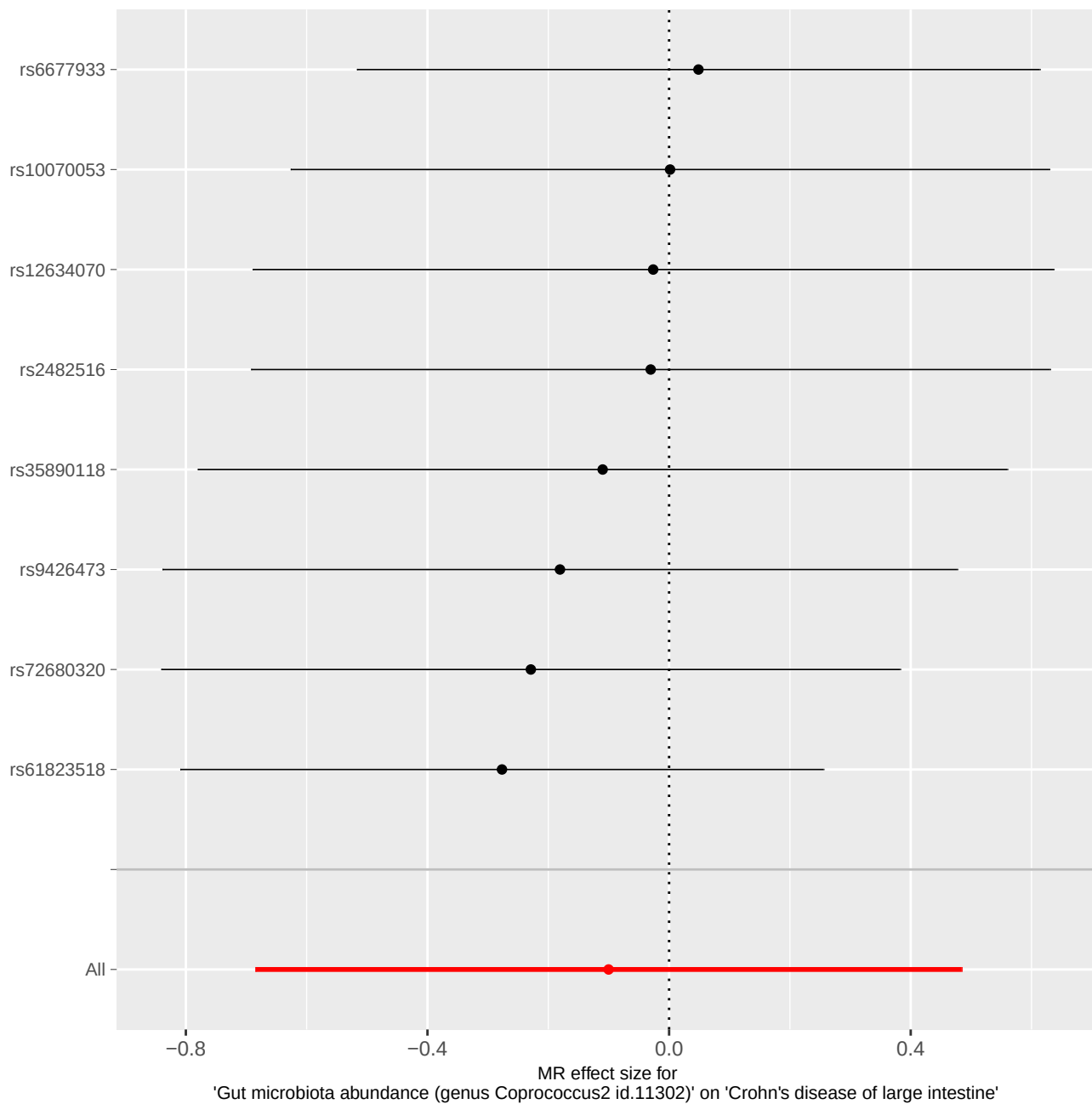
Batch 55 : Gut microbiota abundance (genus Collinsella id.815) on Crohn's disease of large intestine



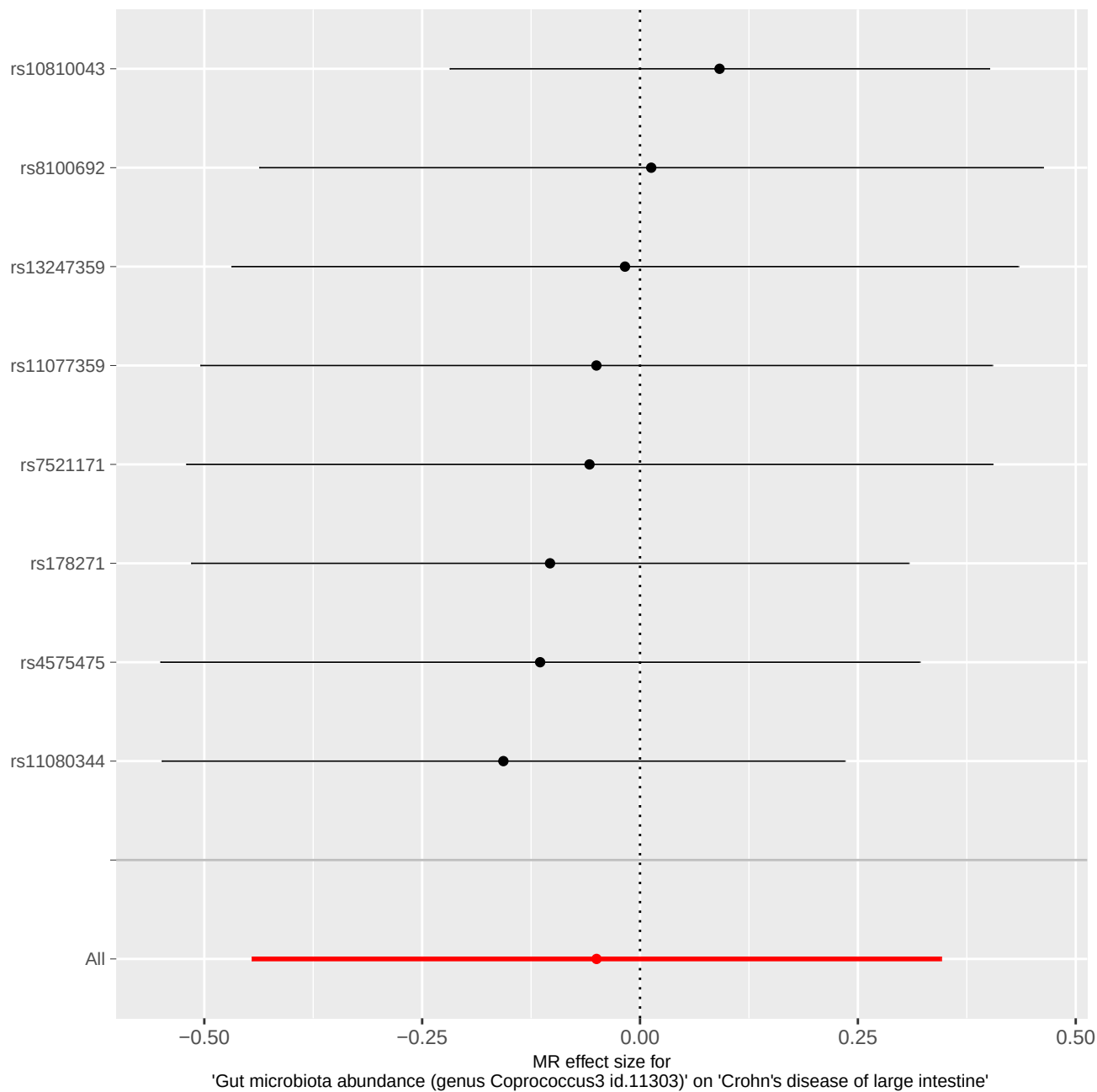


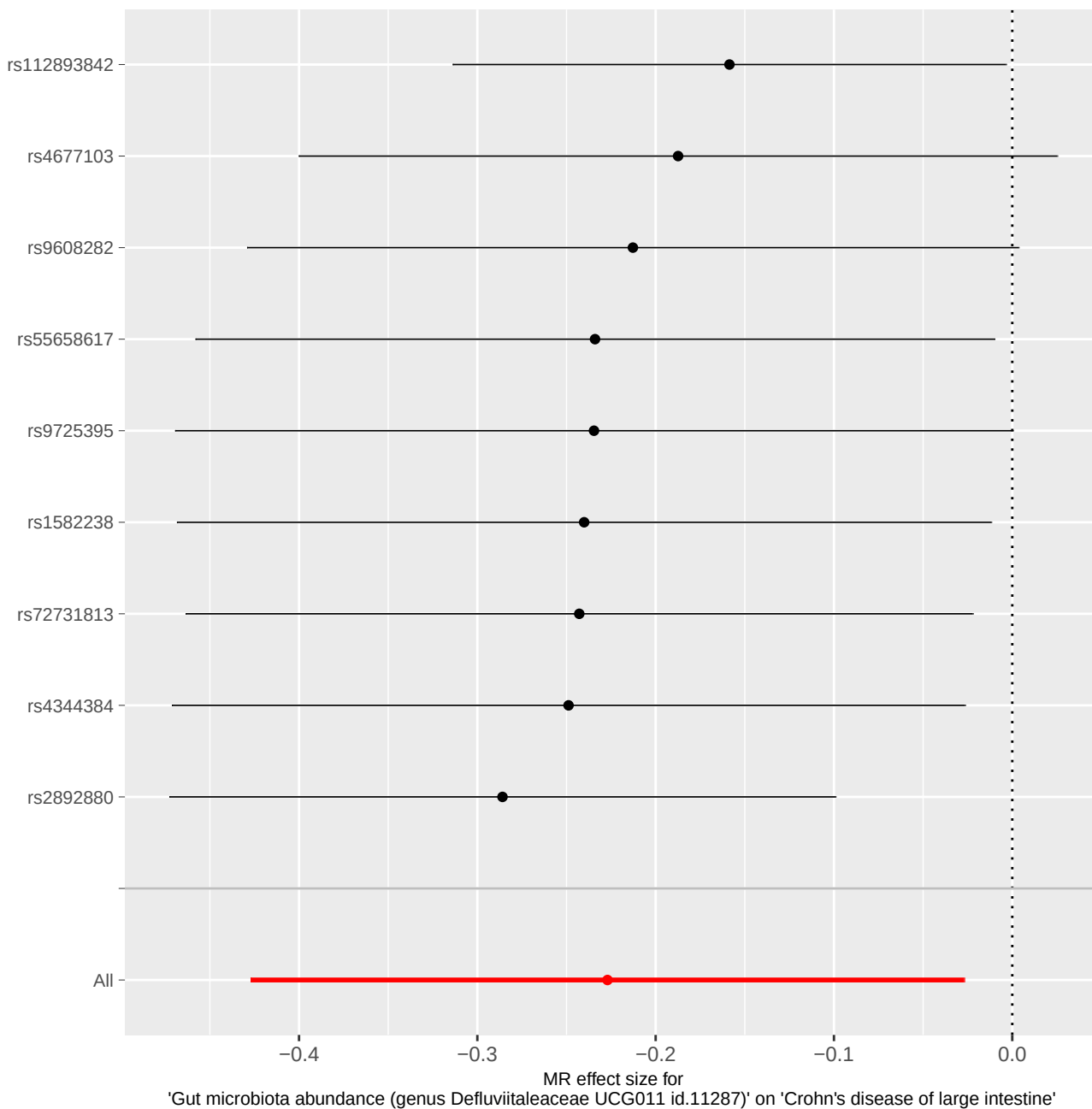
Batch 57 : Gut microbiota abundance (genus Coprococcus1 id.11301) on Crohn's disease of large intestine



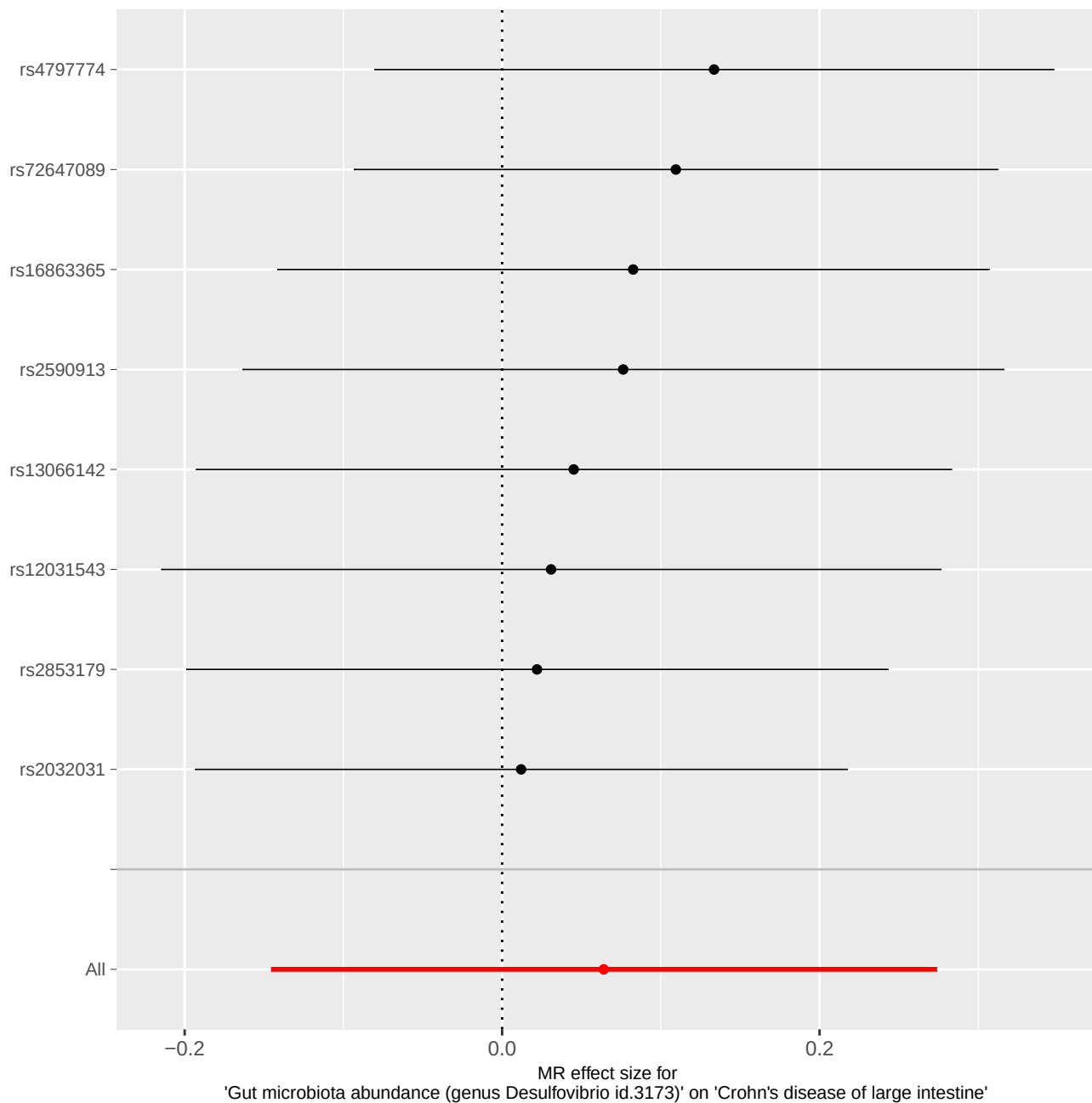


Batch 59 : Gut microbiota abundance (genus Coprococcus3 id.11303) on Crohn's disease of large intestine

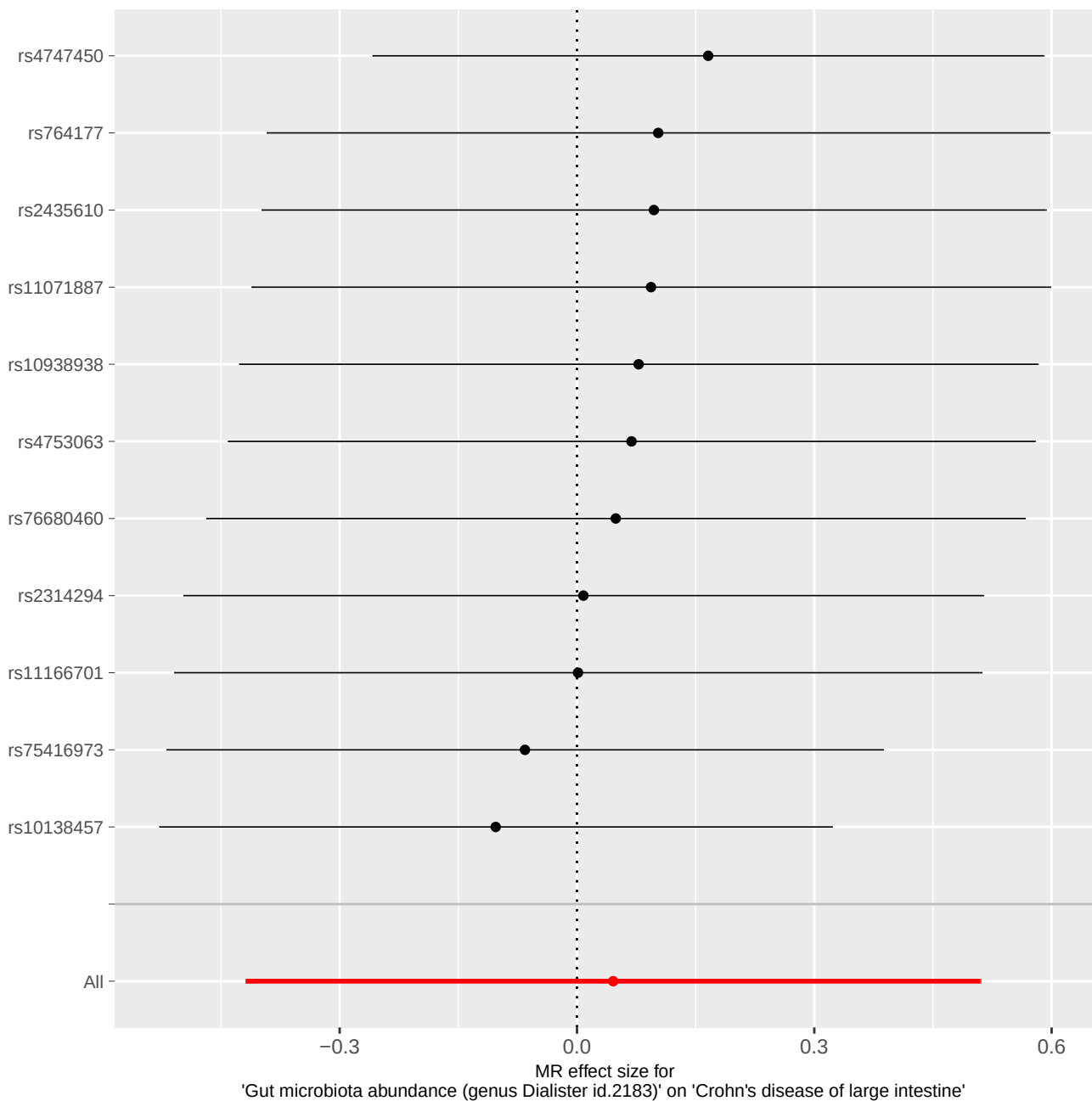




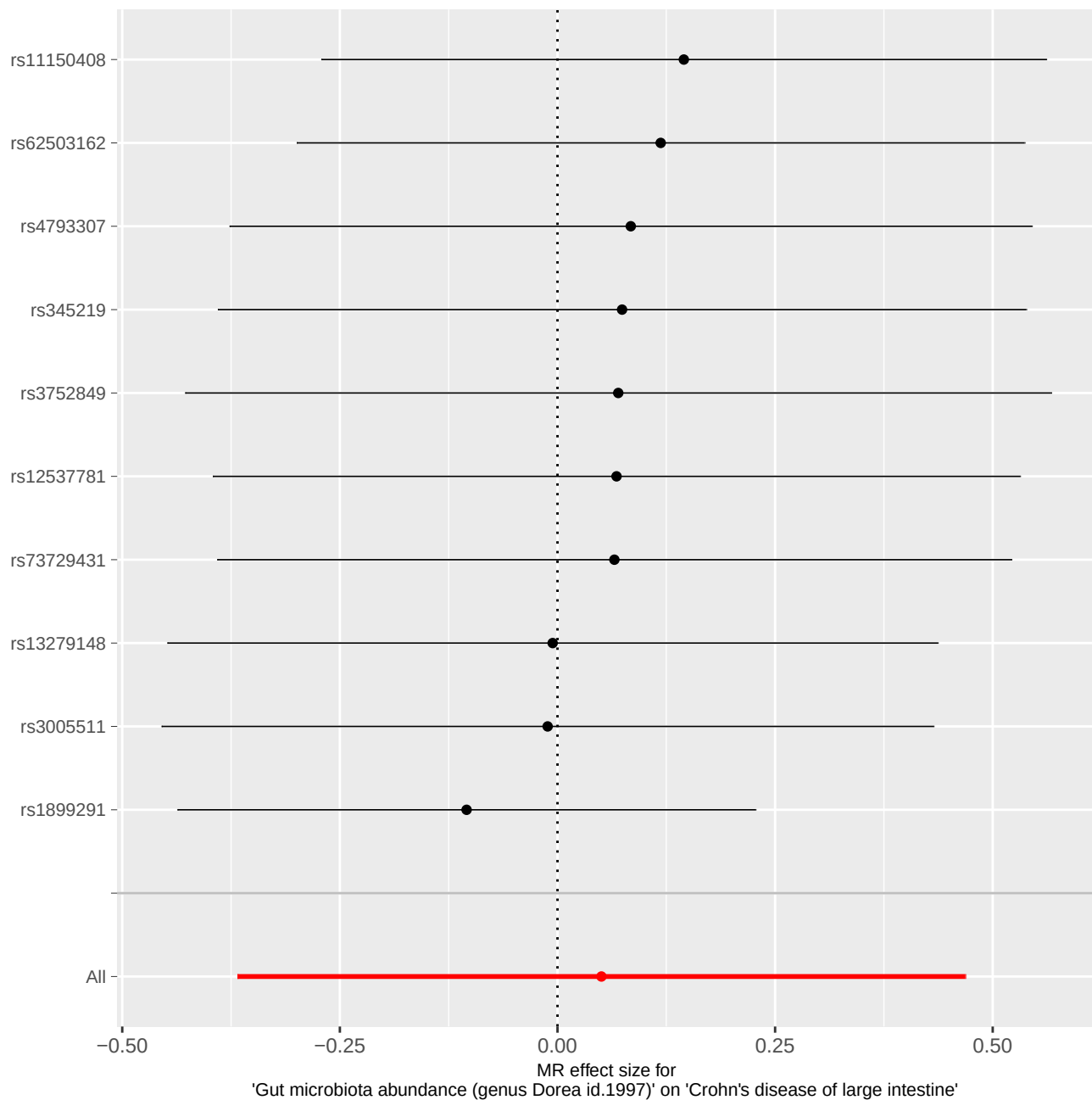
Batch 61 : Gut microbiota abundance (genus Desulfovibrio id.3173) on Crohn's disease of large intestine

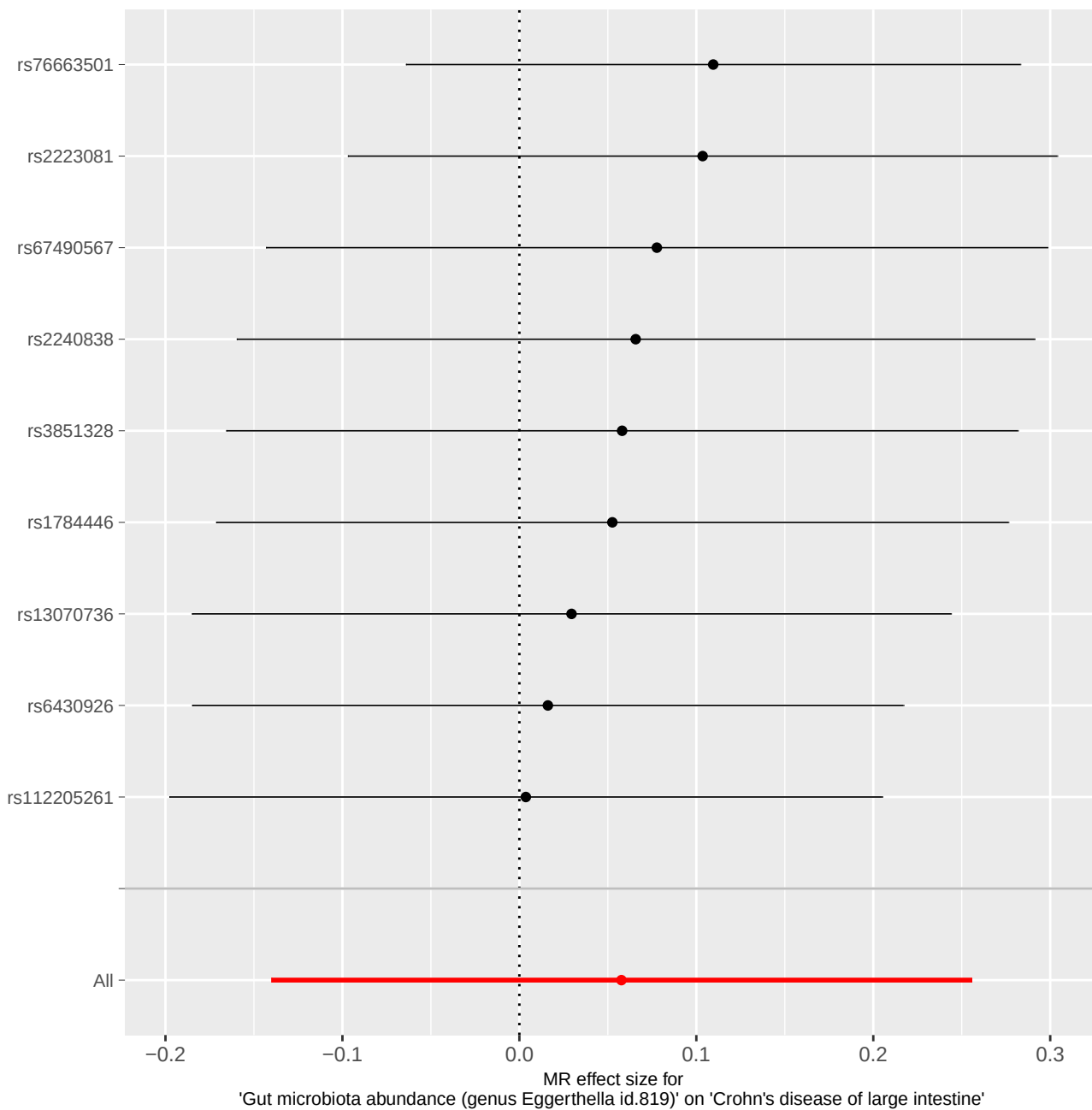


Batch 62 : Gut microbiota abundance (genus Dialister id.2183) on Crohn's disease of large intestine

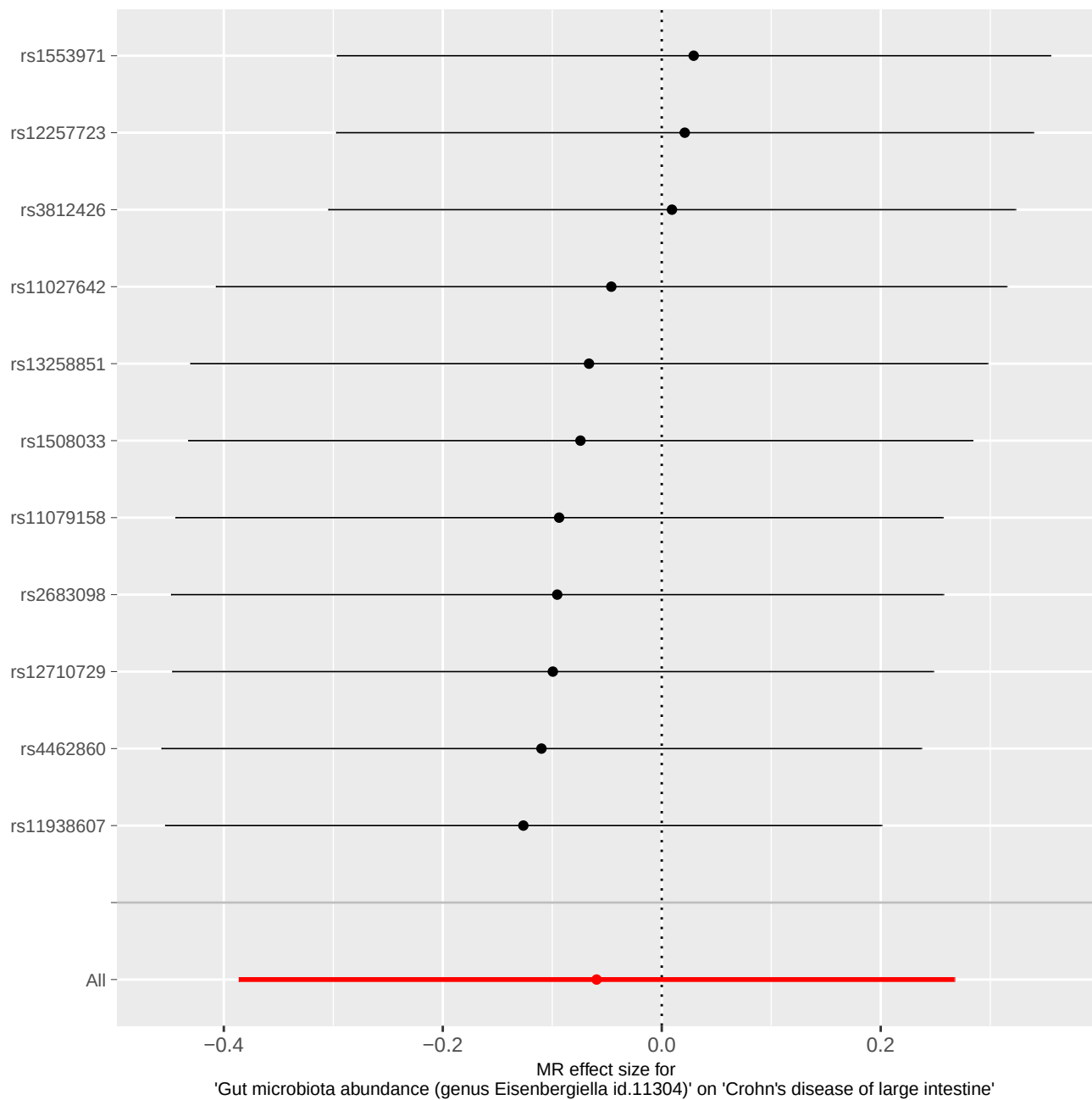


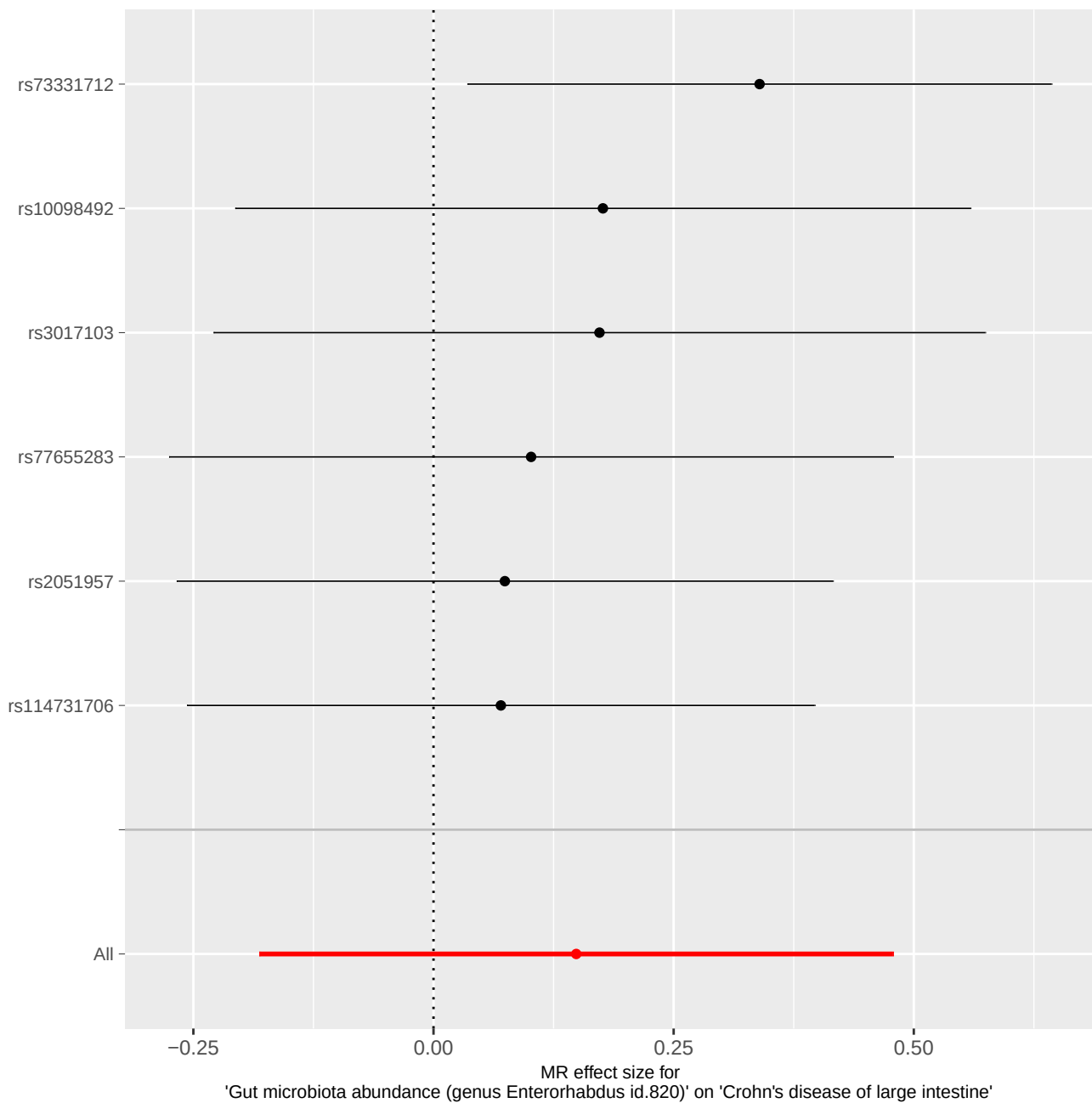
Batch 63 : Gut microbiota abundance (genus Dorea id.1997) on Crohn's disease of large intestine

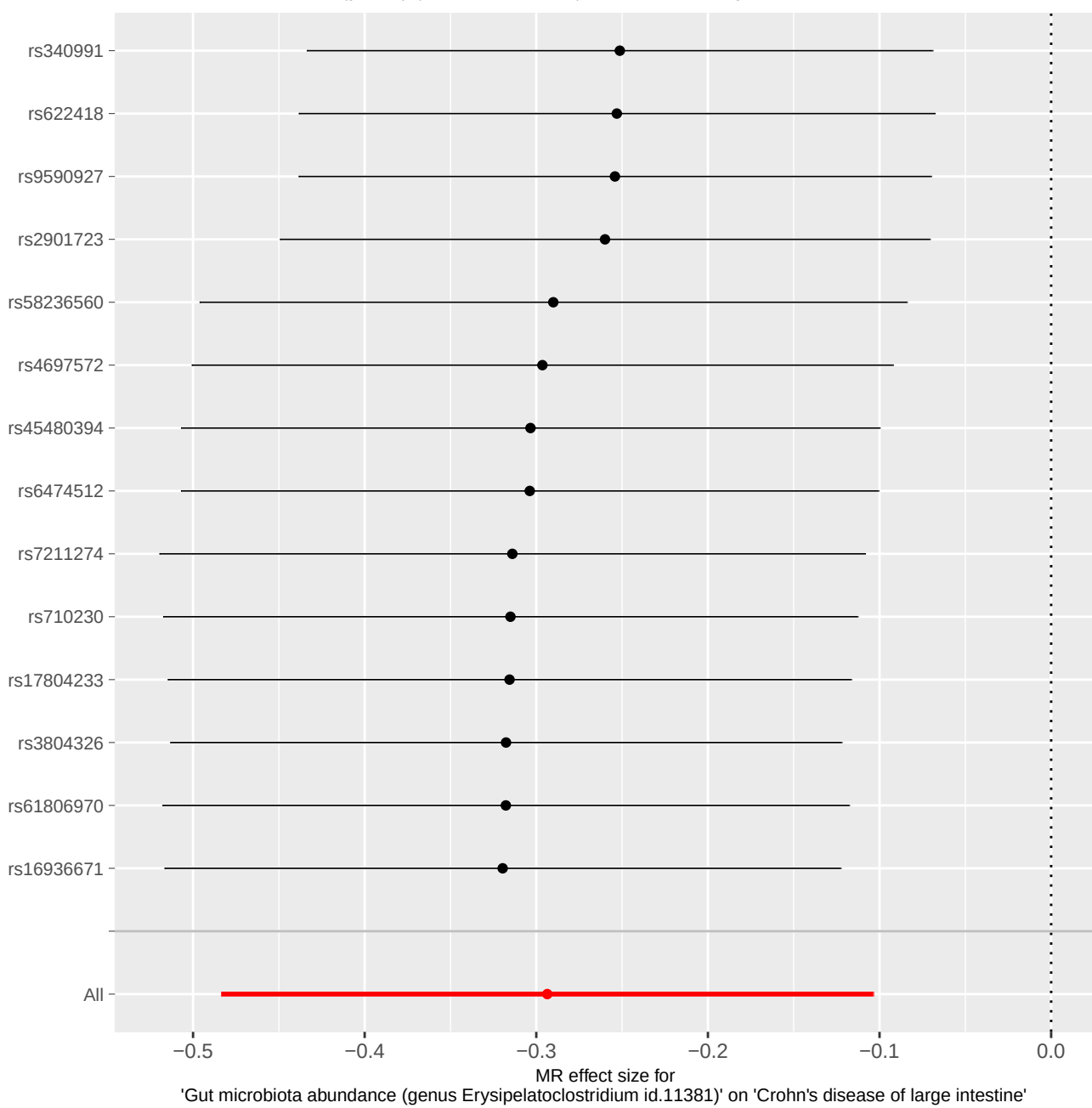


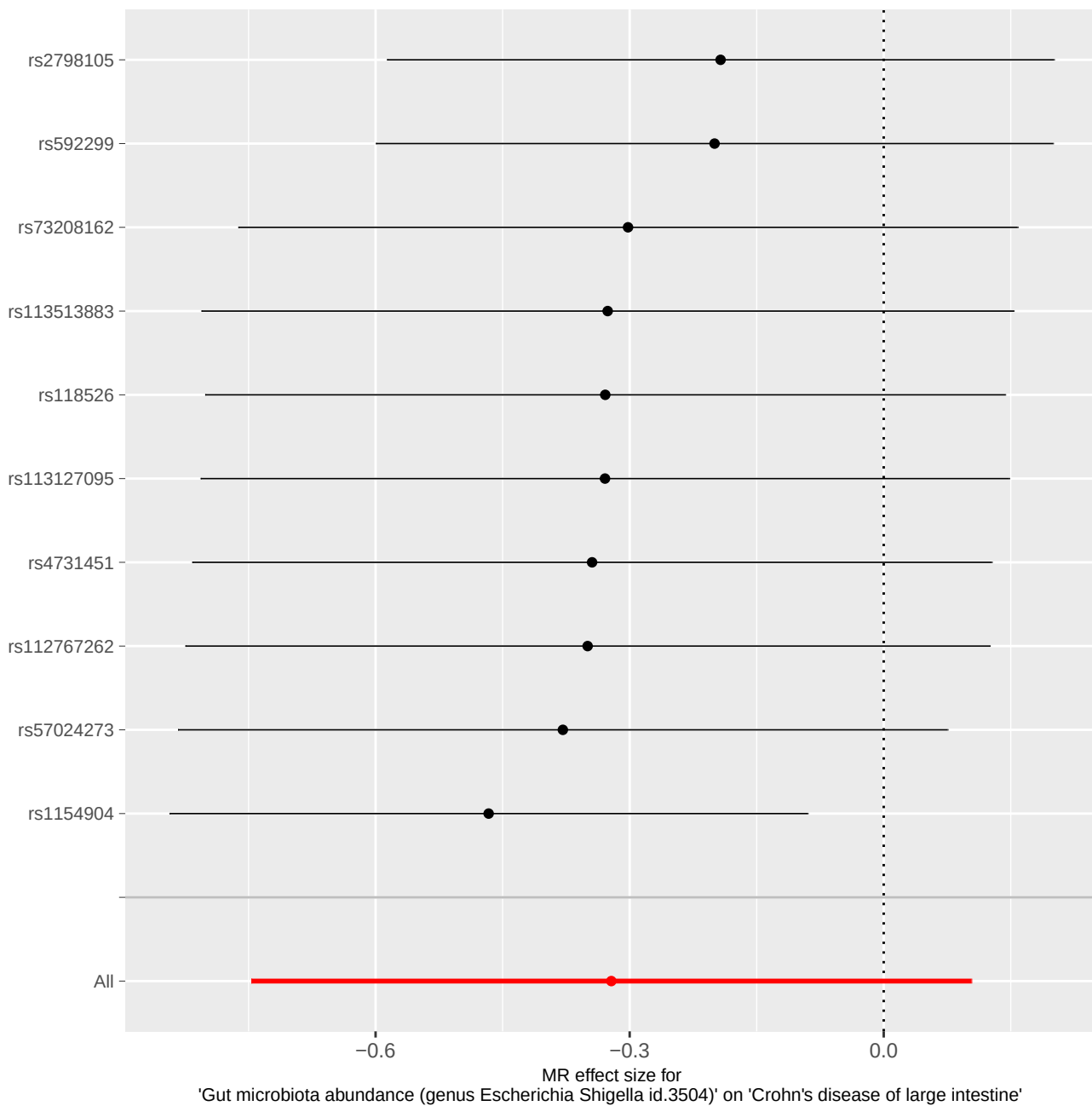


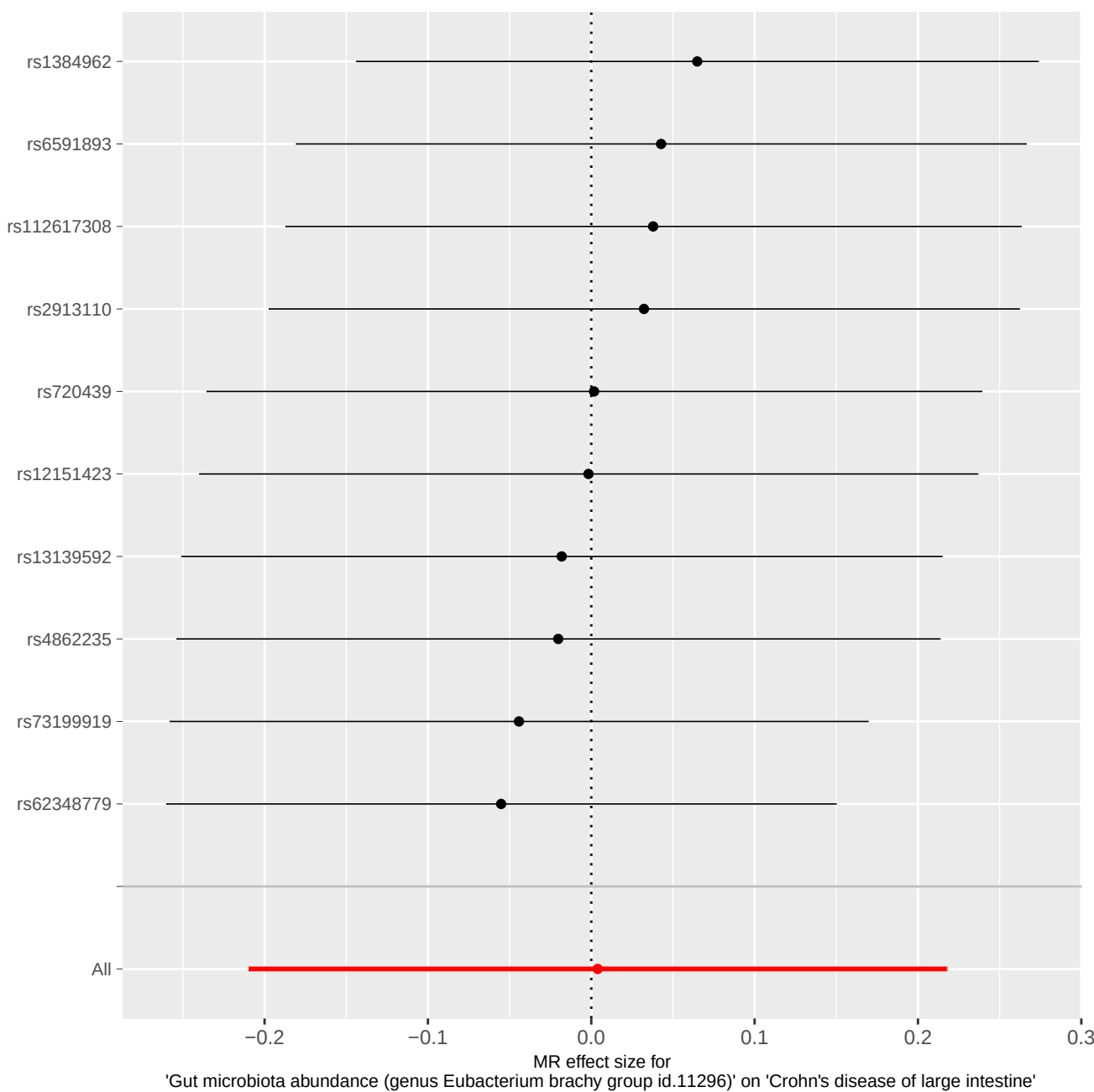
Batch 65 : Gut microbiota abundance (genus Eisenbergiella id.11304) on Crohn's disease of large intestine



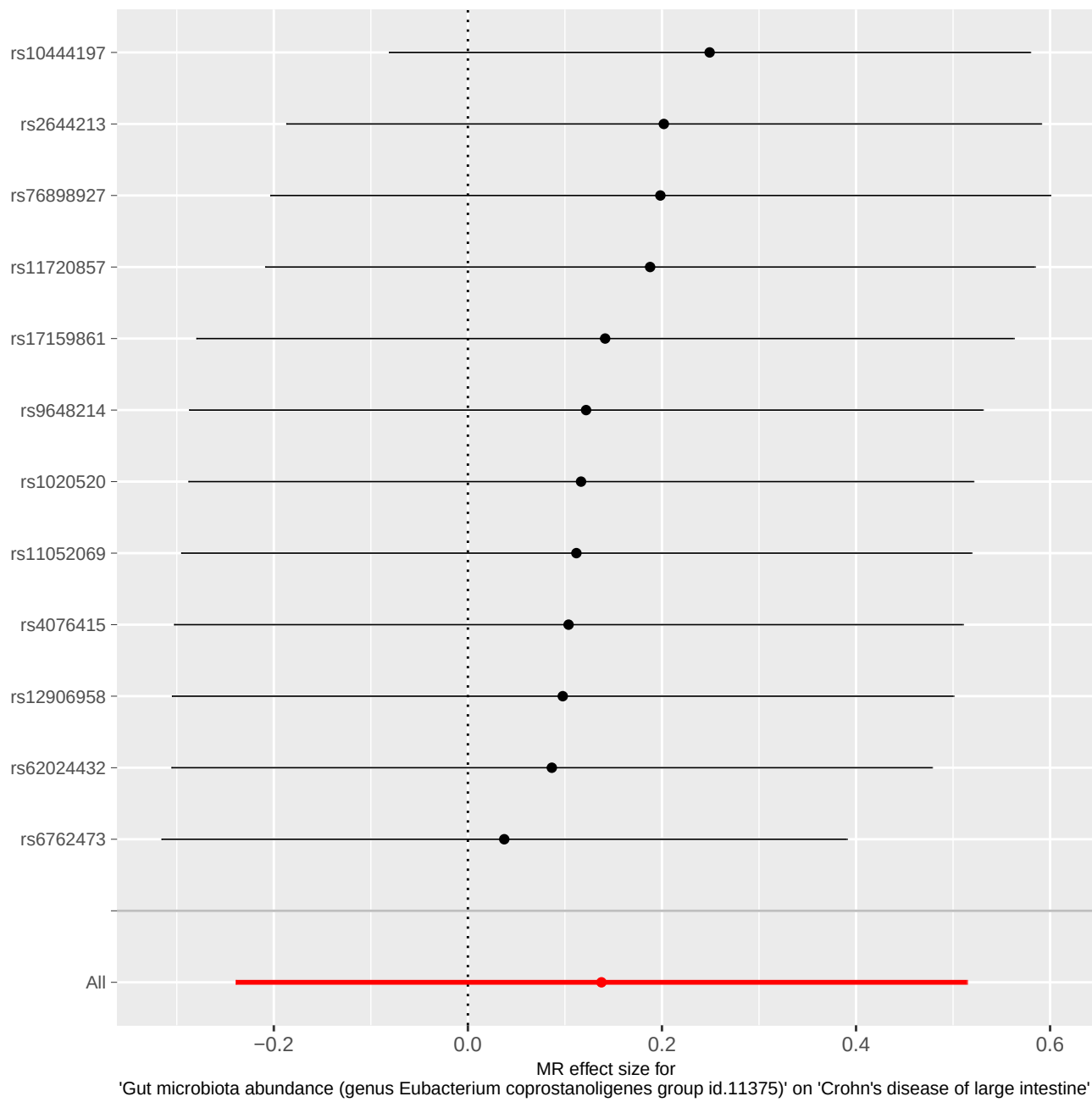


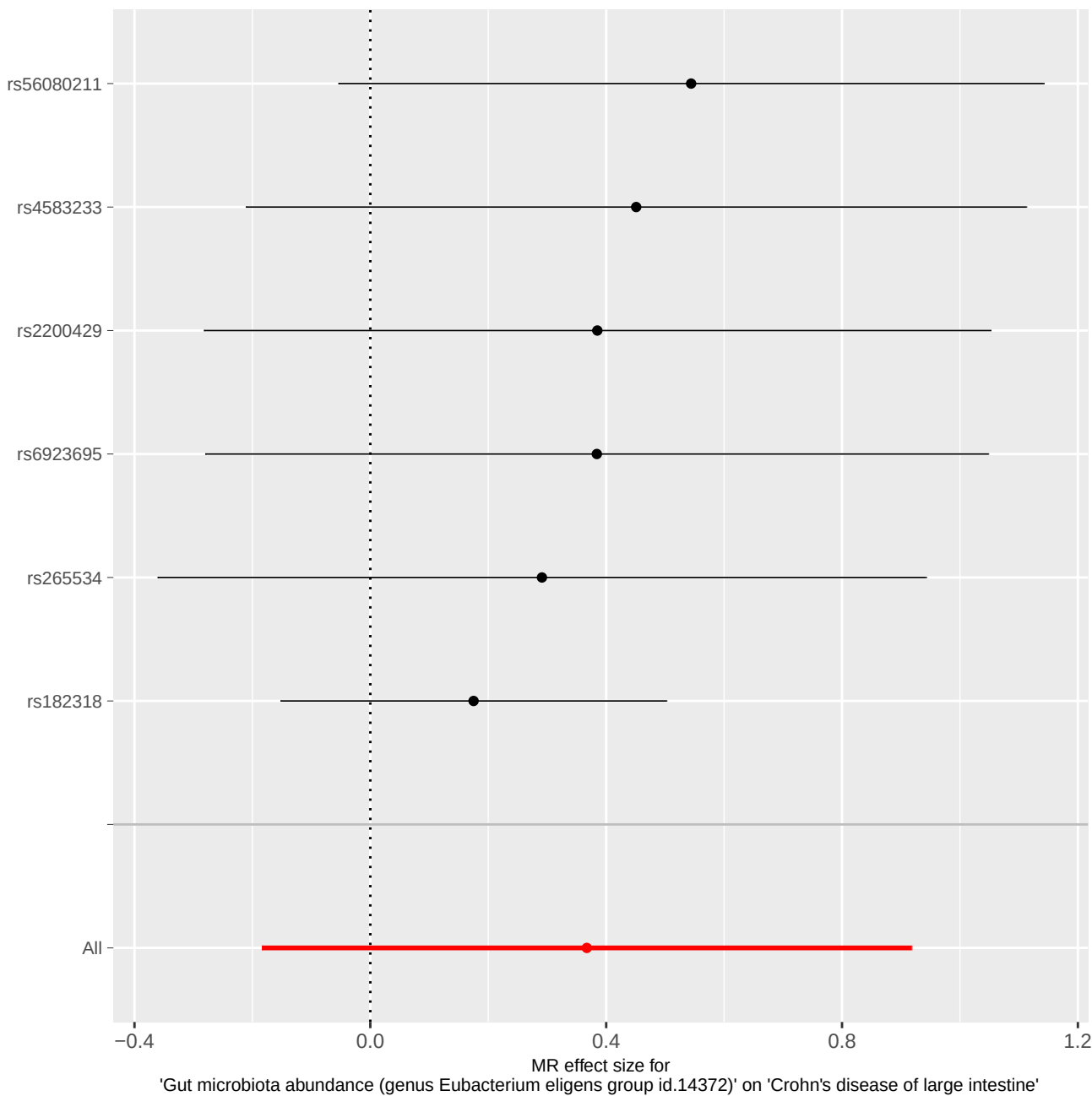




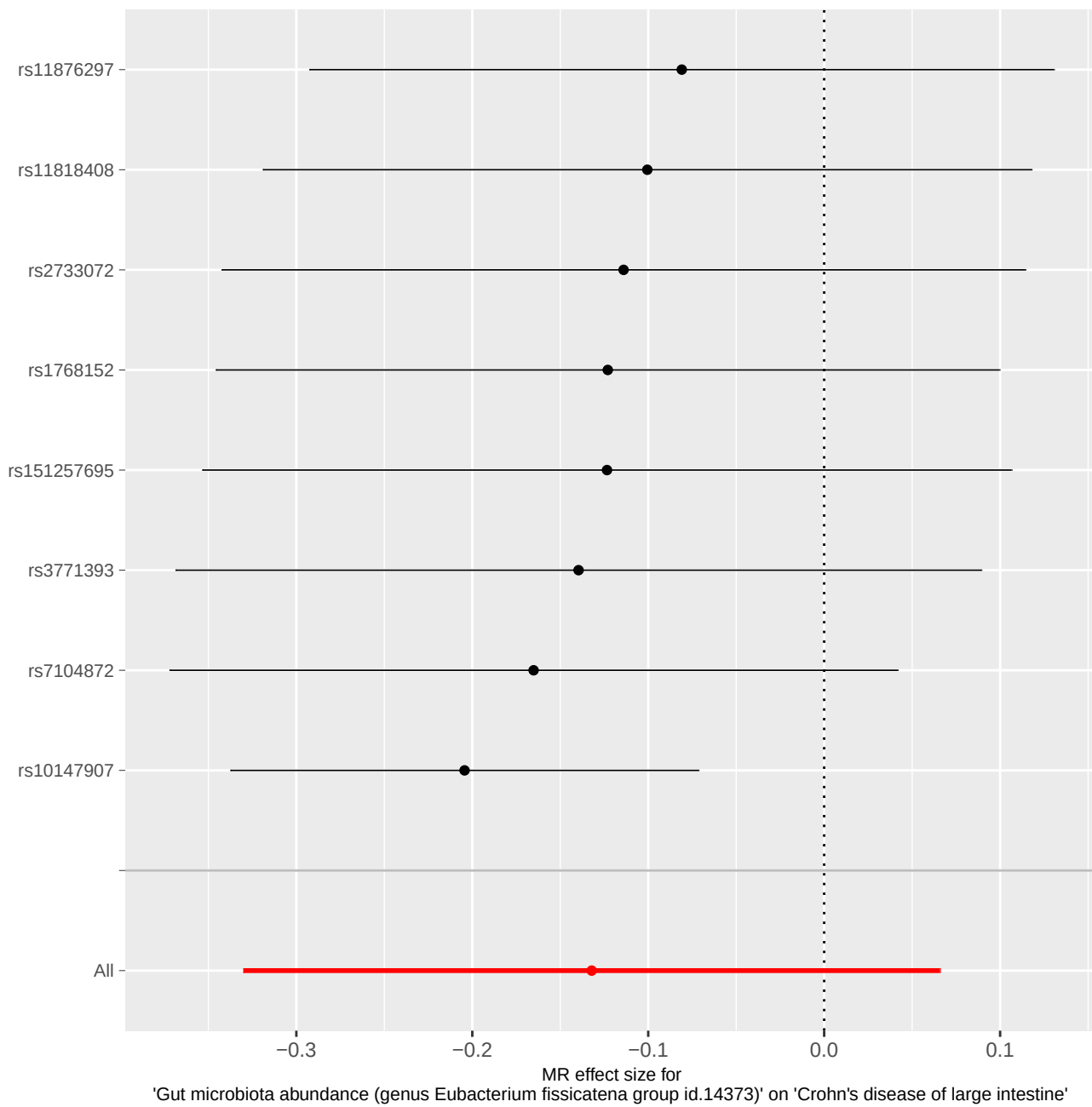


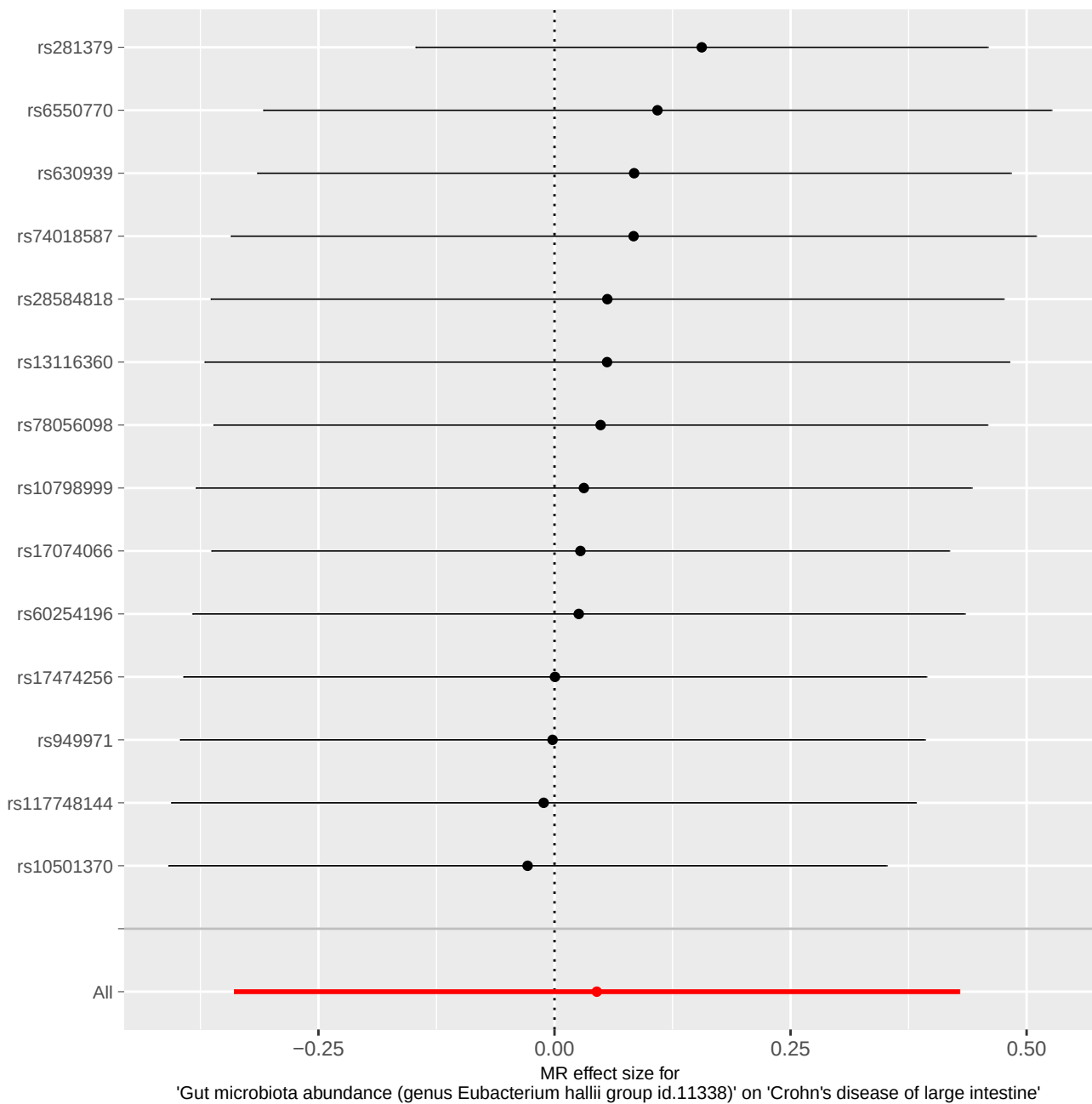
Batch 71 : Gut microbiota abundance (genus Eubacterium coprostanoligenes group id.11375) on Crohn's disease of large intestine

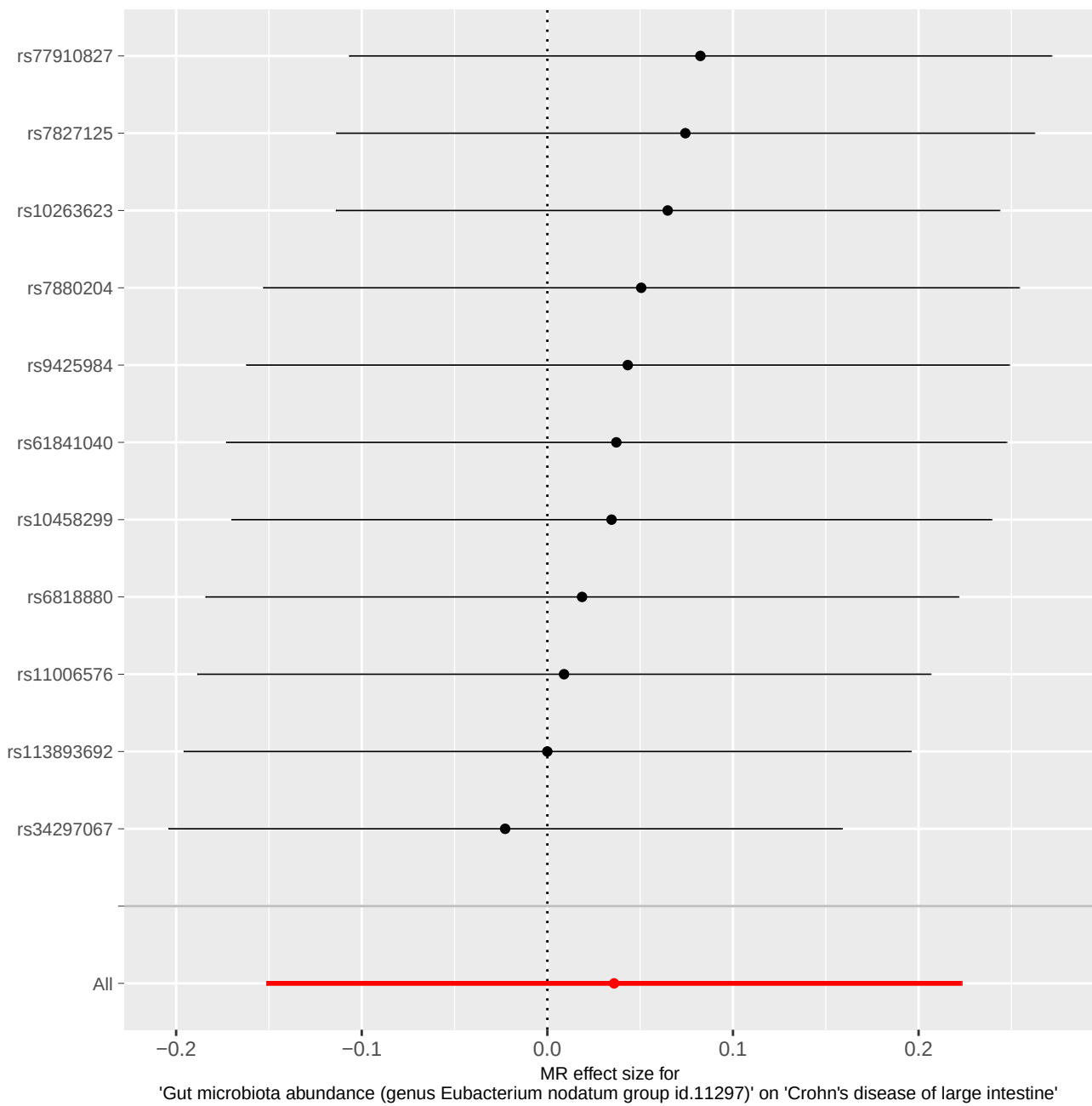


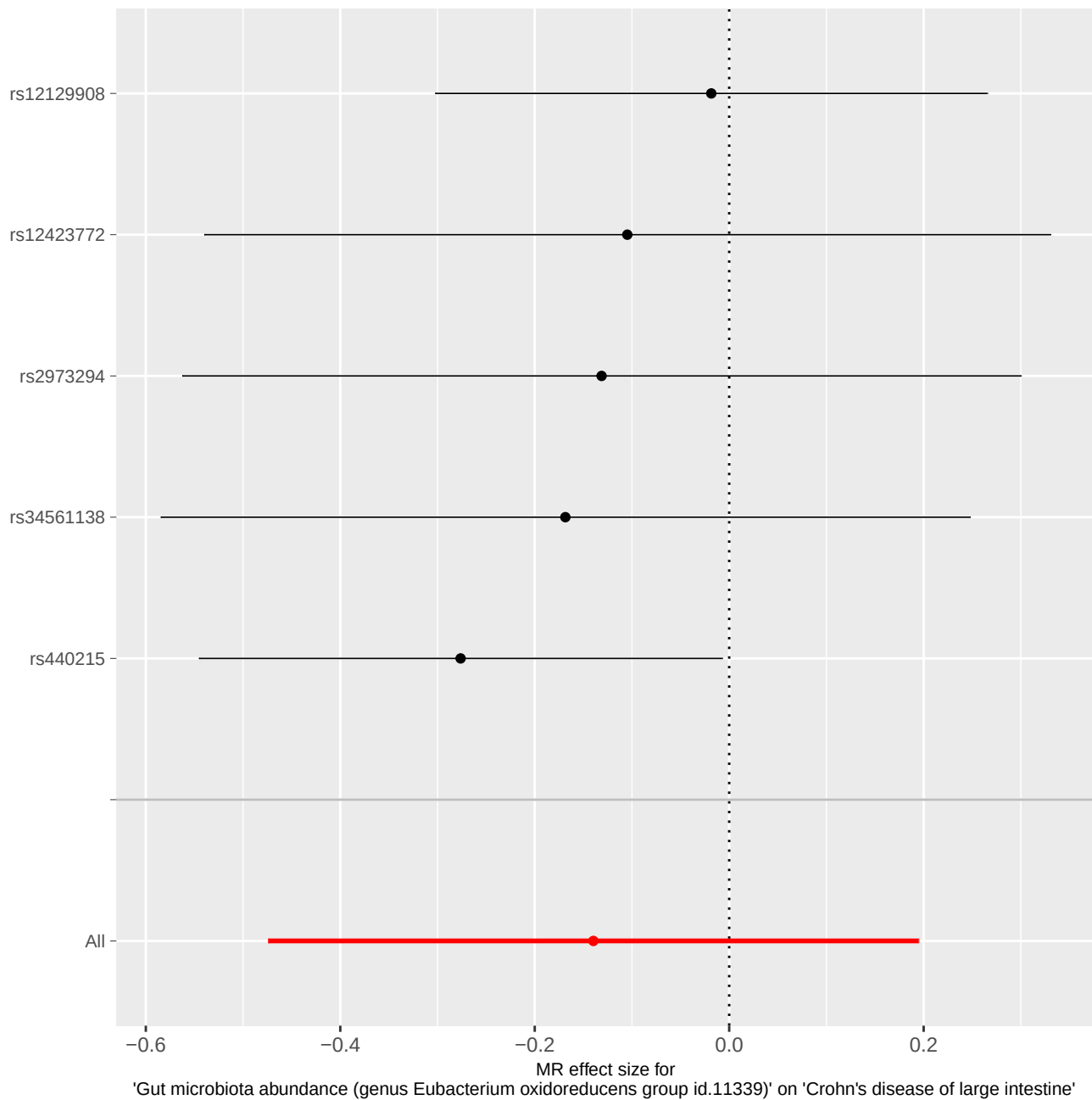


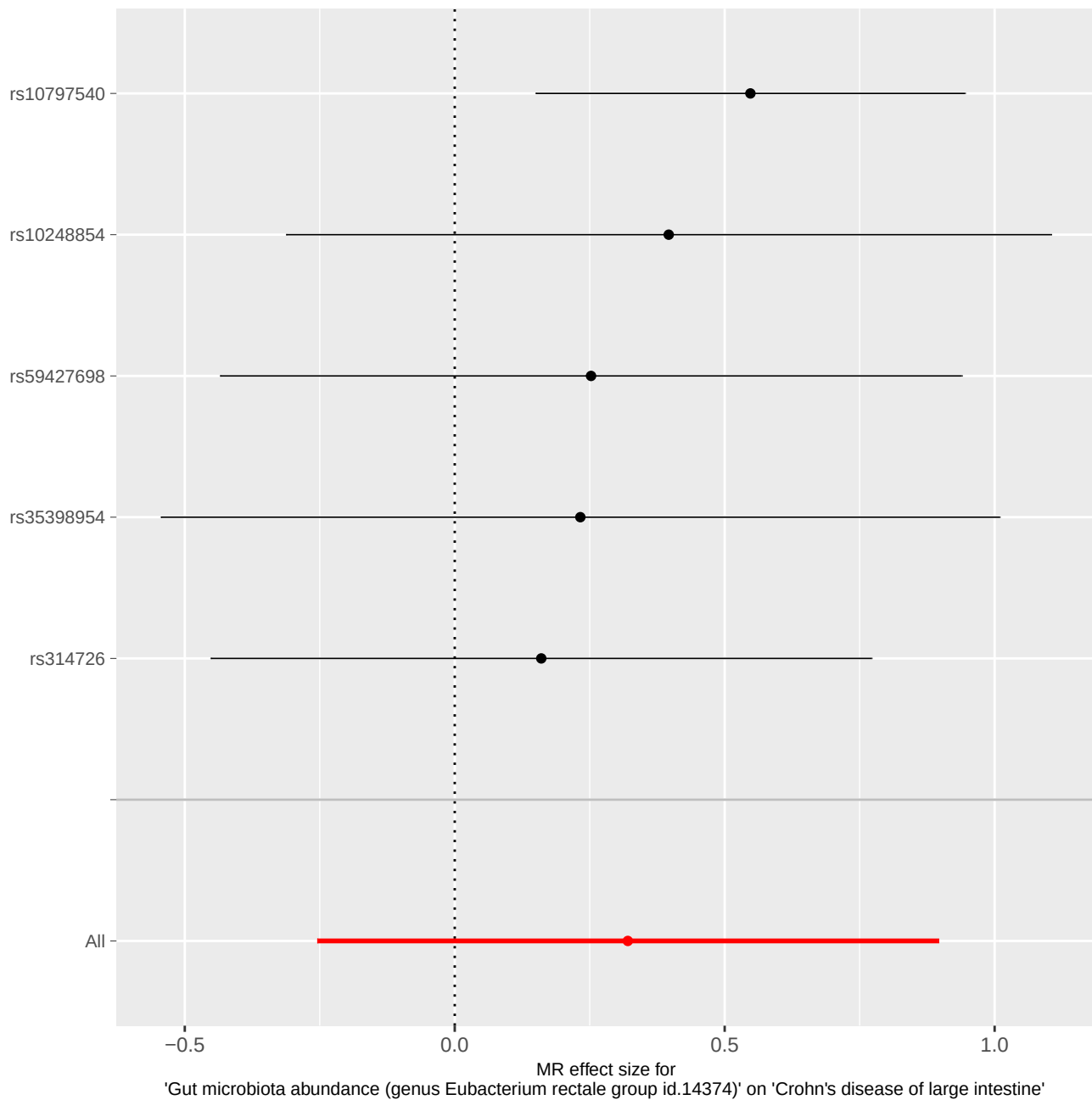
Batch 73 : Gut microbiota abundance (genus Eubacterium fissicatena group id.14373) on Crohn's disease of large intestine



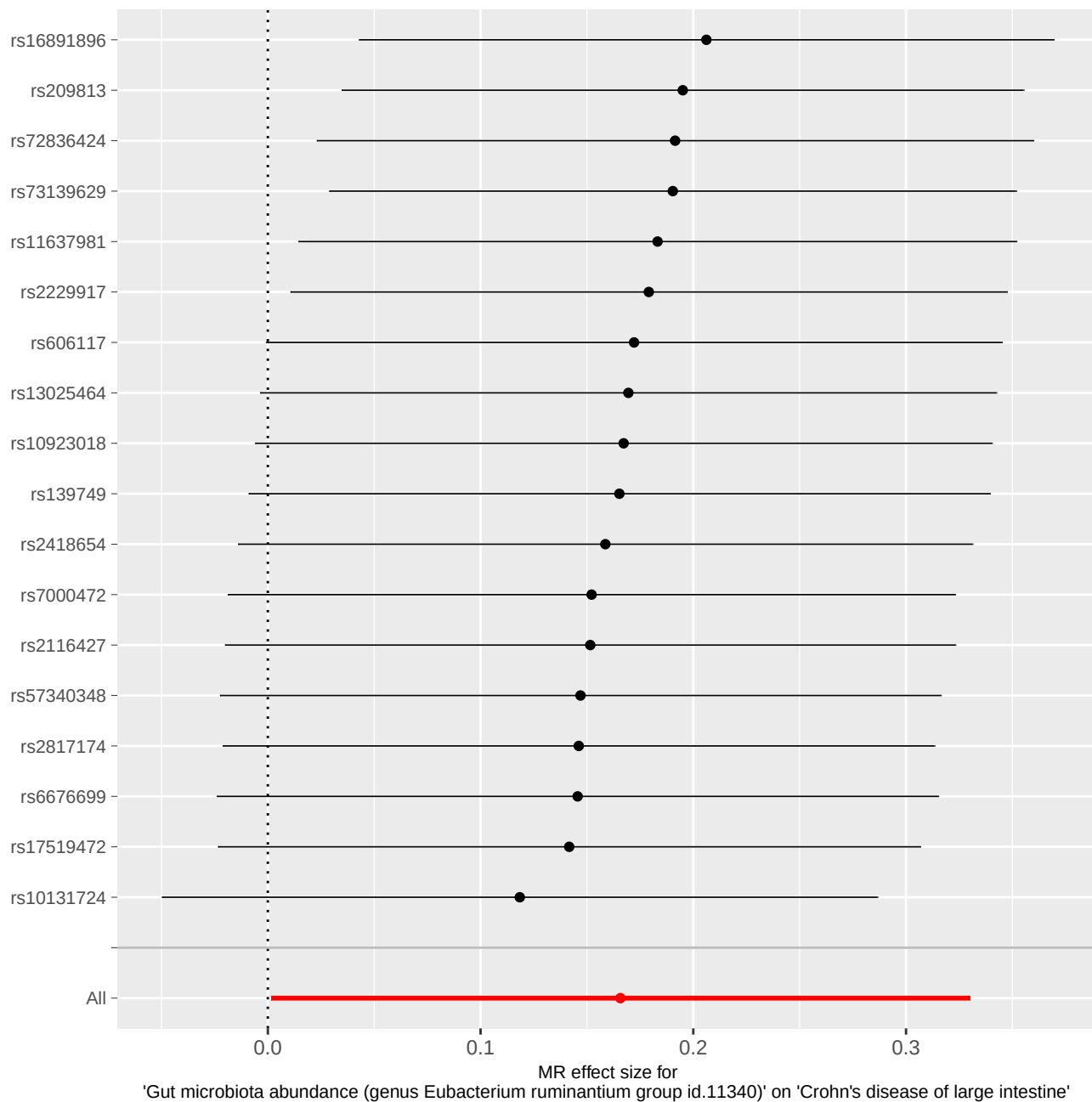


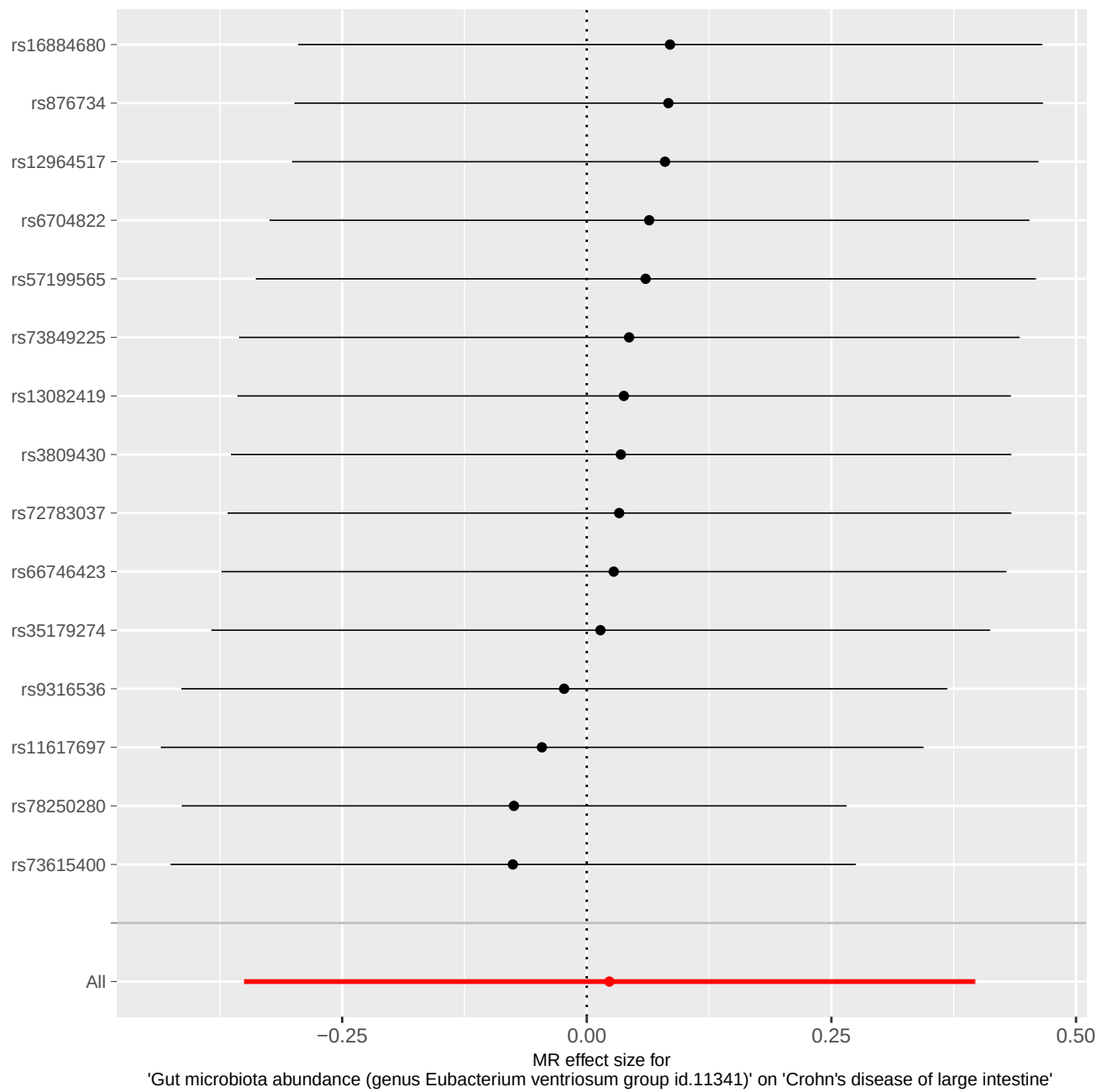




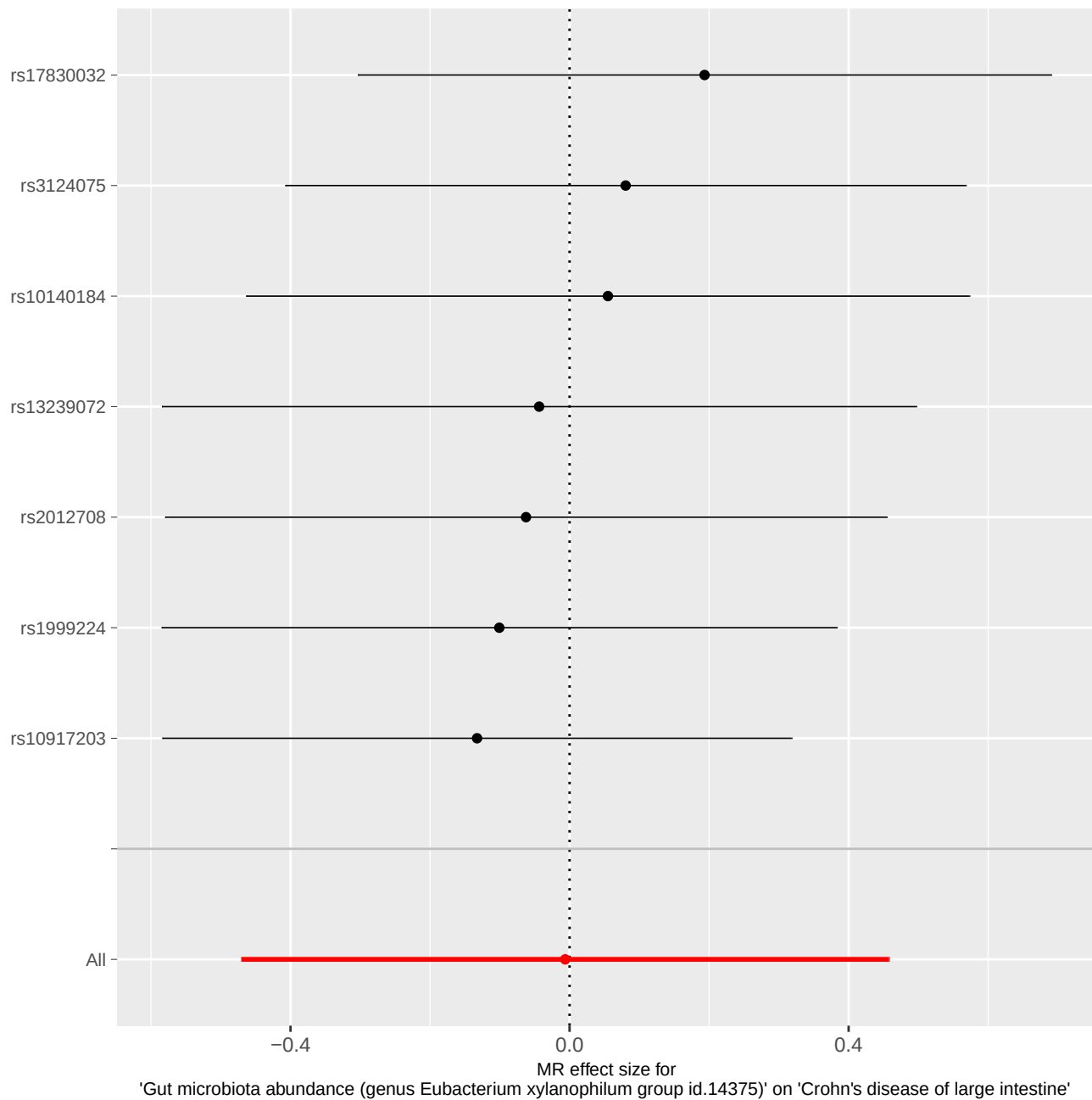


Batch 78 : Gut microbiota abundance (genus Eubacterium ruminantium group id.11340) on Crohn's disease of large intestine

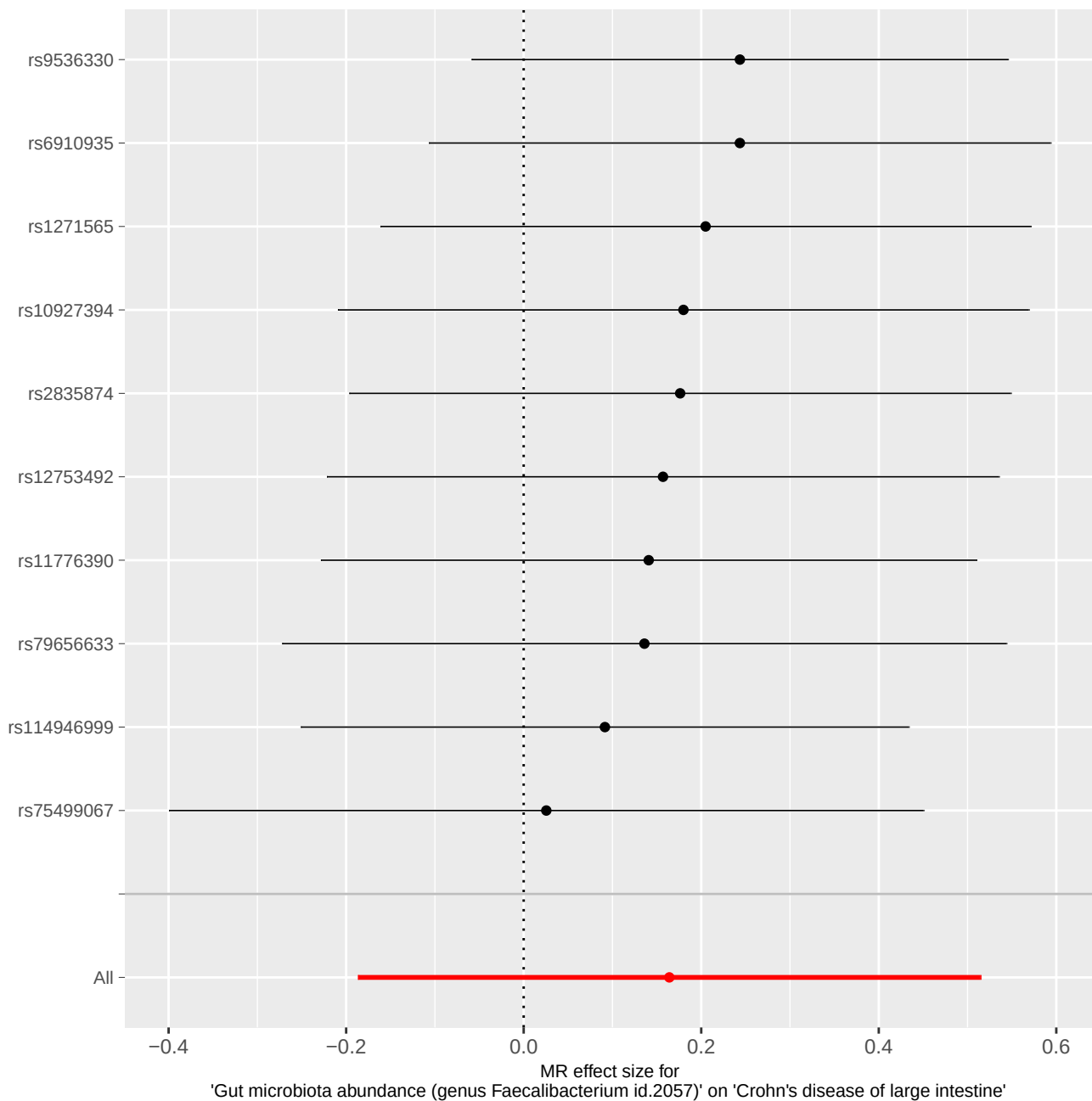




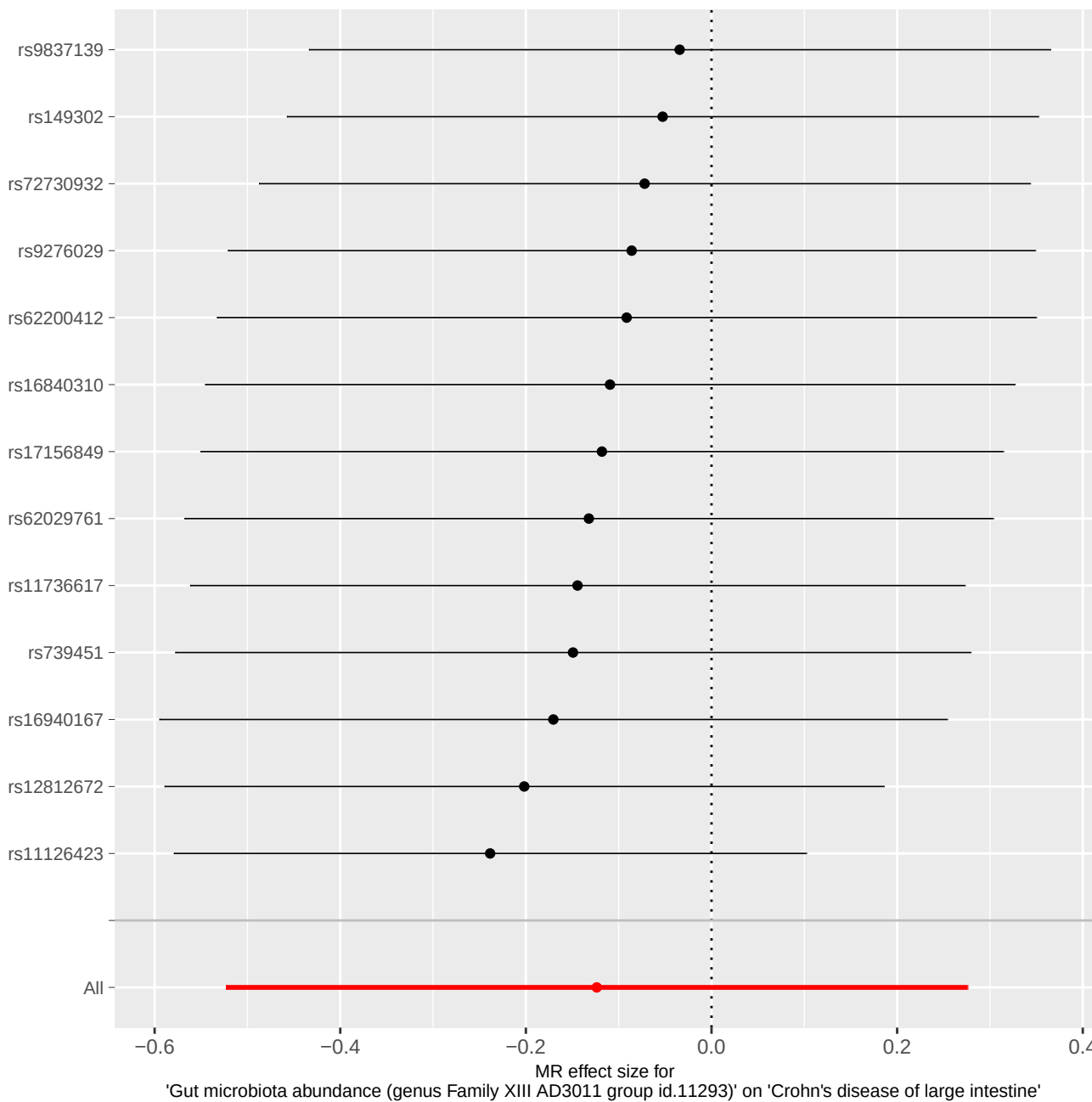
'Gut microbiota abundance (genus Eubacterium ventriosum group id.11341)' on 'Crohn's disease of large intestine'

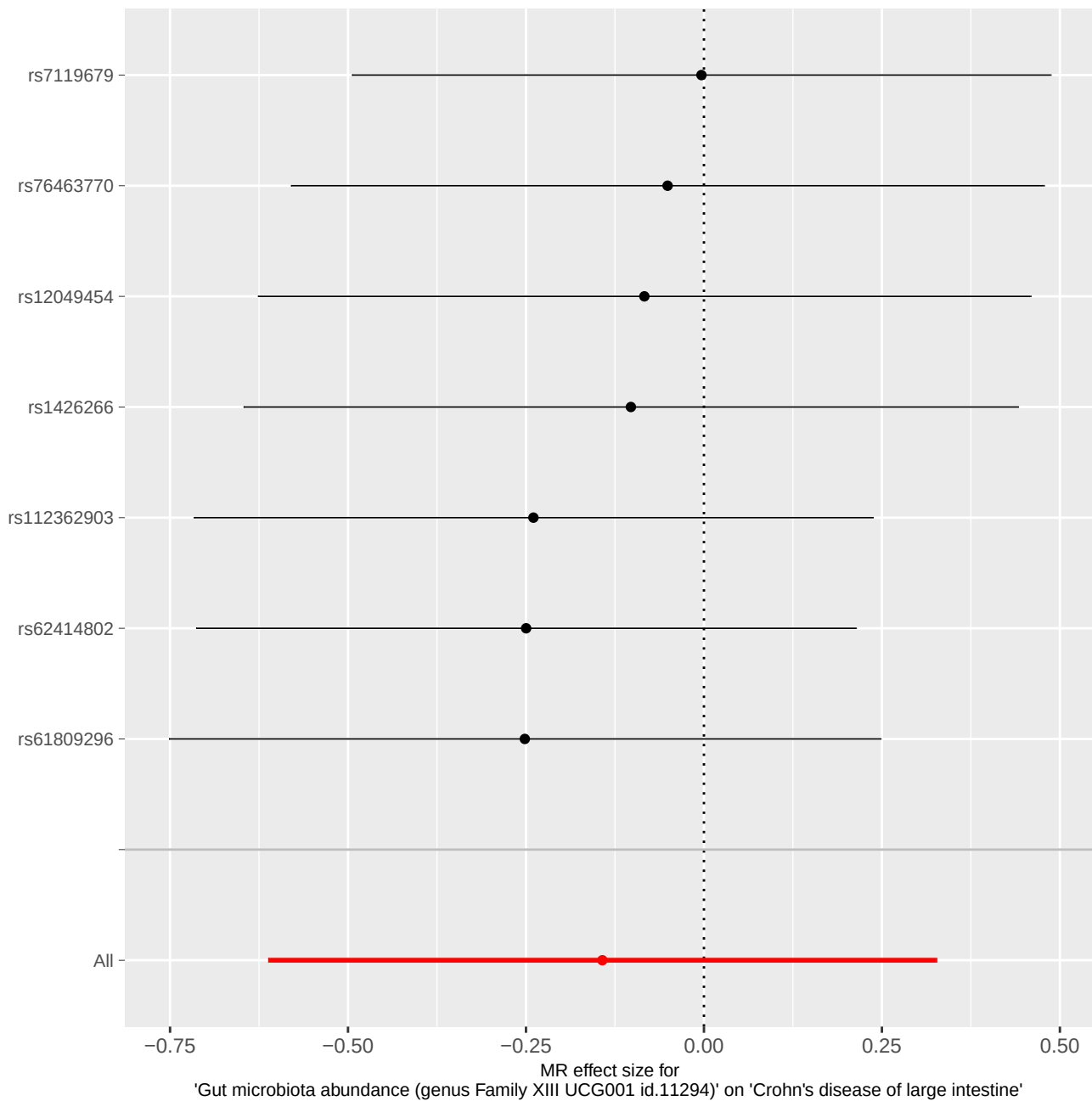


Batch 81 : Gut microbiota abundance (genus Faecalibacterium id.2057) on Crohn's disease of large intestine

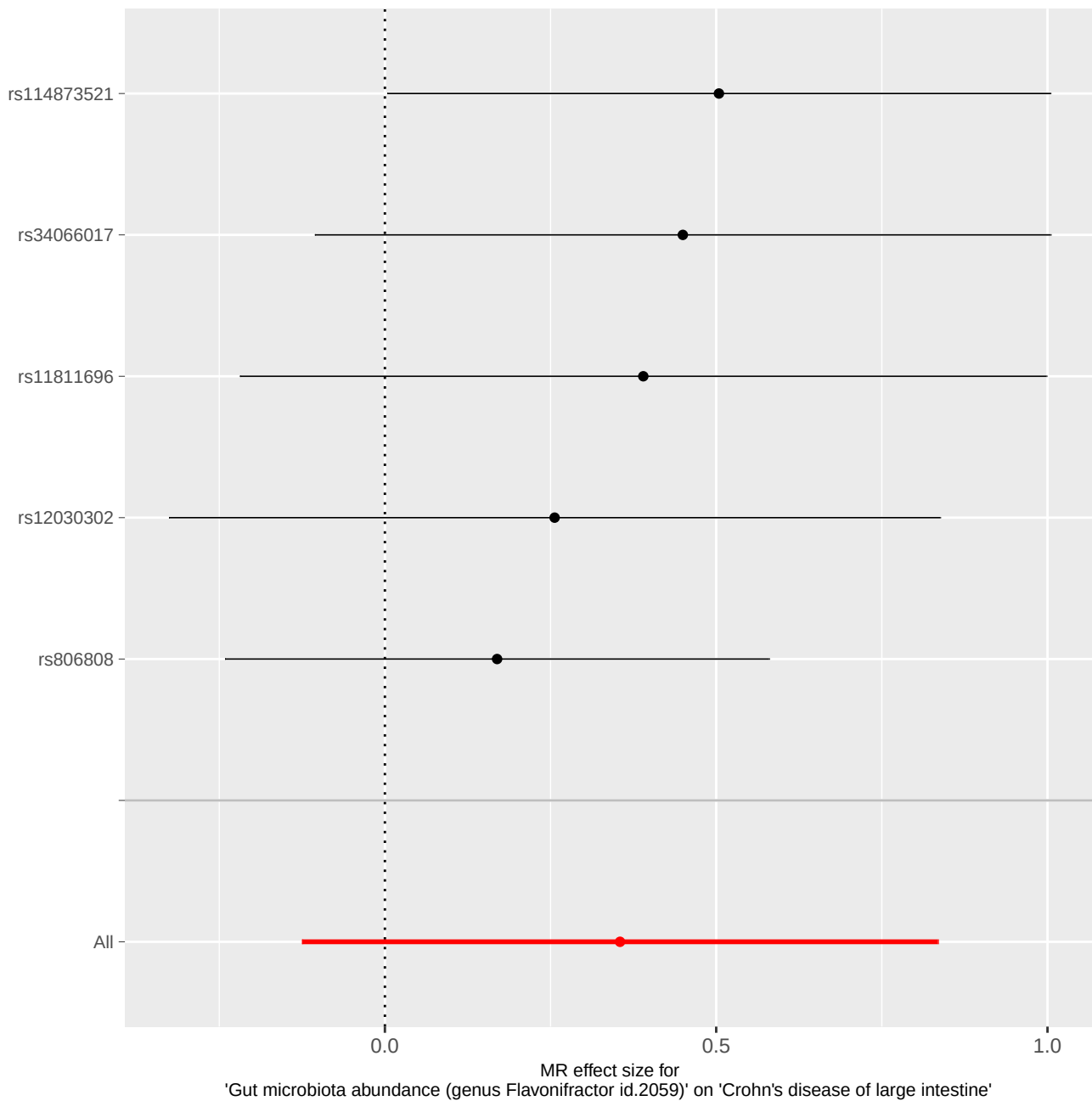


Batch 82 : Gut microbiota abundance (genus Family XIII AD3011 group id.11293) on Crohn's disease of large intestine

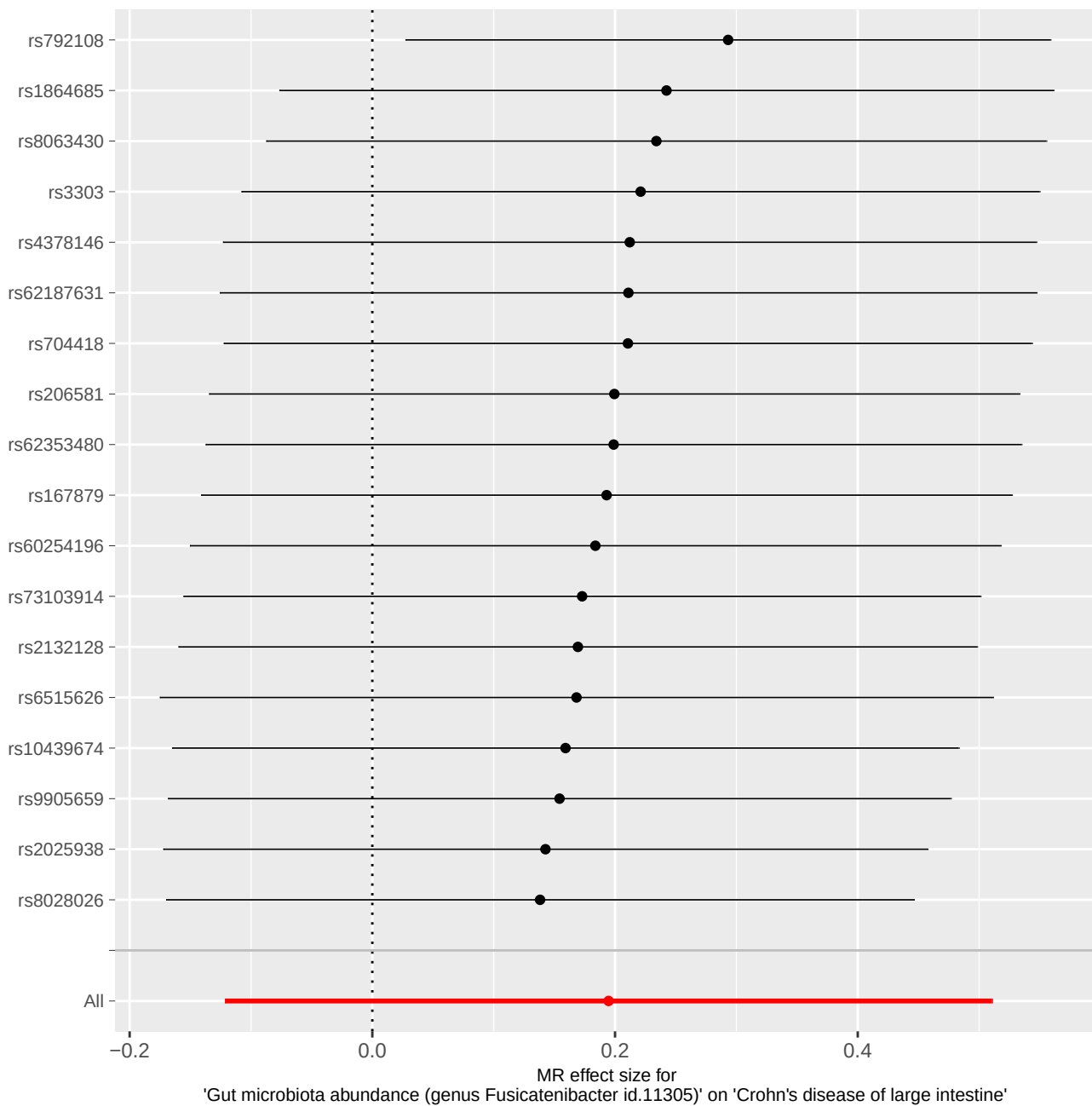




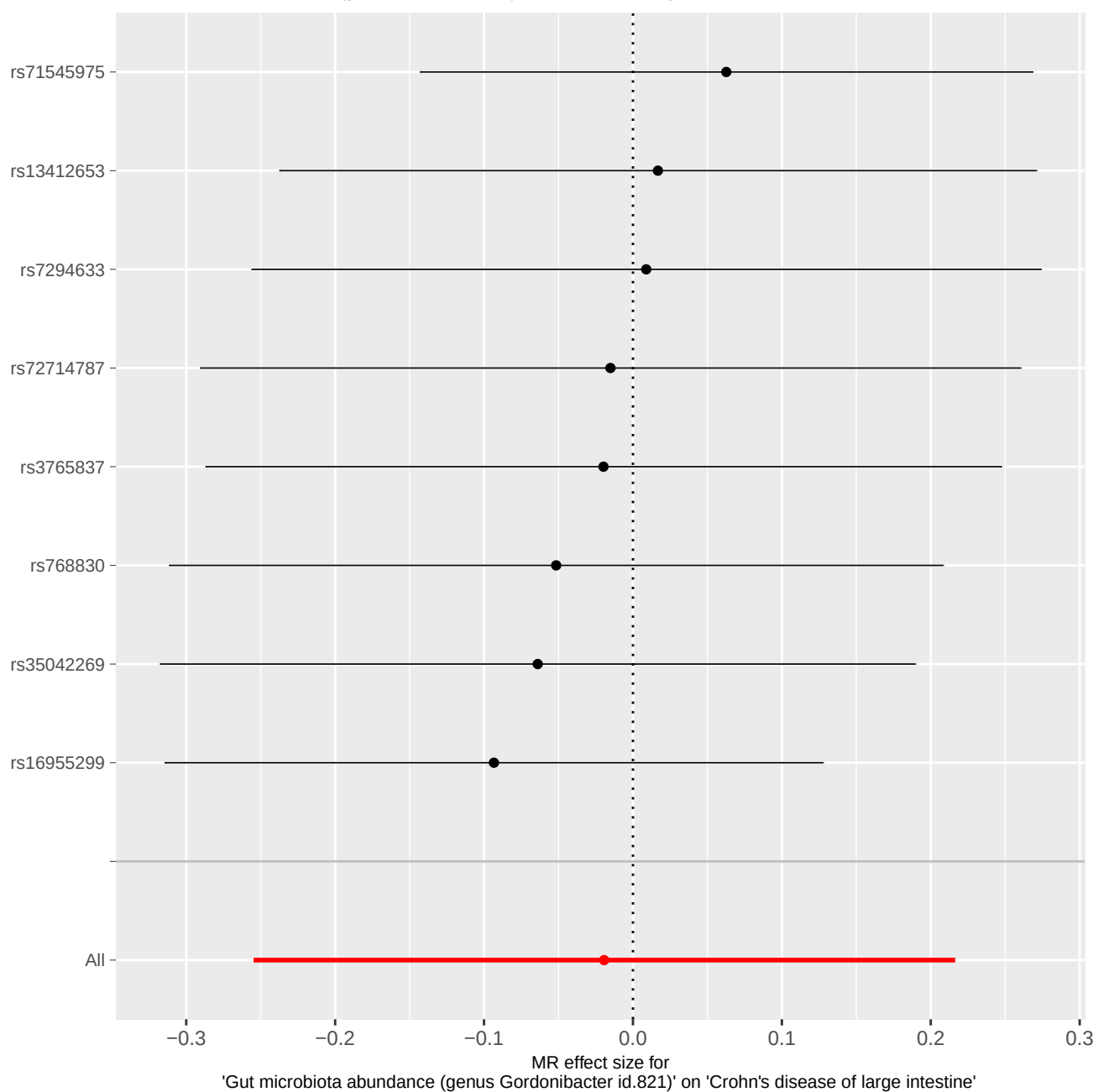
Batch 84 : Gut microbiota abundance (genus Flavonifractor id.2059) on Crohn's disease of large intestine

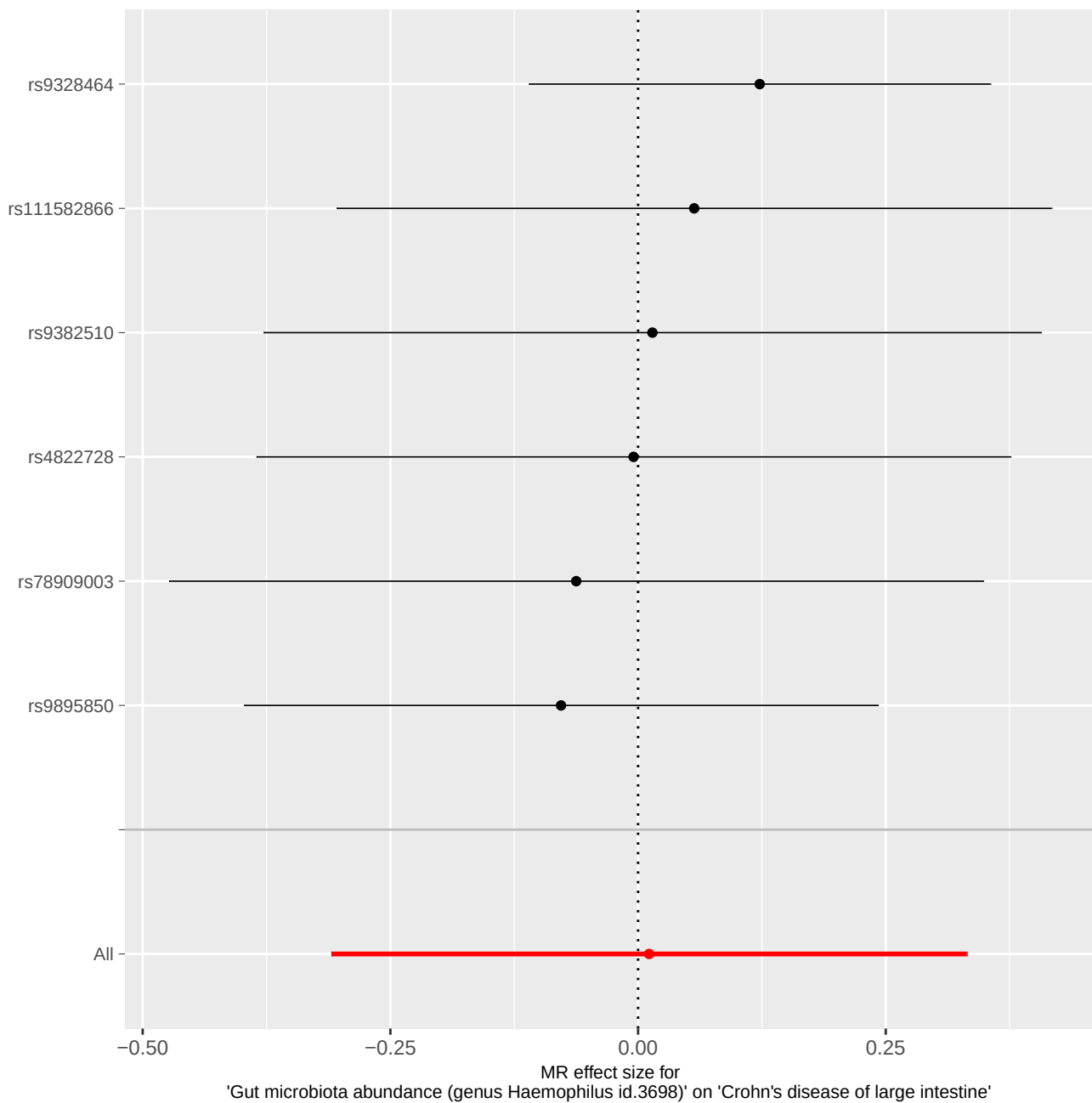


Batch 85 : Gut microbiota abundance (genus Fusicatenibacter id.11305) on Crohn's disease of large intestine

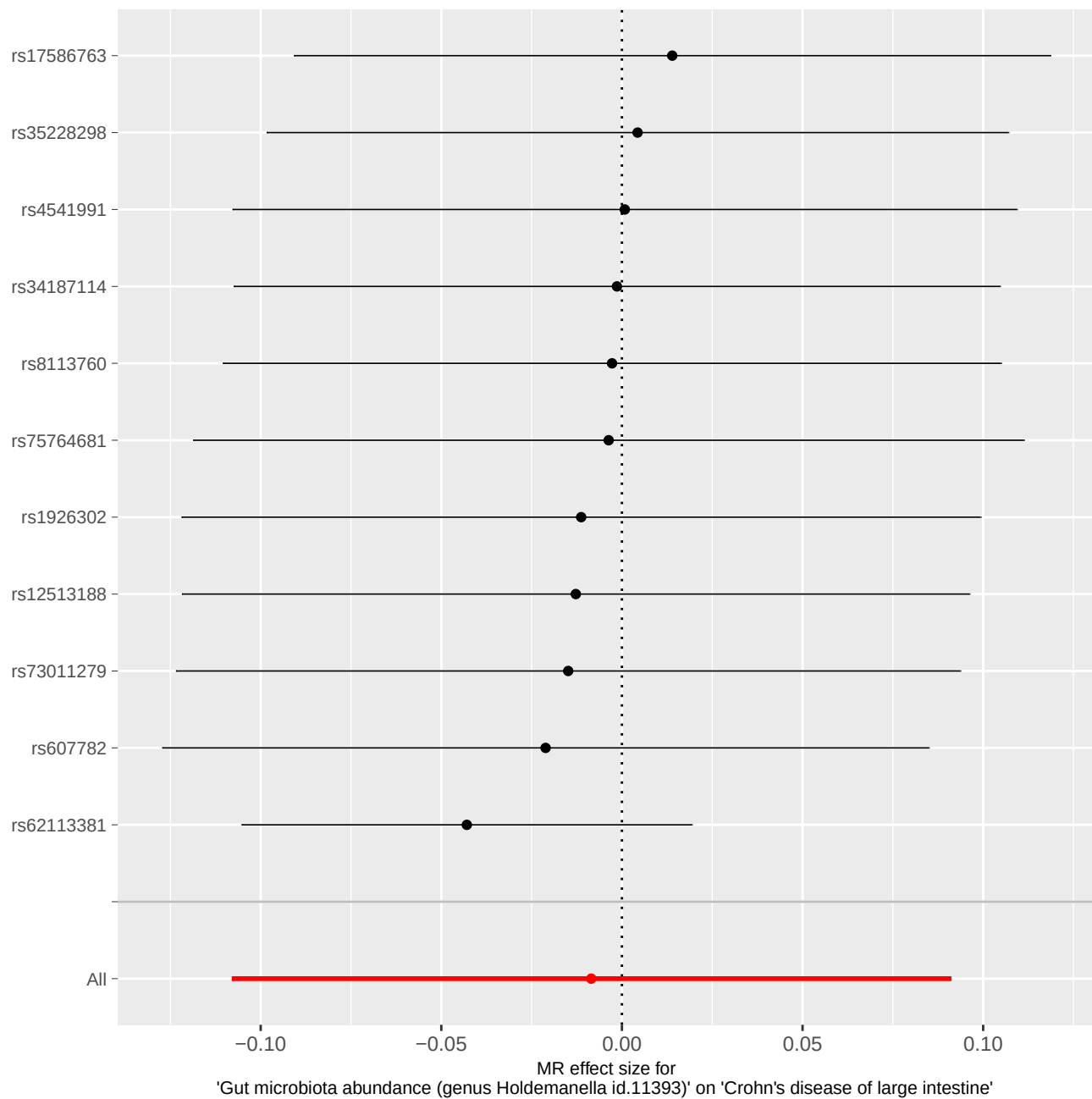


Batch 86 : Gut microbiota abundance (genus Gordonibacter id.821) on Crohn's disease of large intestine

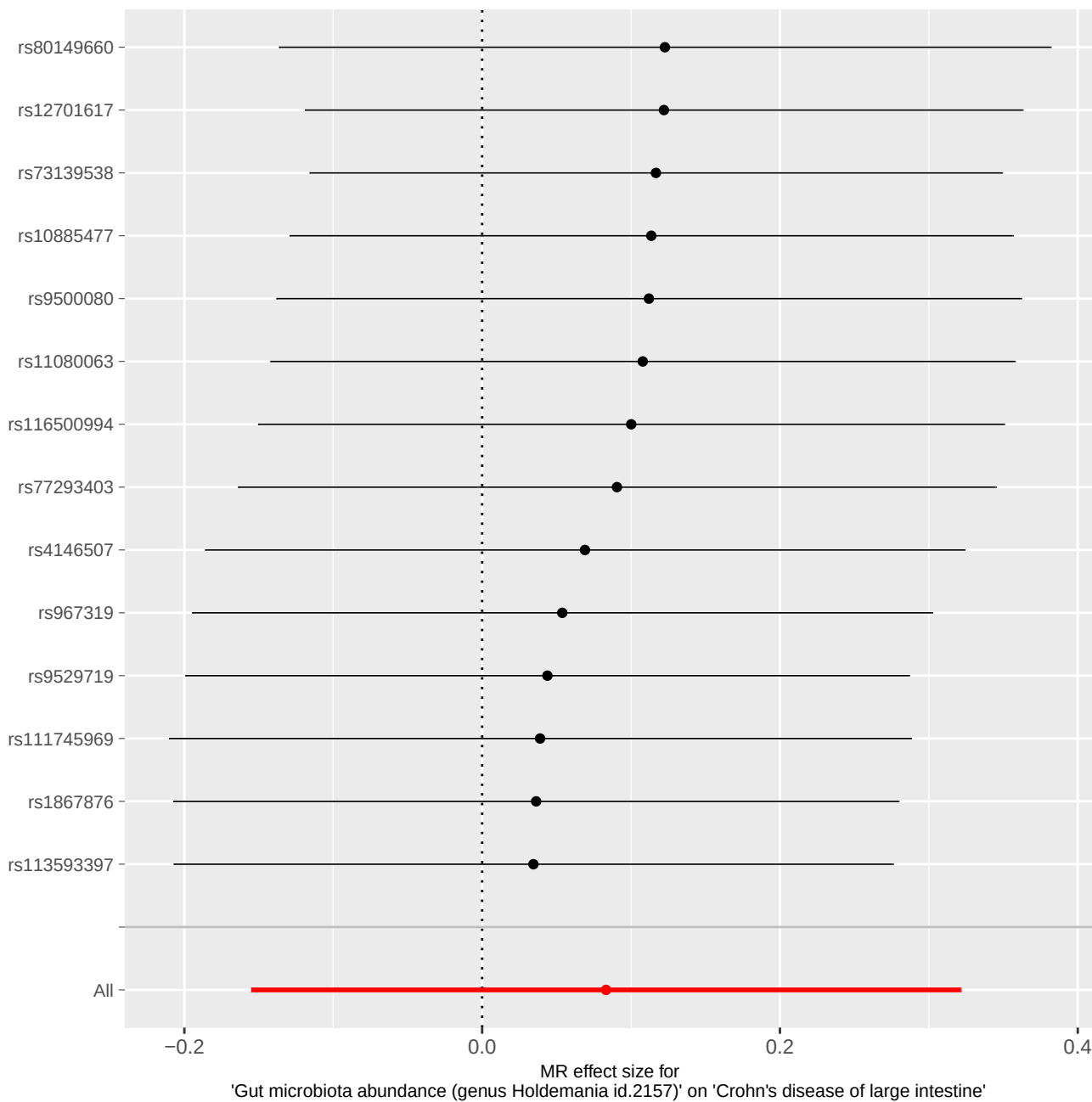


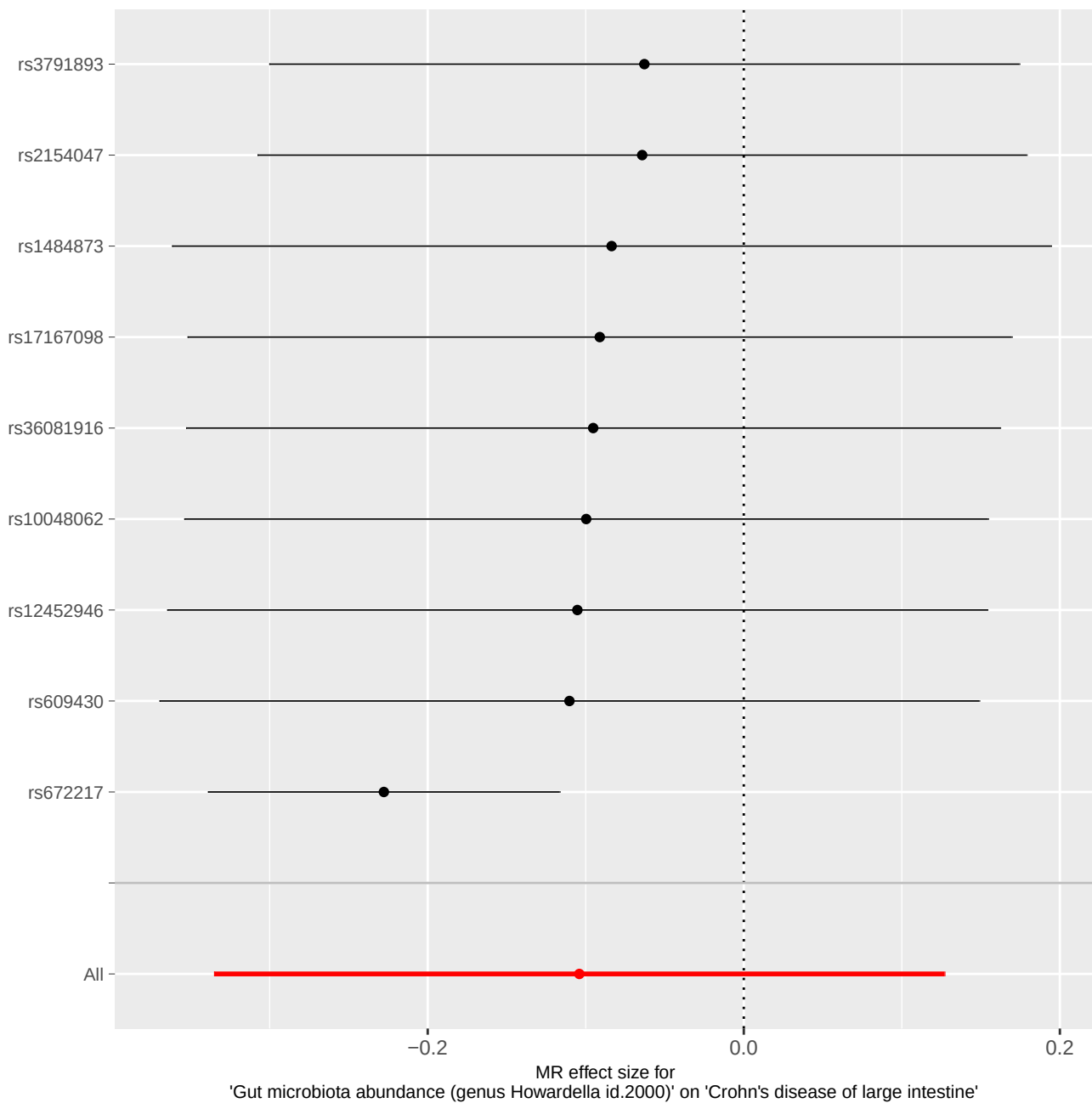


Batch 88 : Gut microbiota abundance (genus Holdemanella id.11393) on Crohn's disease of large intestine

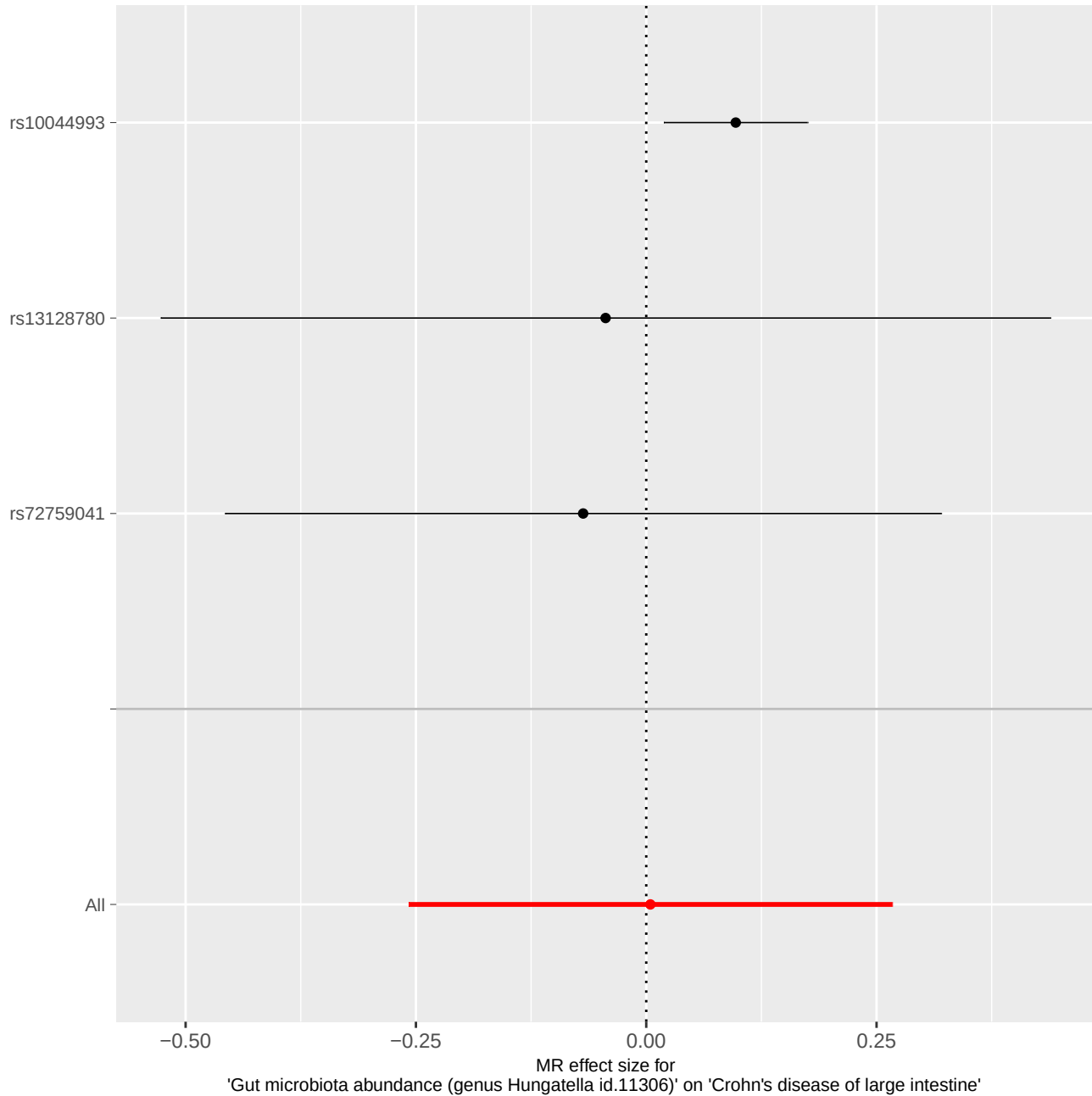


Batch 89 : Gut microbiota abundance (genus Holdemania id.2157) on Crohn's disease of large intestine

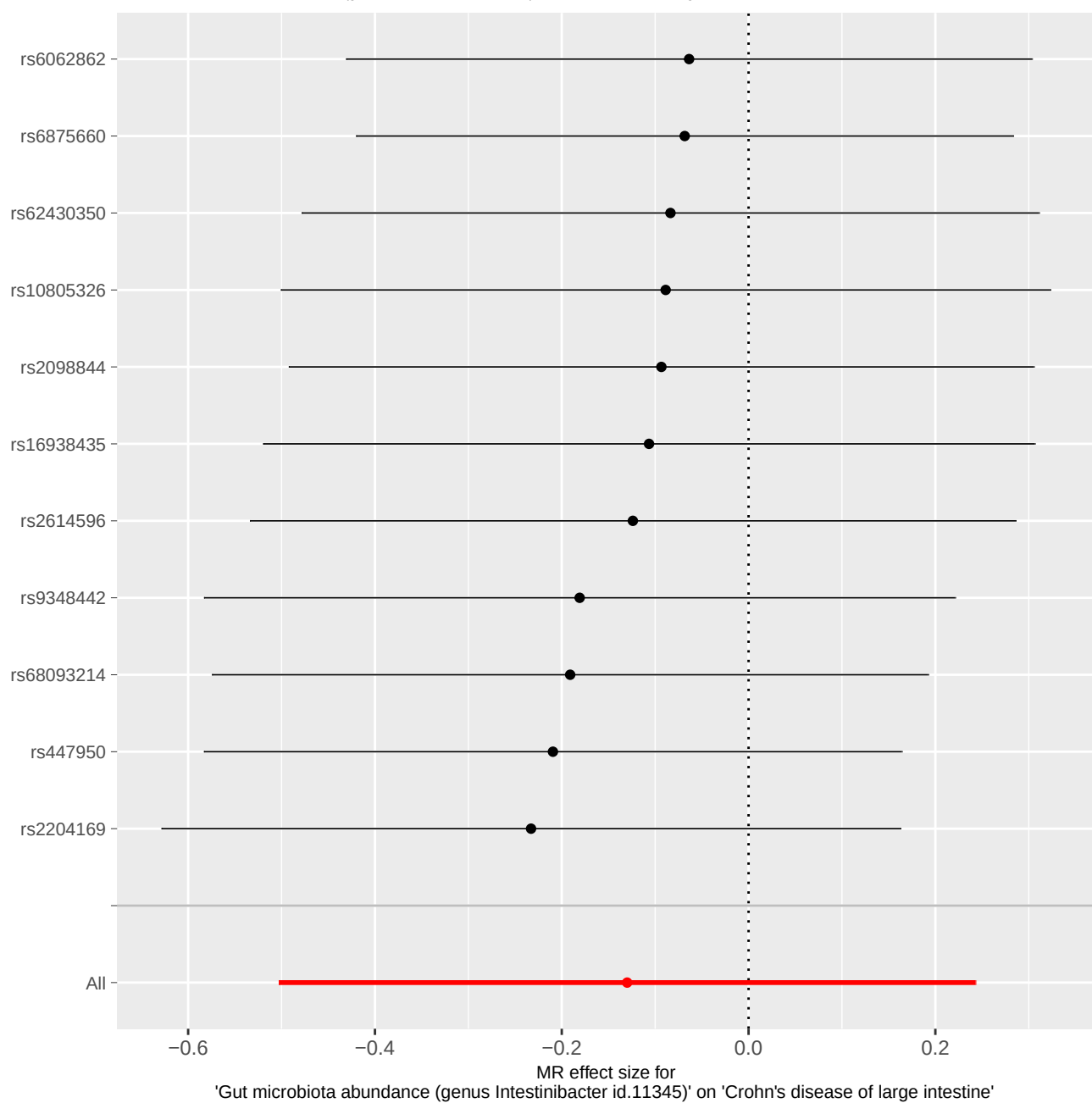




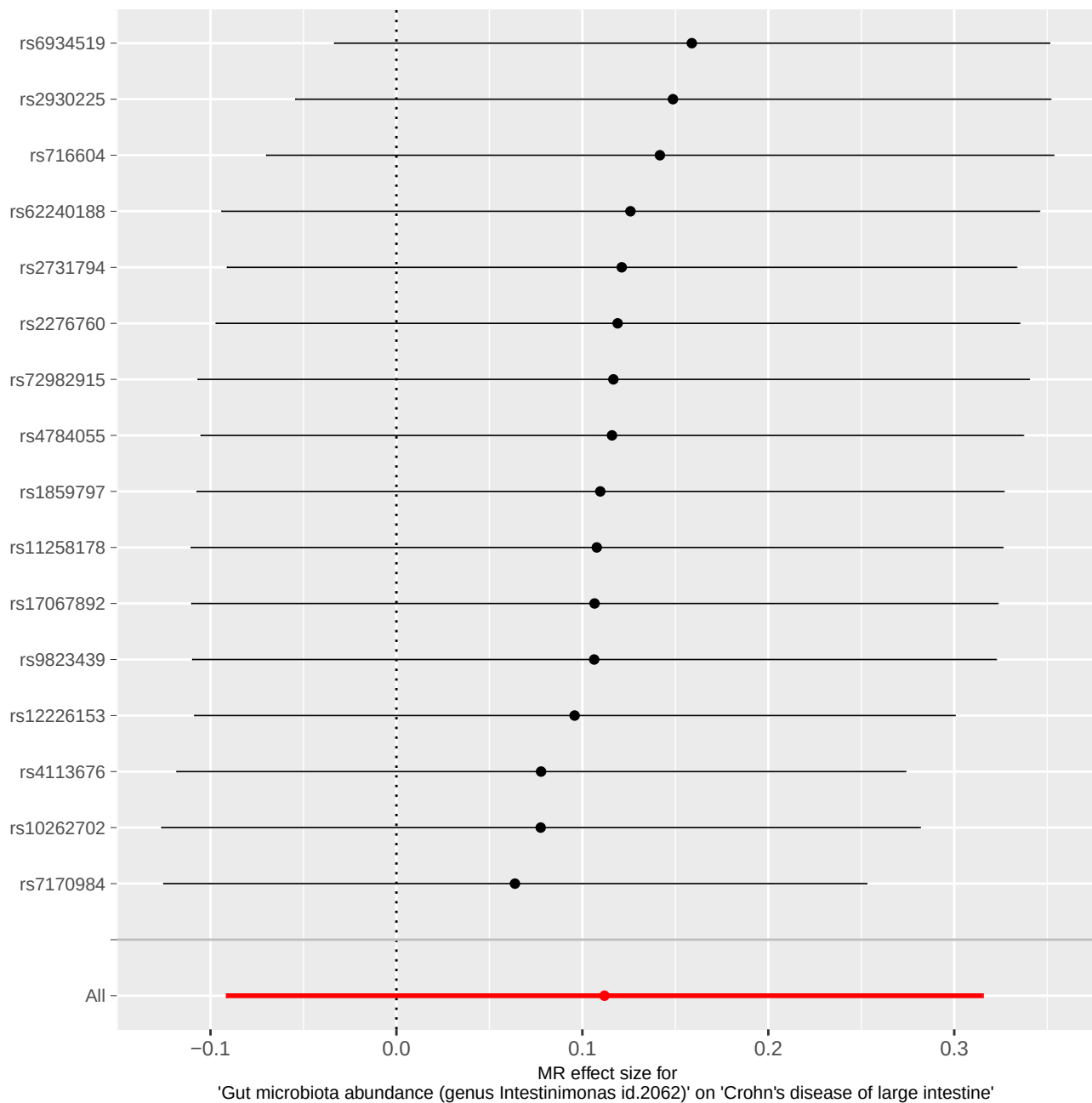
Batch 91 : Gut microbiota abundance (genus Hungatella id.11306) on Crohn's disease of large intestine



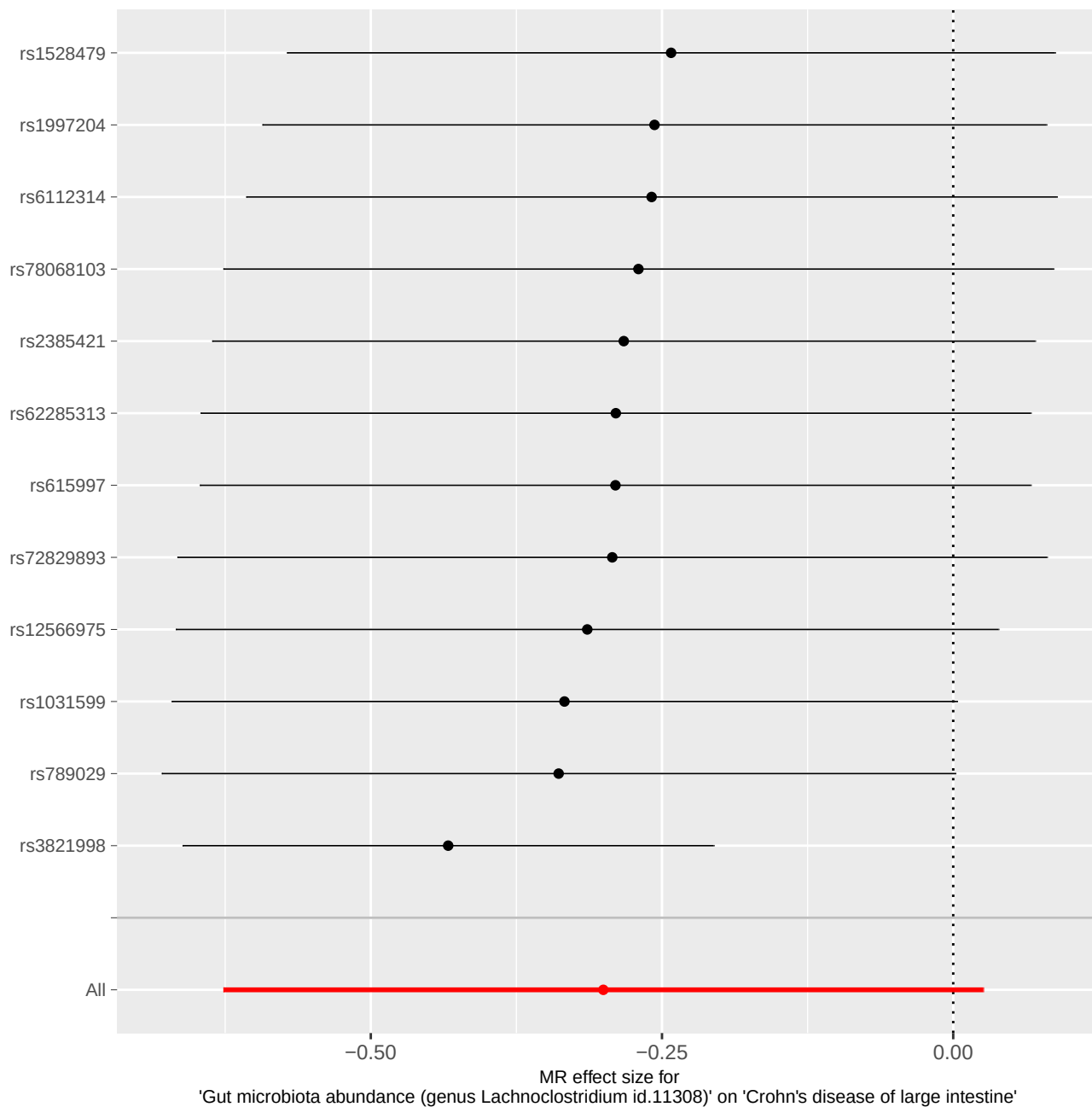
Batch 92 : Gut microbiota abundance (genus Intestinibacter id.11345) on Crohn's disease of large intestine



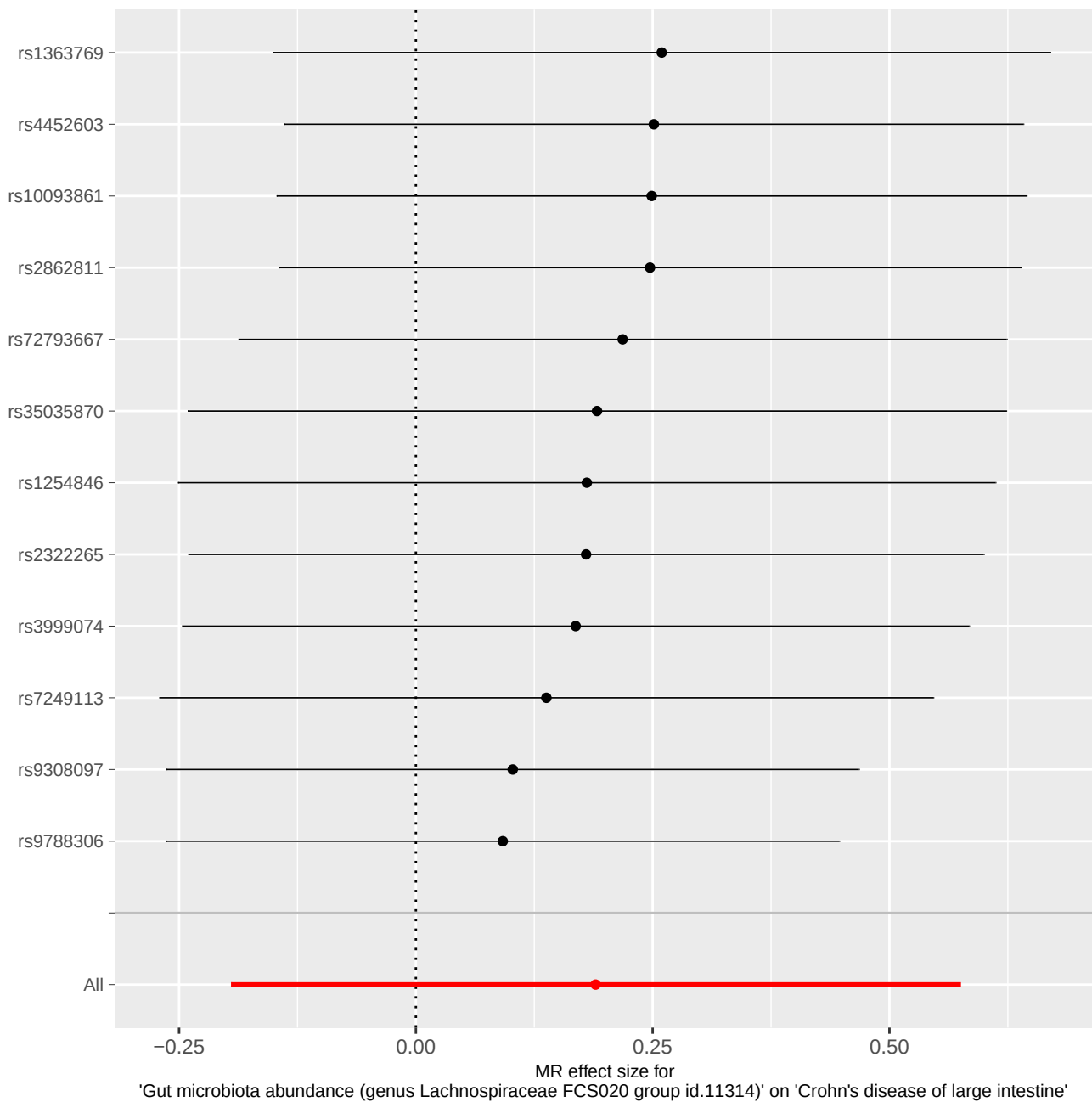
Batch 93 : Gut microbiota abundance (genus *Intestinimonas* id.2062) on Crohn's disease of large intestine

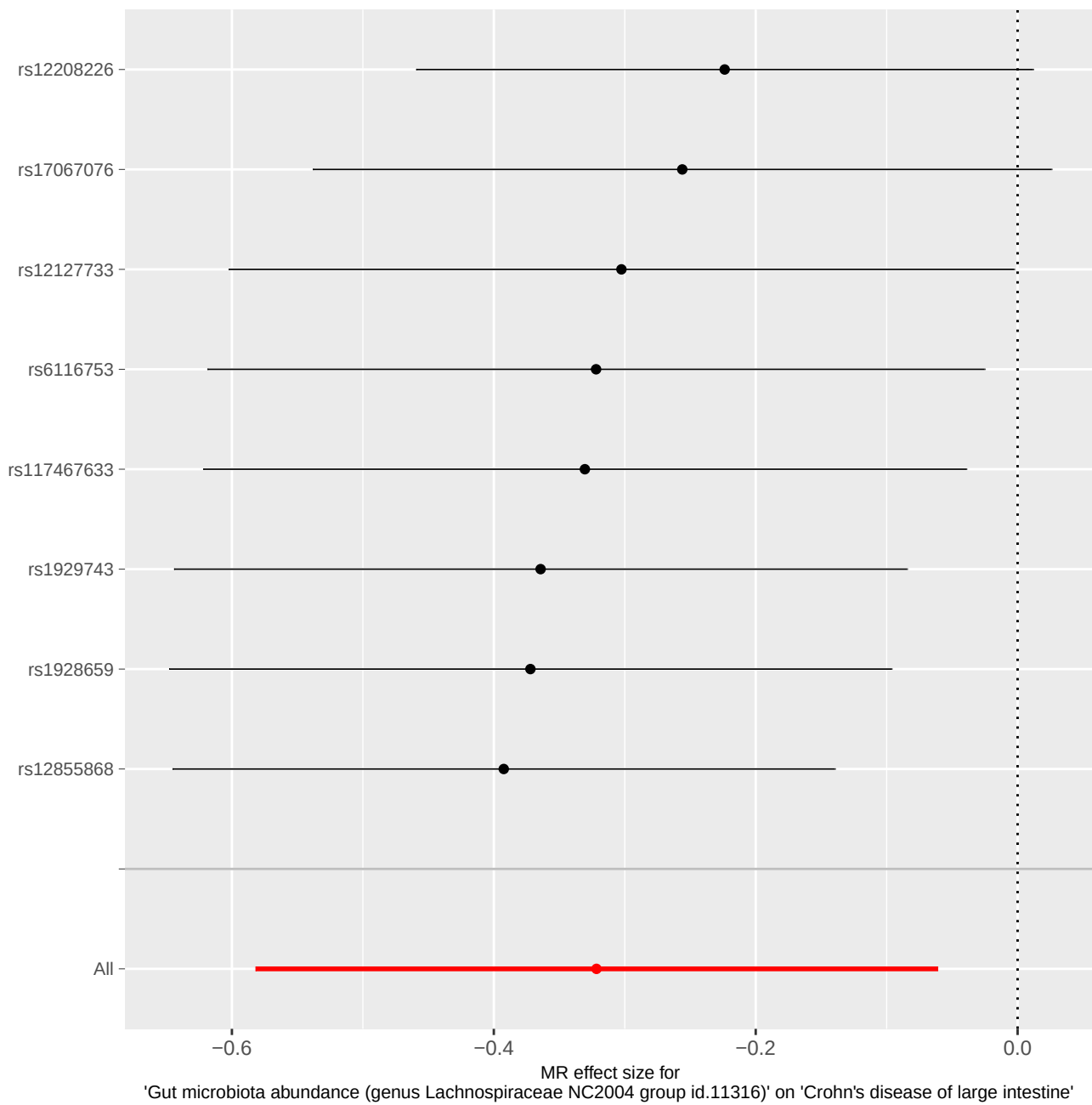


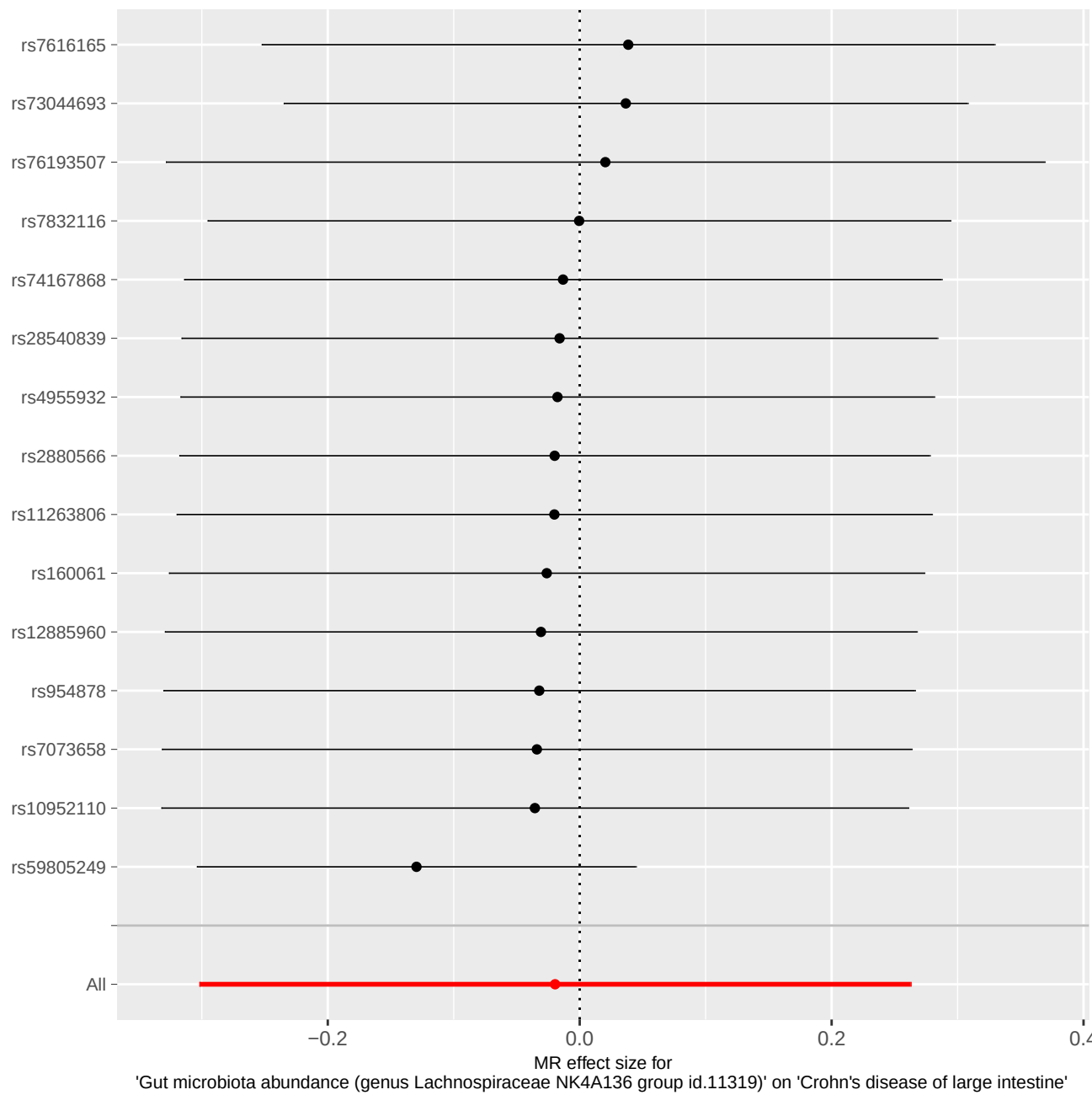
Batch 94 : Gut microbiota abundance (genus Lachnoclostridium id.11308) on Crohn's disease of large intestine

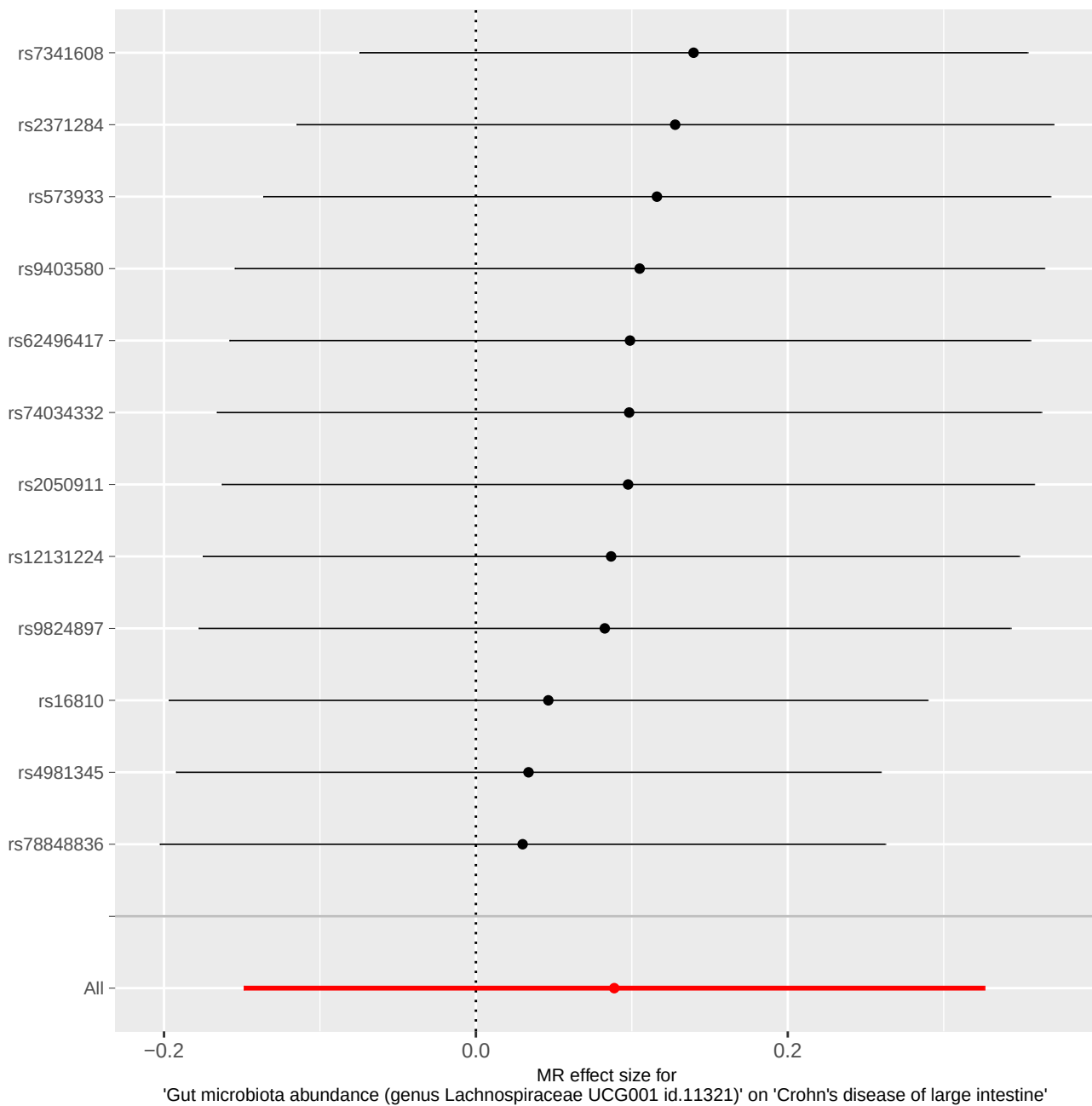


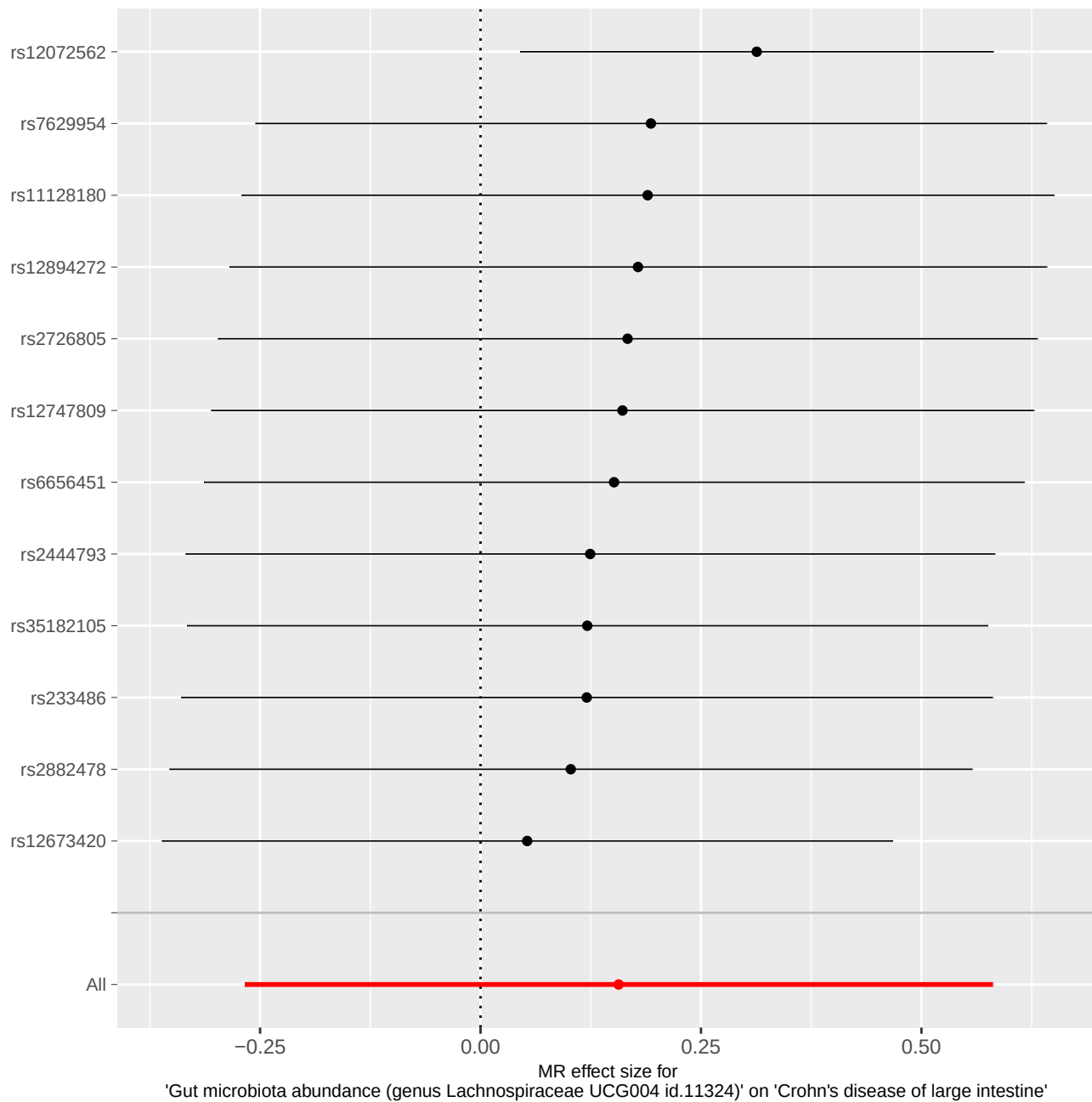
Batch 95 : Gut microbiota abundance (genus Lachnospiraceae FCS020 group id.11314) on Crohn's disease of large intestine

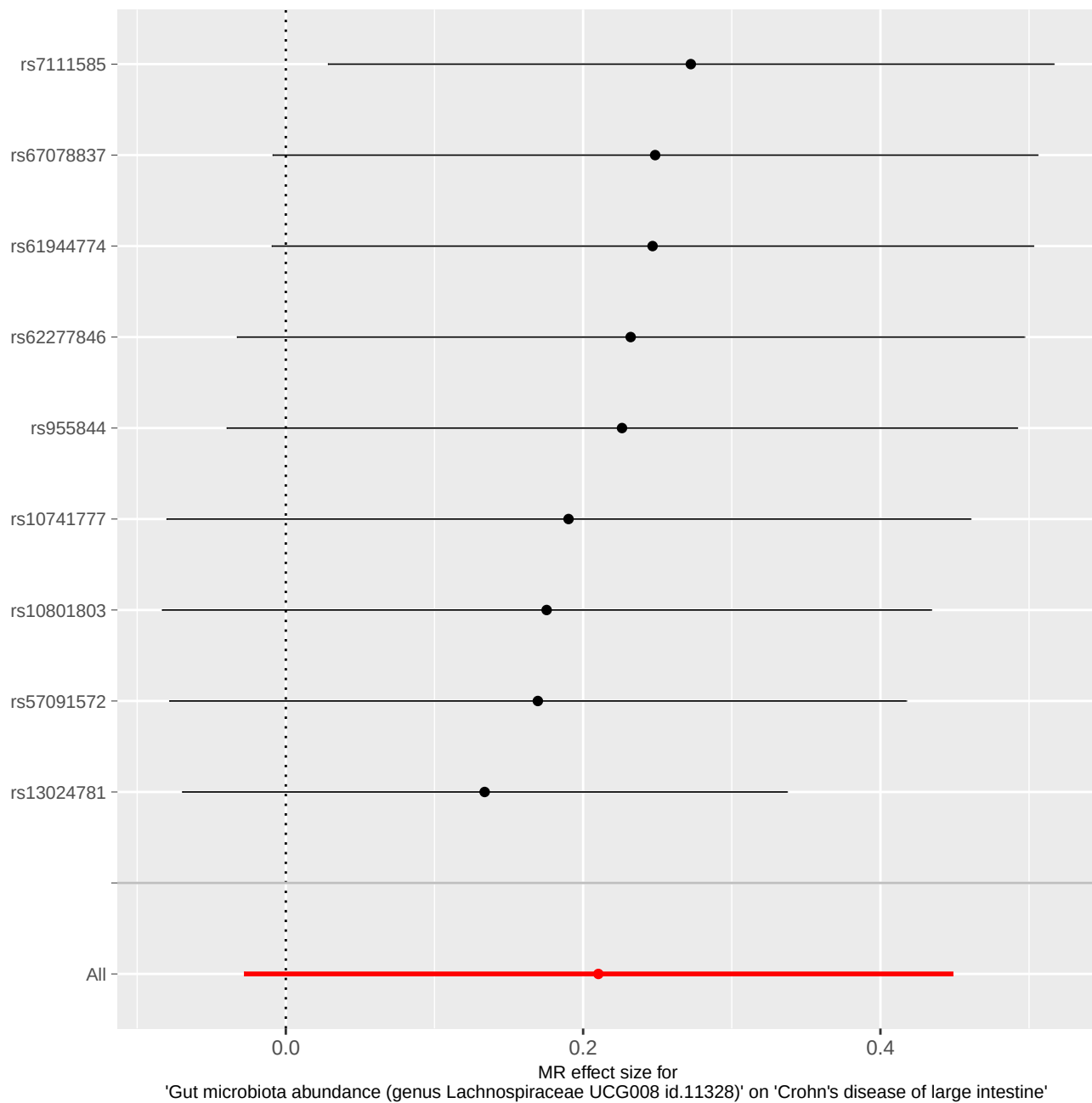


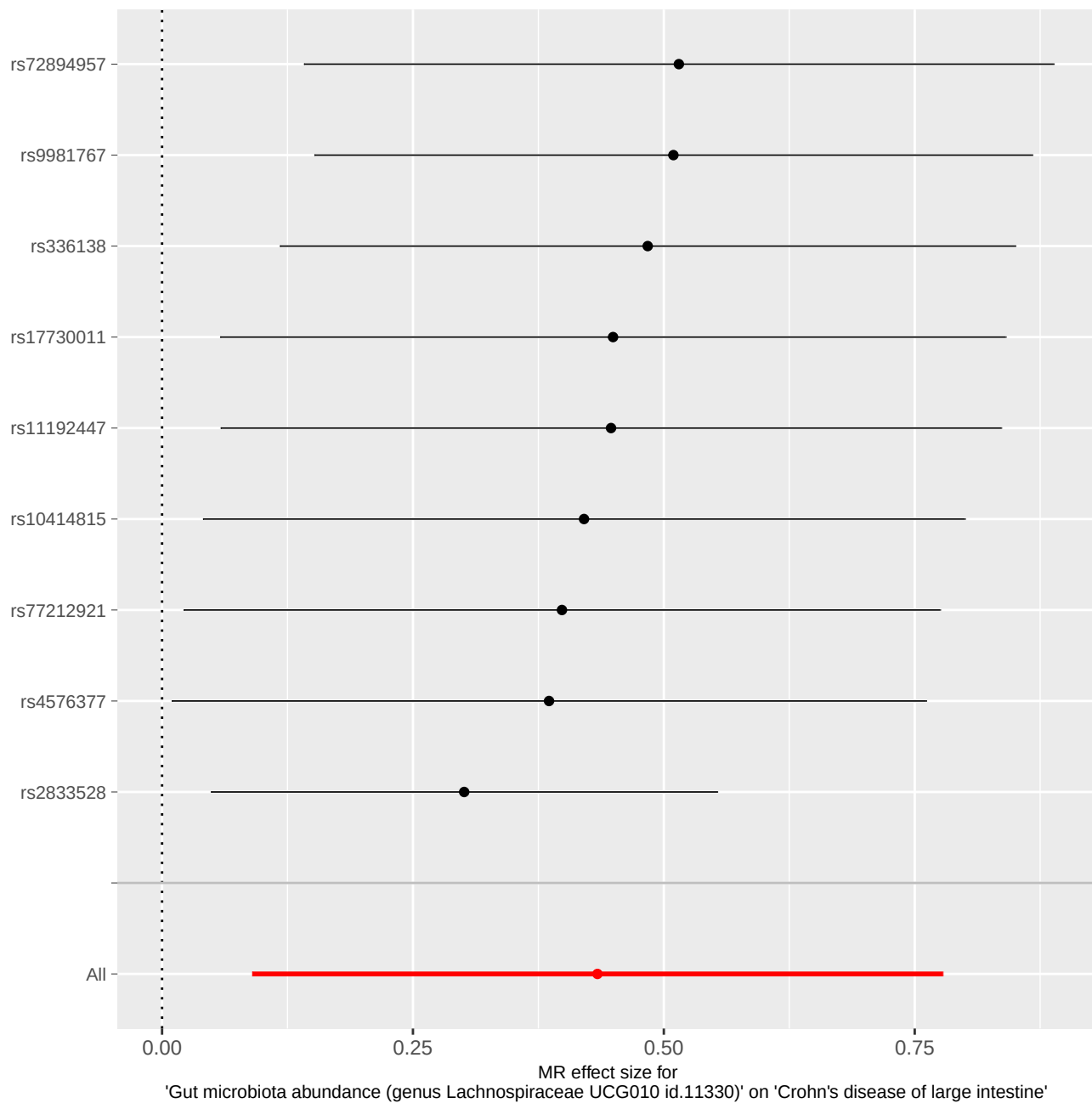


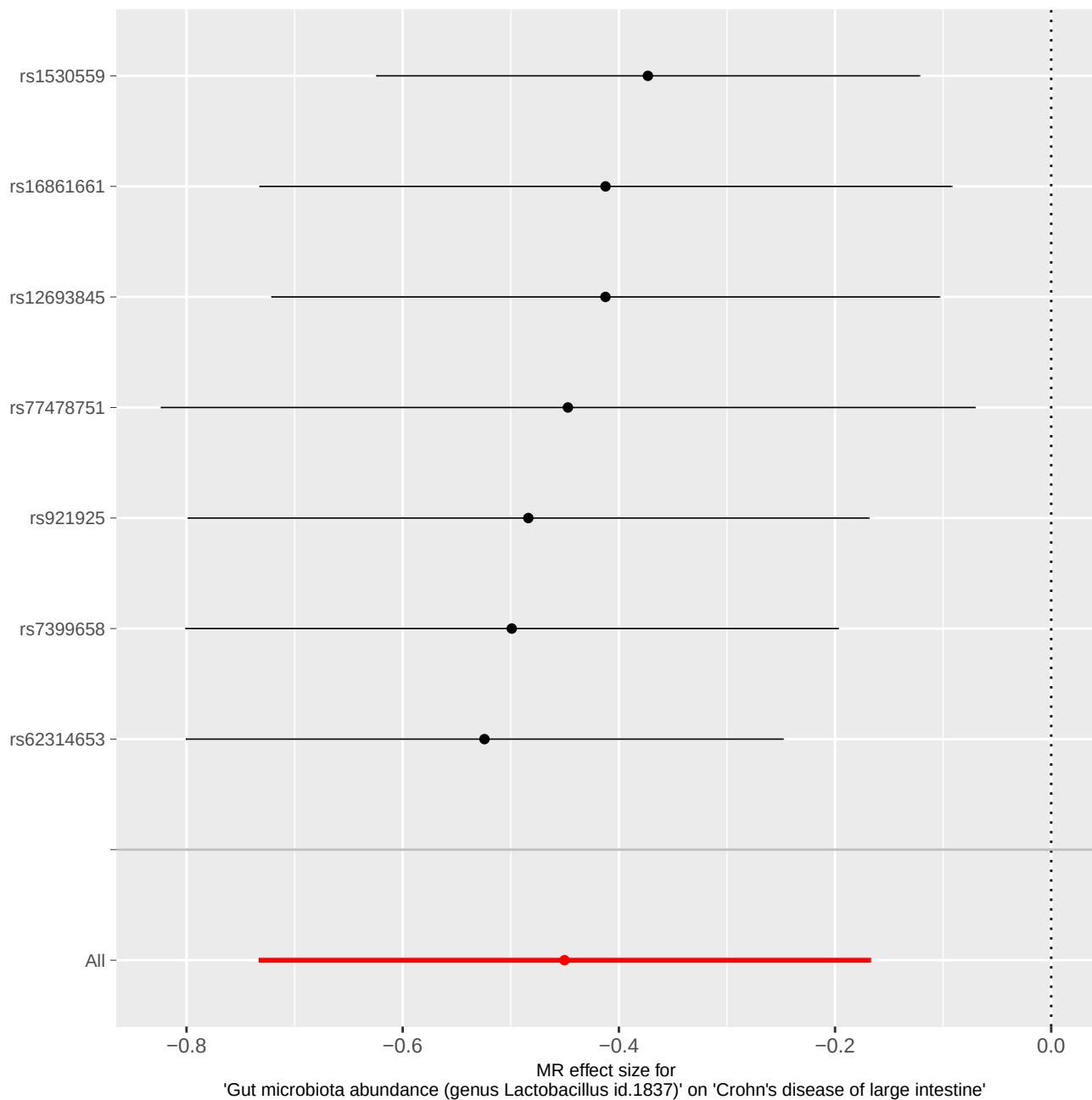


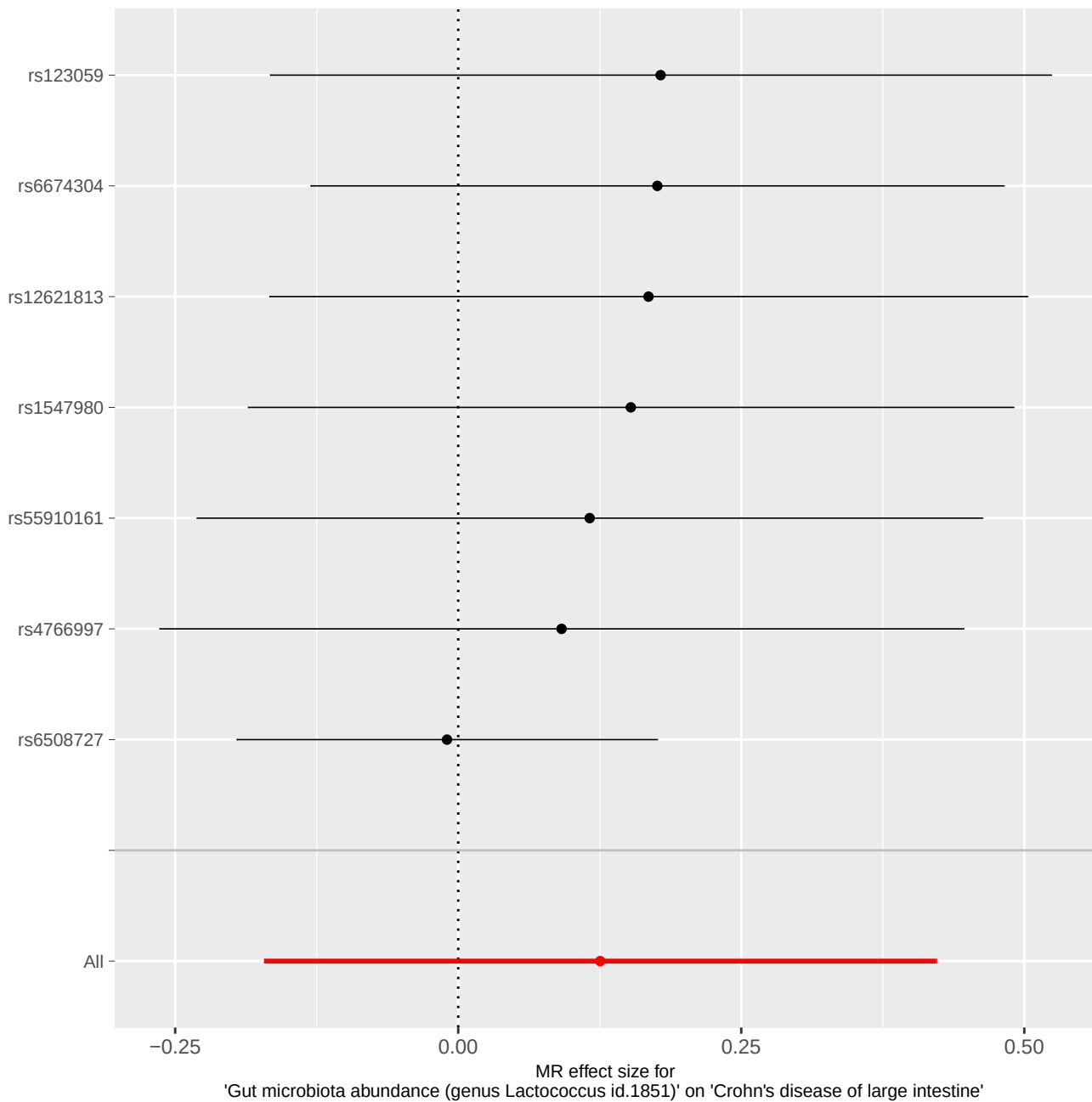


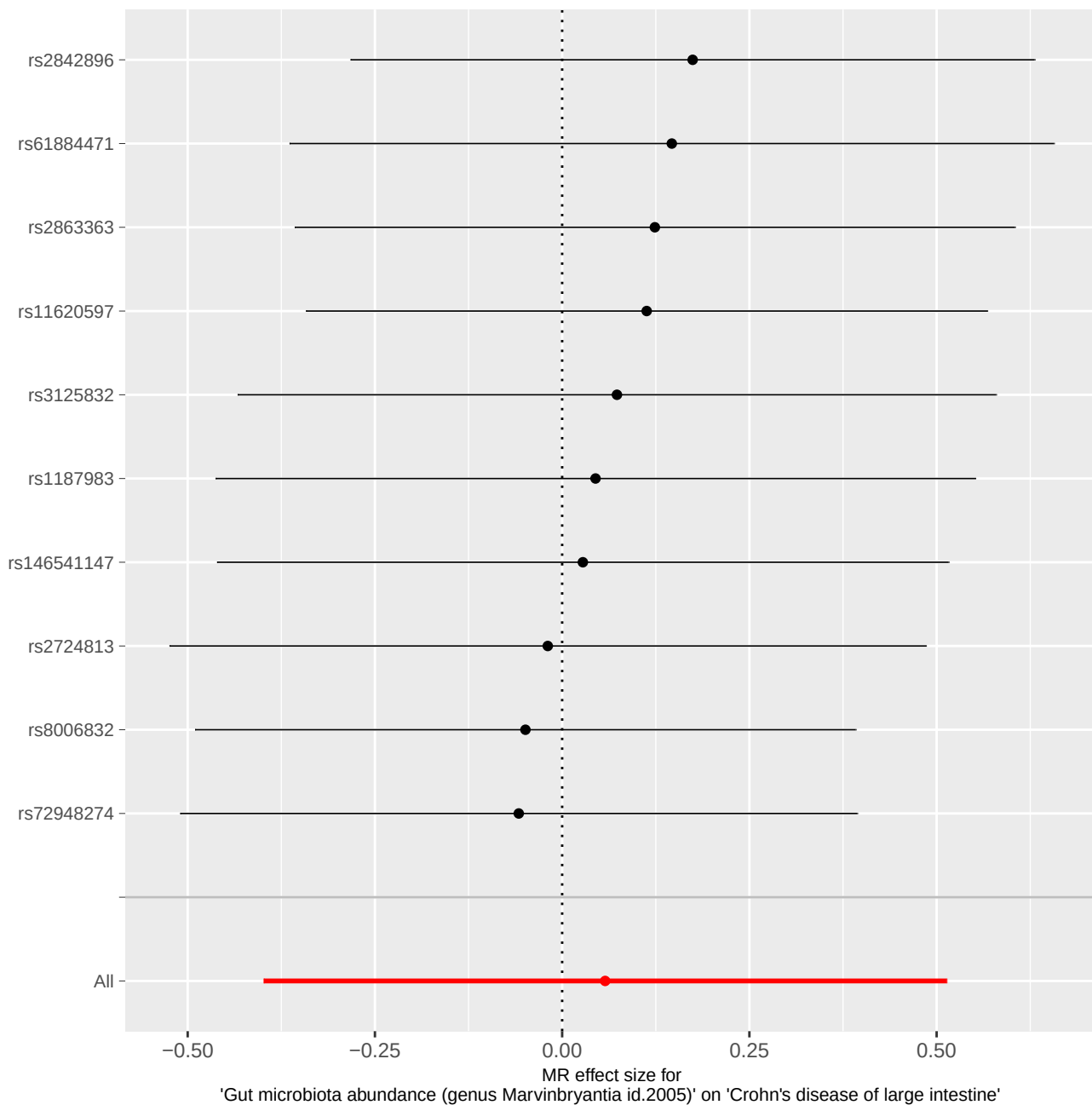


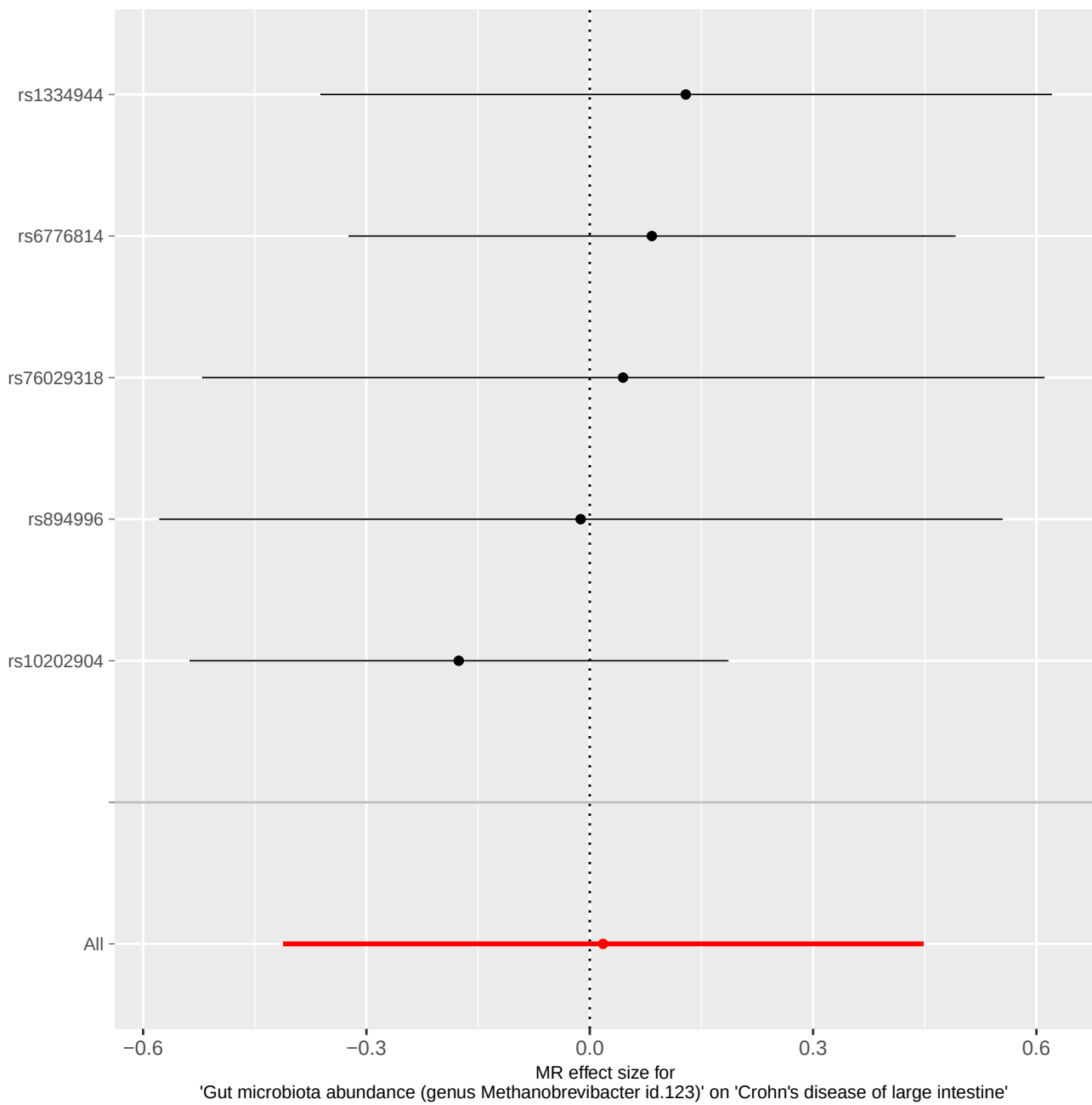


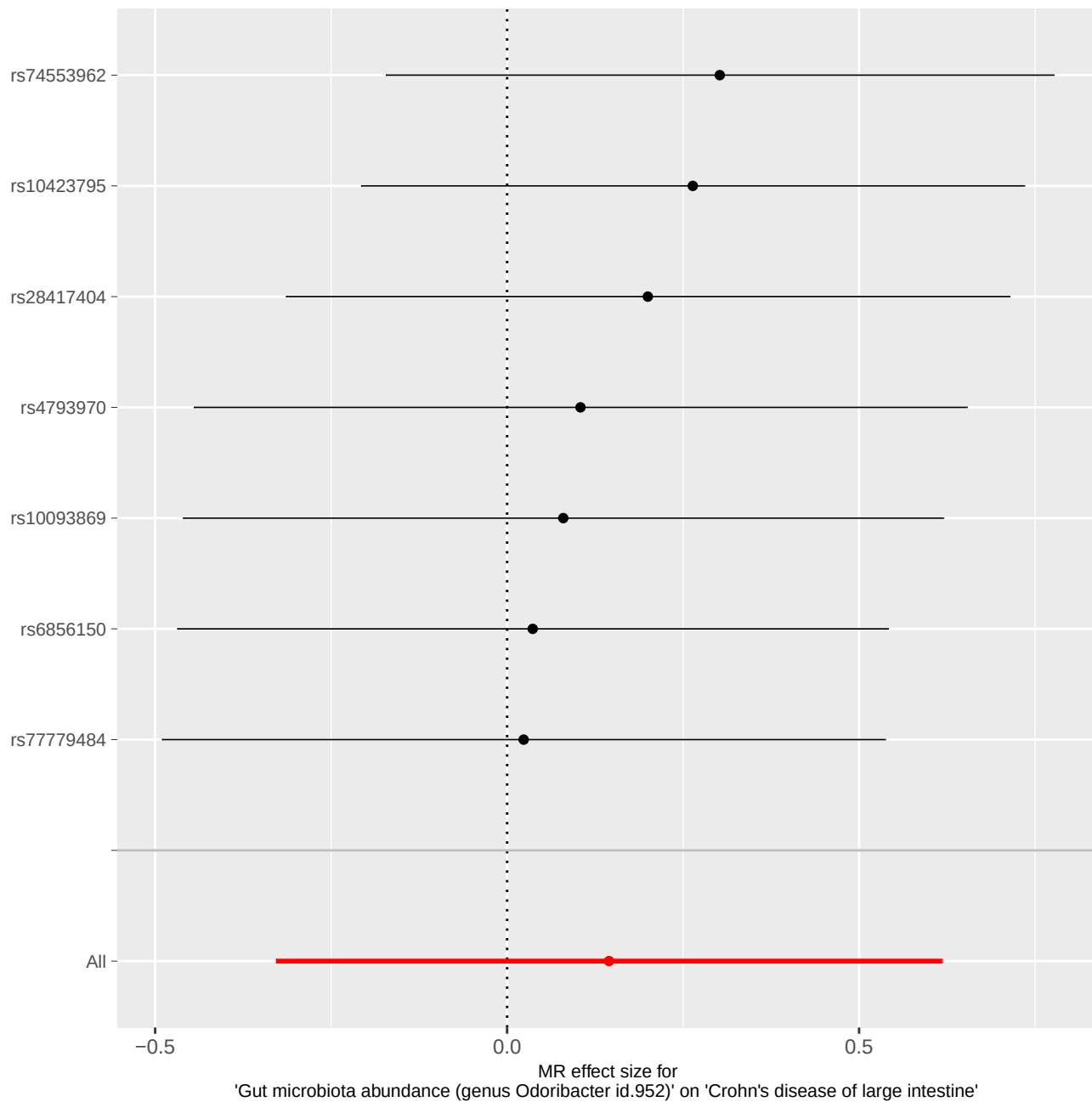


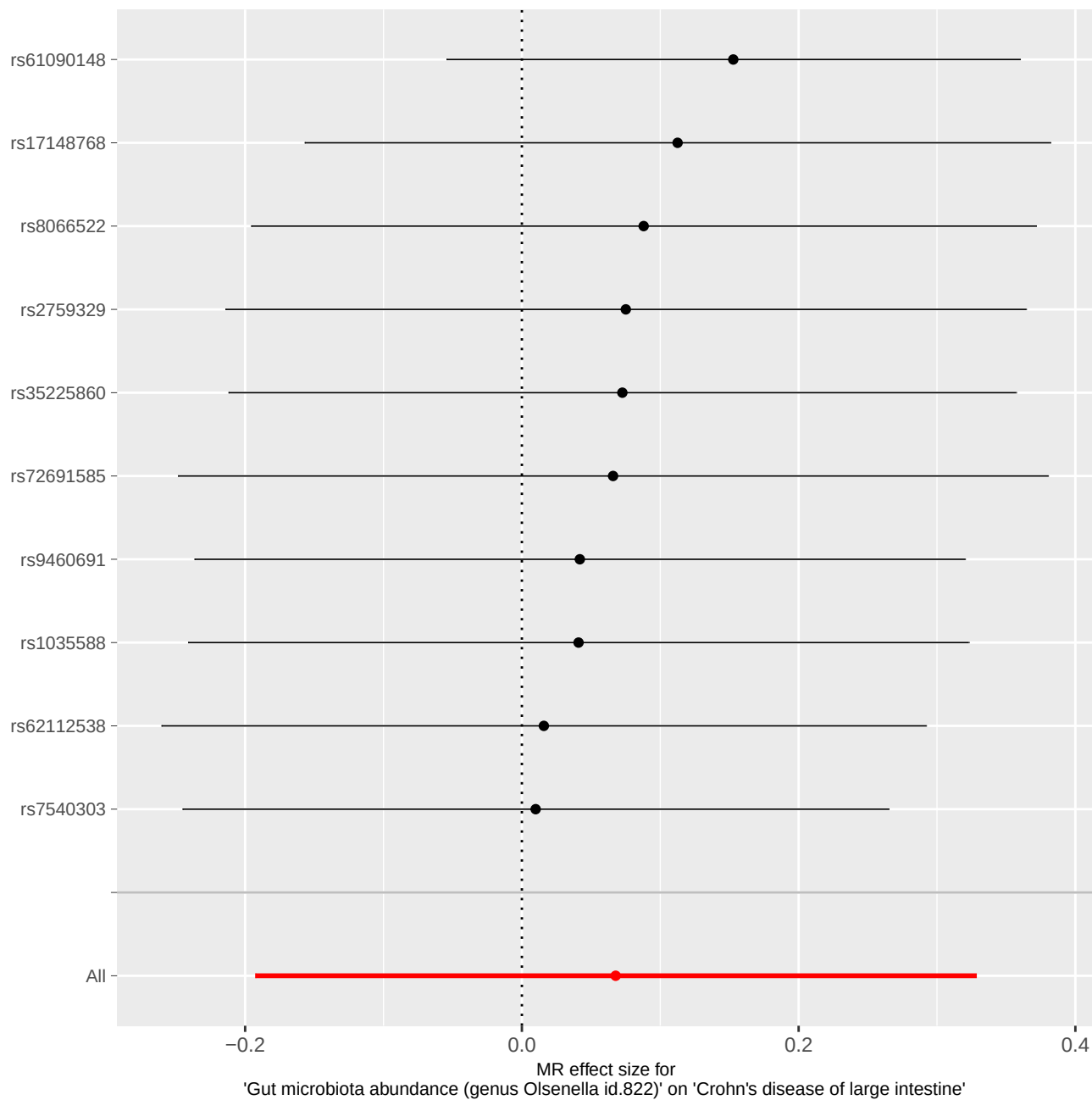


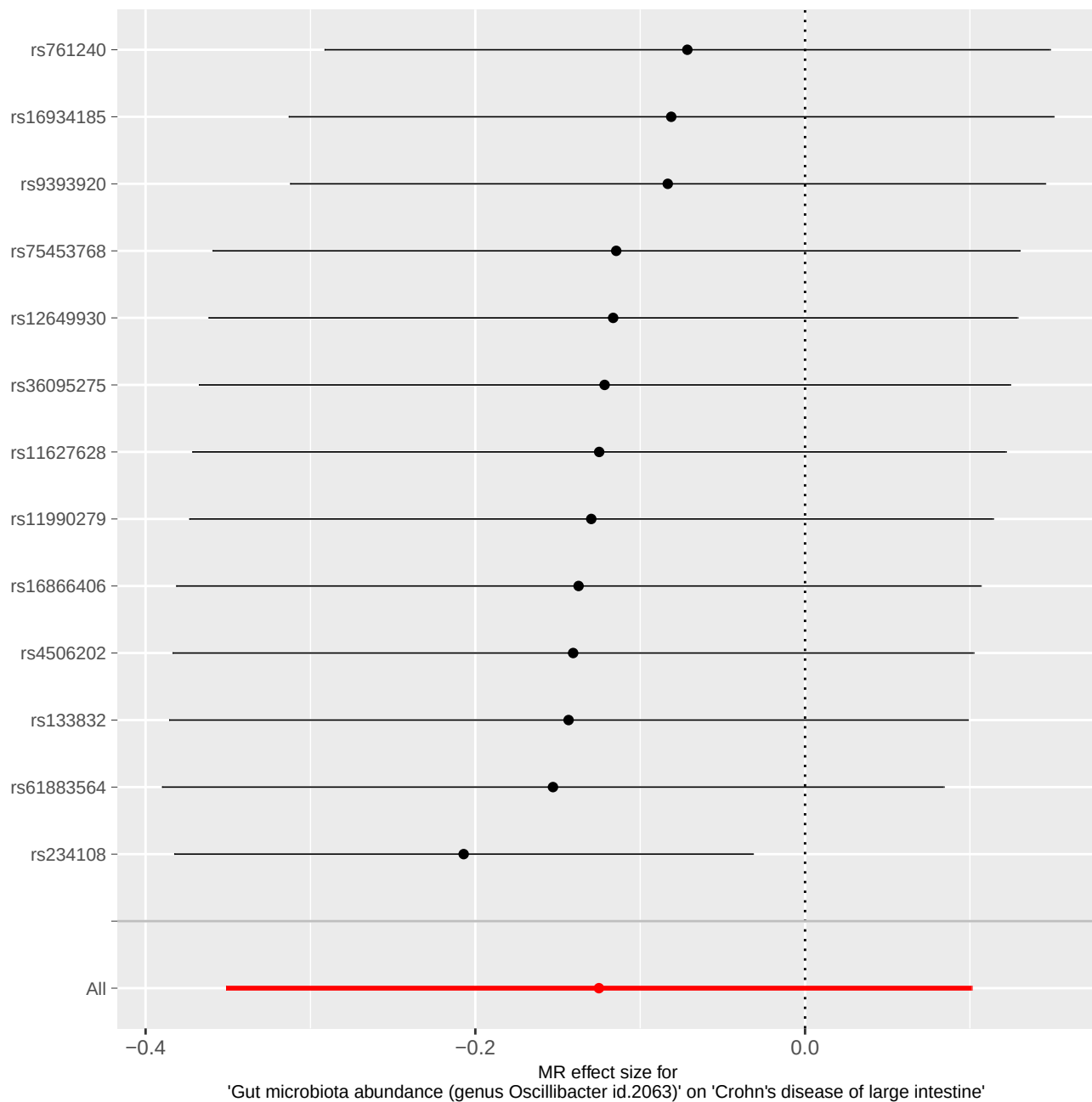


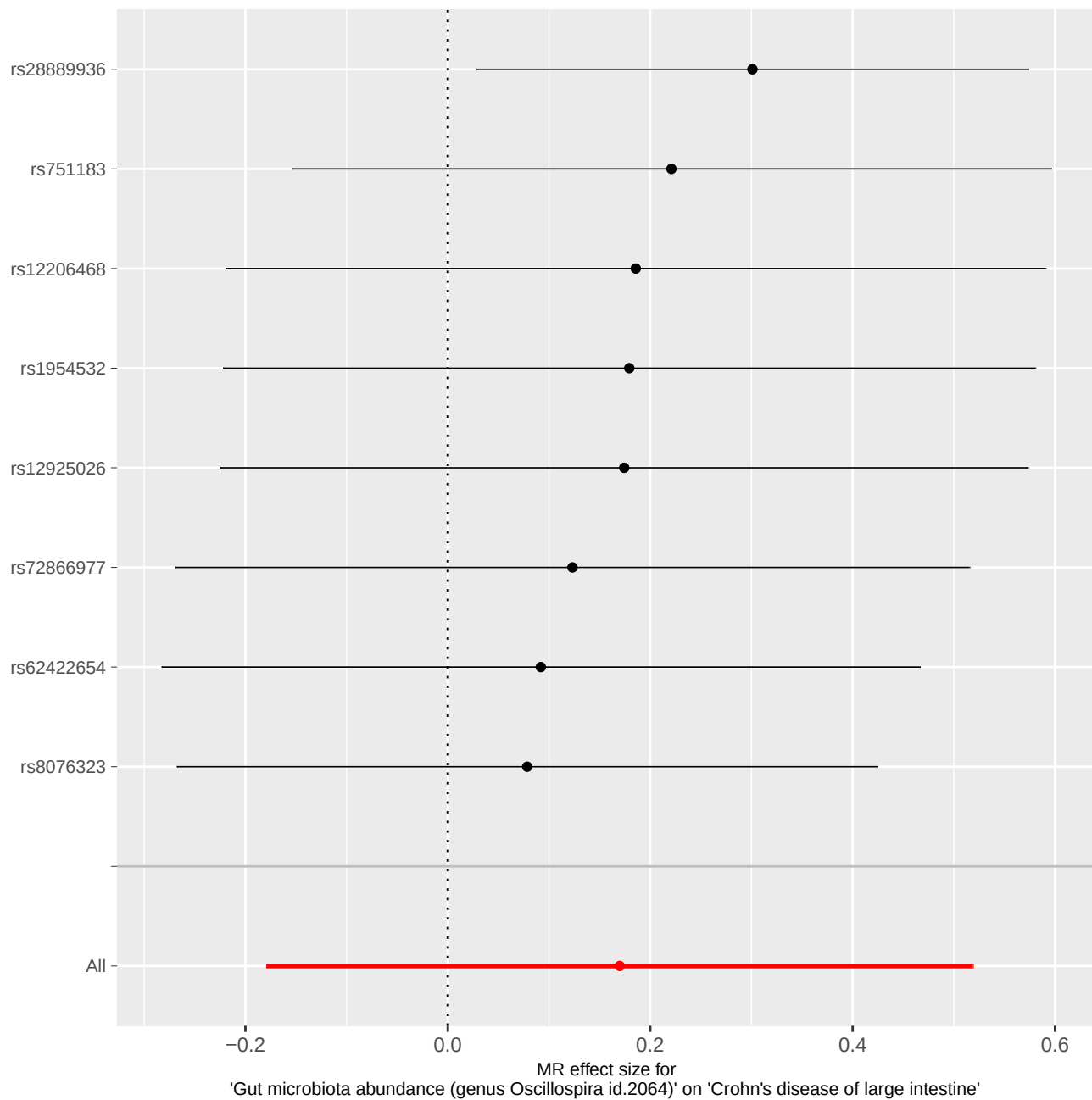


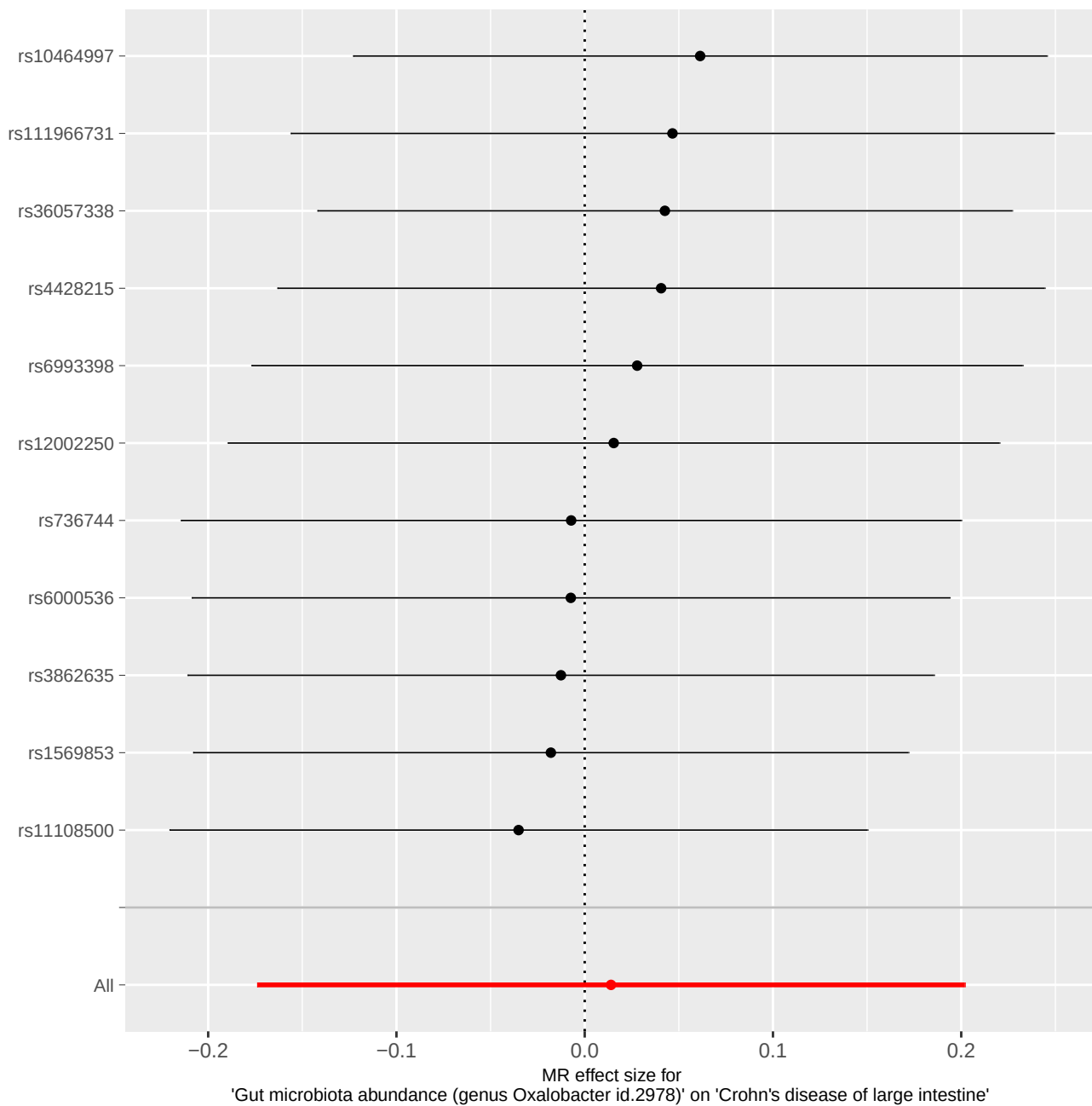


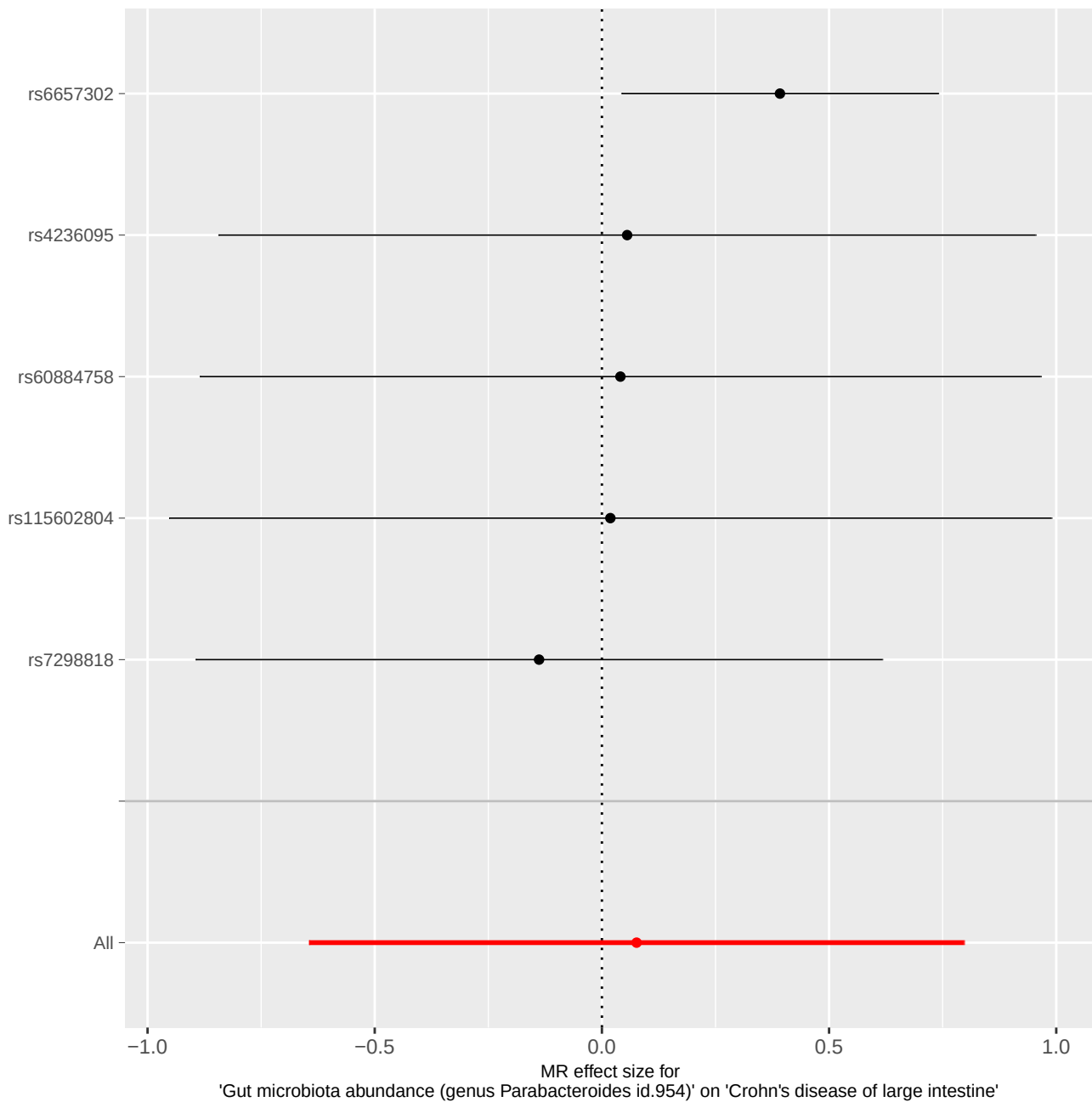


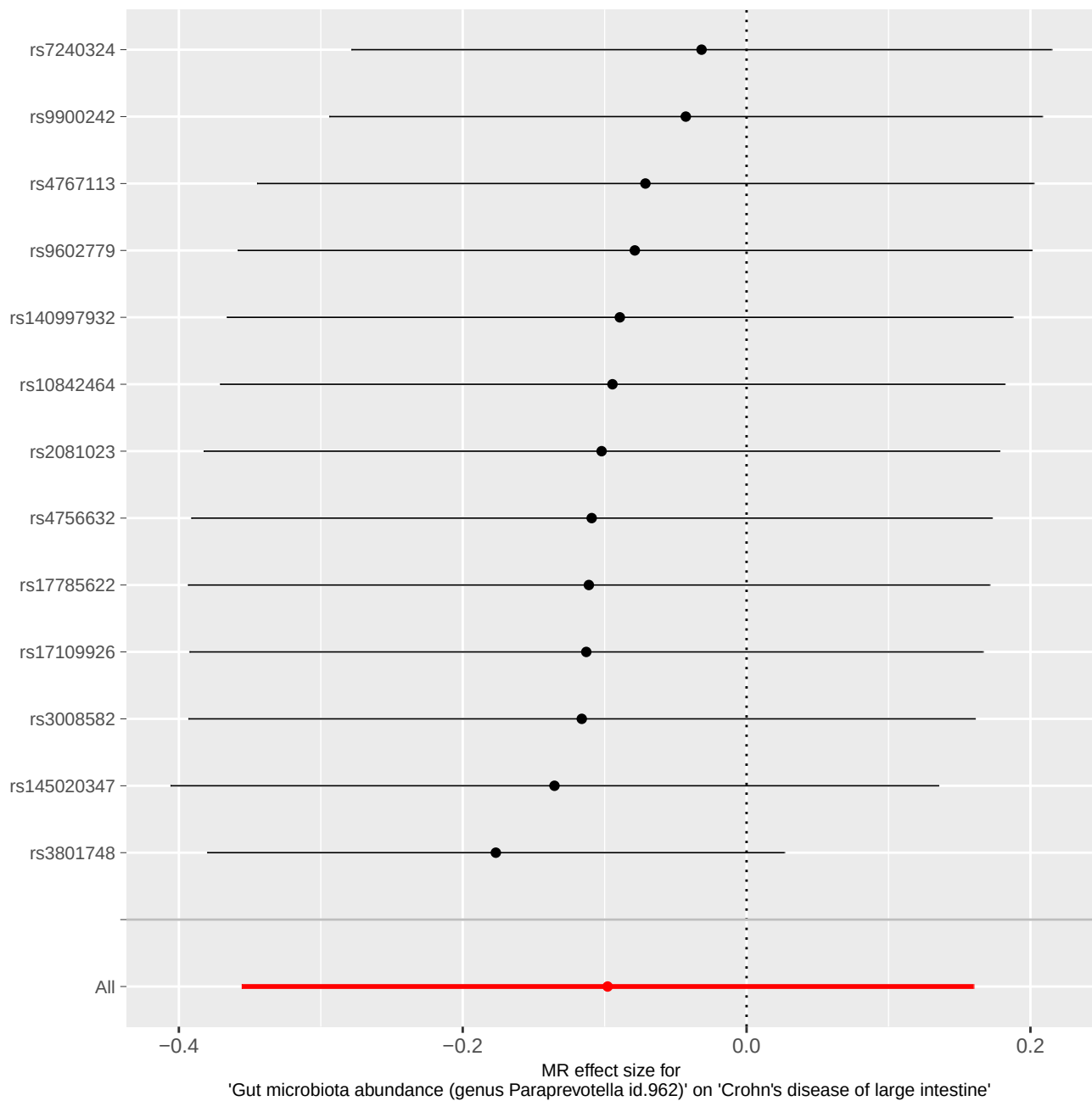


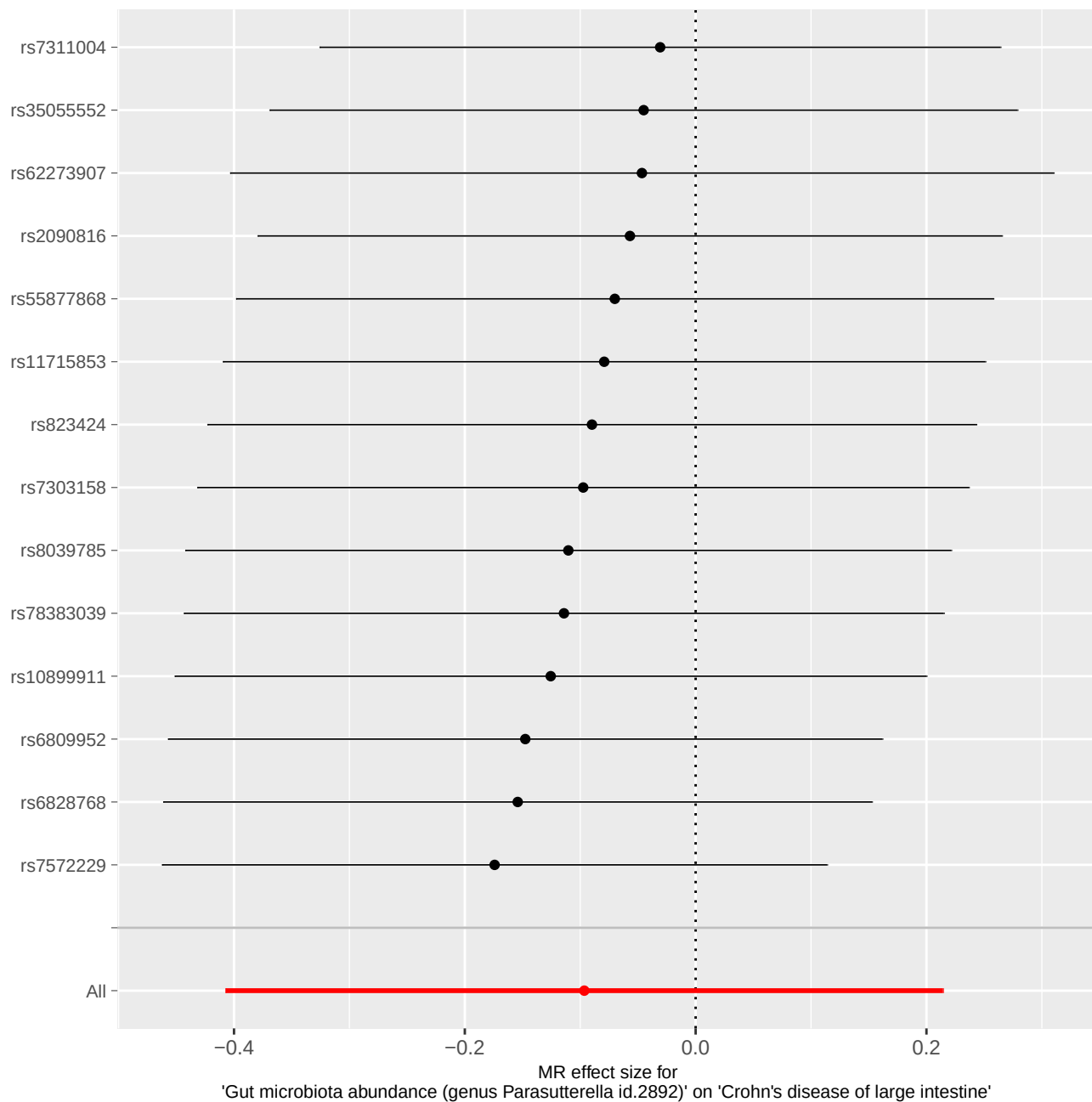


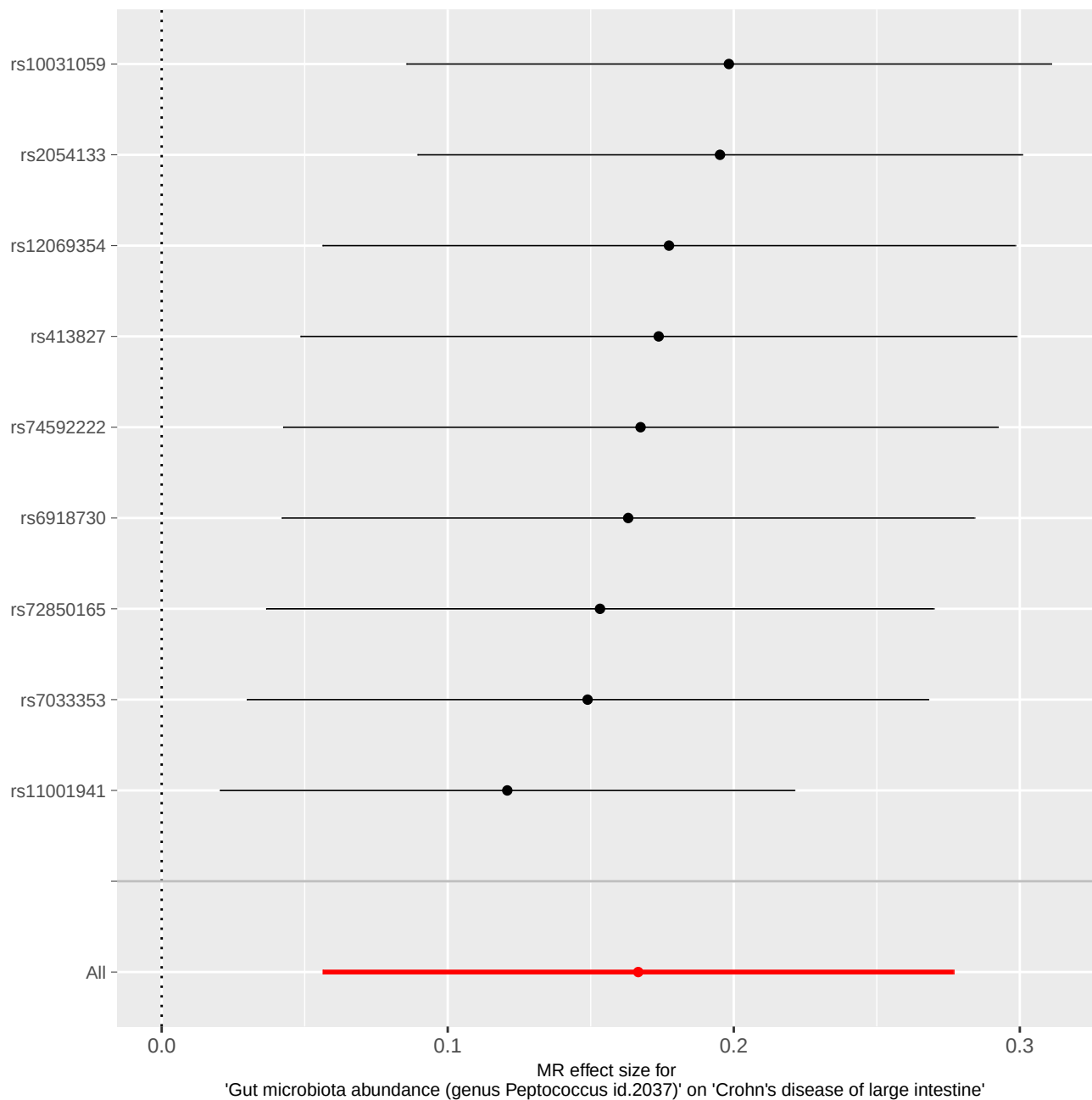


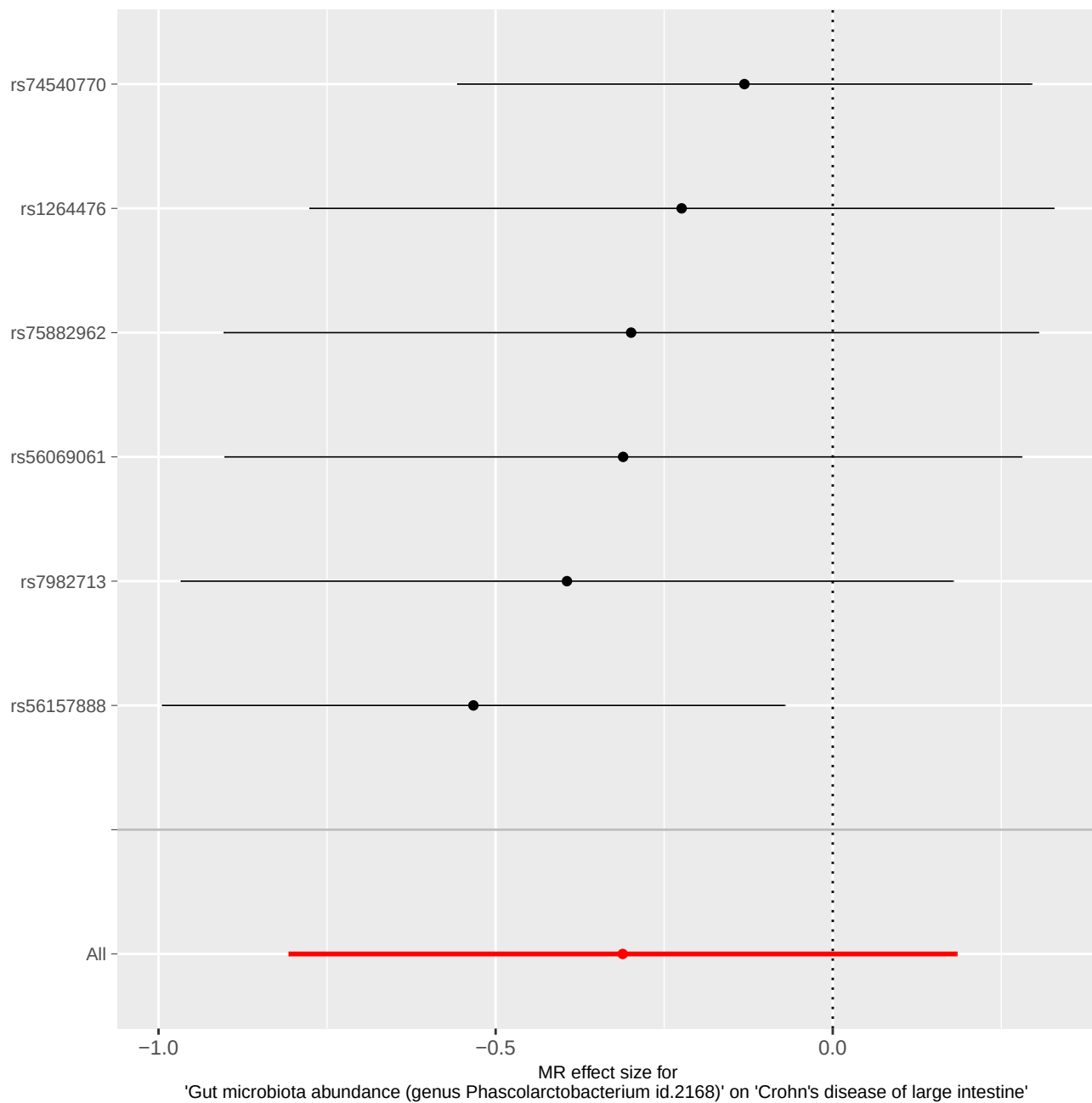


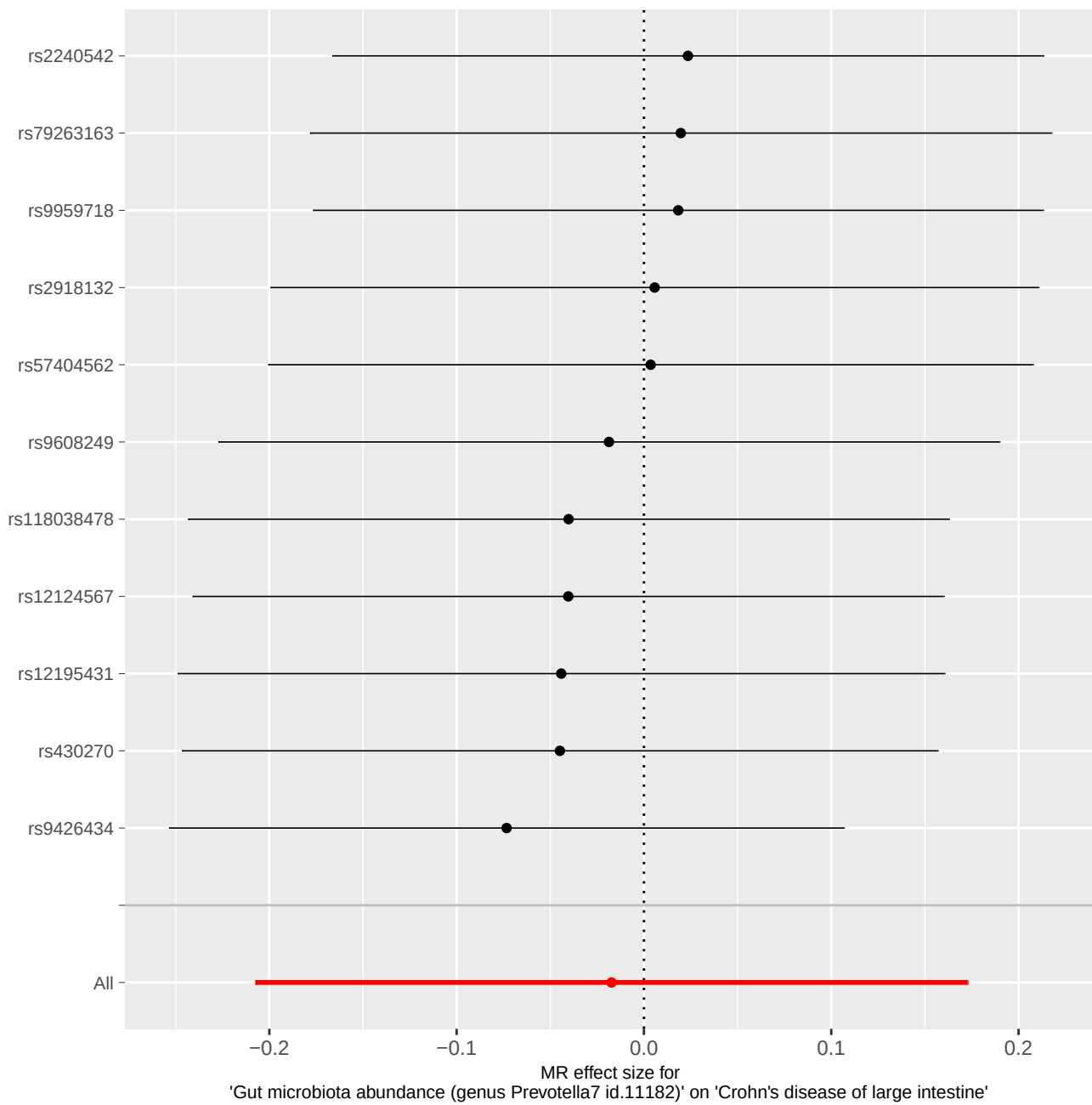


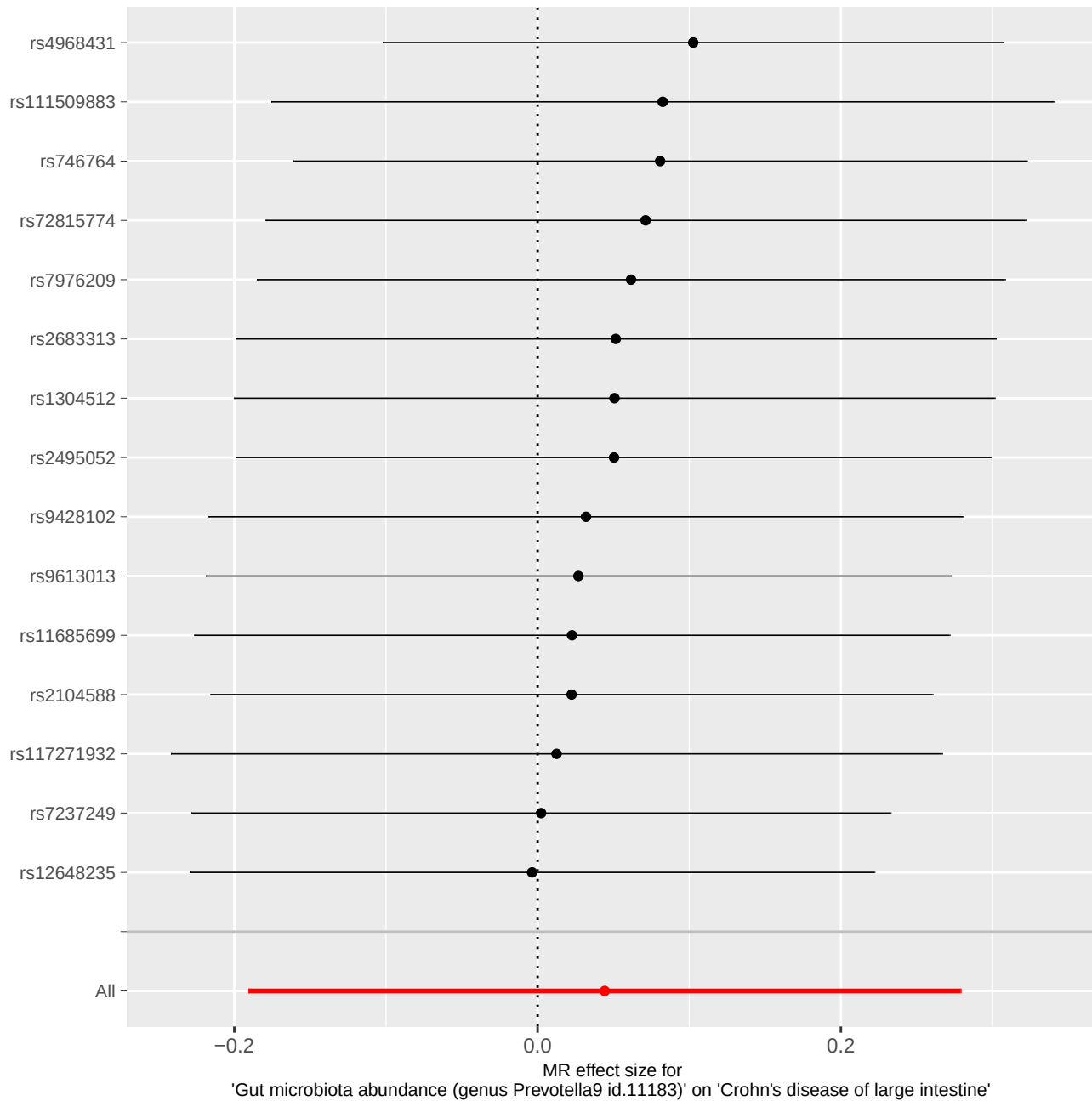


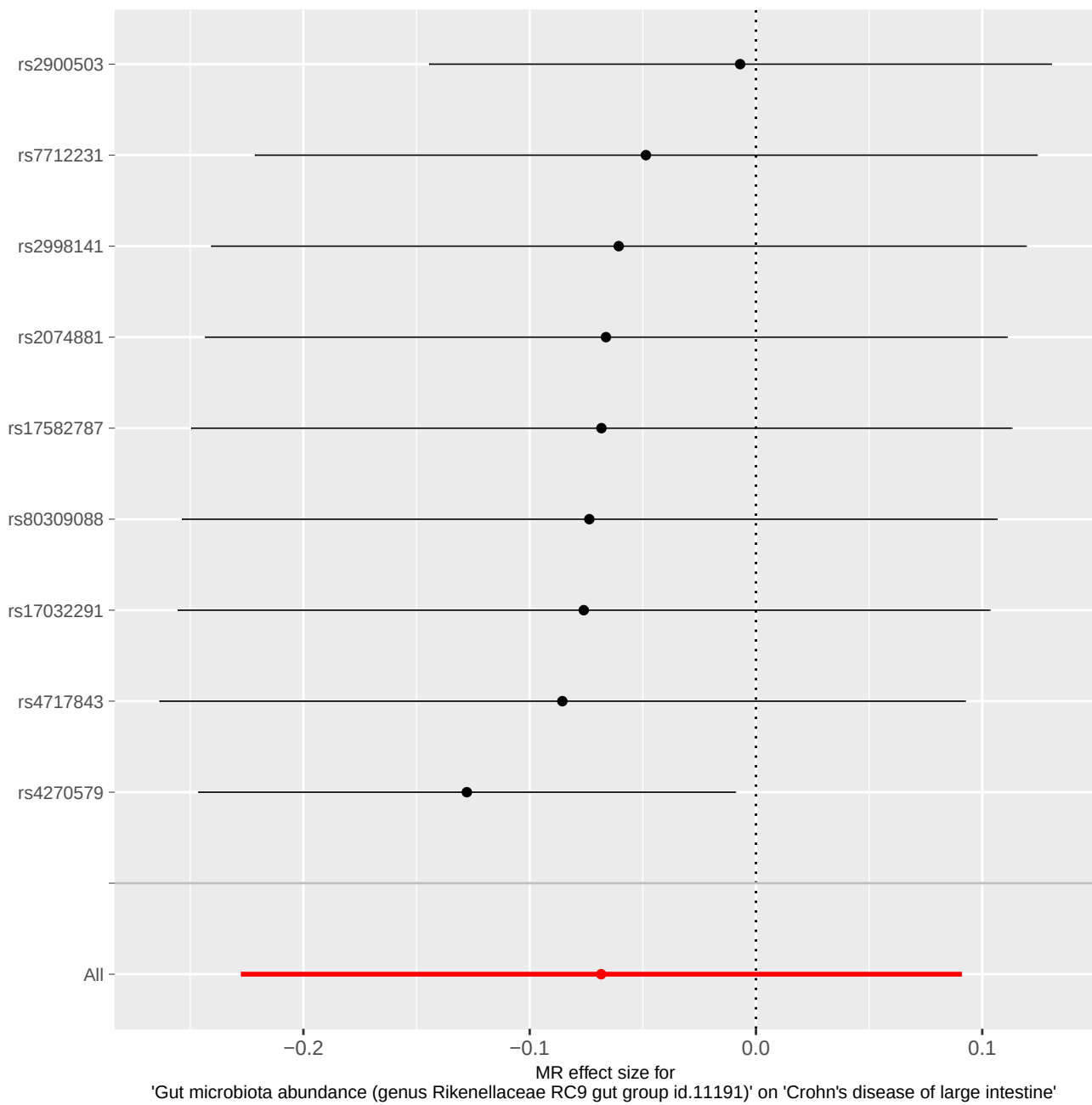




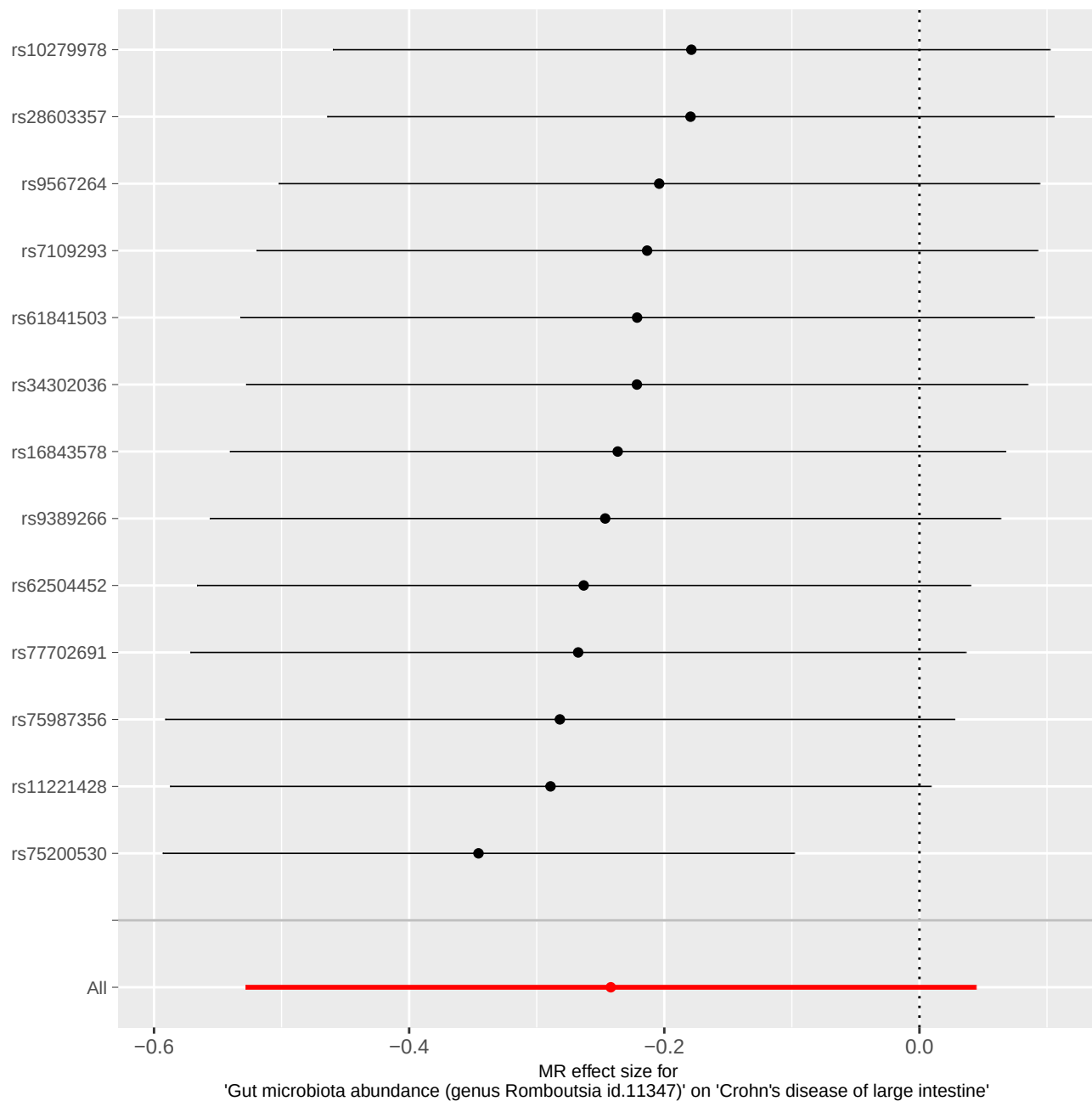


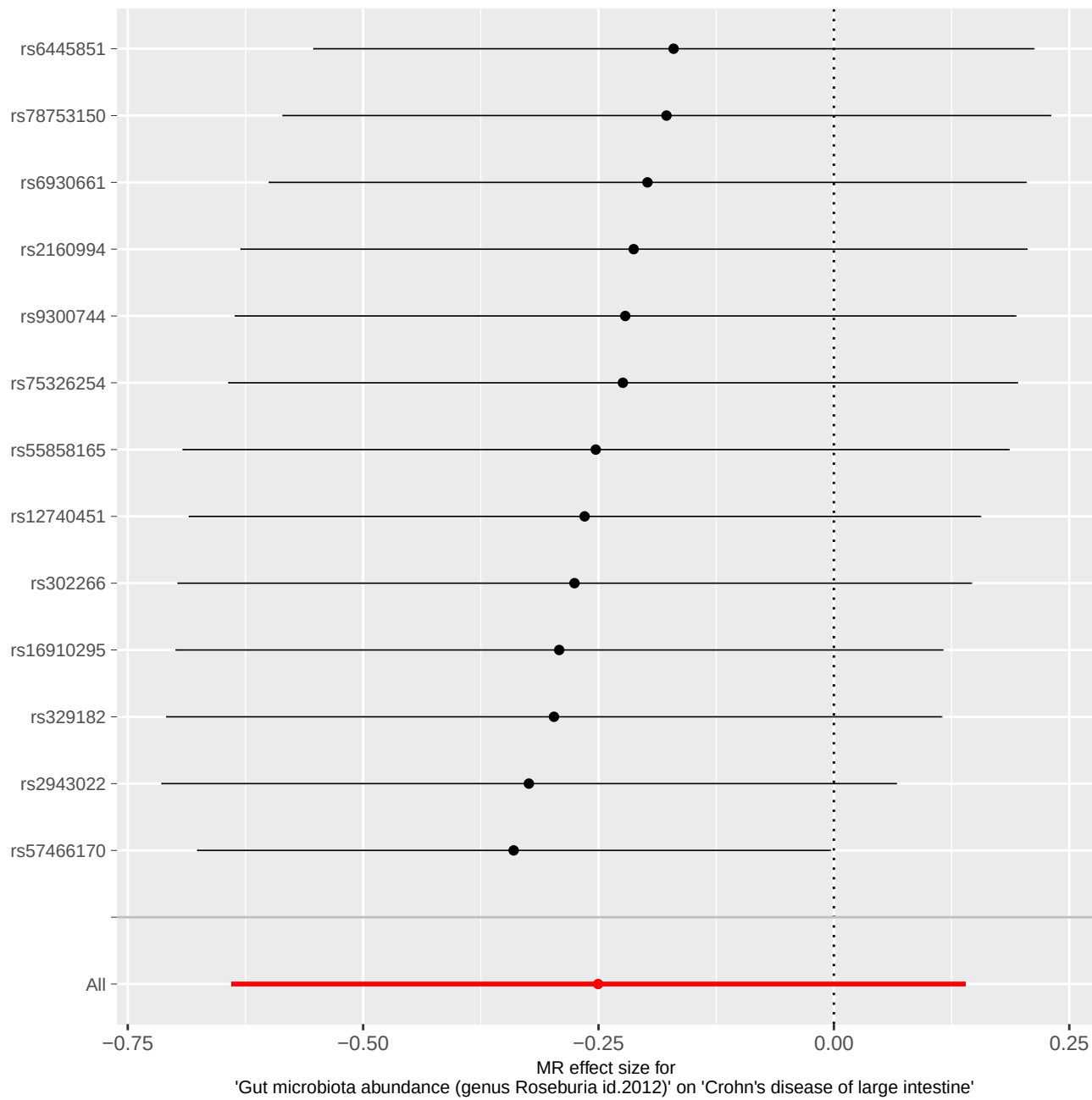




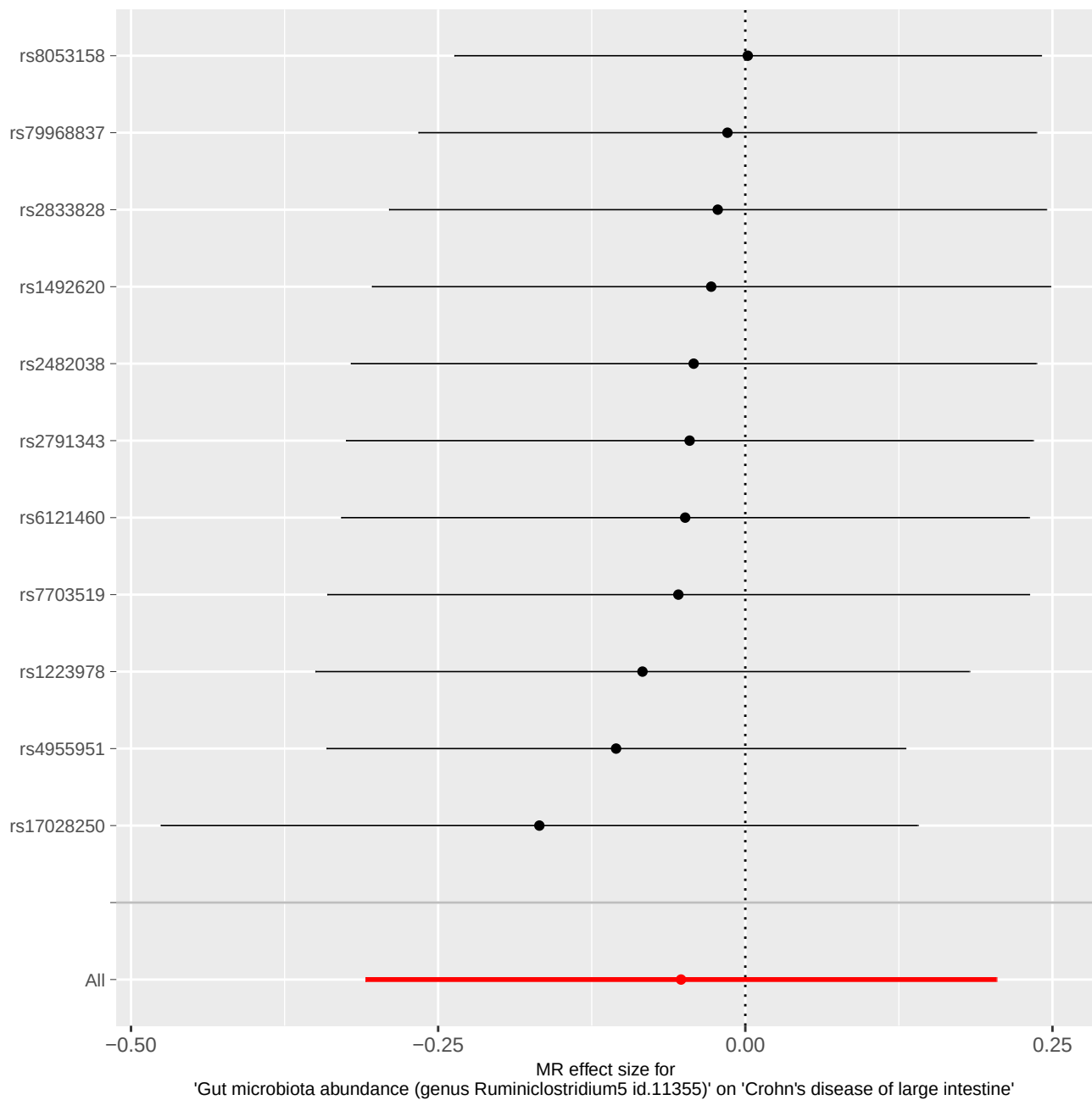


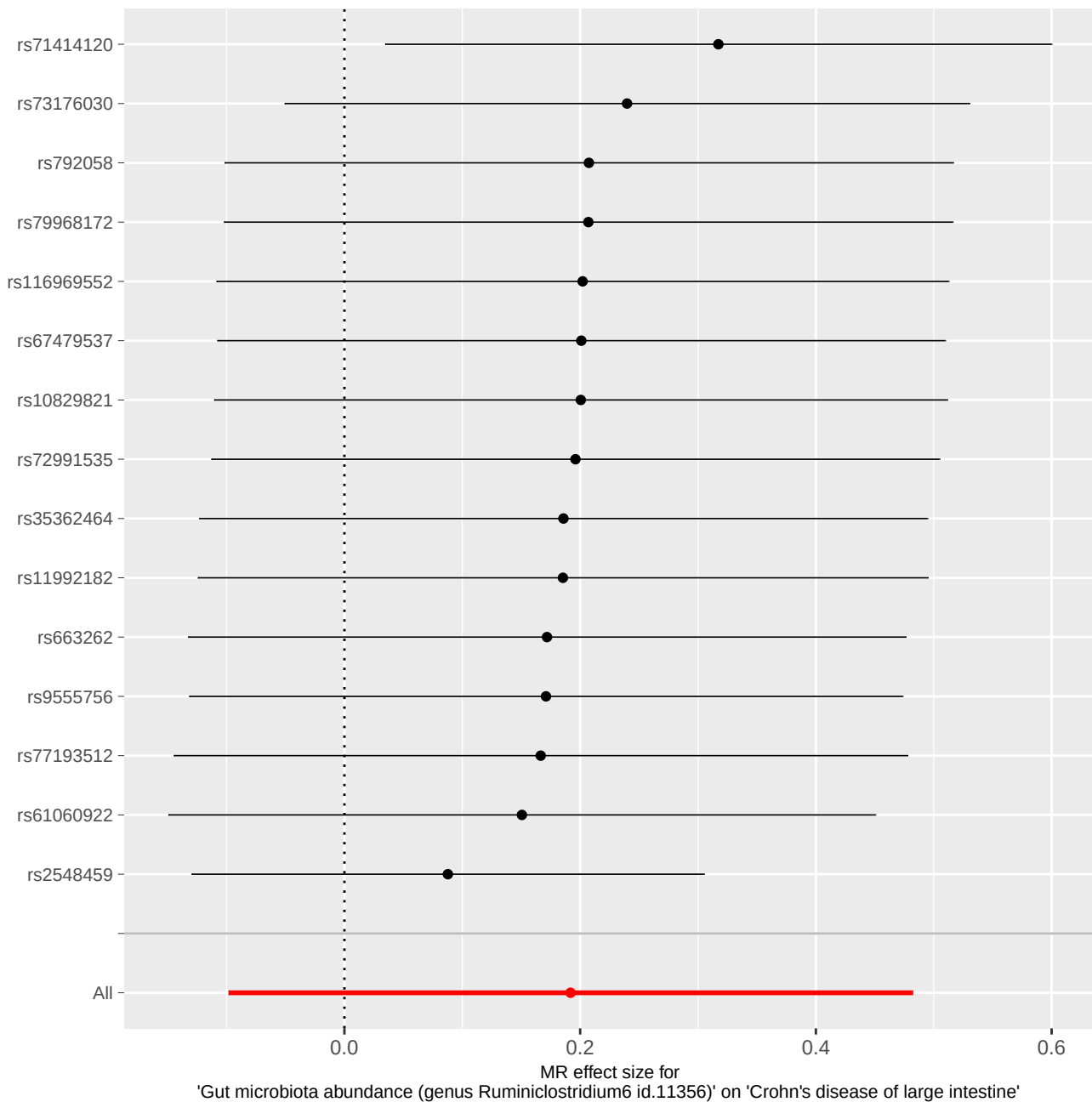
Batch 121 : Gut microbiota abundance (genus Romboutsia id.11347) on Crohn's disease of large intestine



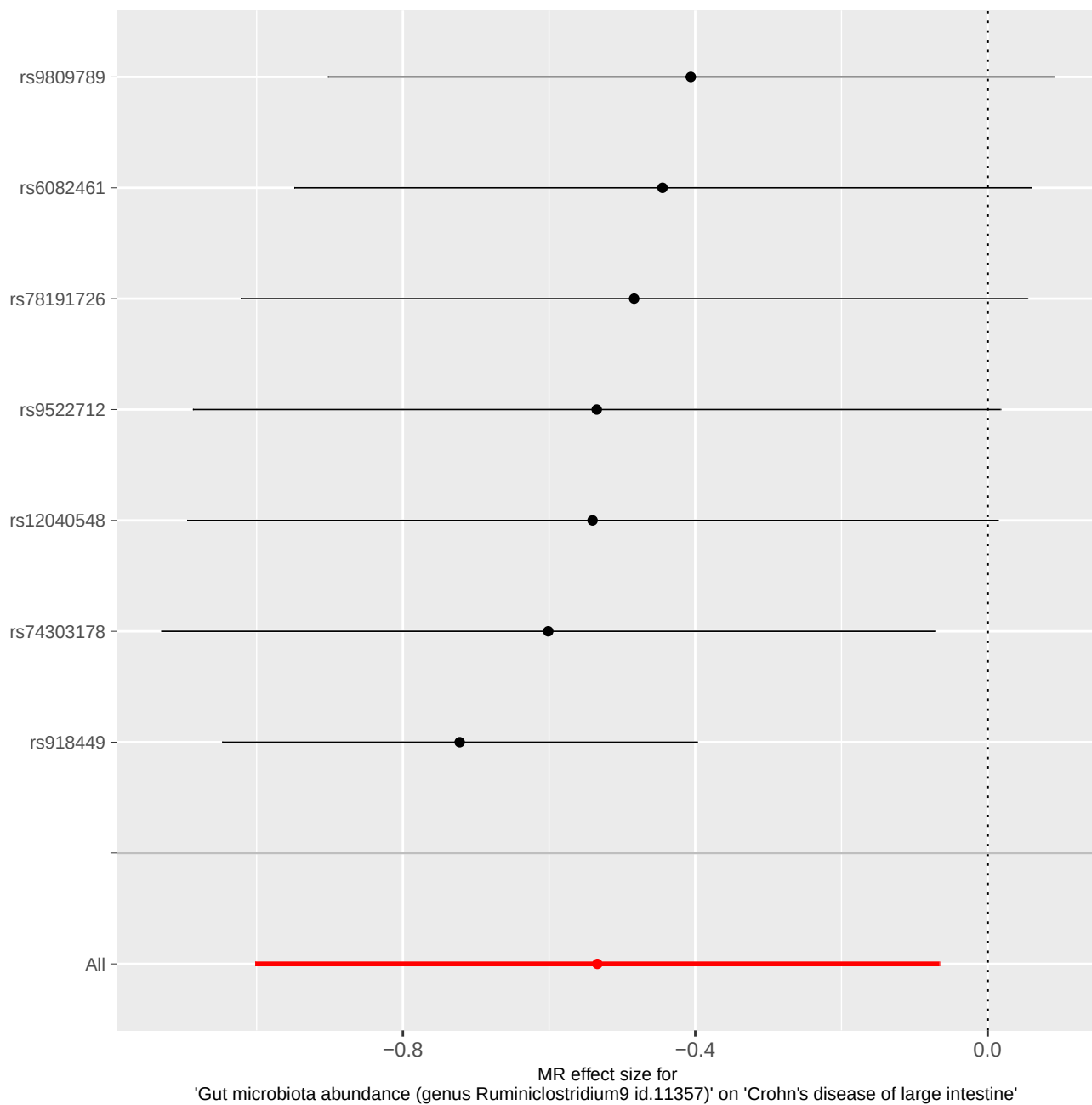


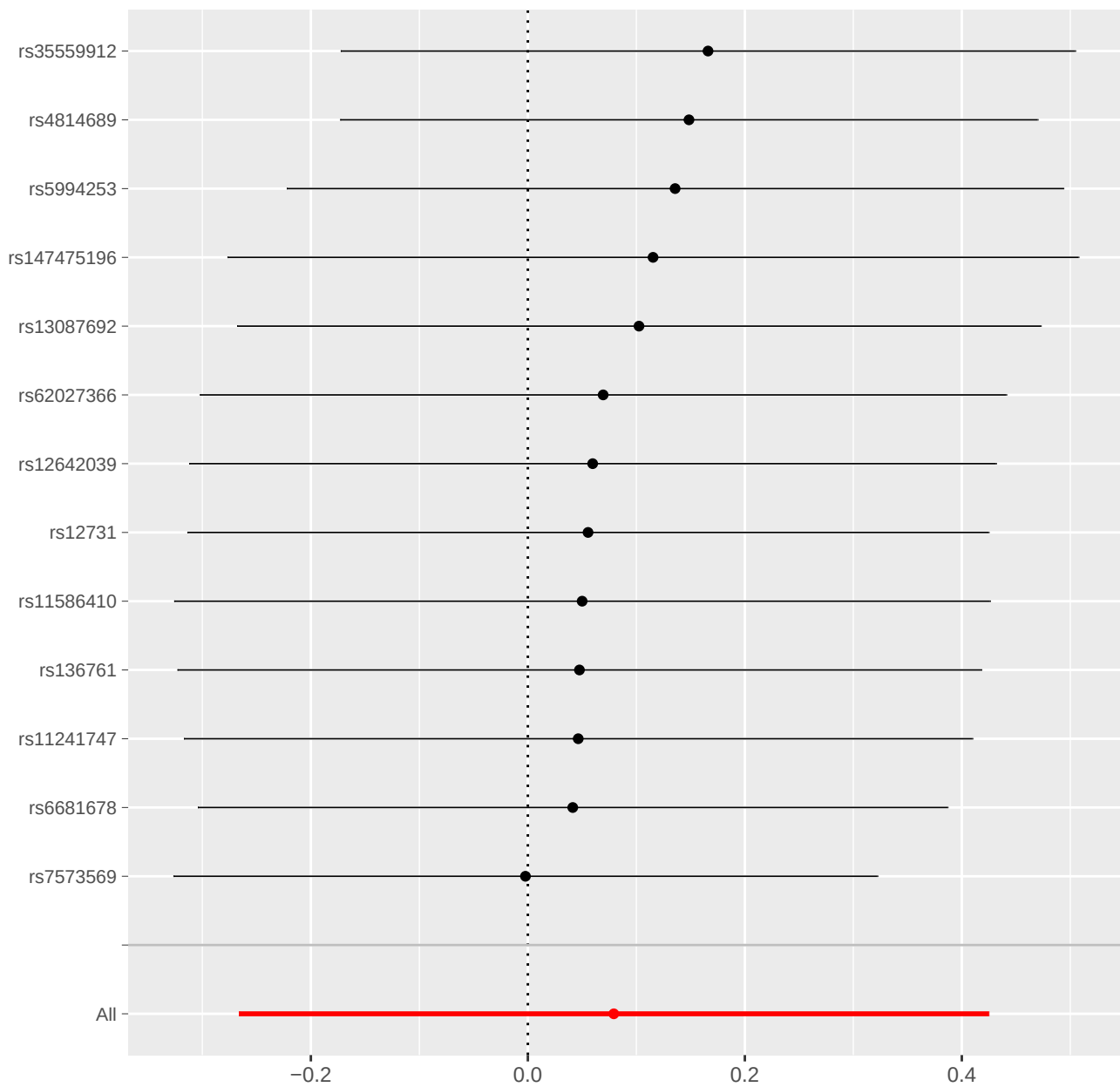
Batch 123 : Gut microbiota abundance (genus Ruminiclostridium5 id.11355) on Crohn's disease of large intestine



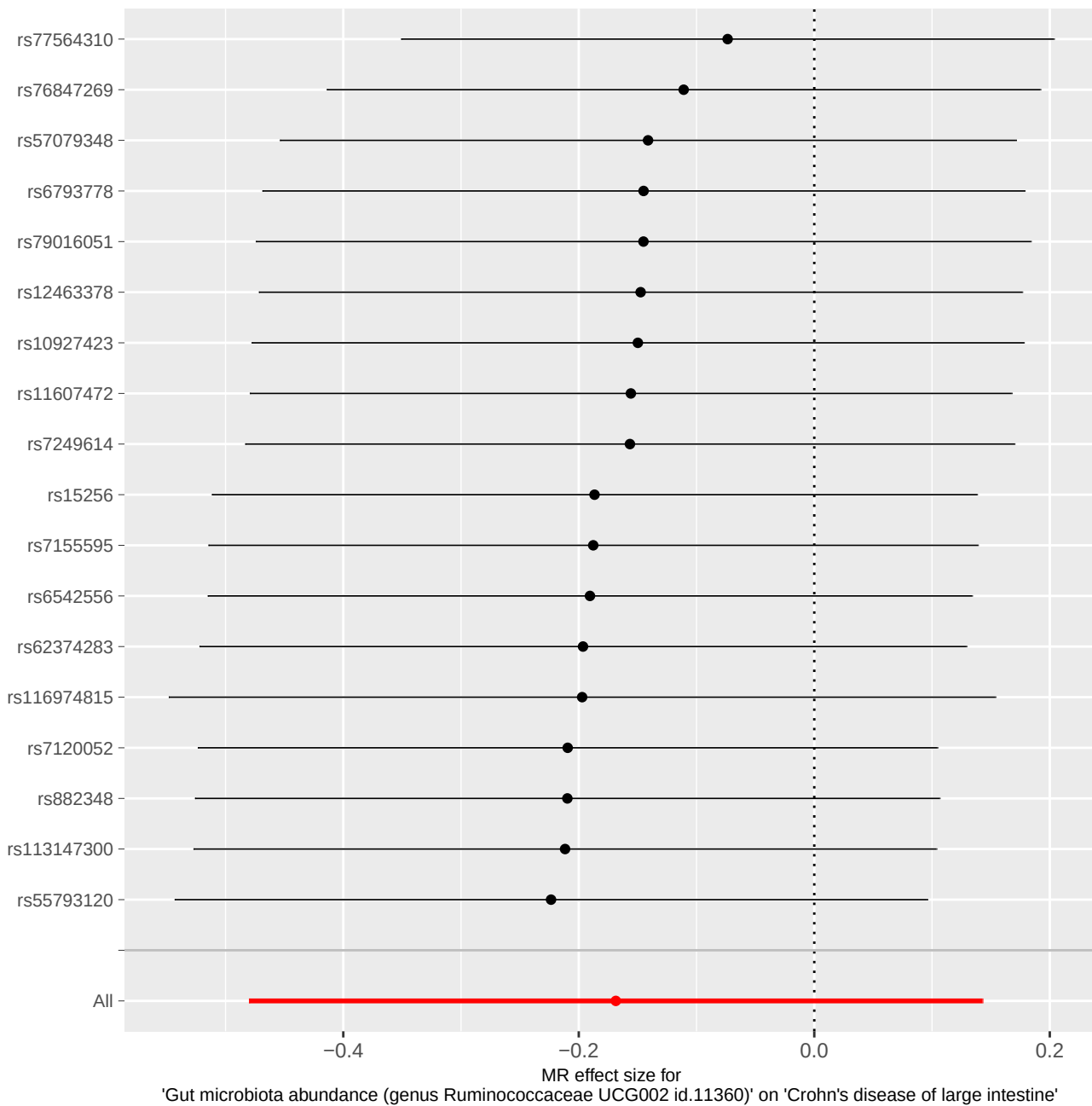


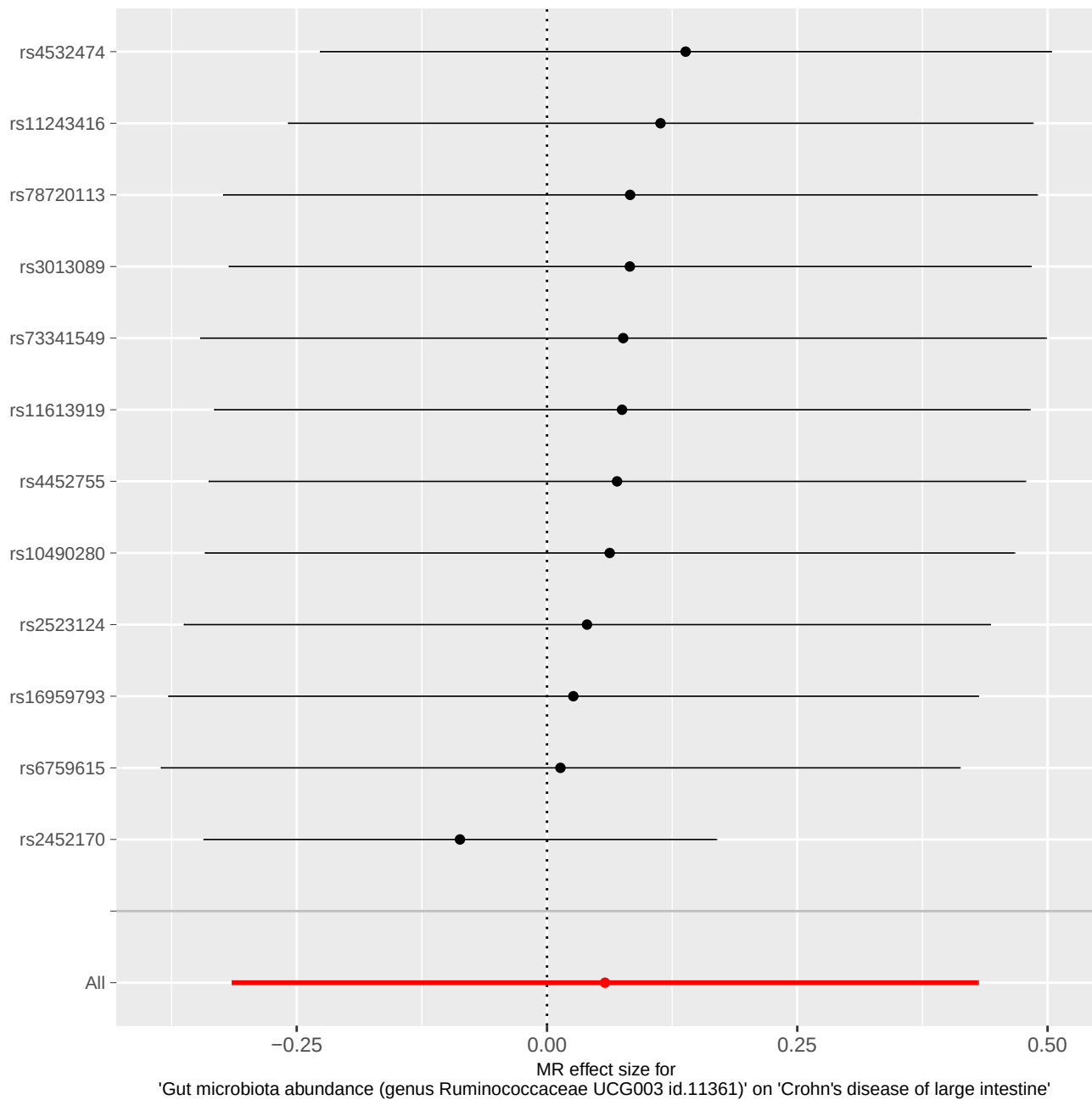
Batch 125 : Gut microbiota abundance (genus Ruminiclostridium9 id.11357) on Crohn's disease of large intestine

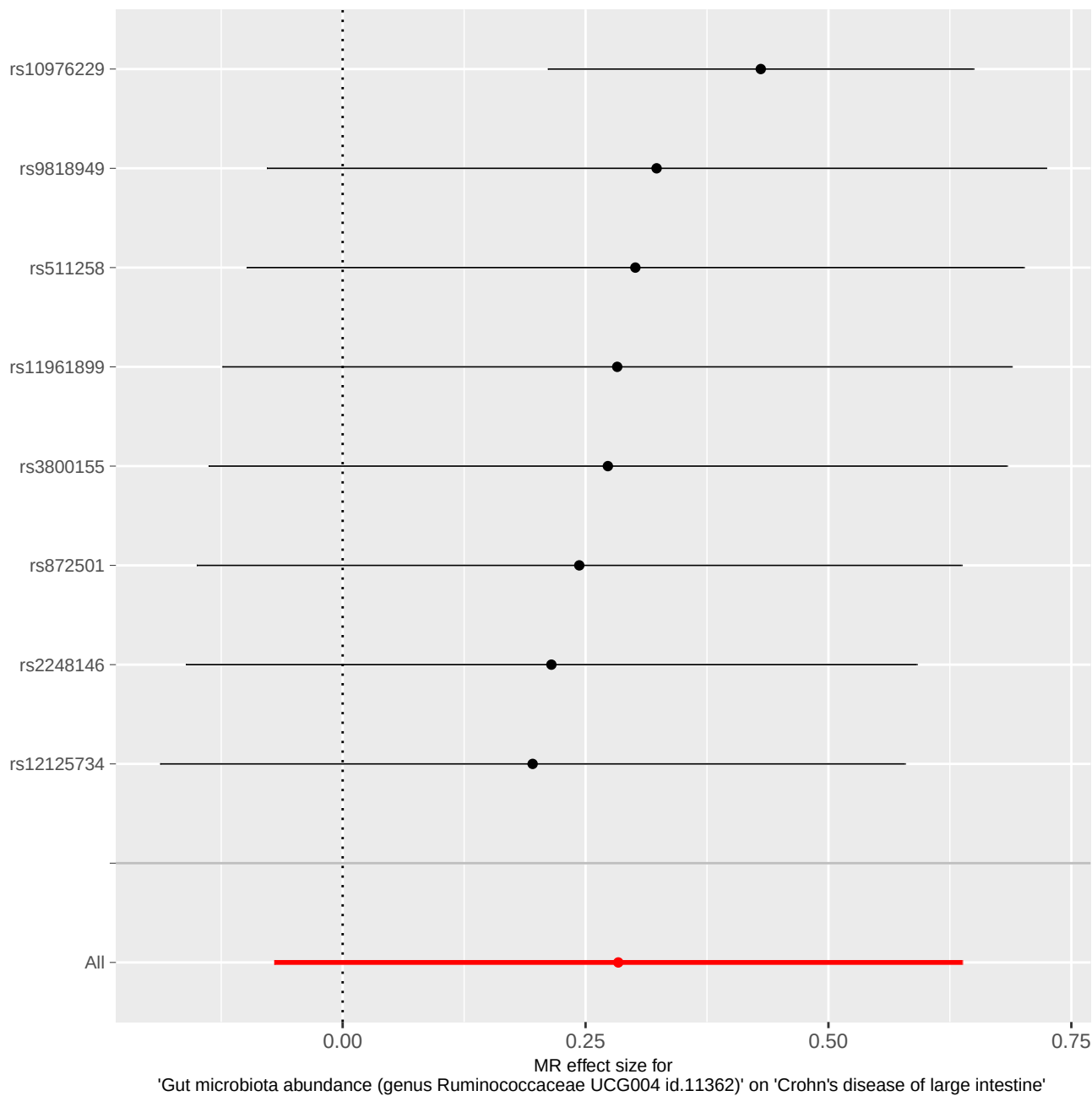




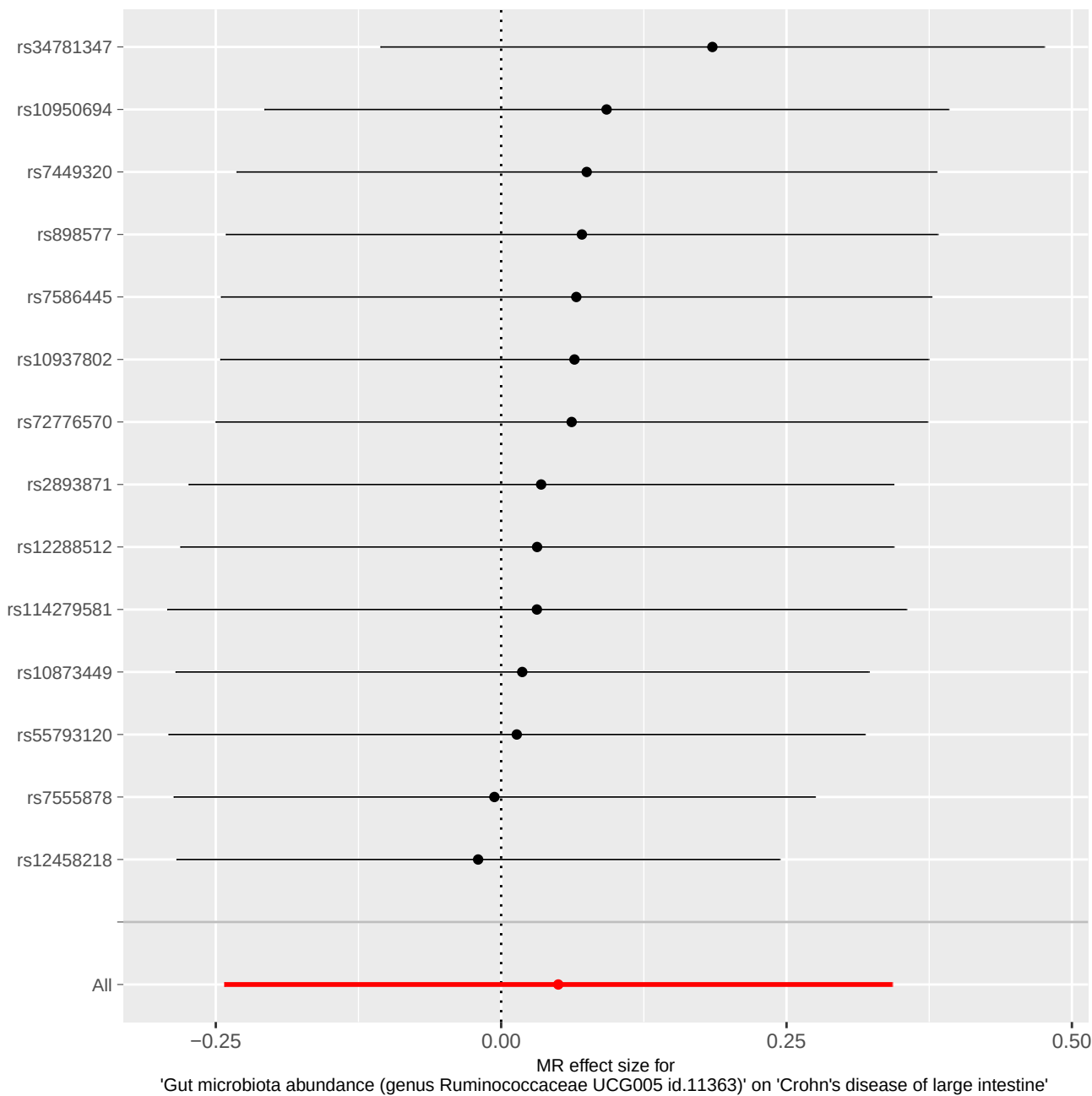
MR effect size for
'Gut microbiota abundance (genus Ruminococcaceae NK4A214 group id.11358)' on 'Crohn's disease of large intestine'



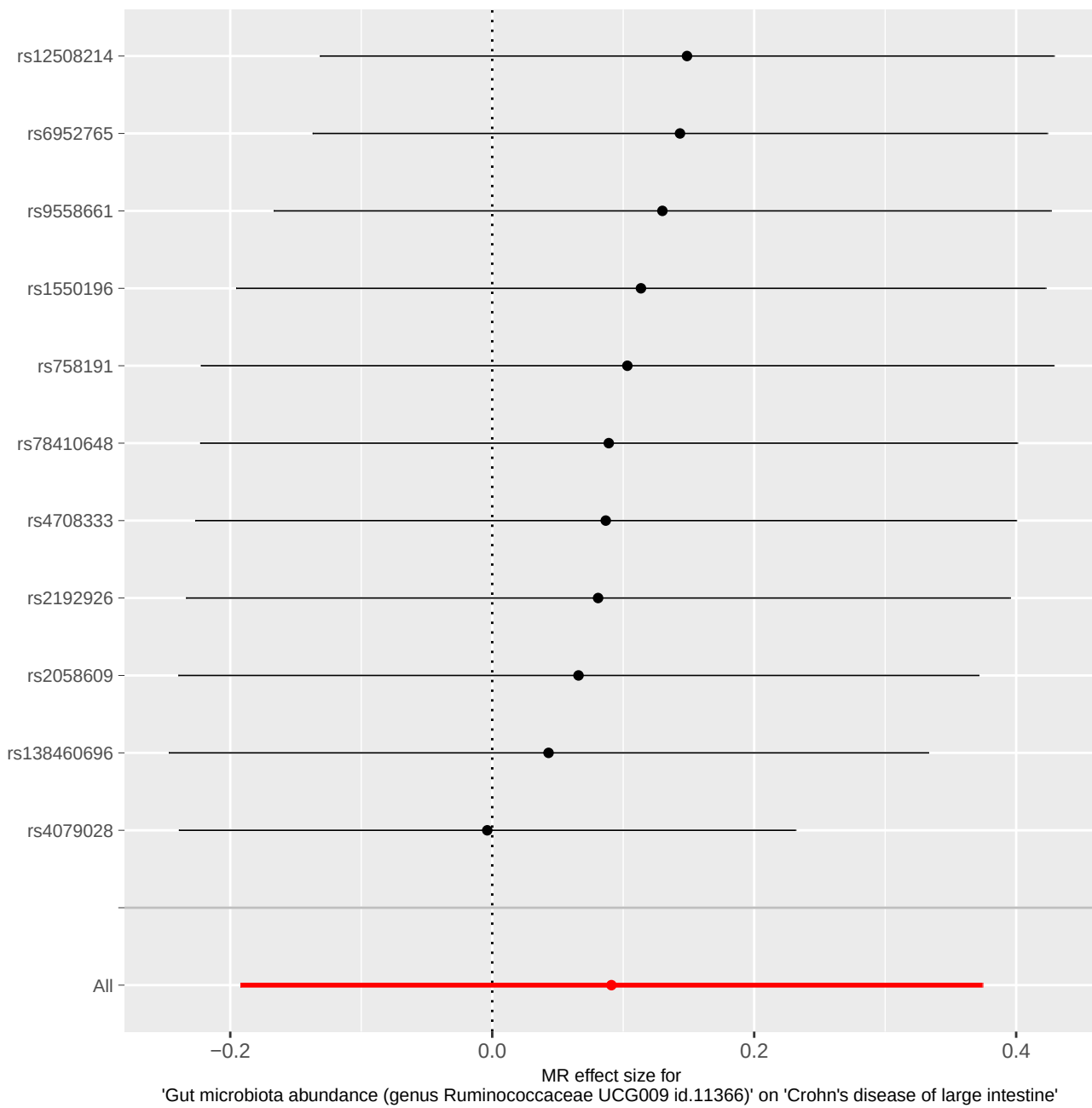


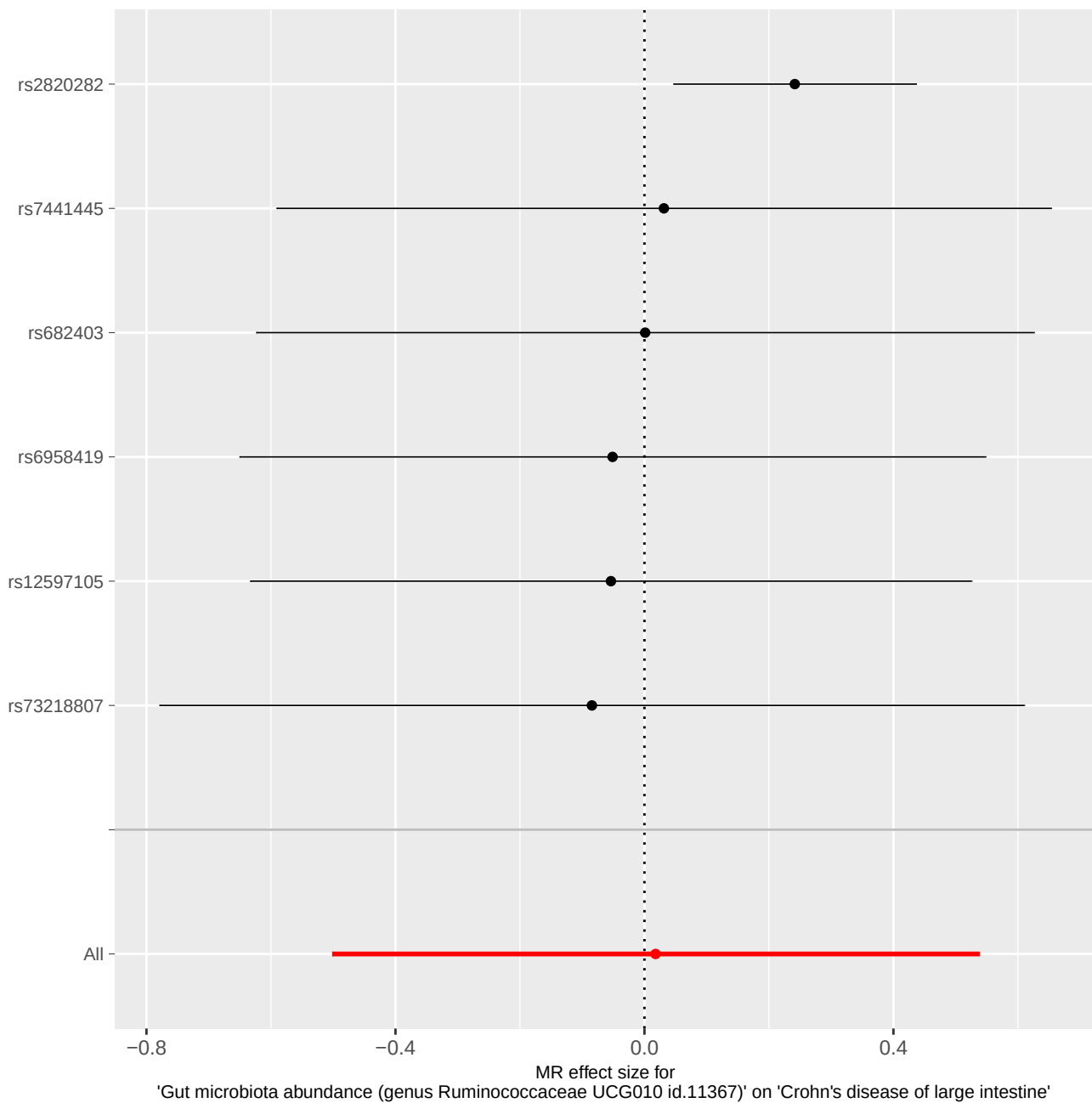


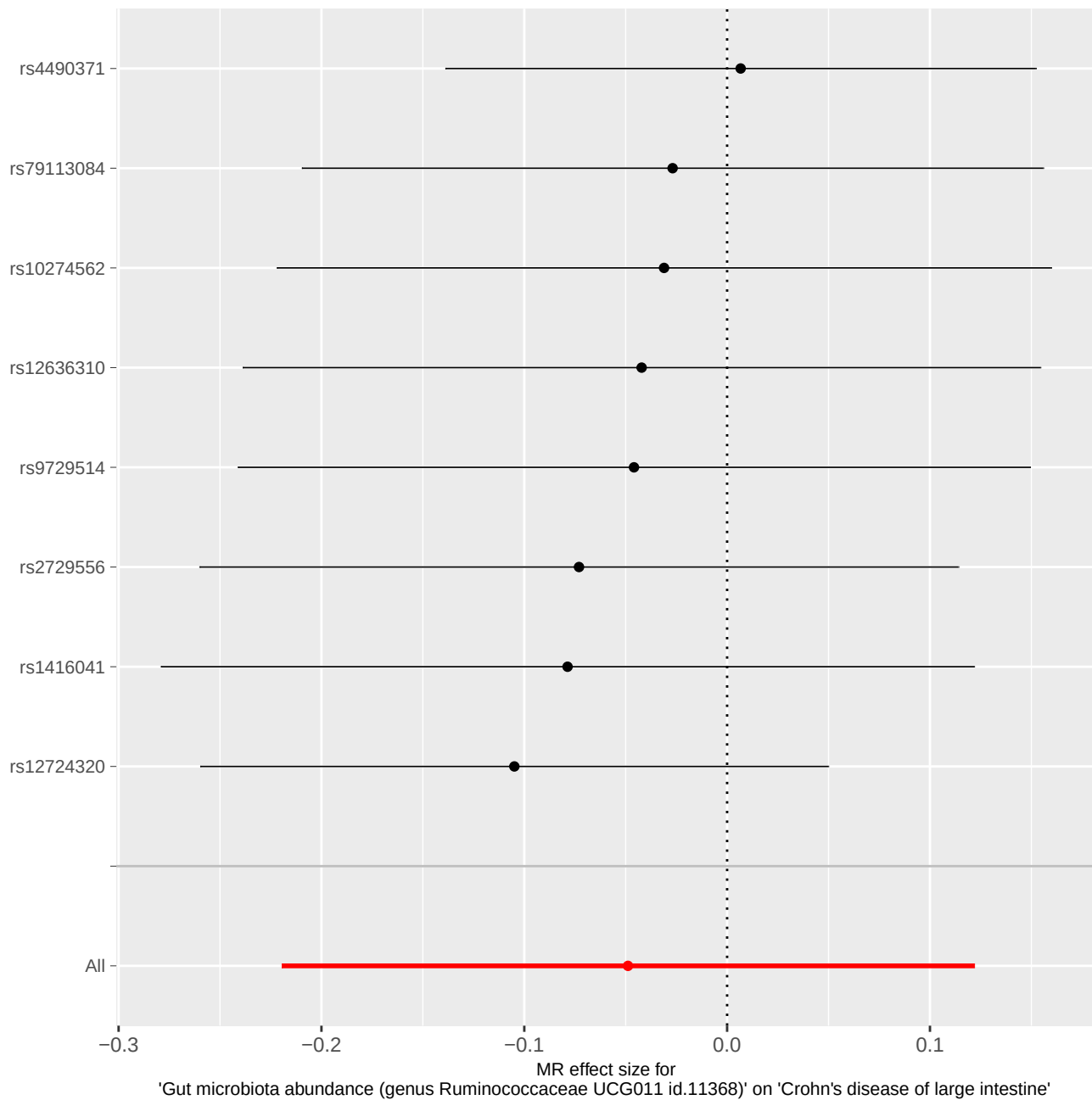
MR effect size for
'Gut microbiota abundance (genus Ruminococcaceae UCG004 id.11362)' on 'Crohn's disease of large intestine'

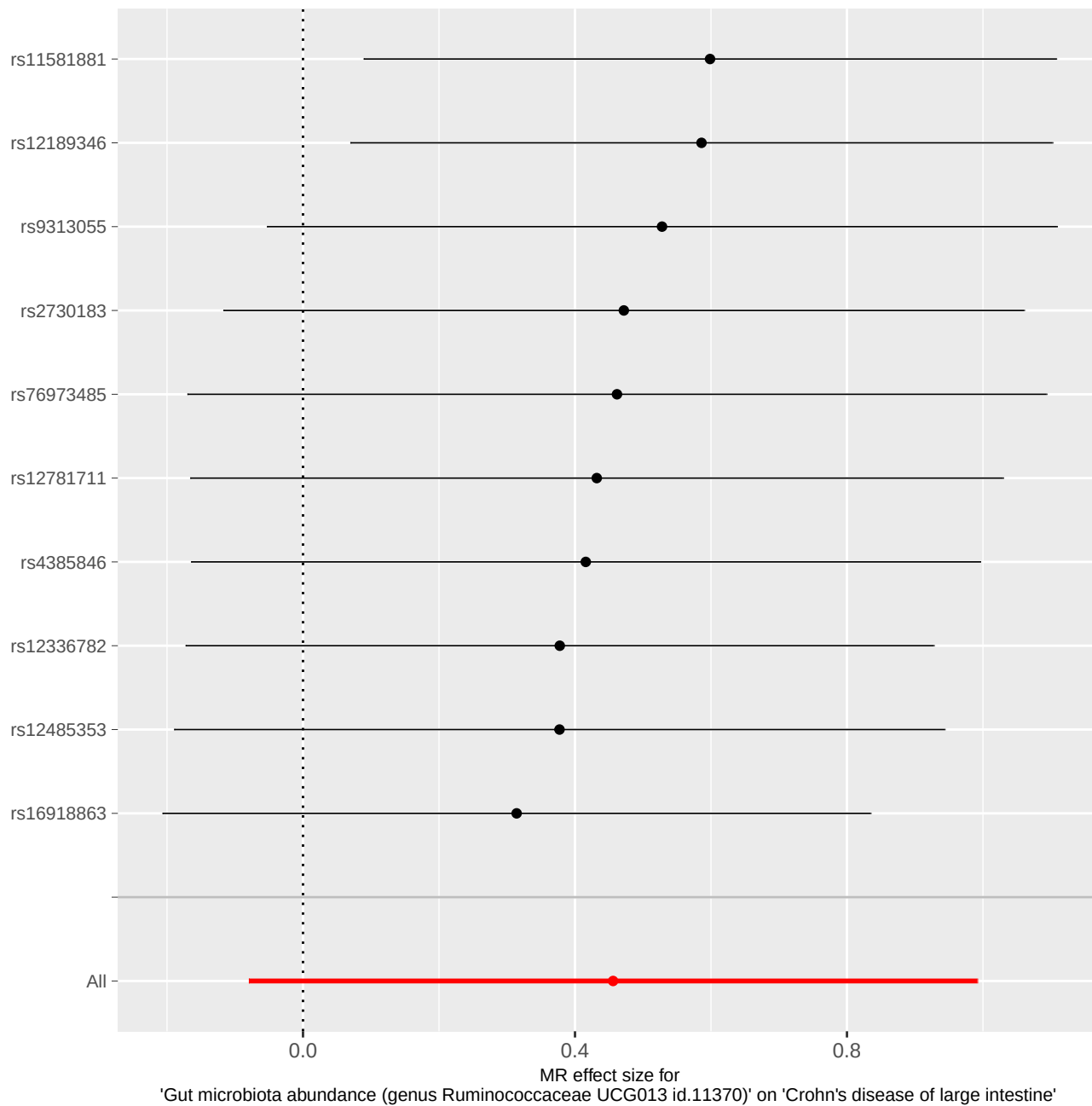


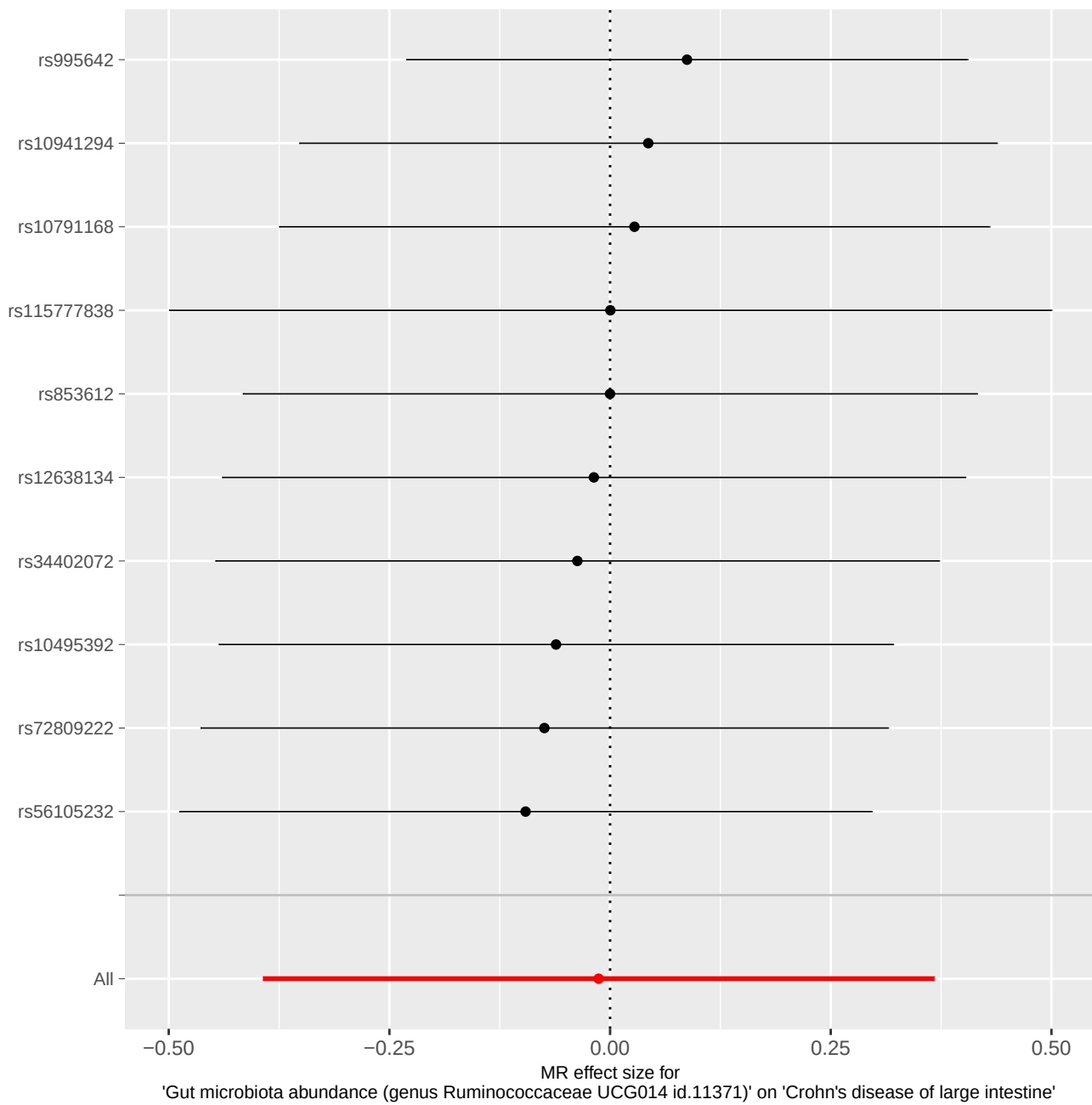
Batch 131 : Gut microbiota abundance (genus Ruminococcaceae UCG009 id.11366) on Crohn's disease of large intestine

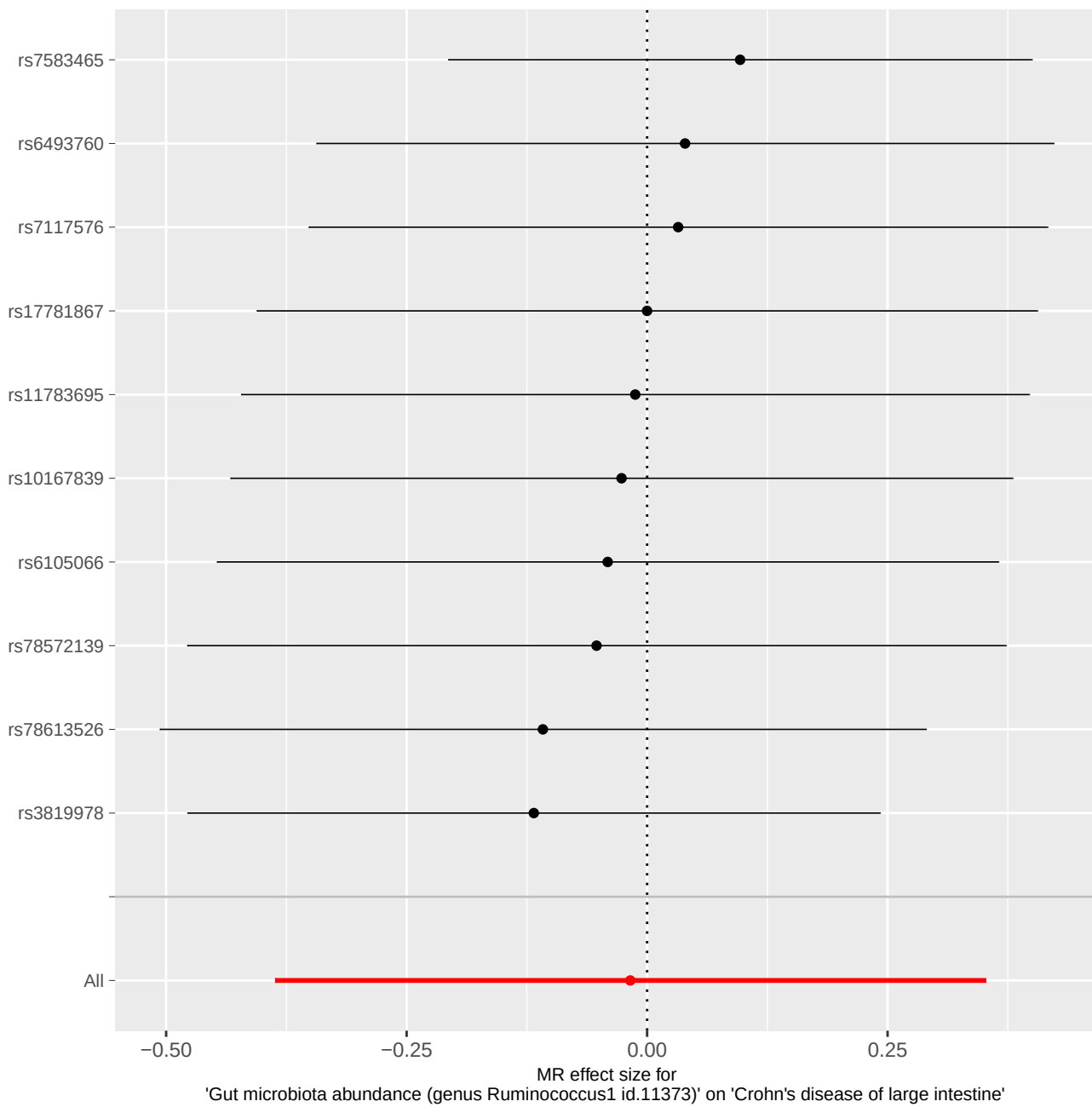




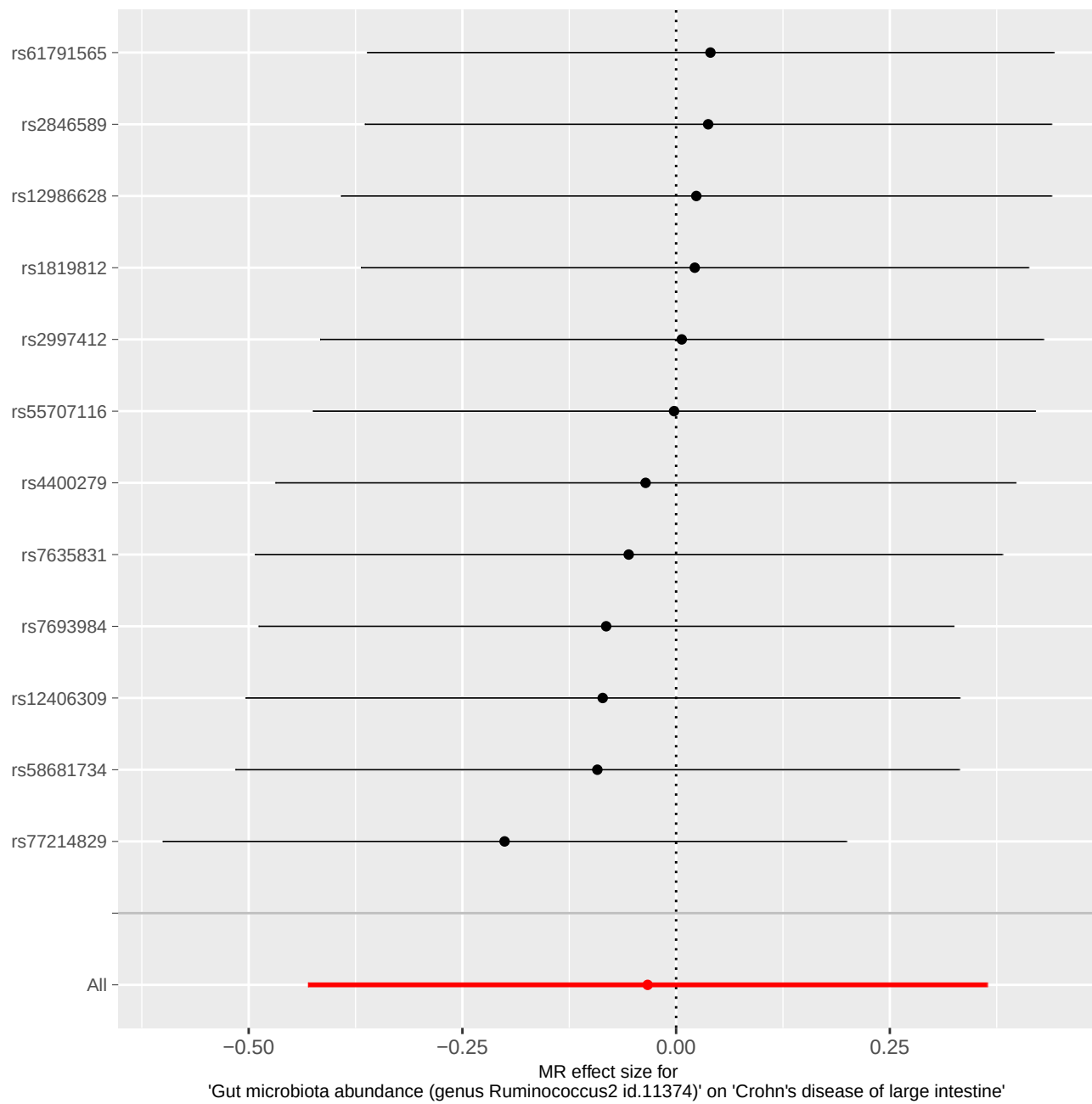


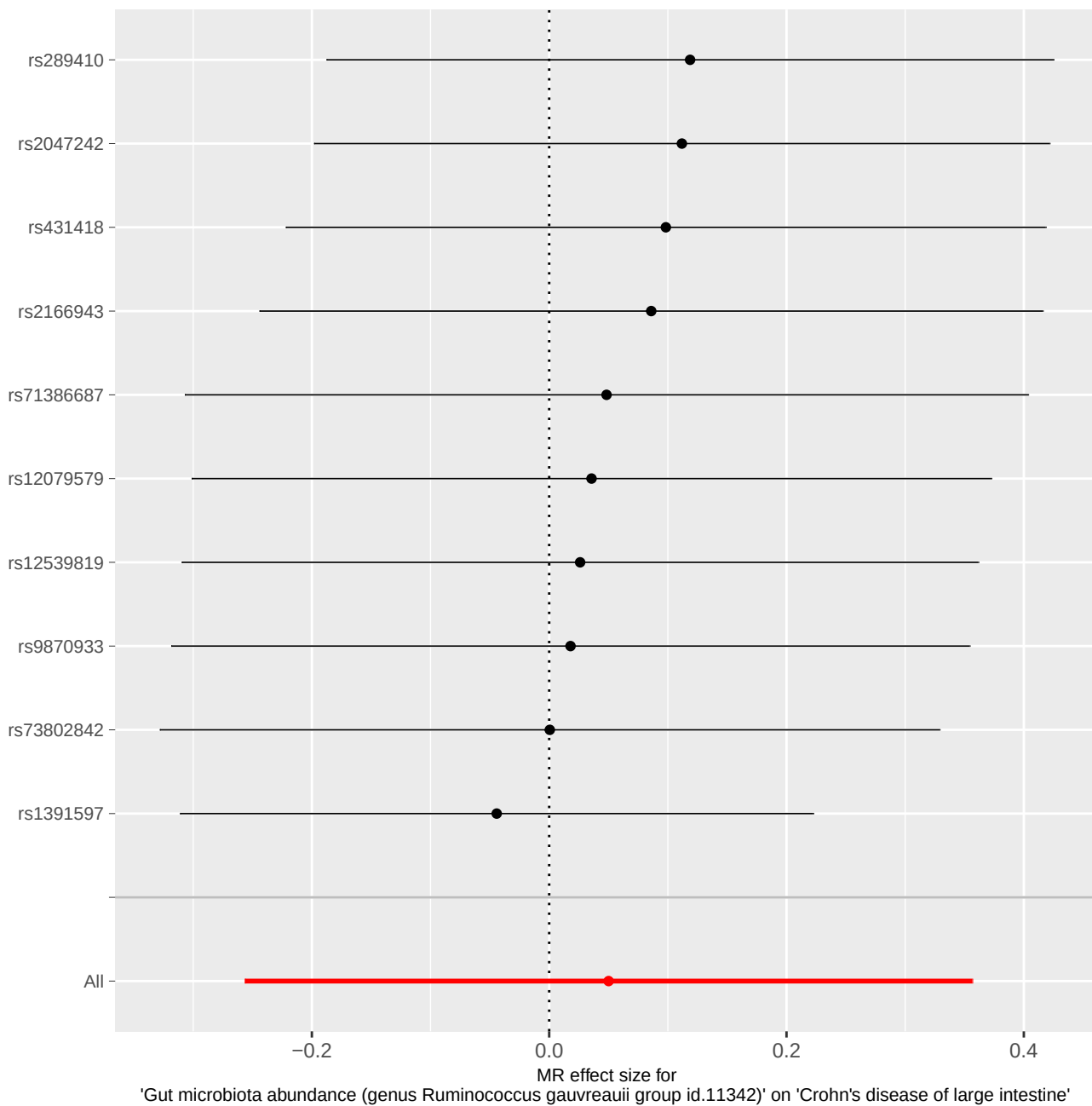


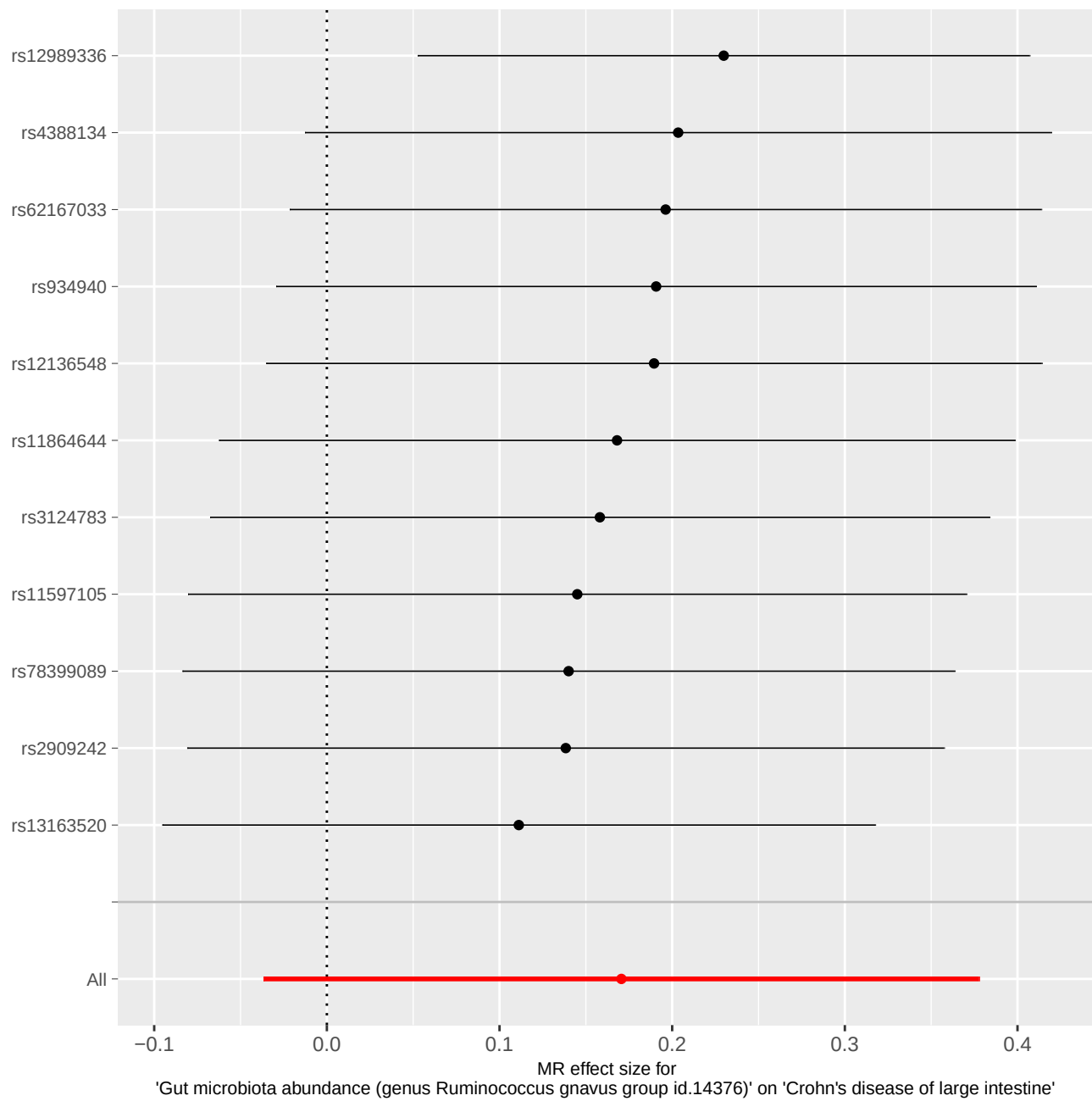


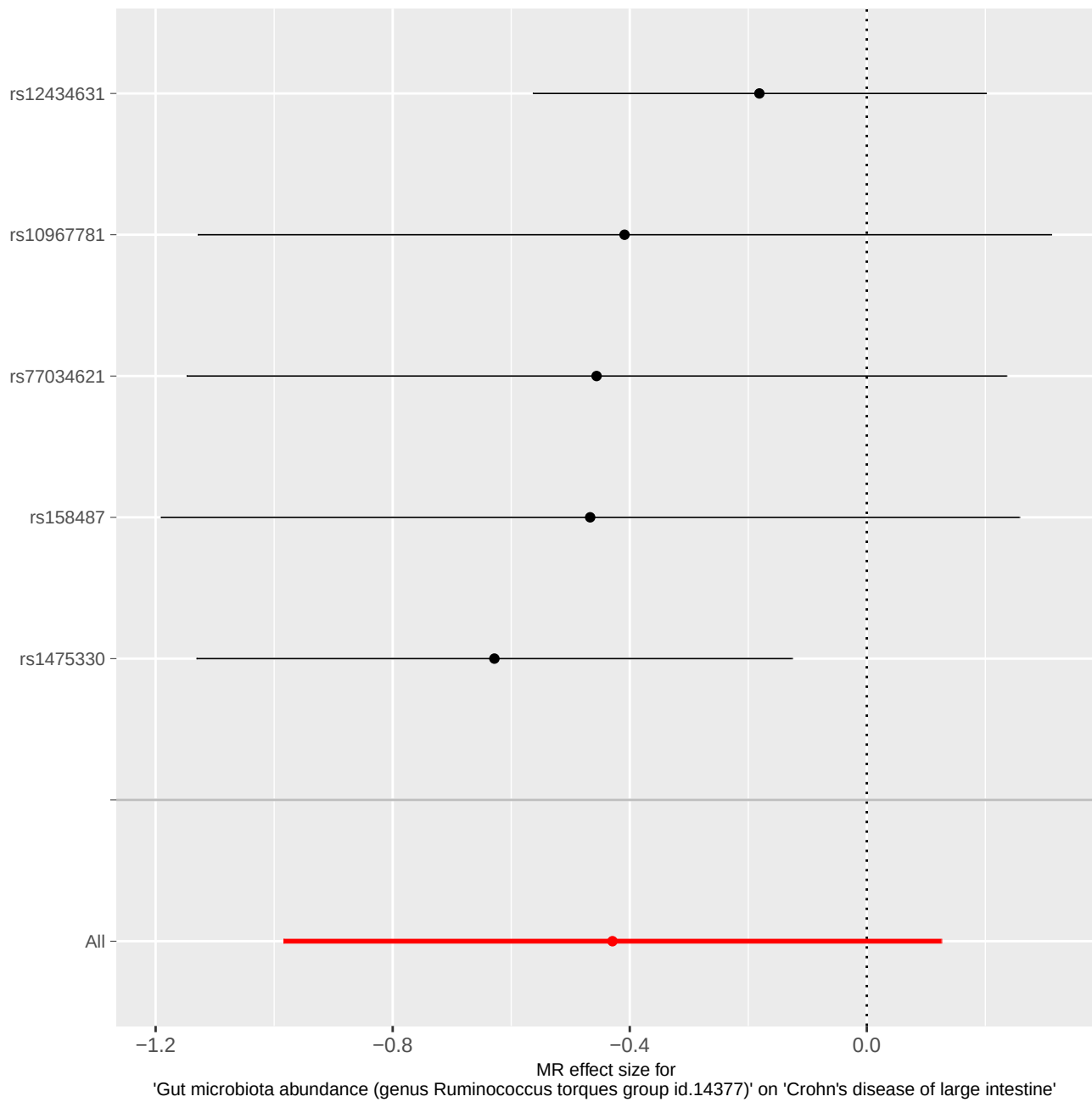


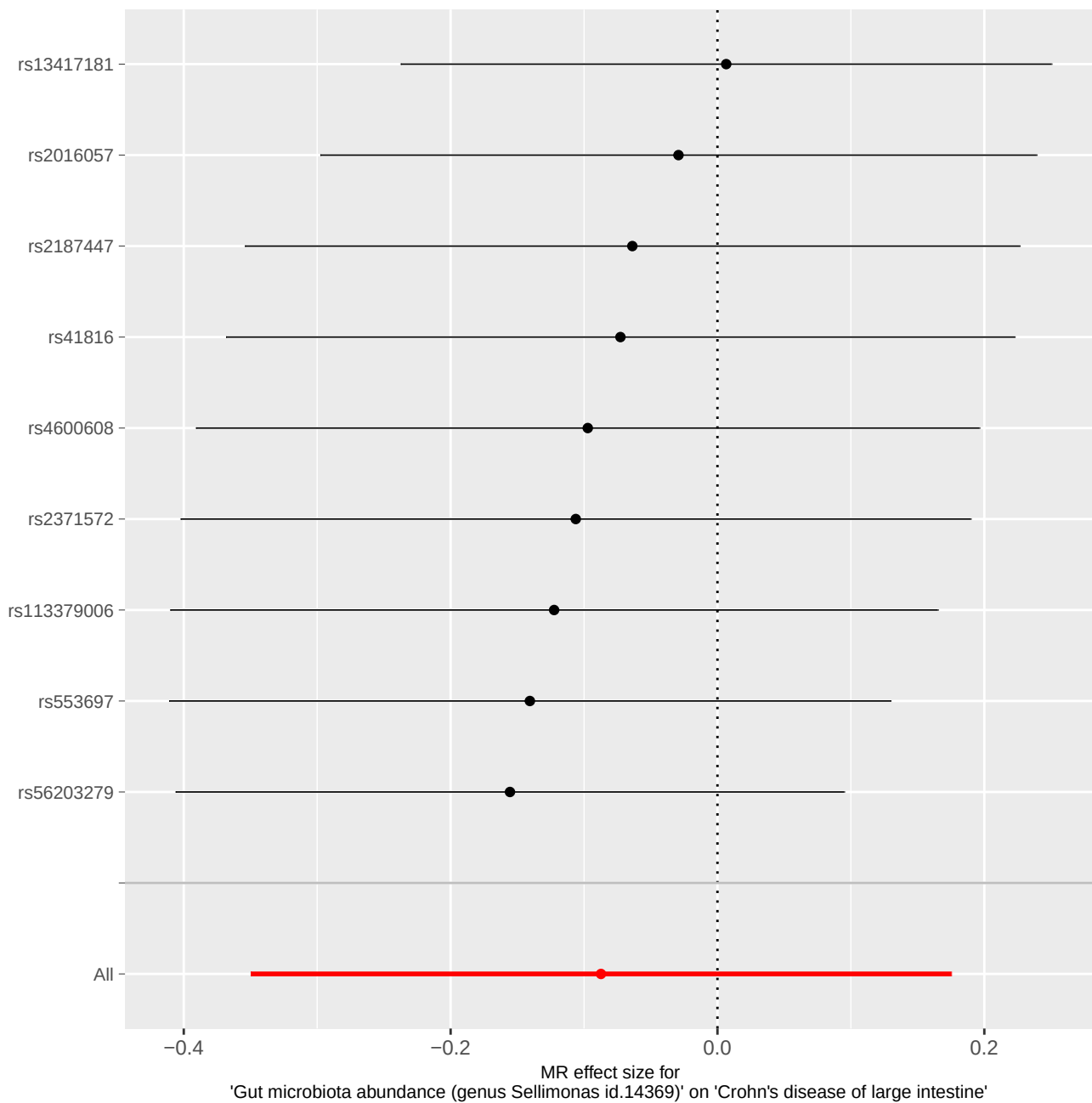
Batch 137 : Gut microbiota abundance (genus Ruminococcus2 id.11374) on Crohn's disease of large intestine

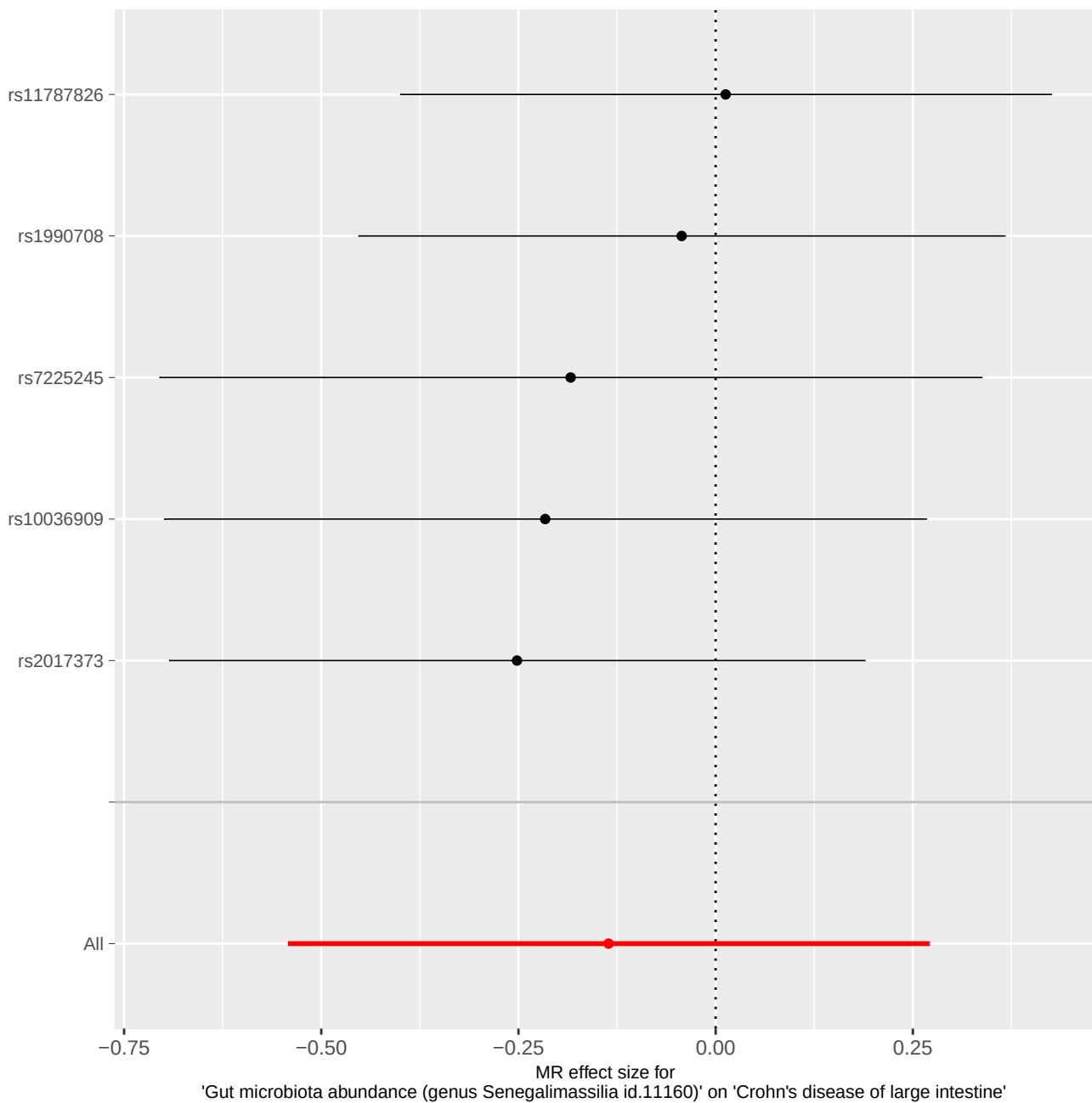




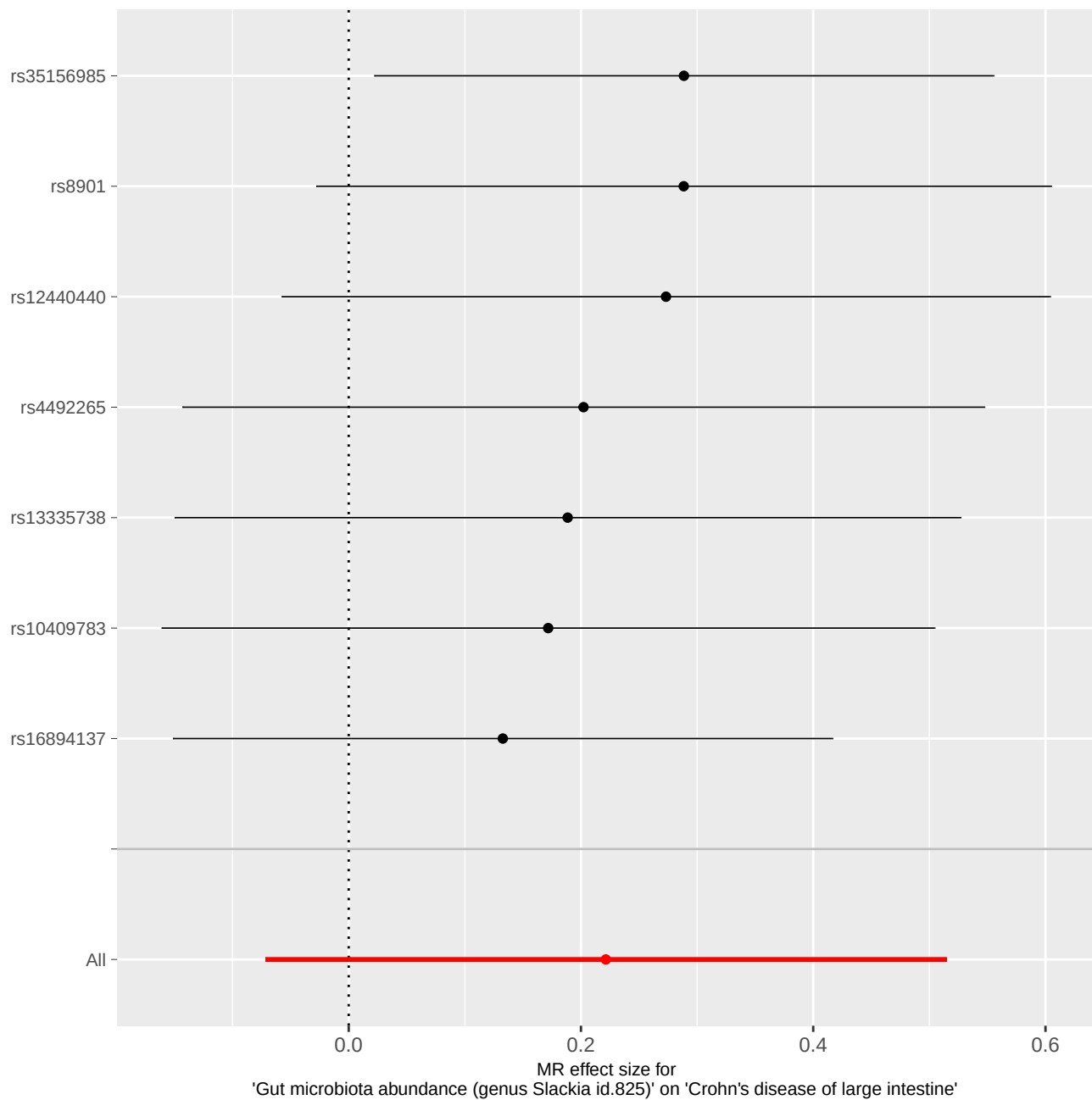


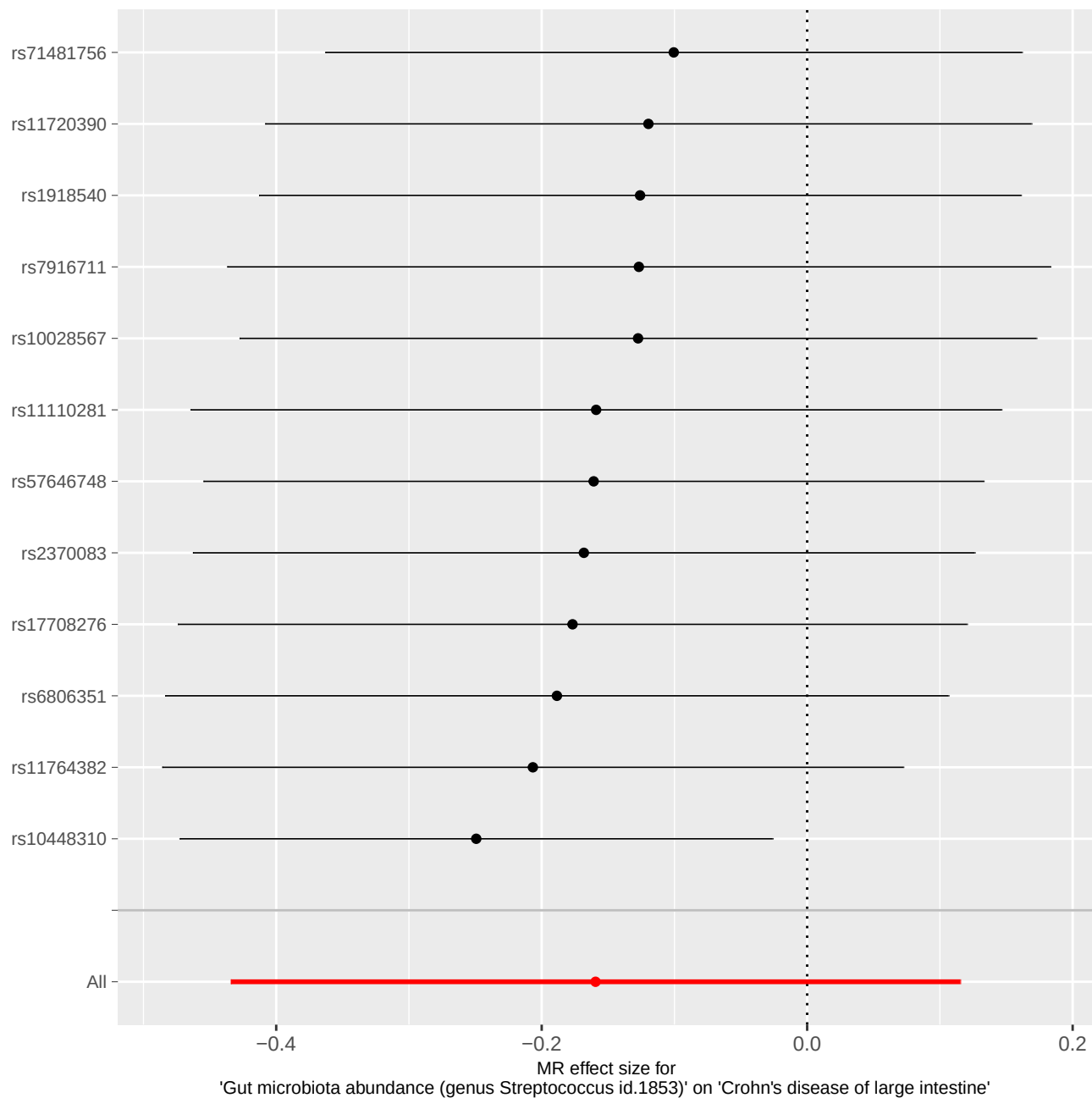


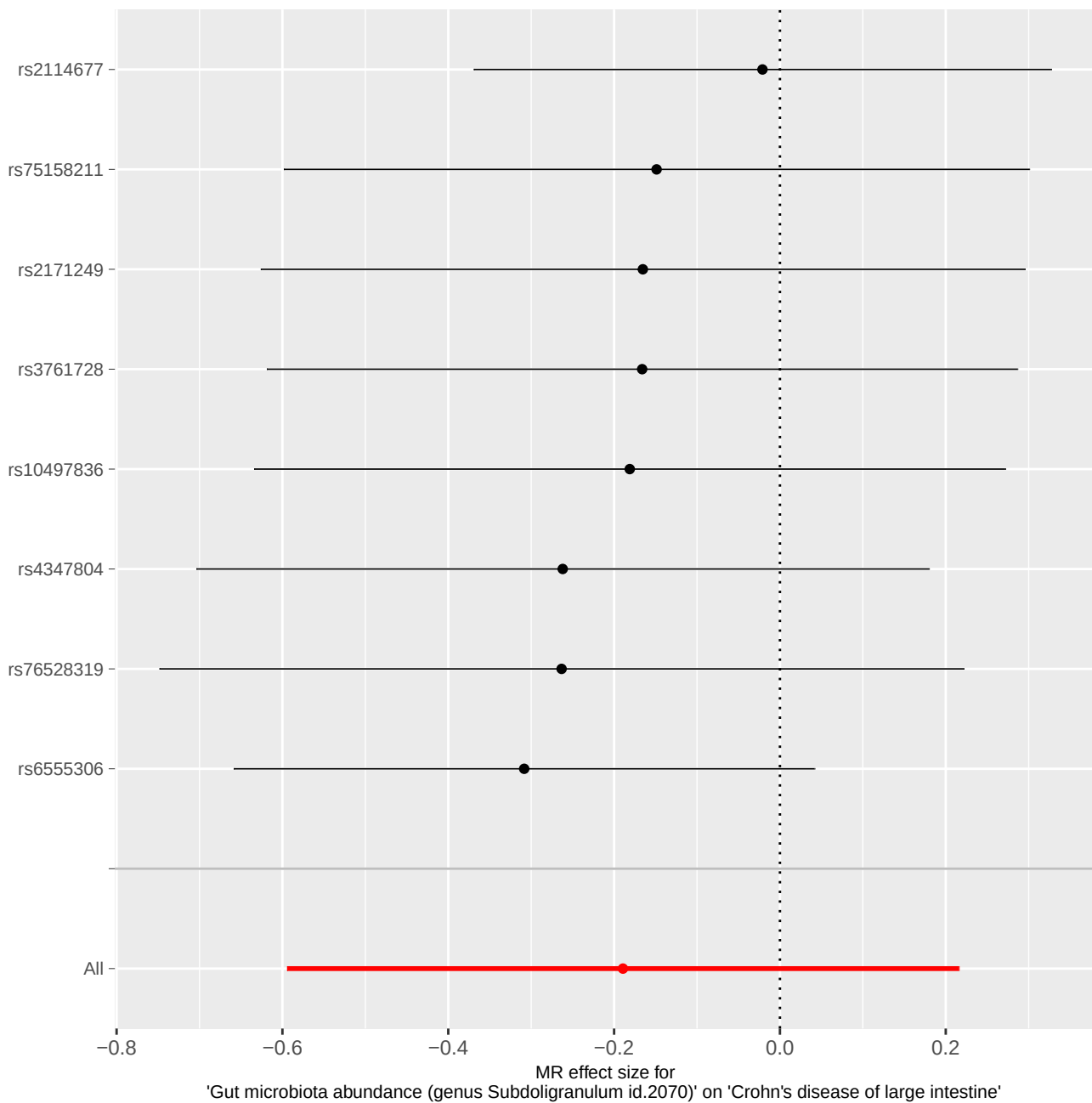


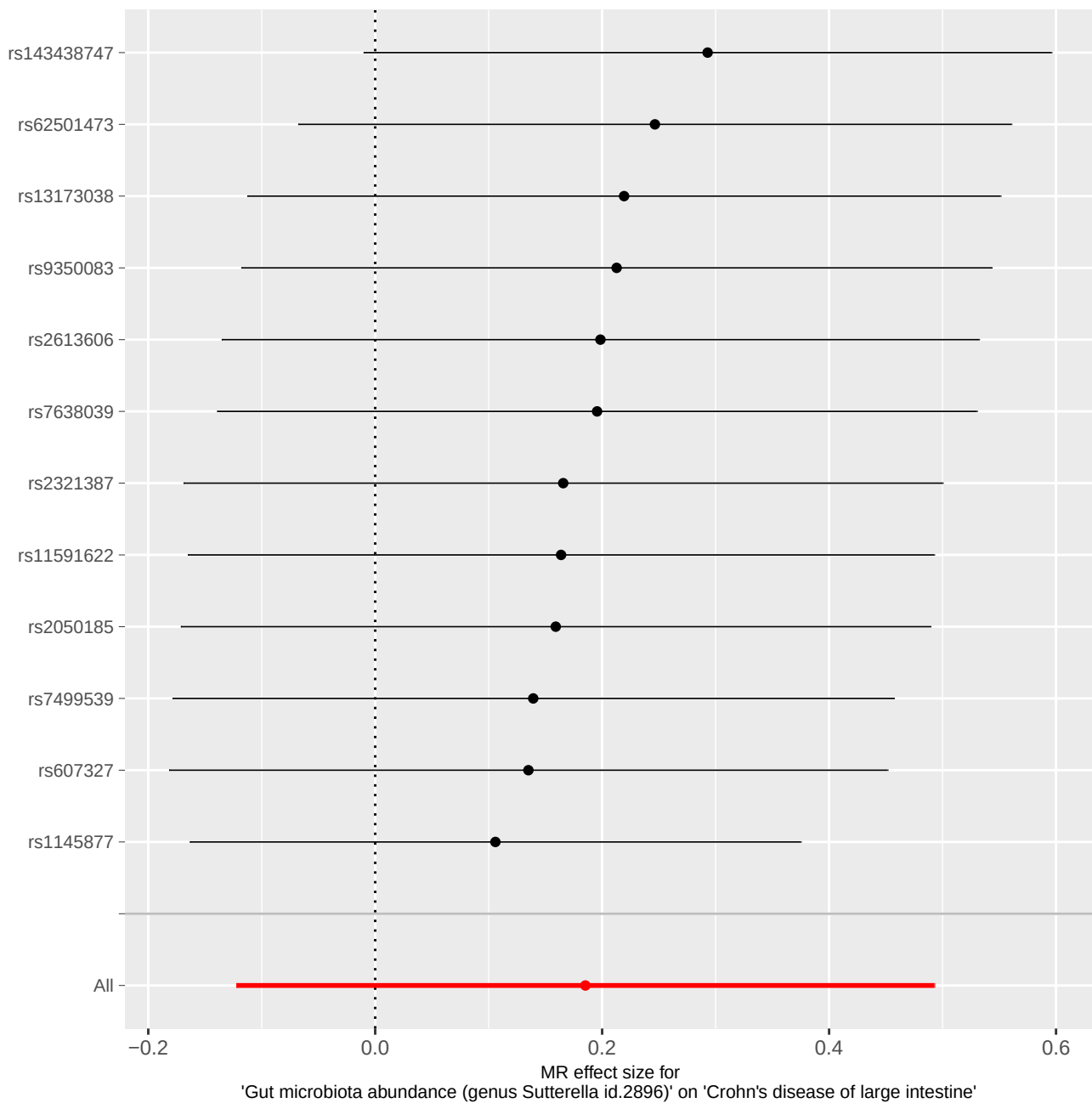


Batch 143 : Gut microbiota abundance (genus Slackia id.825) on Crohn's disease of large intestine

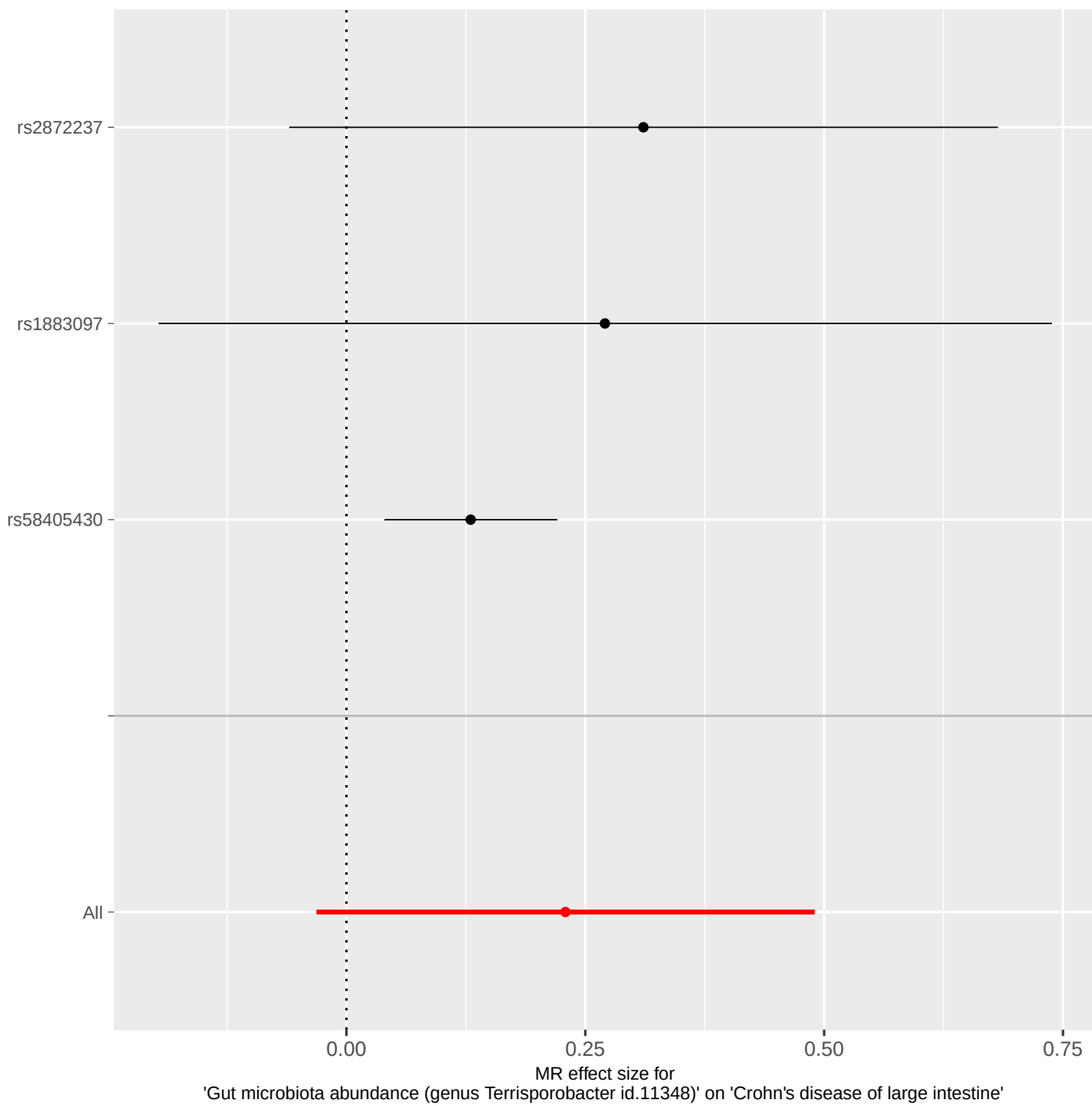


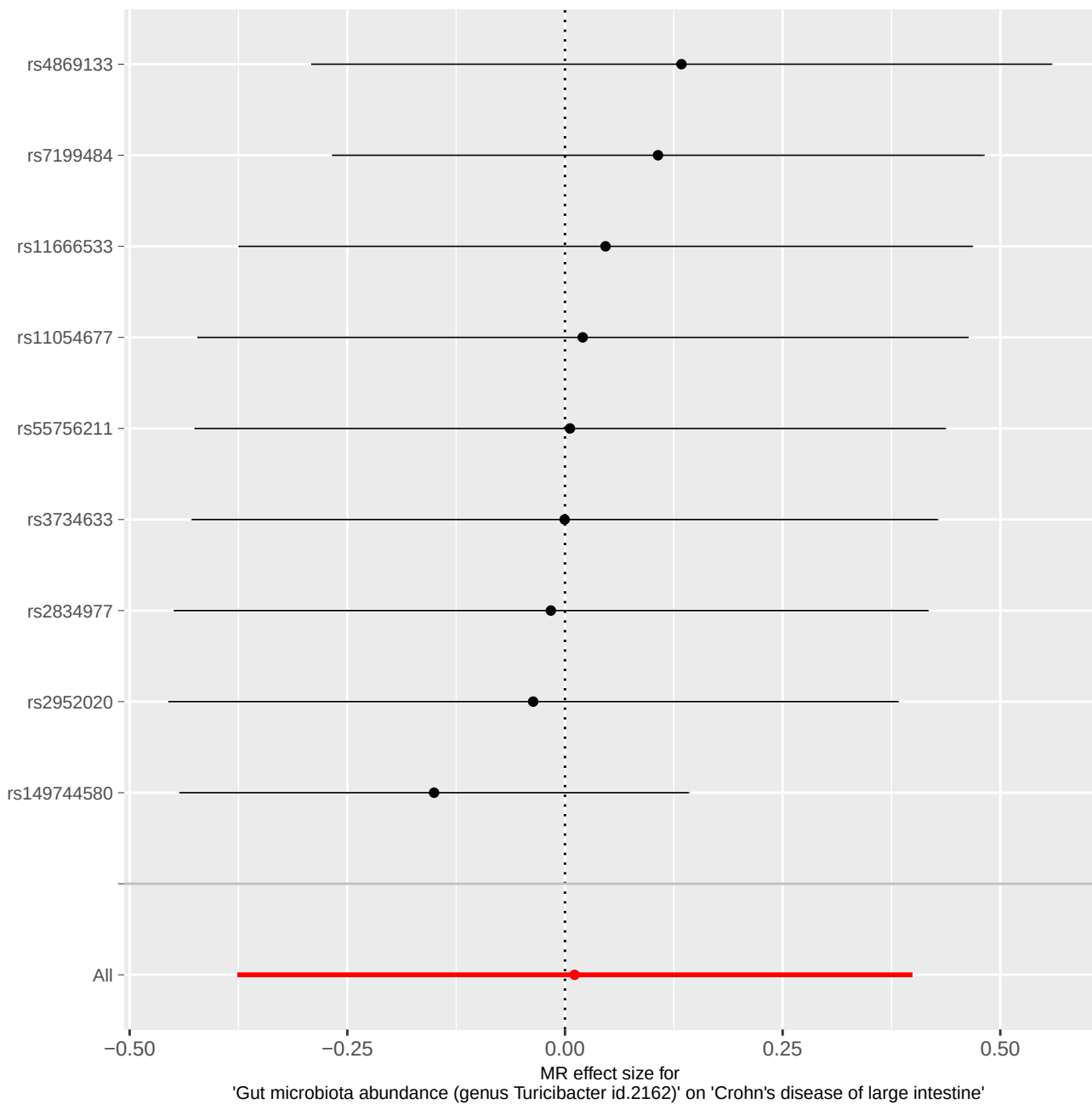


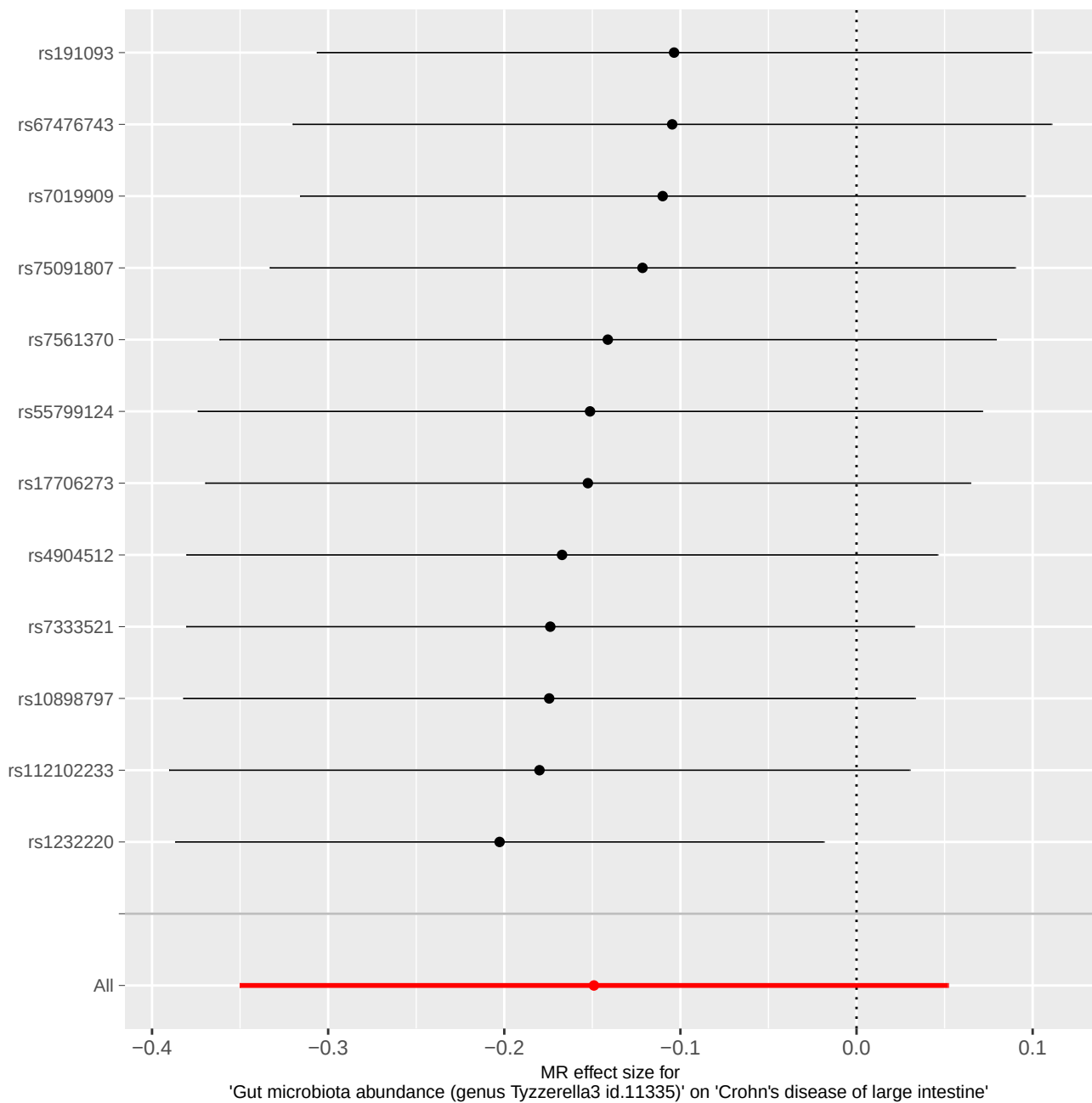


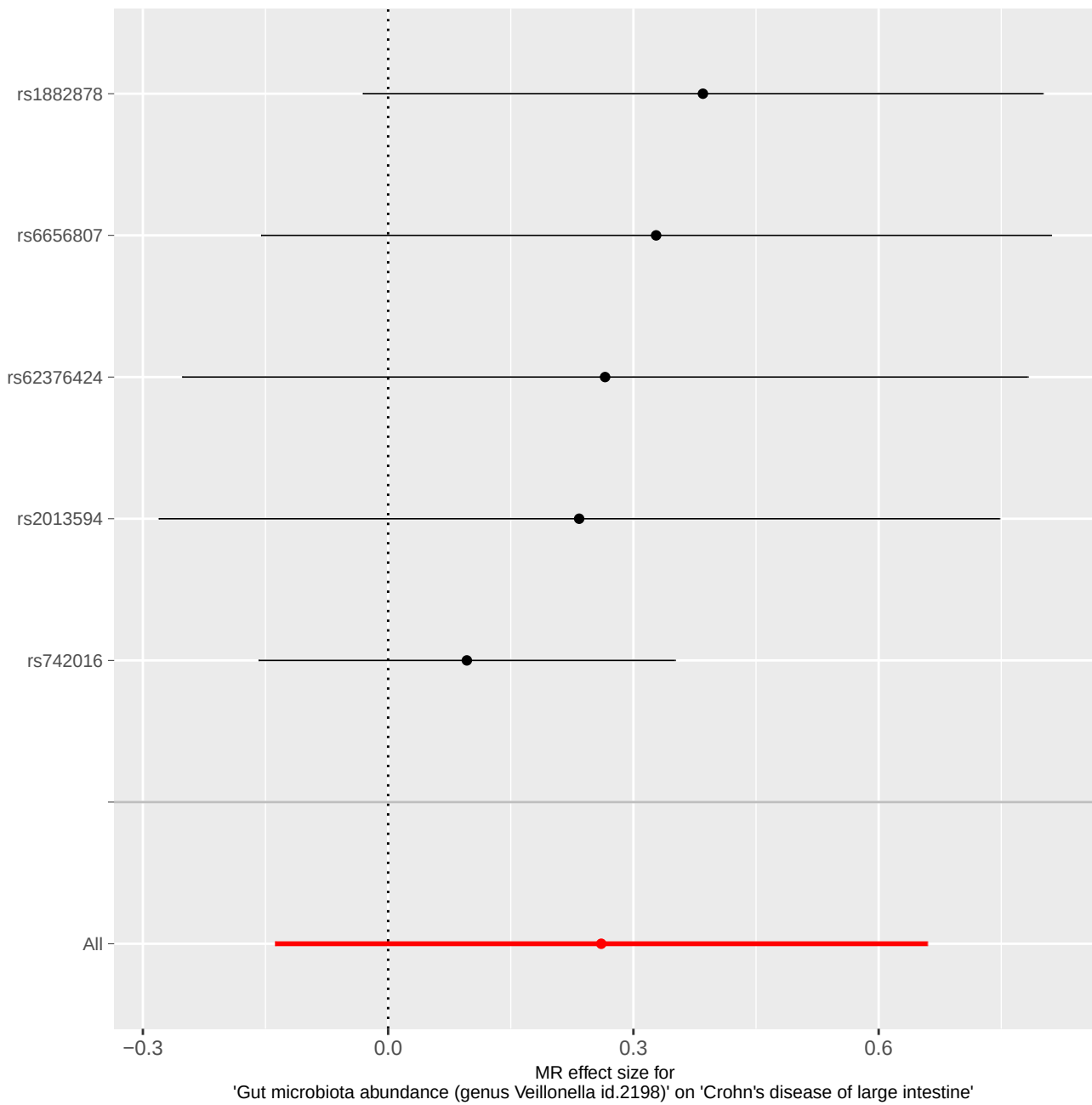


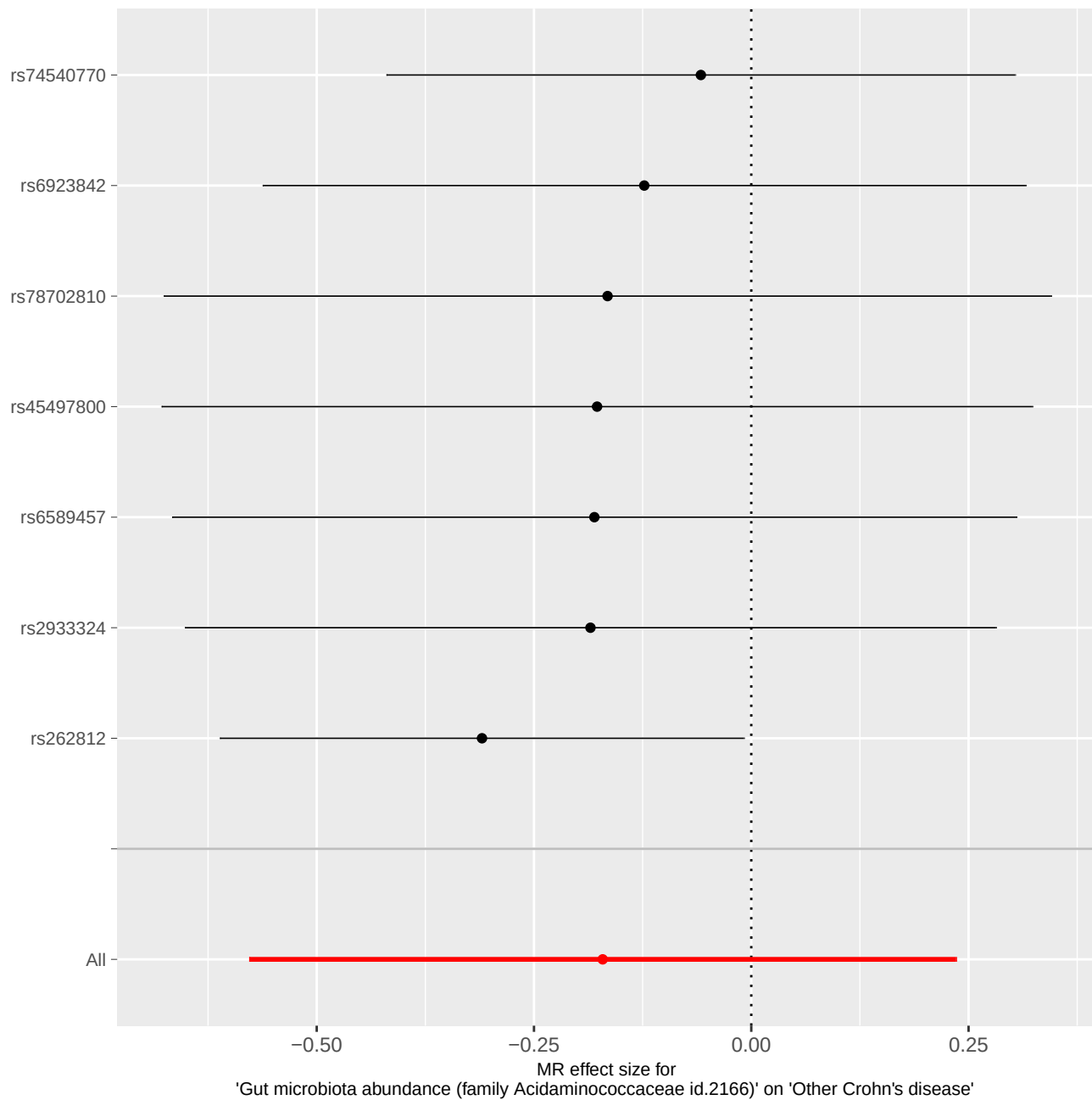
Batch 147 : Gut microbiota abundance (genus Terrisporobacter id.11348) on Crohn's disease of large intestine

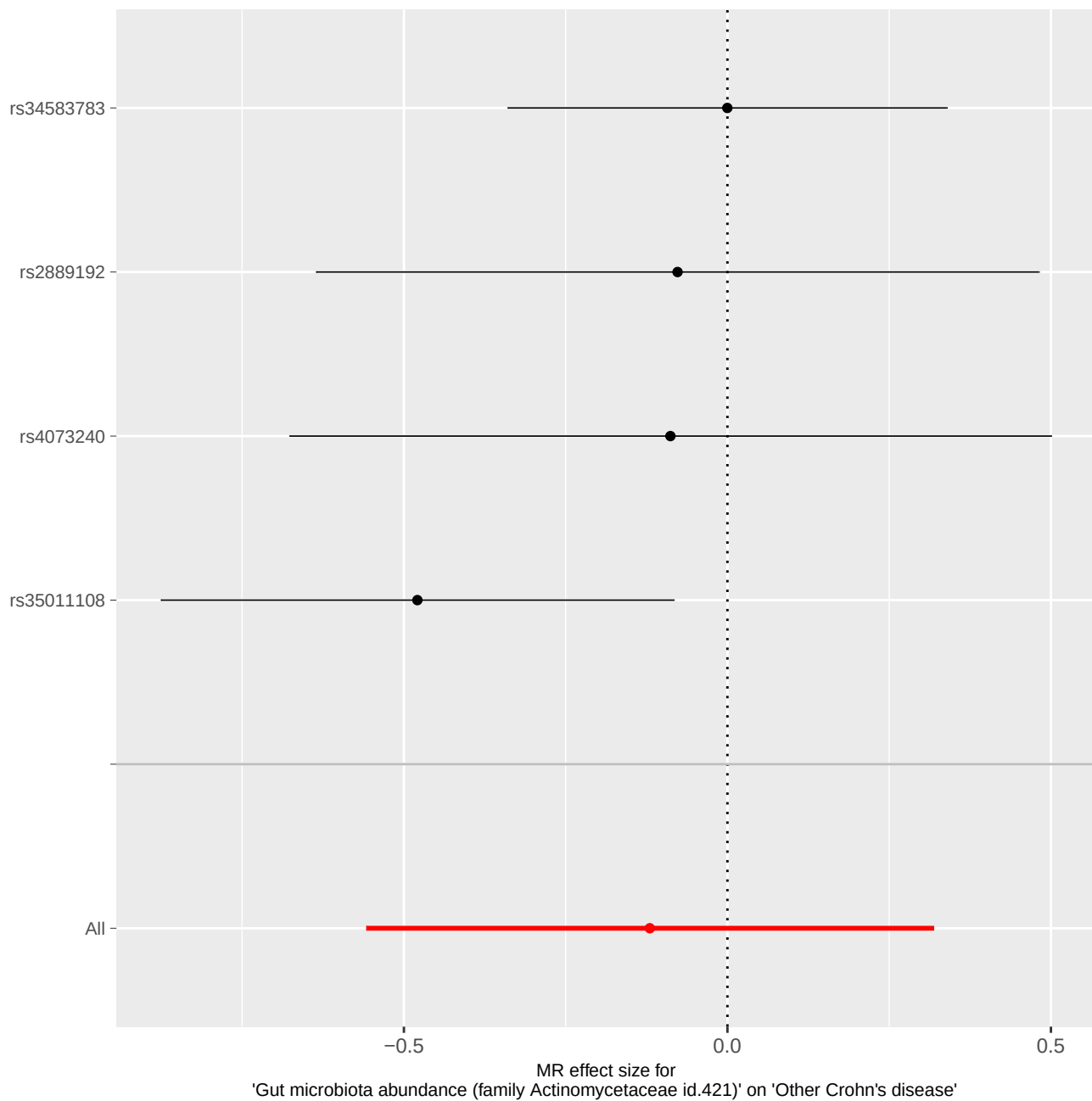


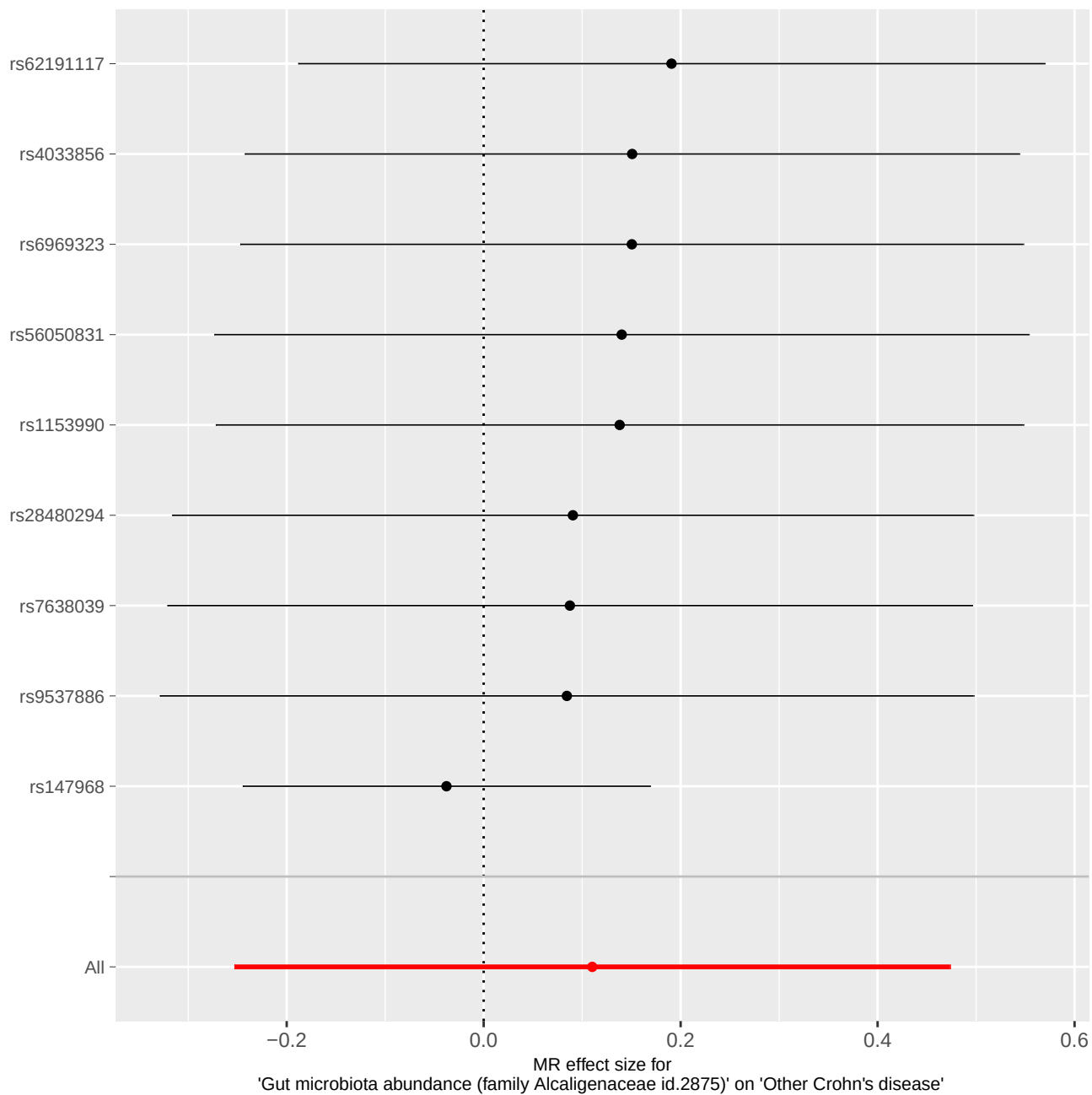




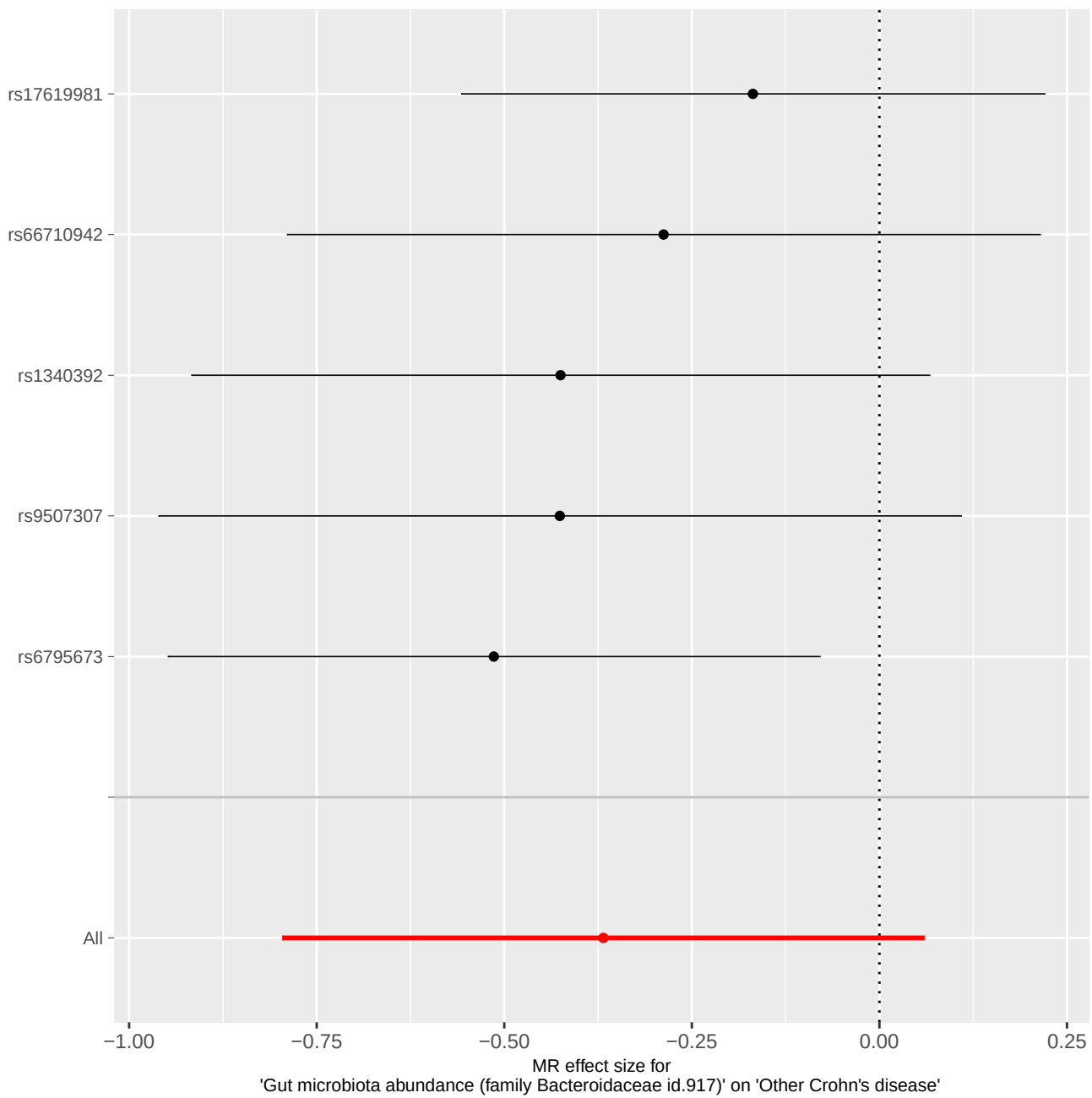


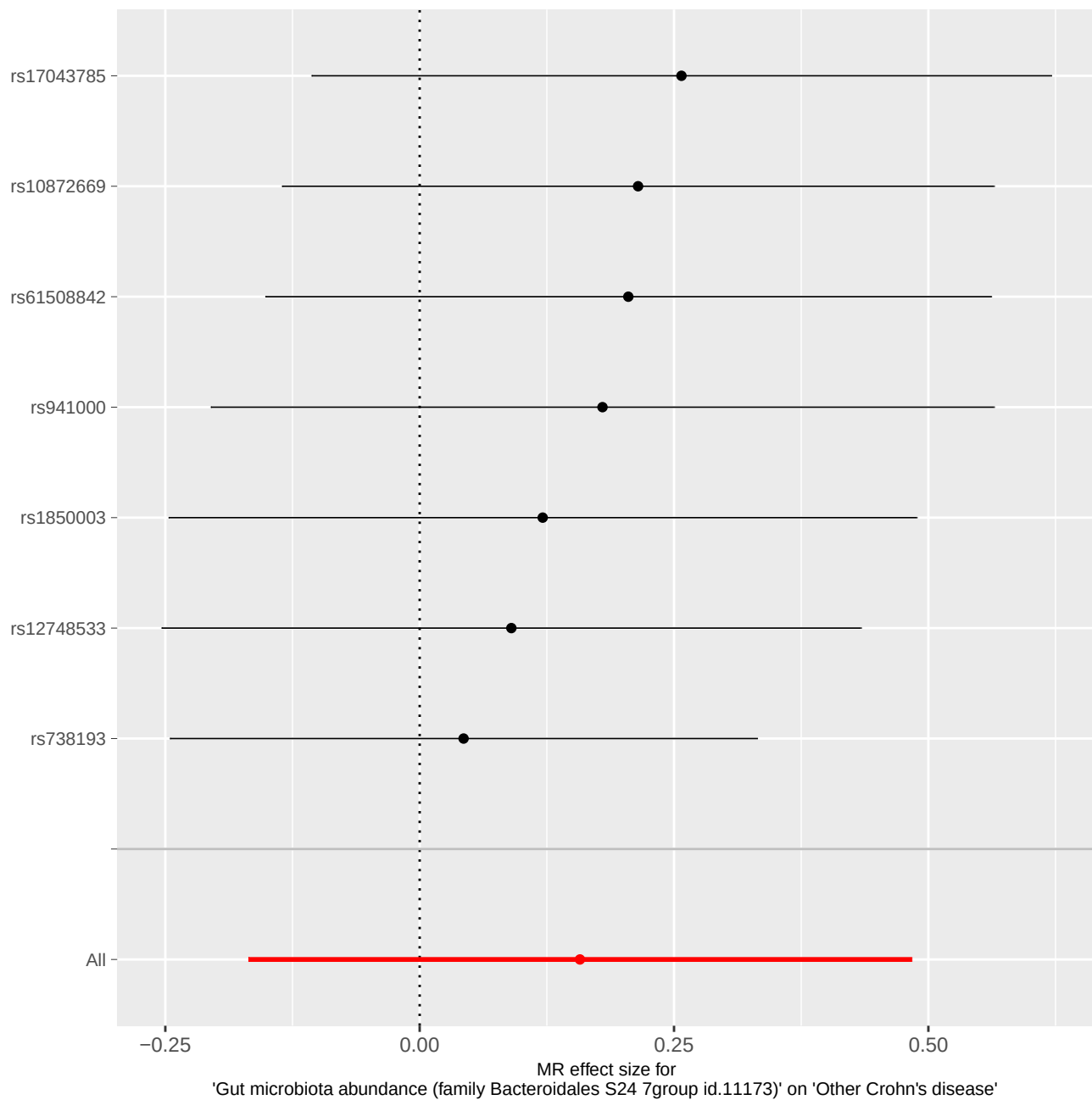


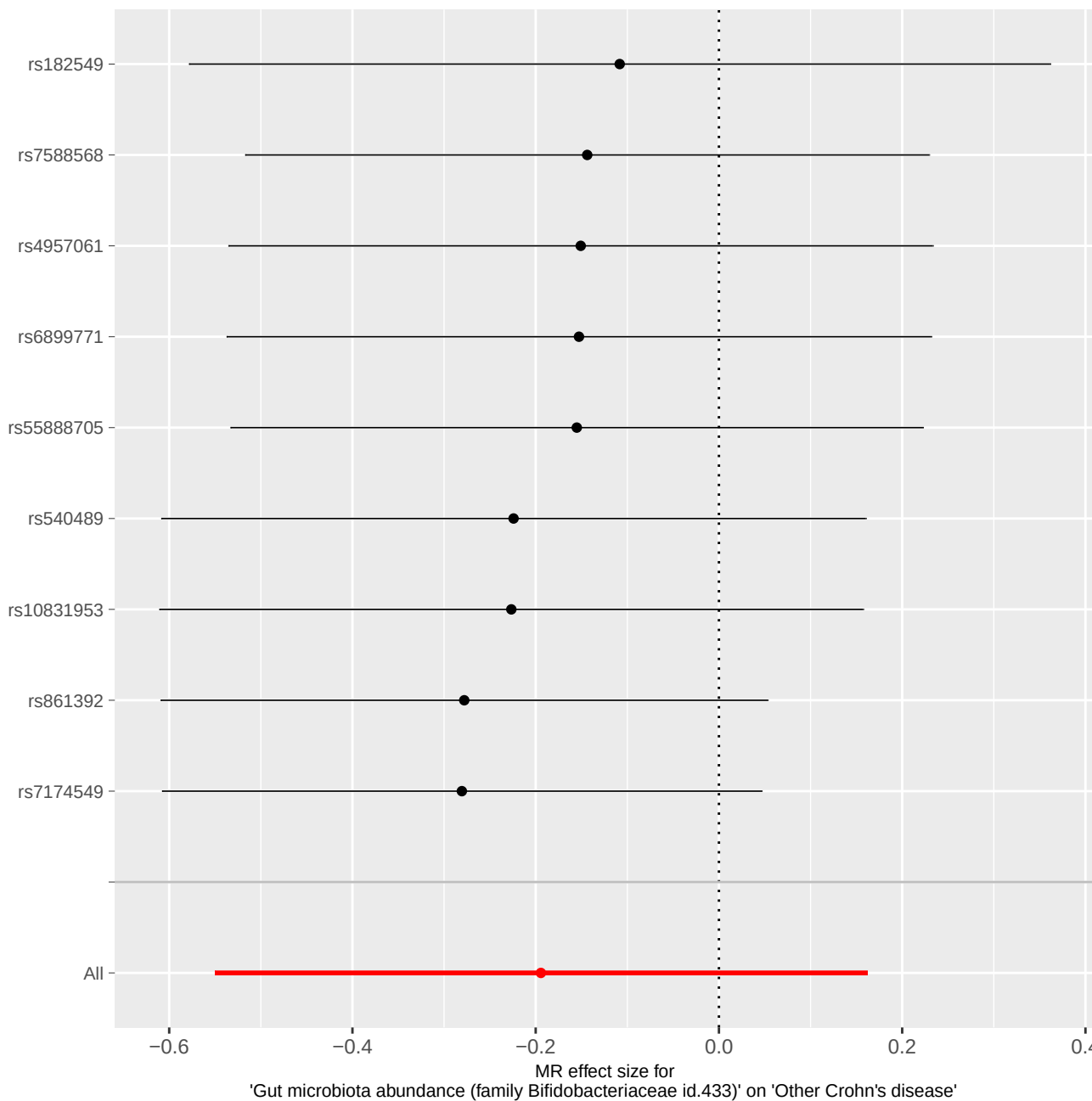


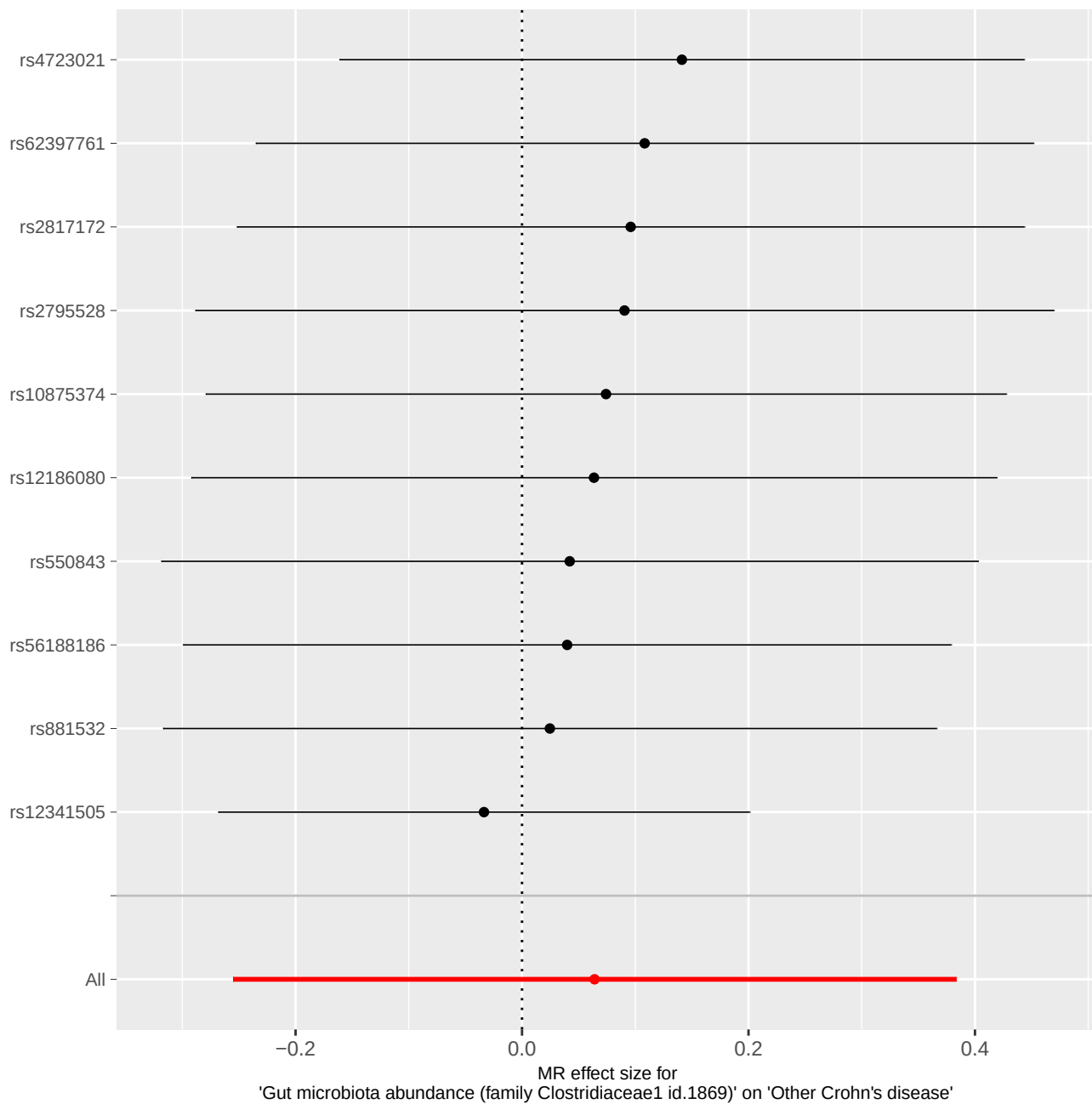


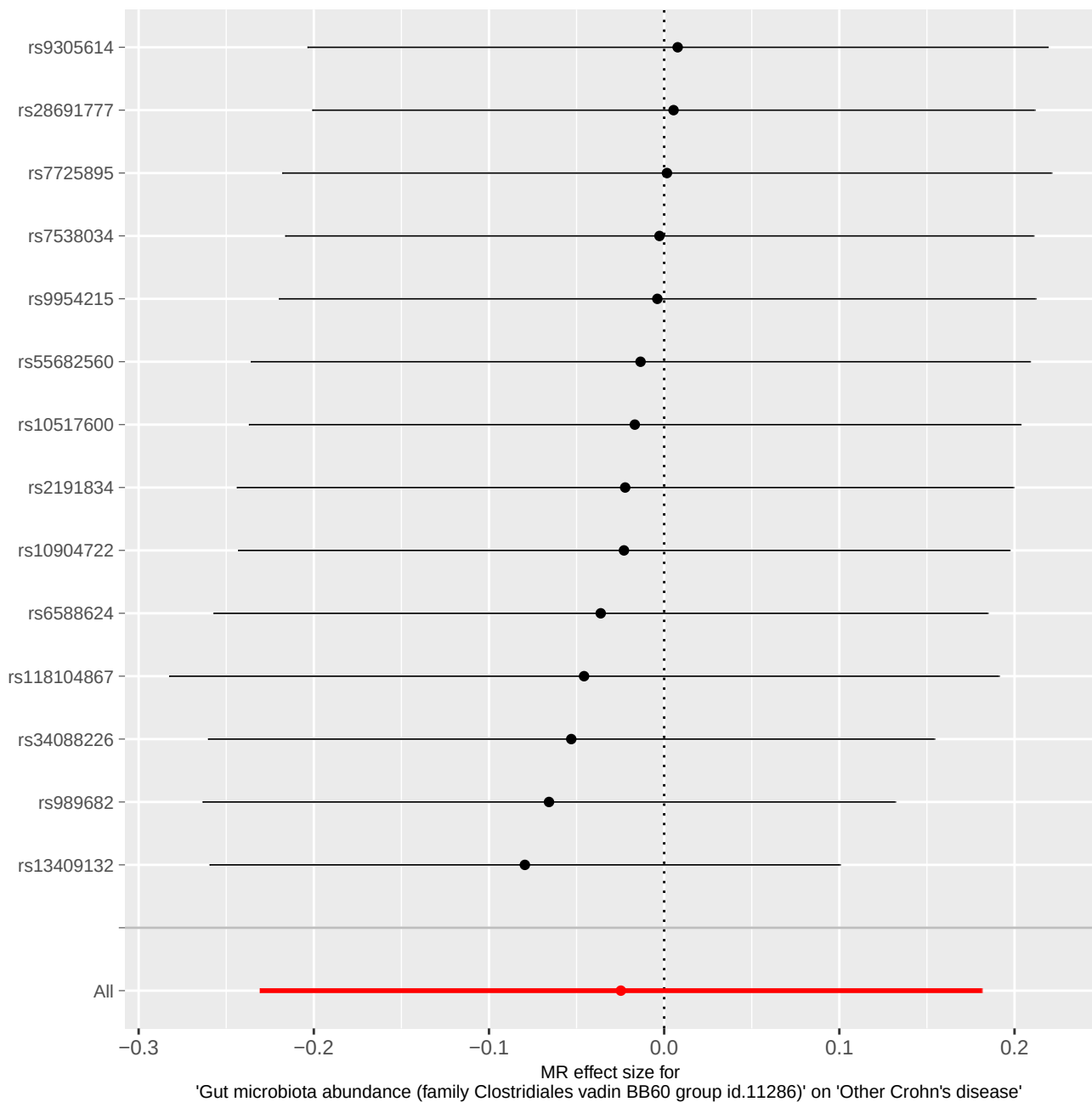
MR effect size for
'Gut microbiota abundance (family Alcaligenaceae id.2875)' on 'Other Crohn's disease'



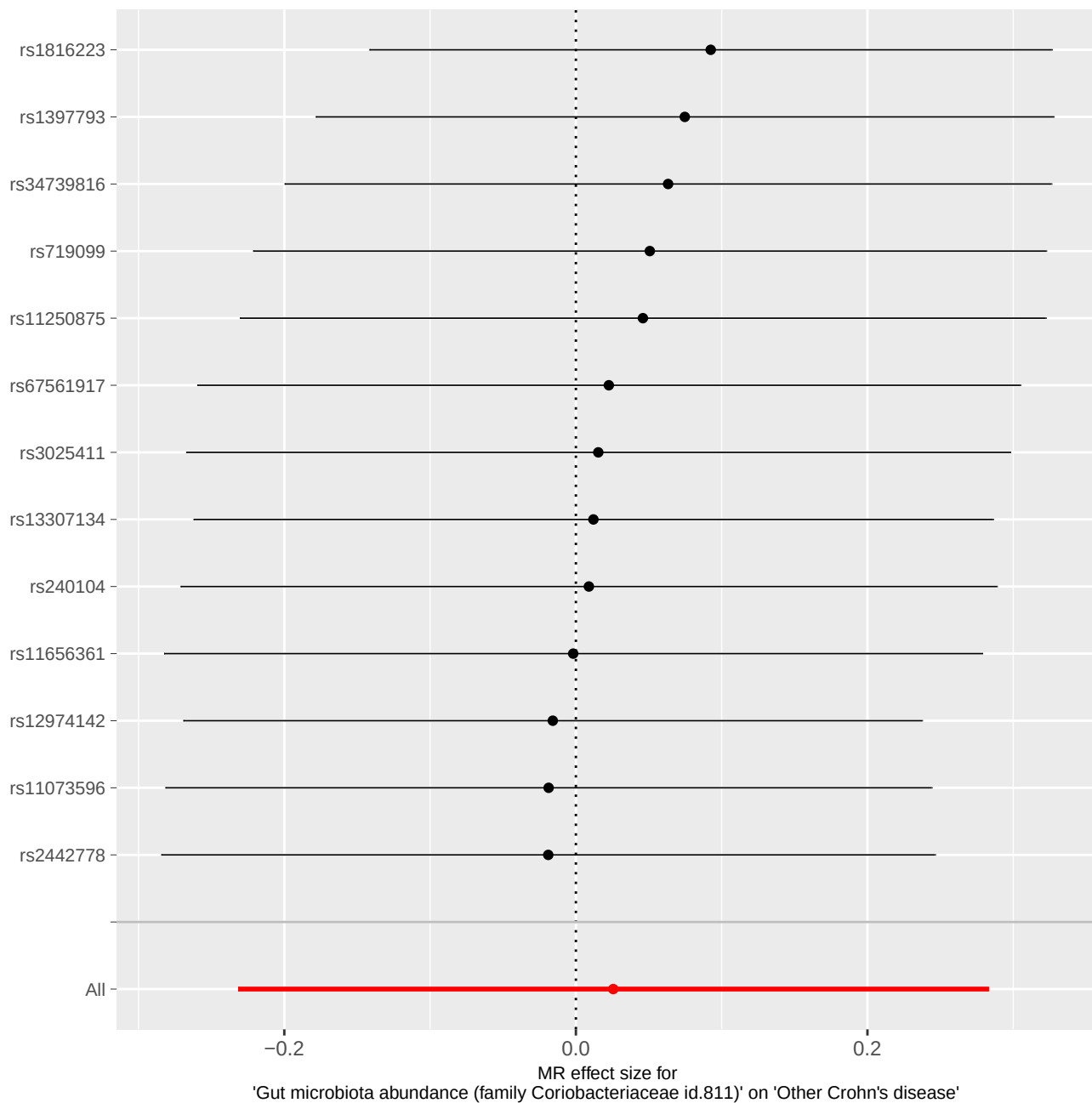


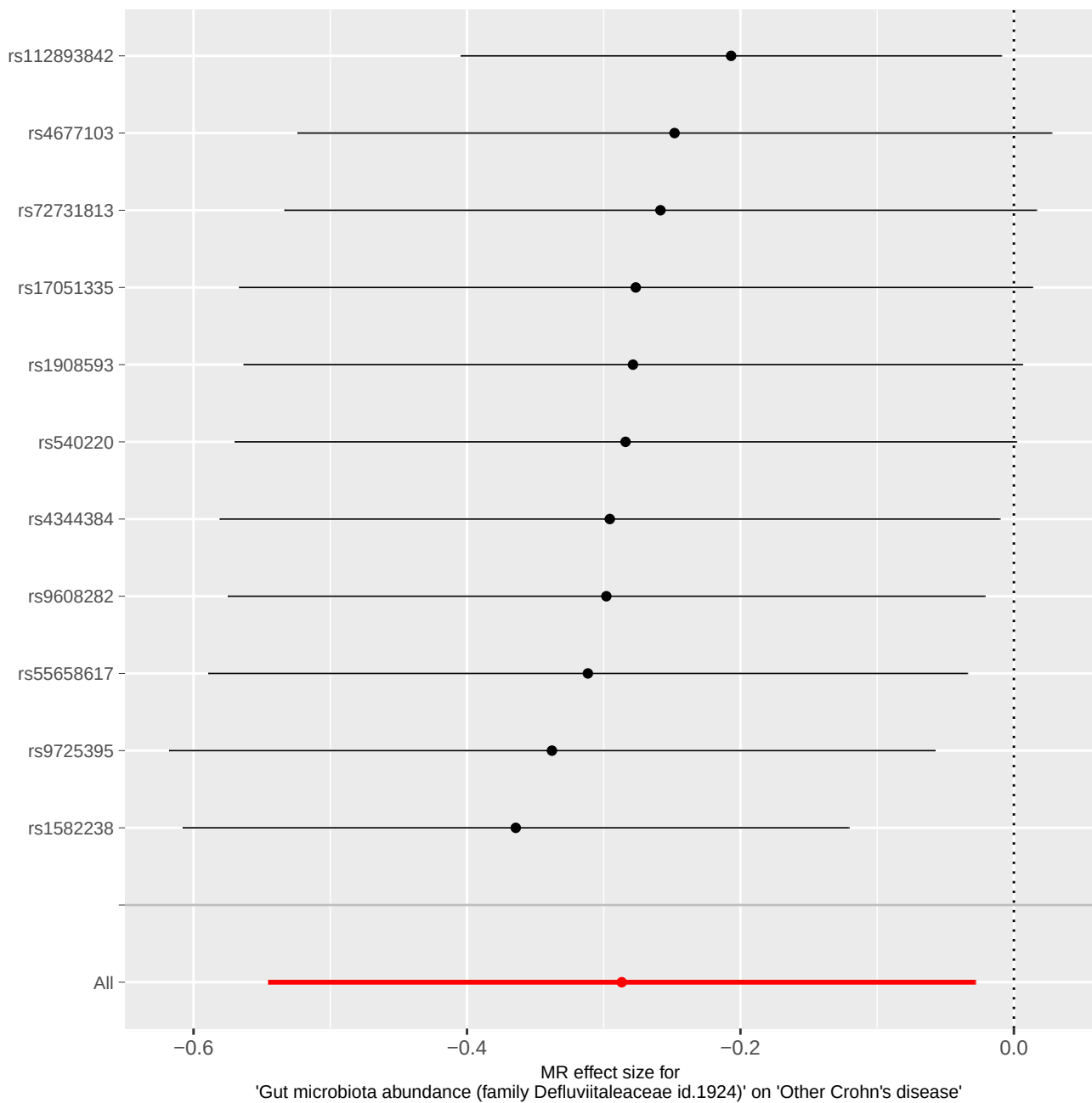


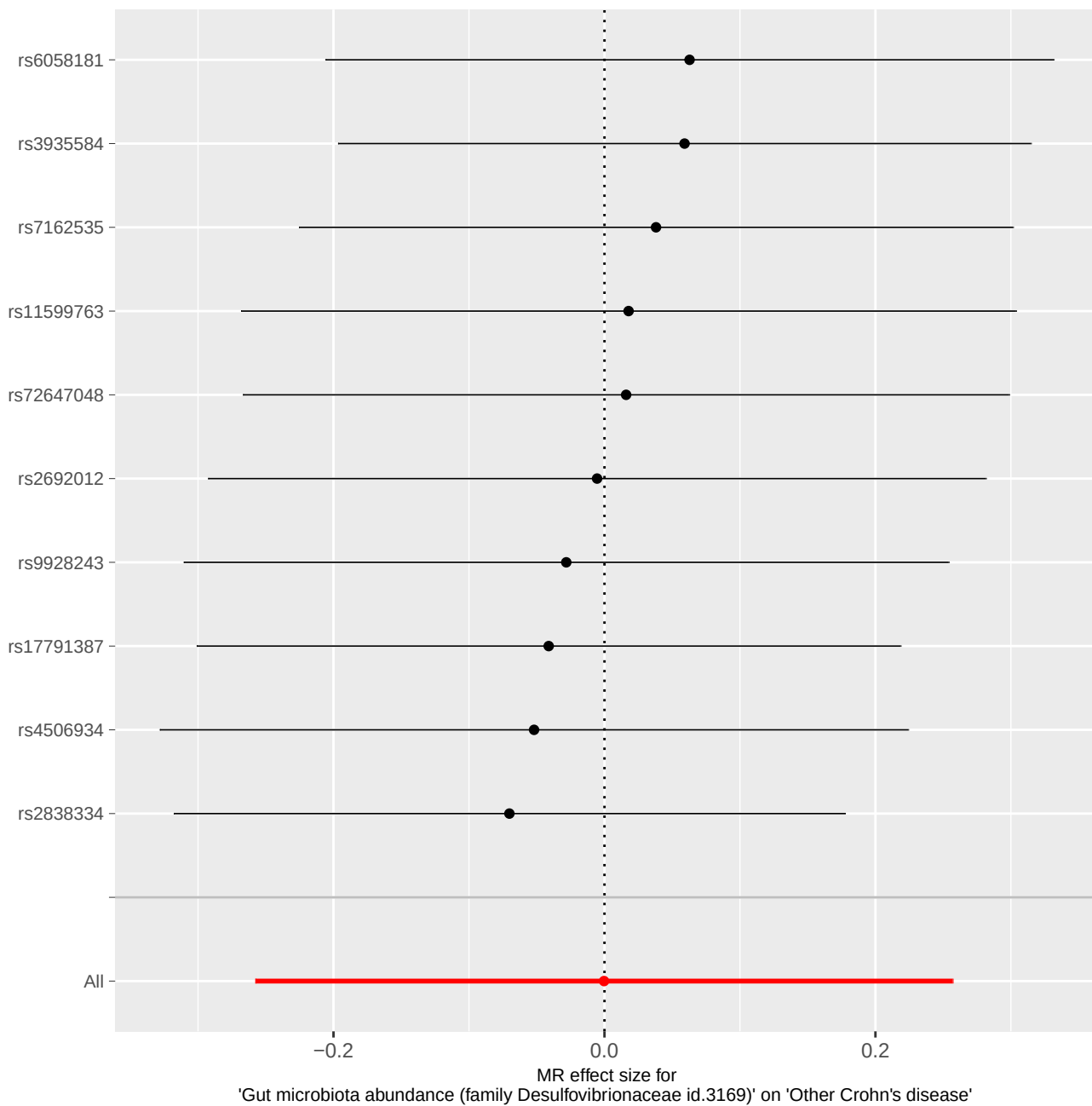


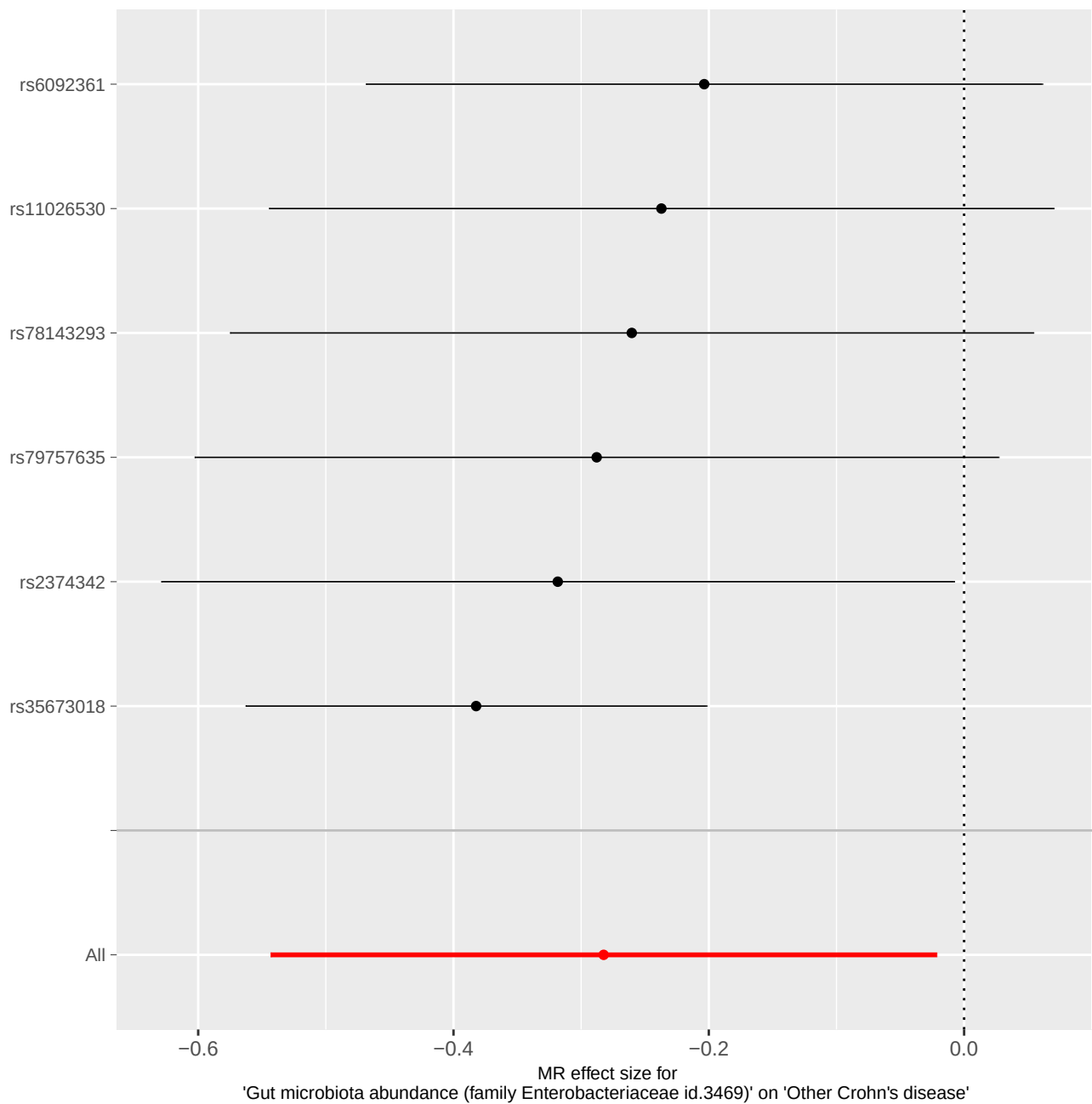


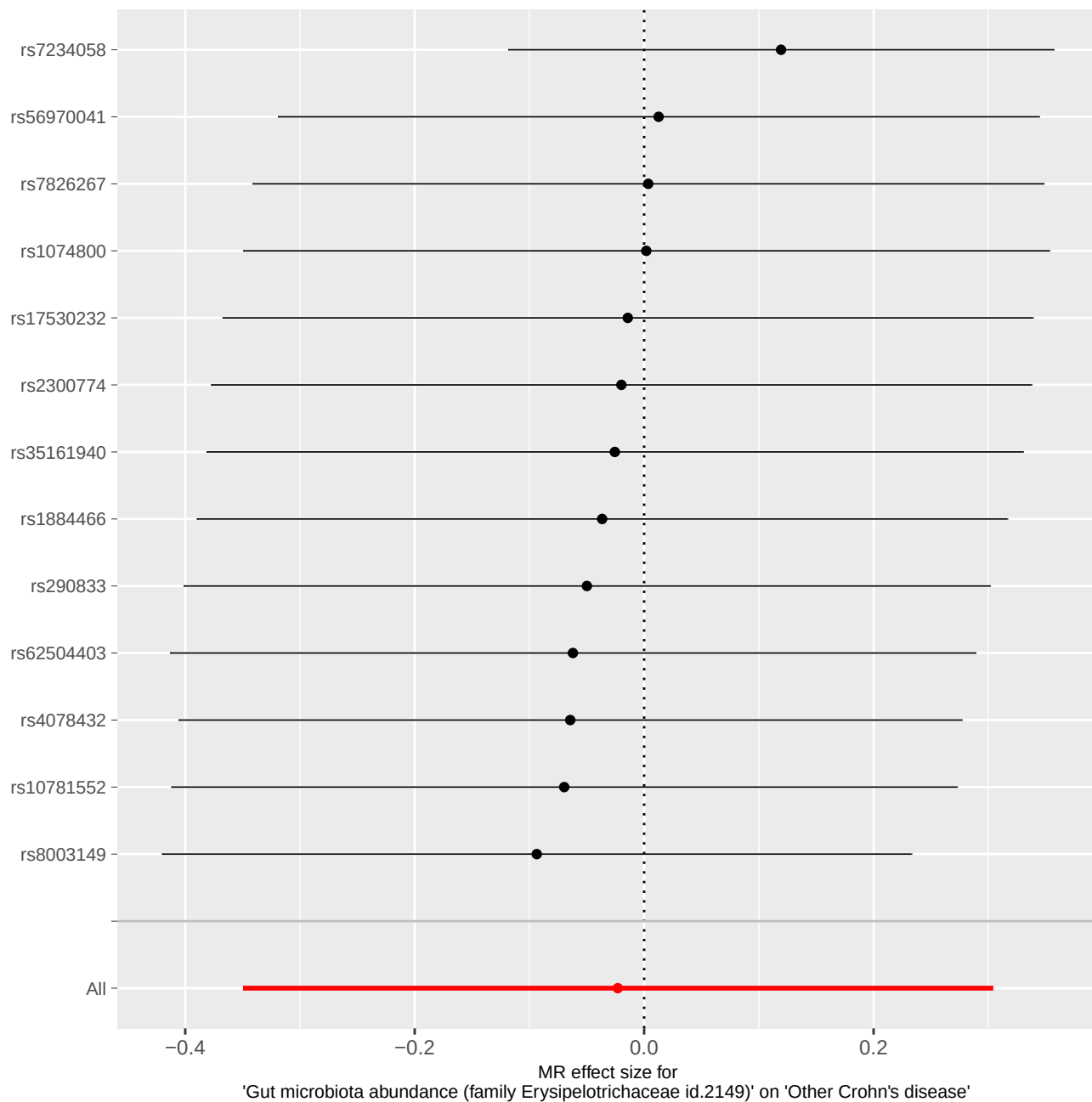
Batch 160 : Gut microbiota abundance (family Coriobacteriaceae id.811) on Other Crohn's disease

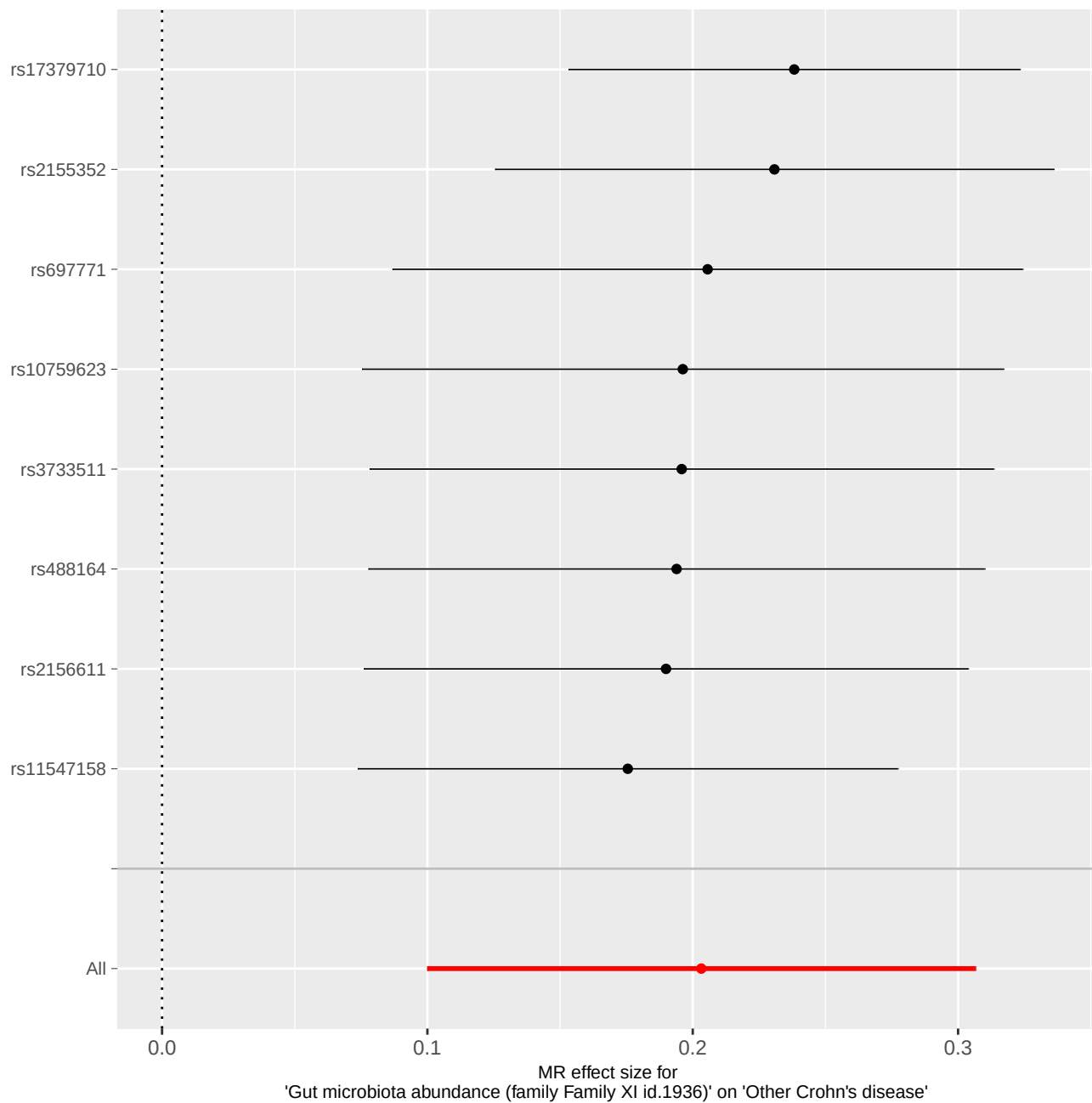


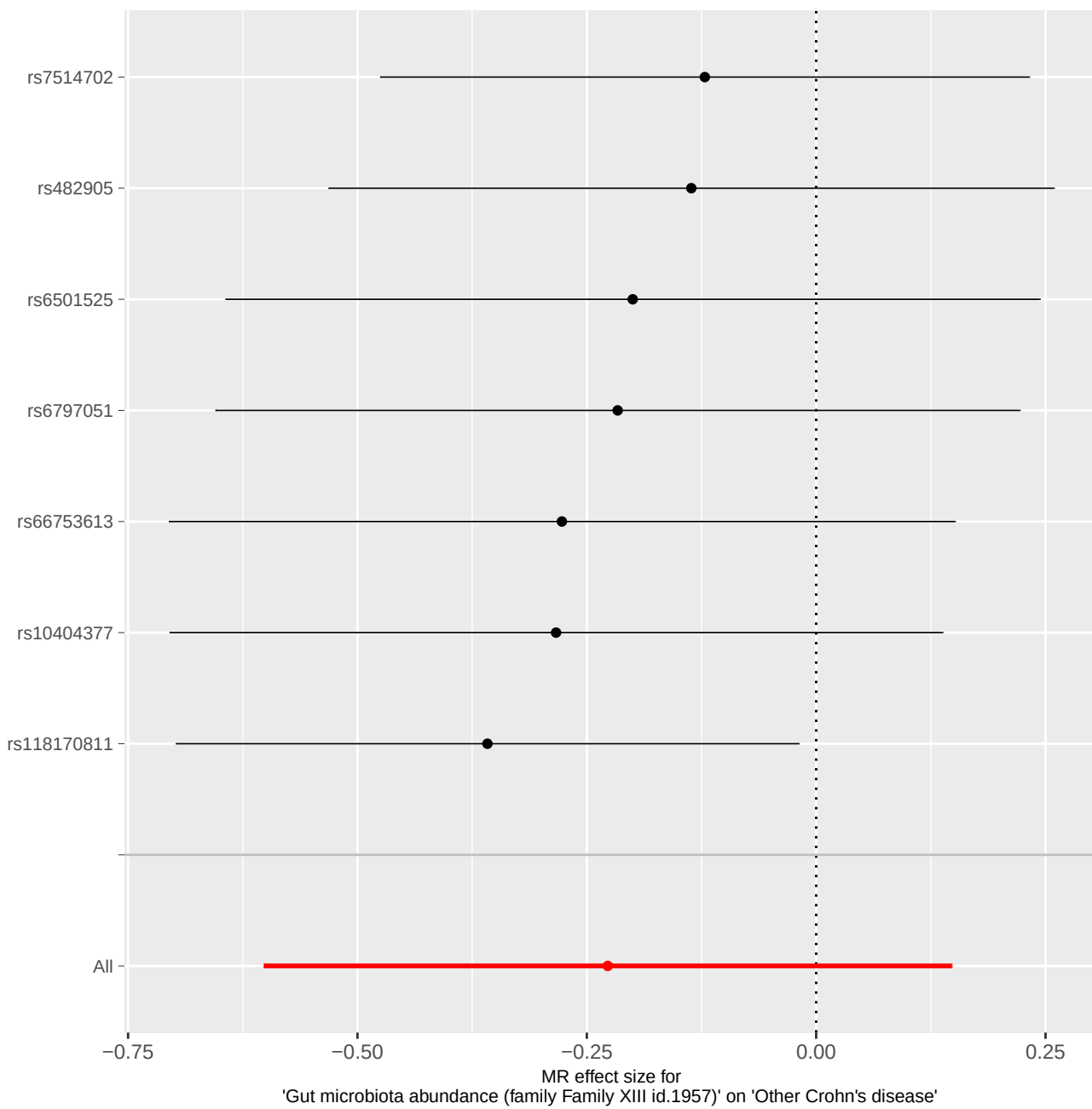




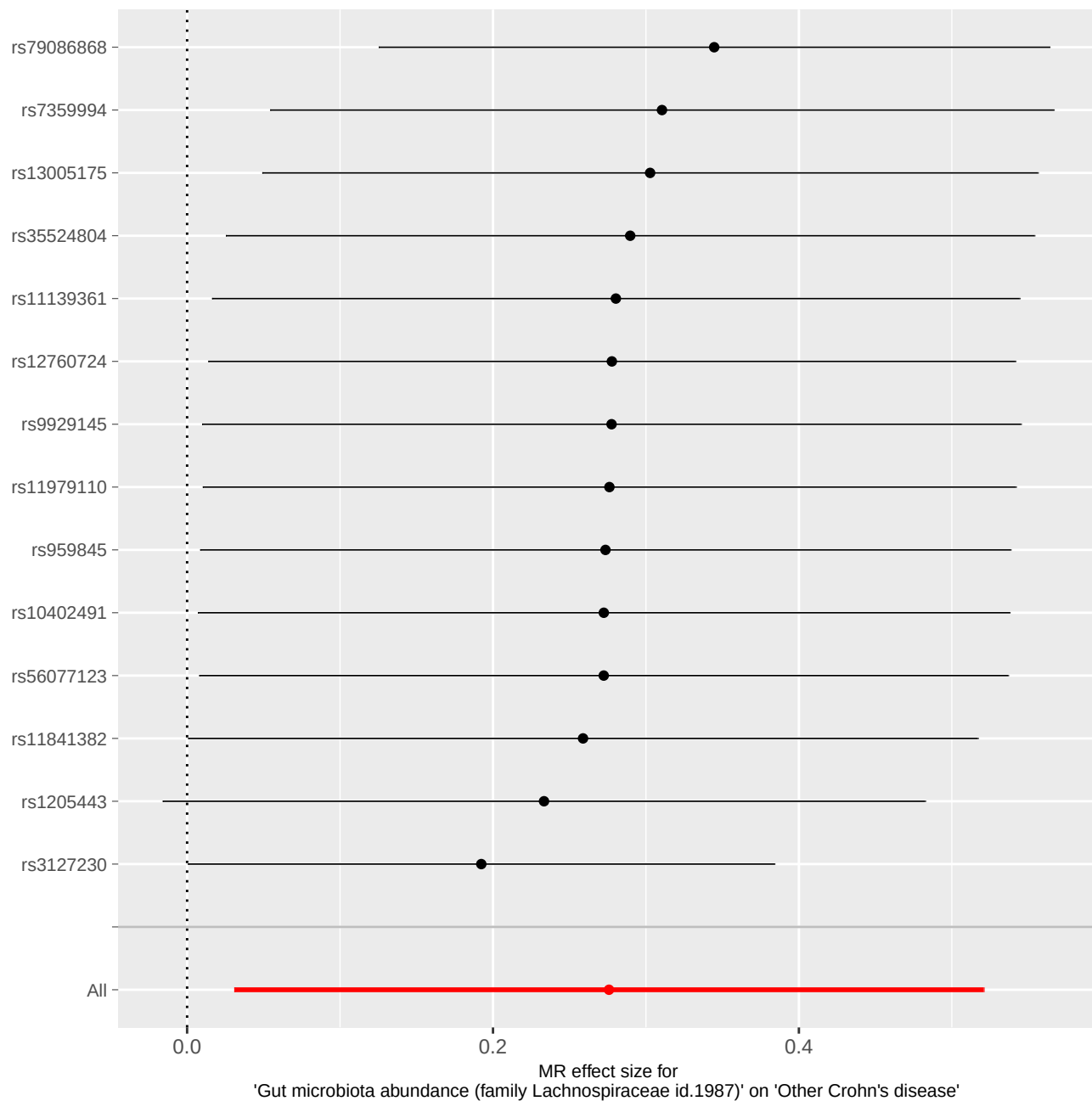


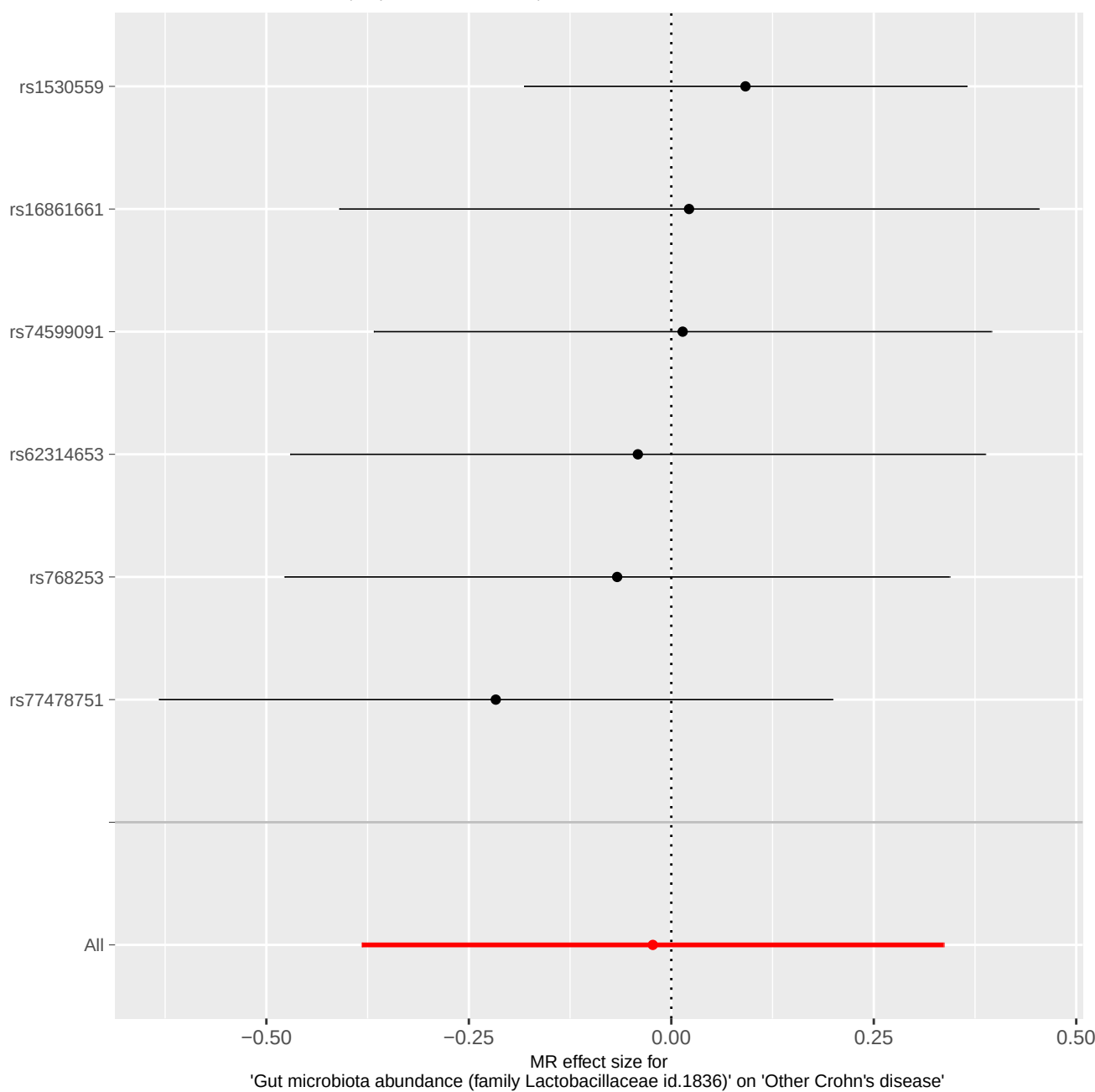


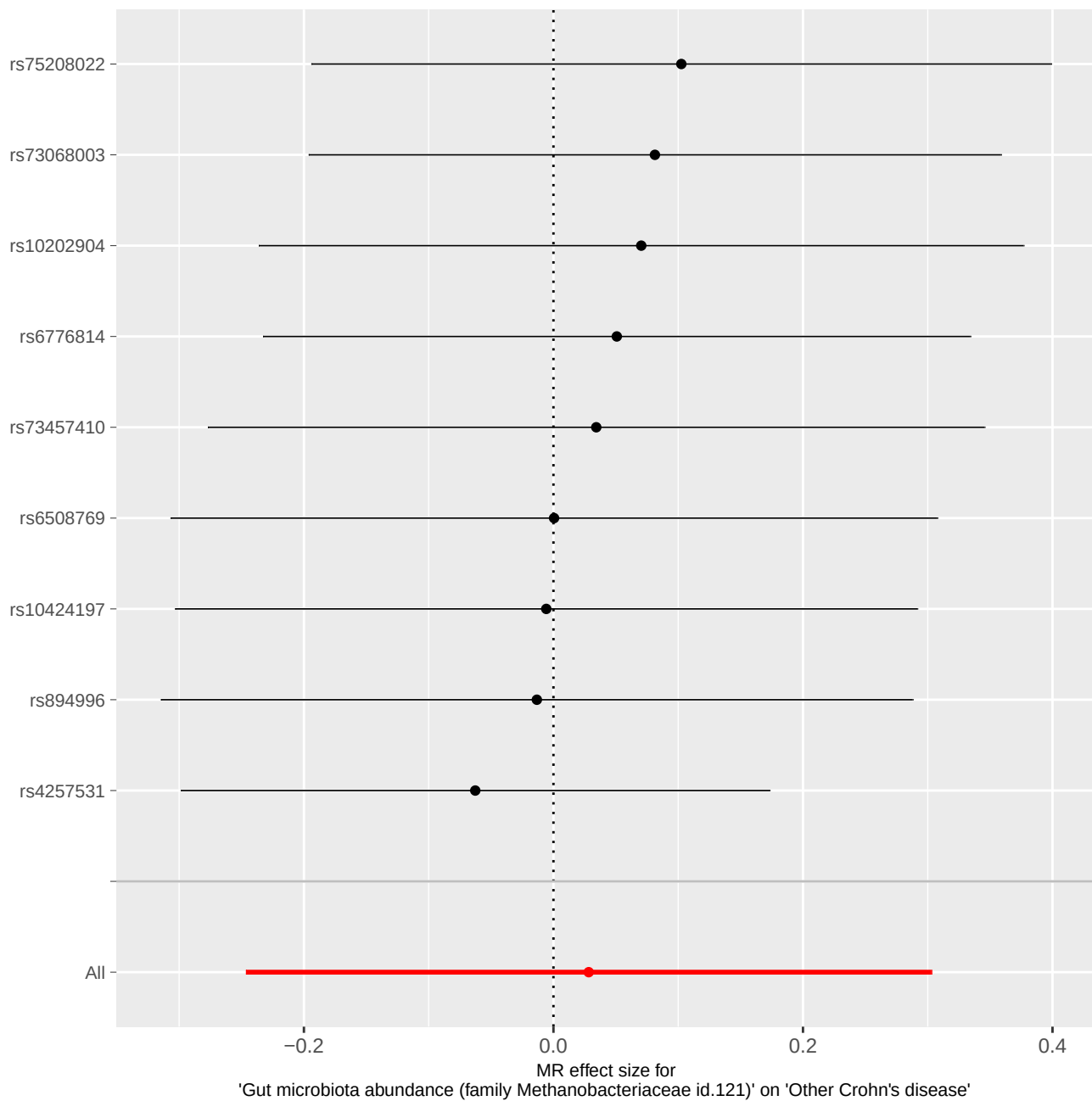




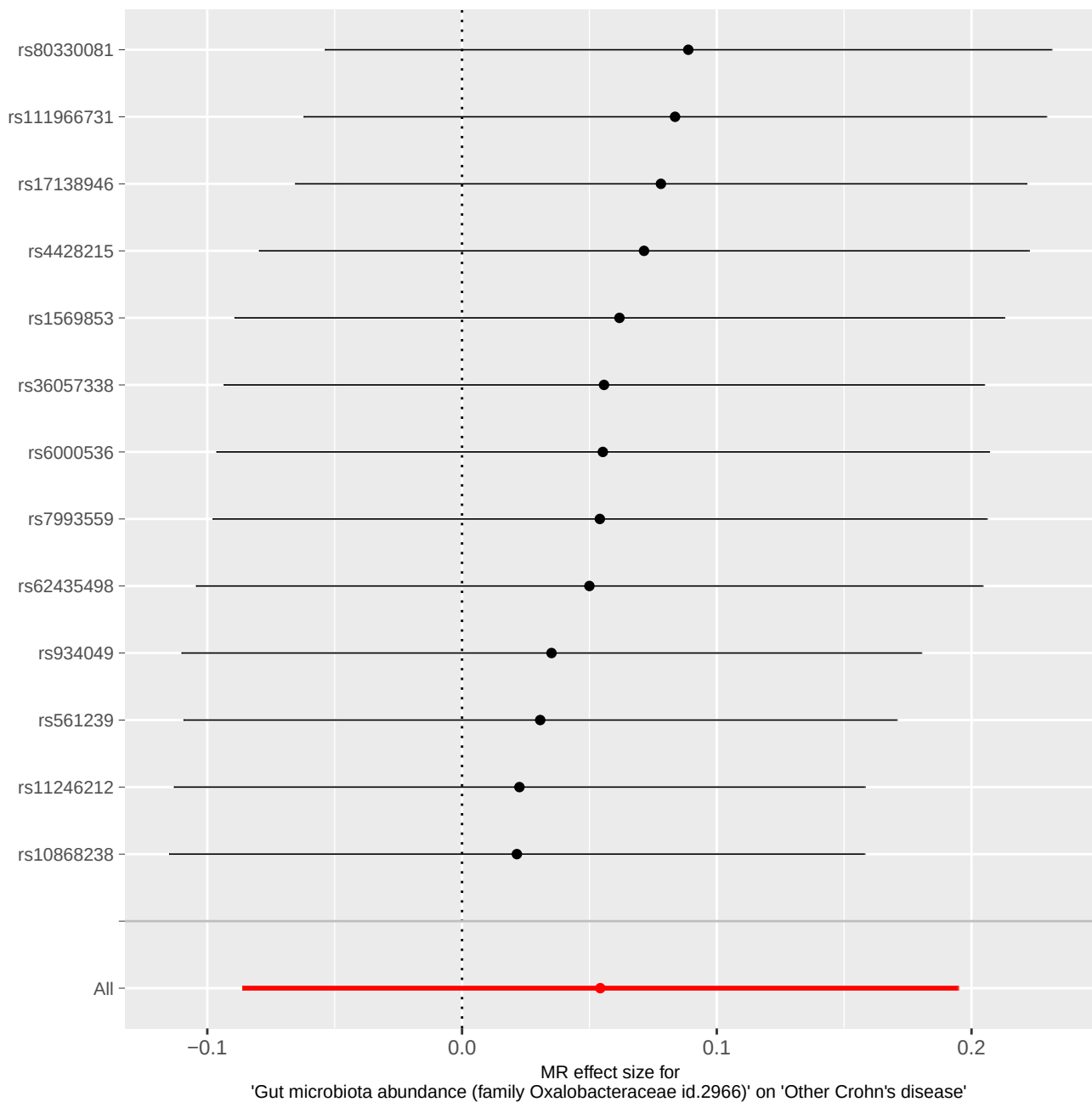
Batch 167 : Gut microbiota abundance (family Lachnospiraceae id.1987) on Other Crohn's disease

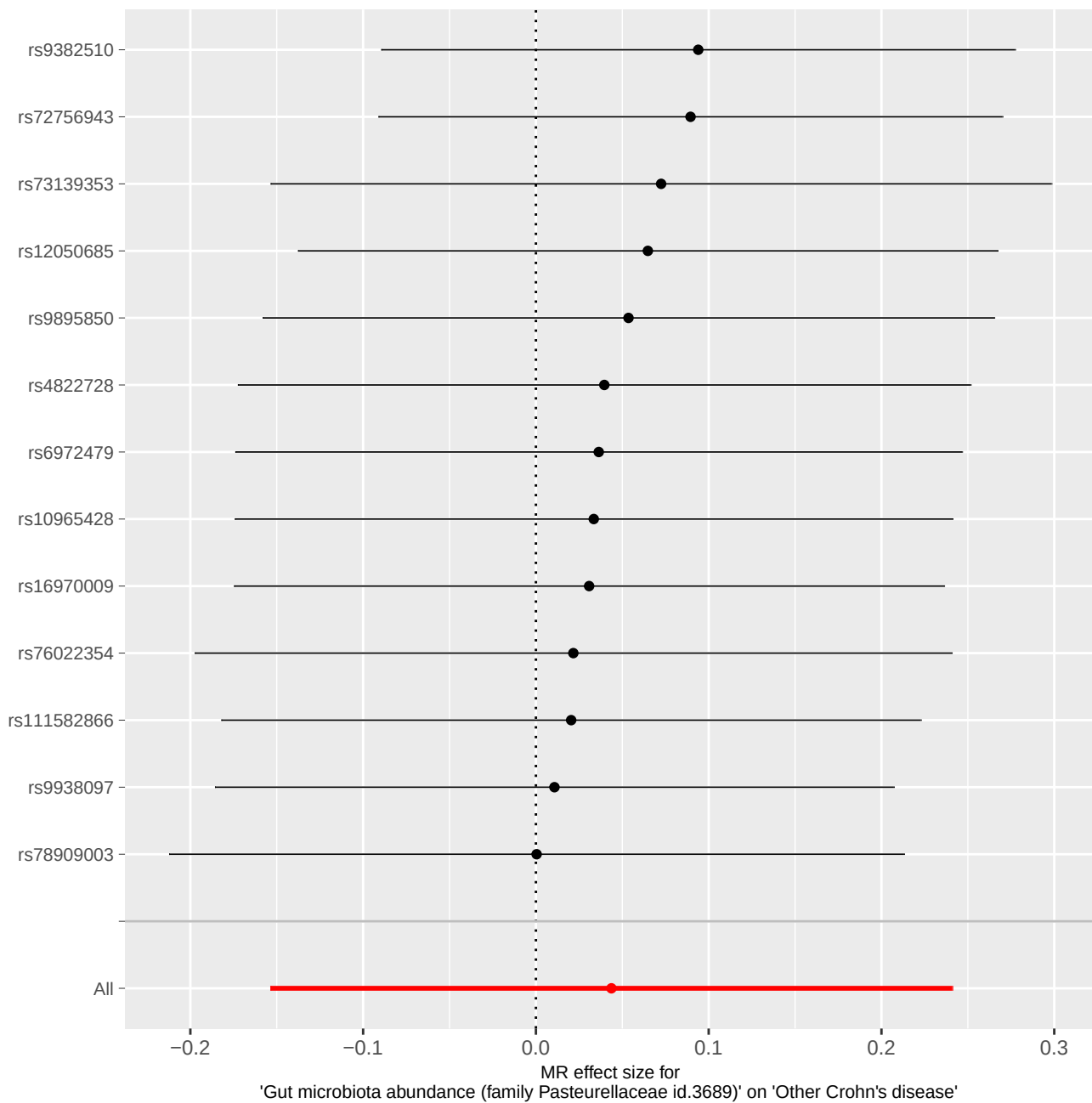




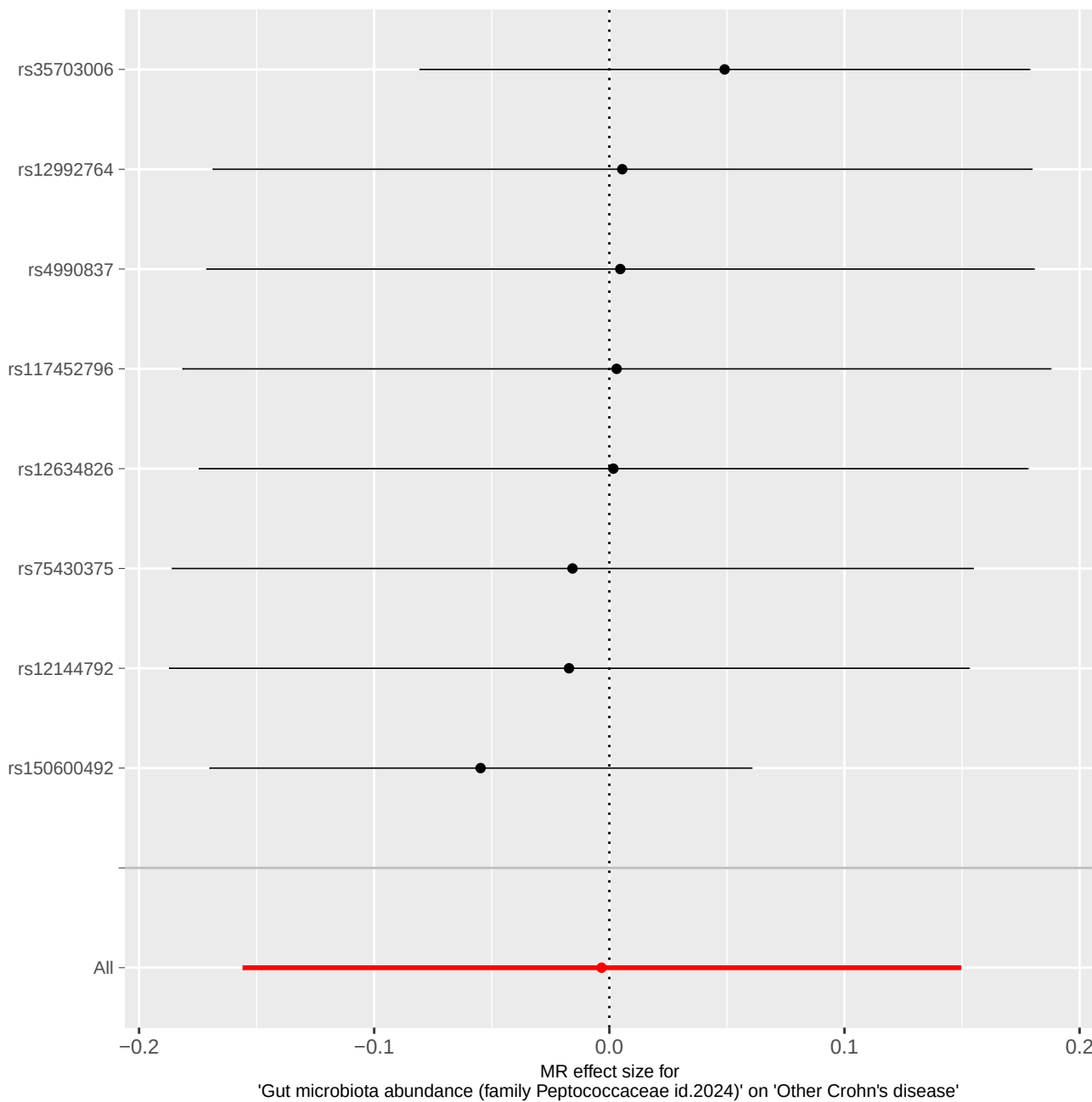


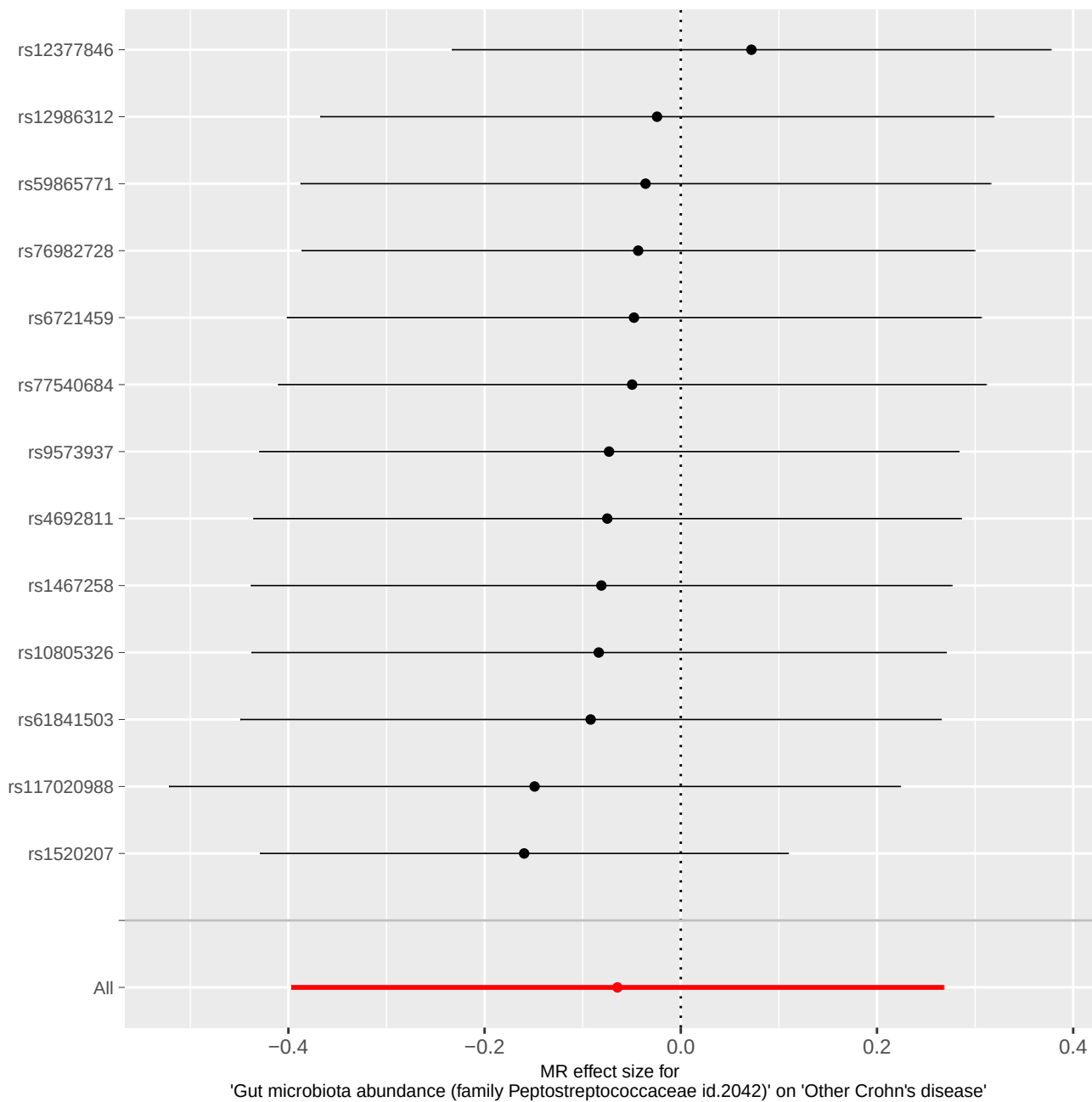
MR effect size for
'Gut microbiota abundance (family Methanobacteriaceae id.121)' on 'Other Crohn's disease'

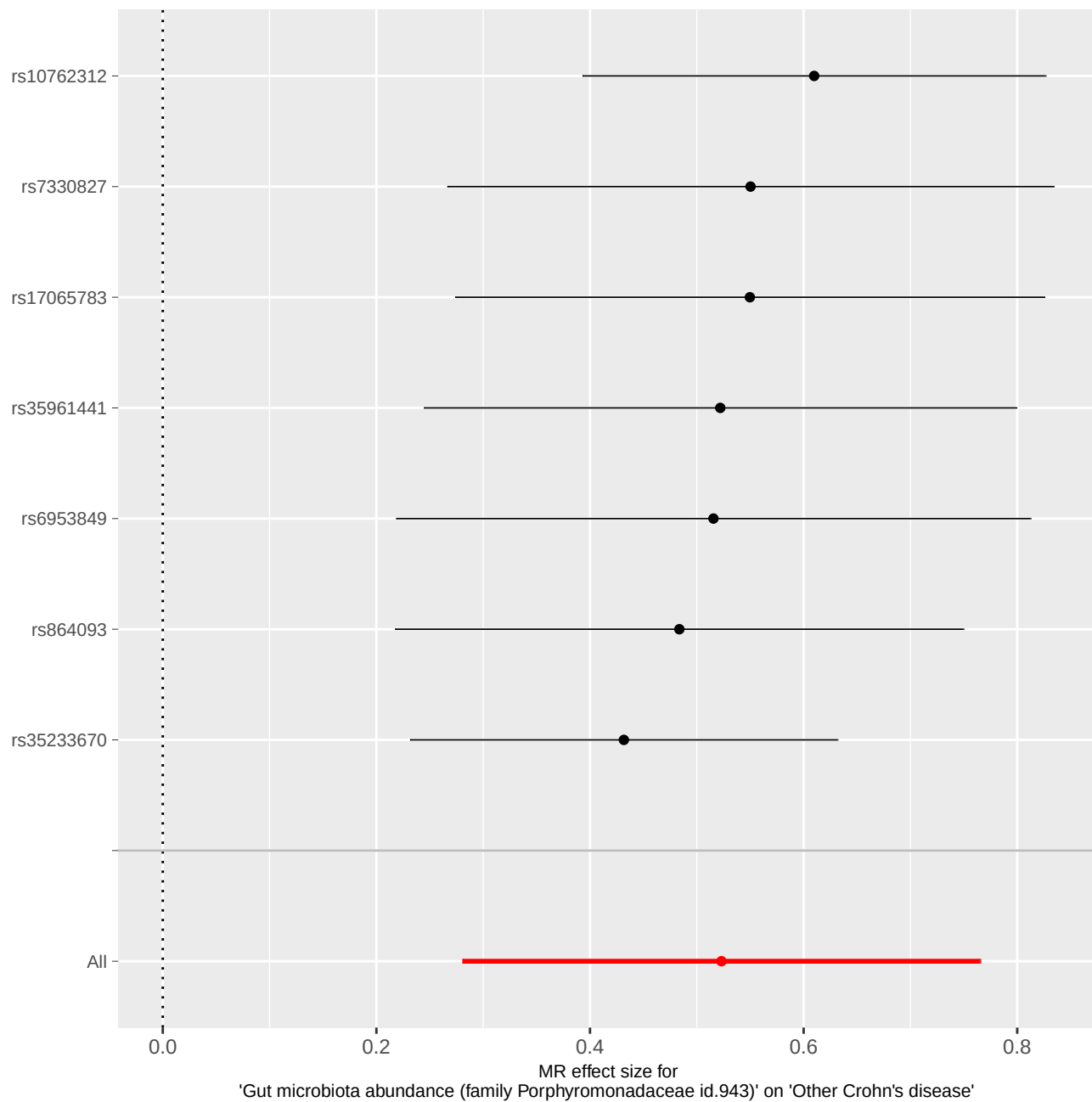




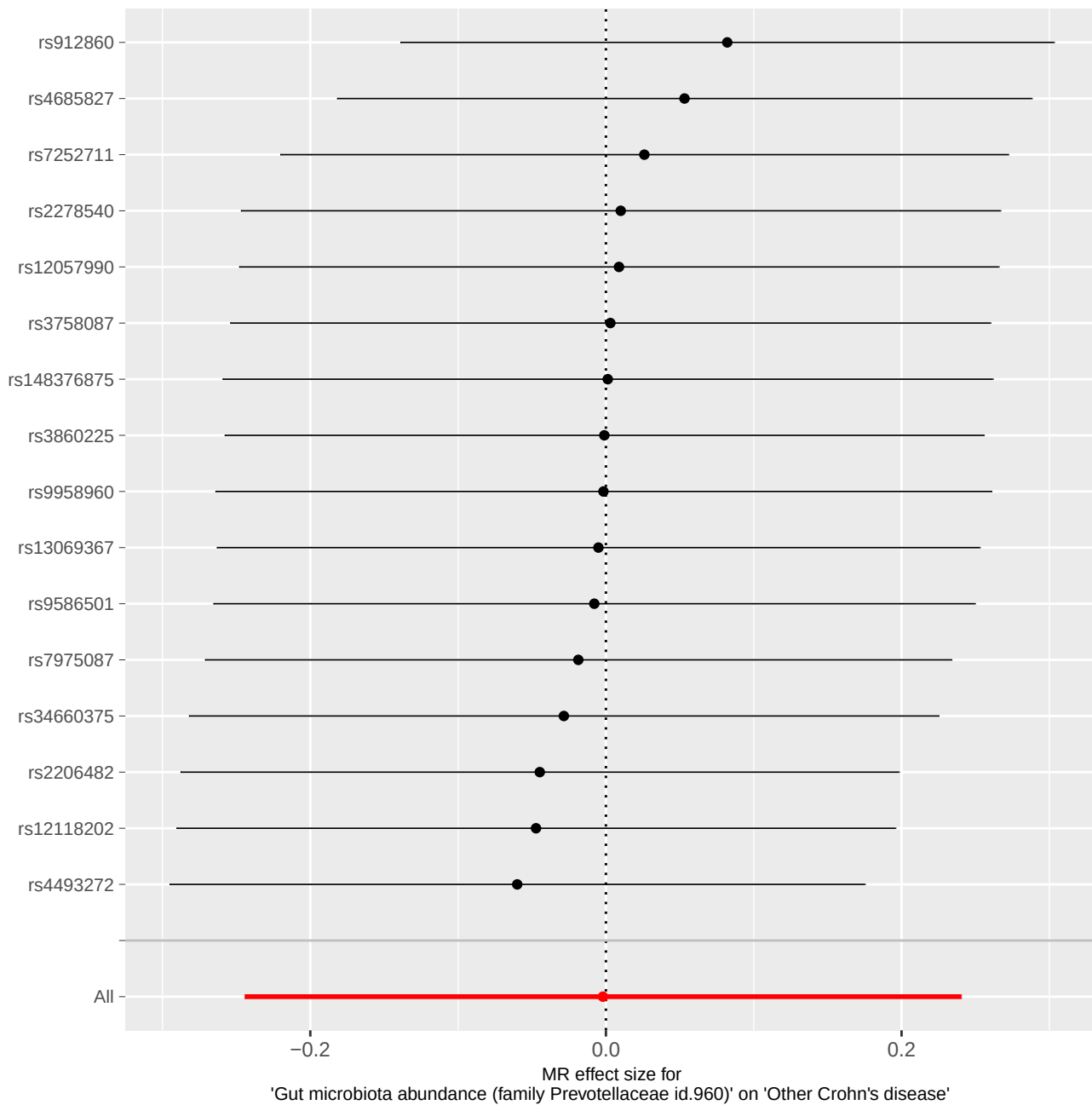
Batch 172 : Gut microbiota abundance (family Peptococcaceae id.2024) on Other Crohn's disease

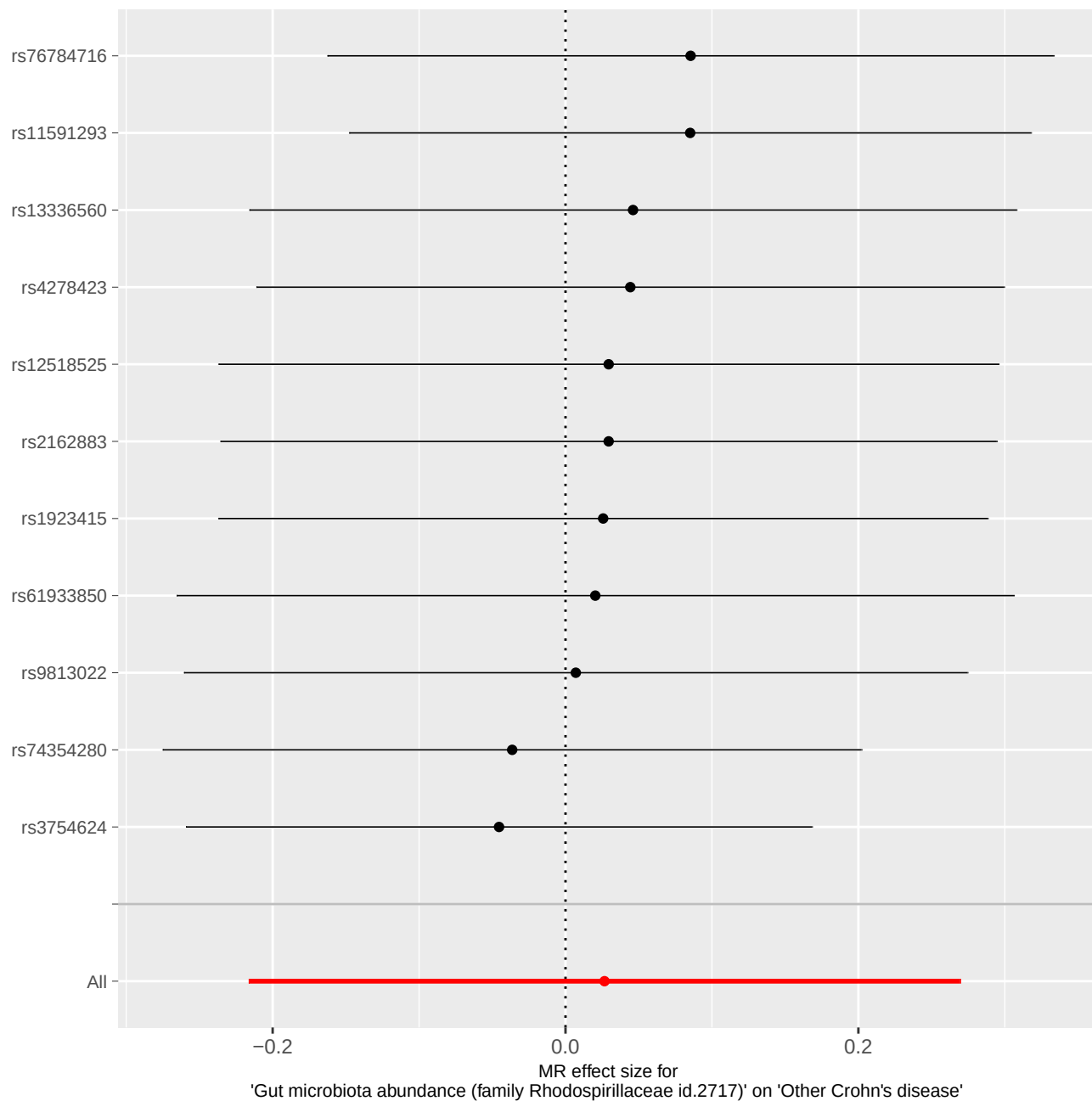




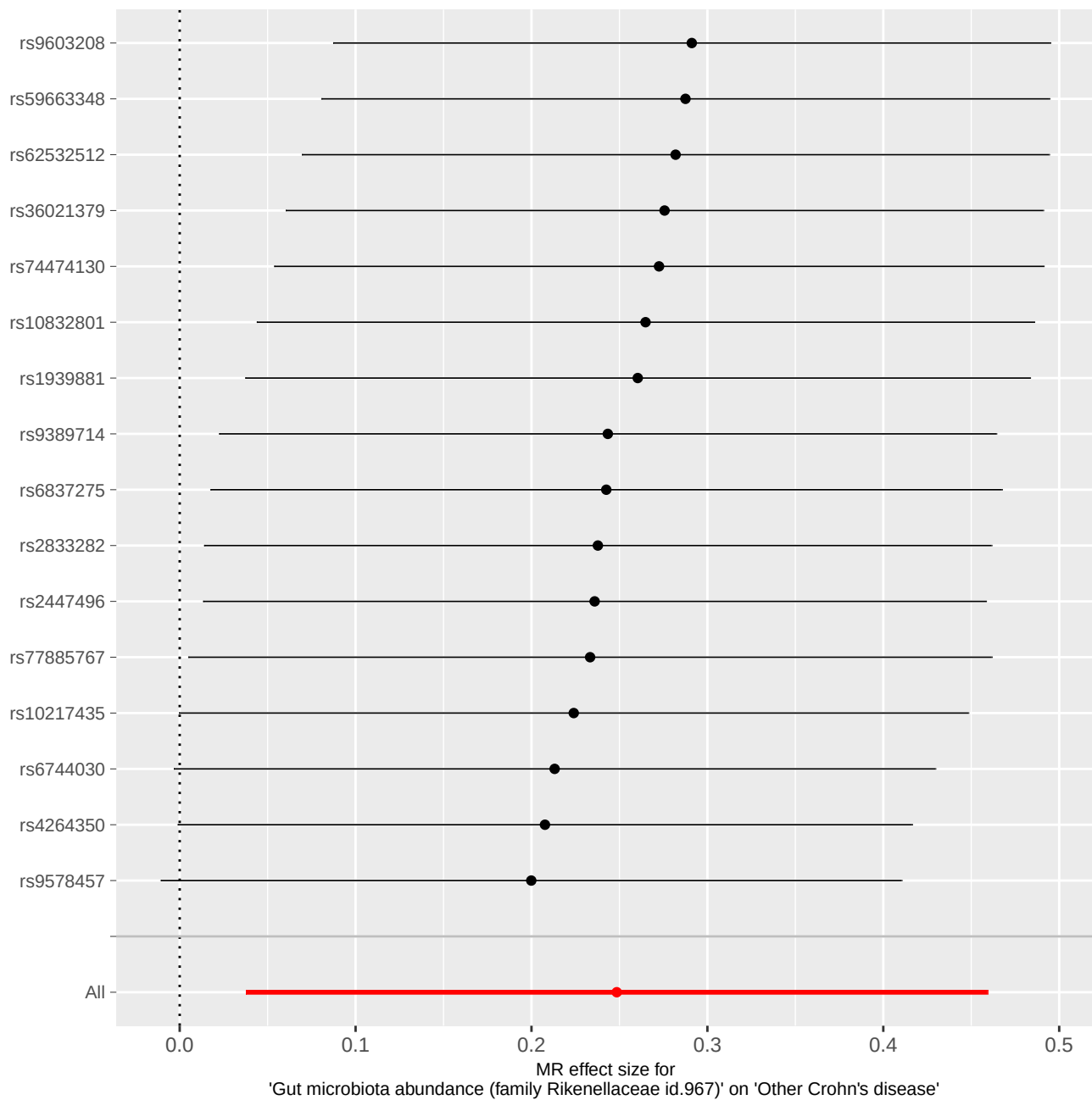


MR effect size for
'Gut microbiota abundance (family Porphyromonadaceae id.943)' on 'Other Crohn's disease'

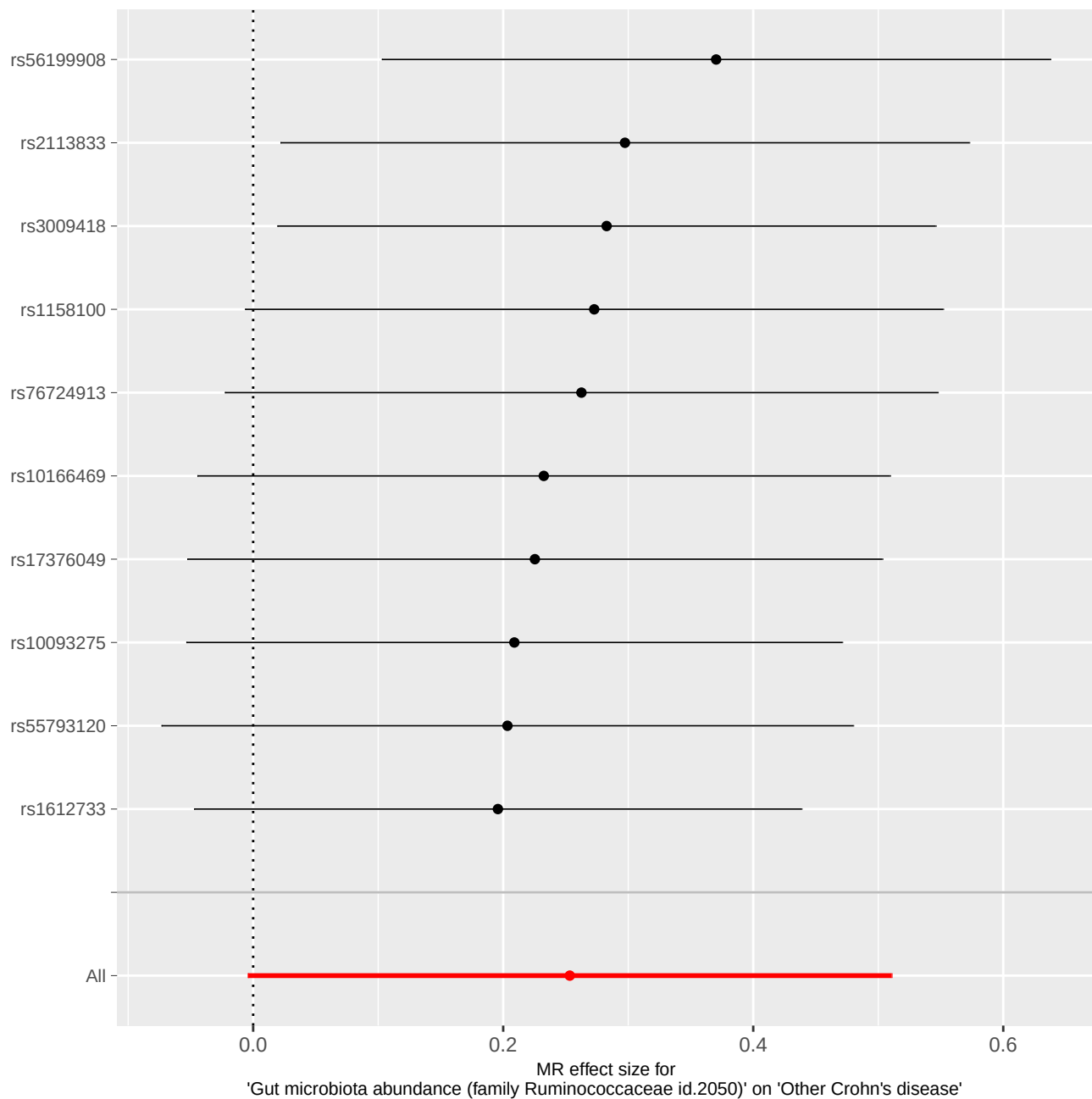


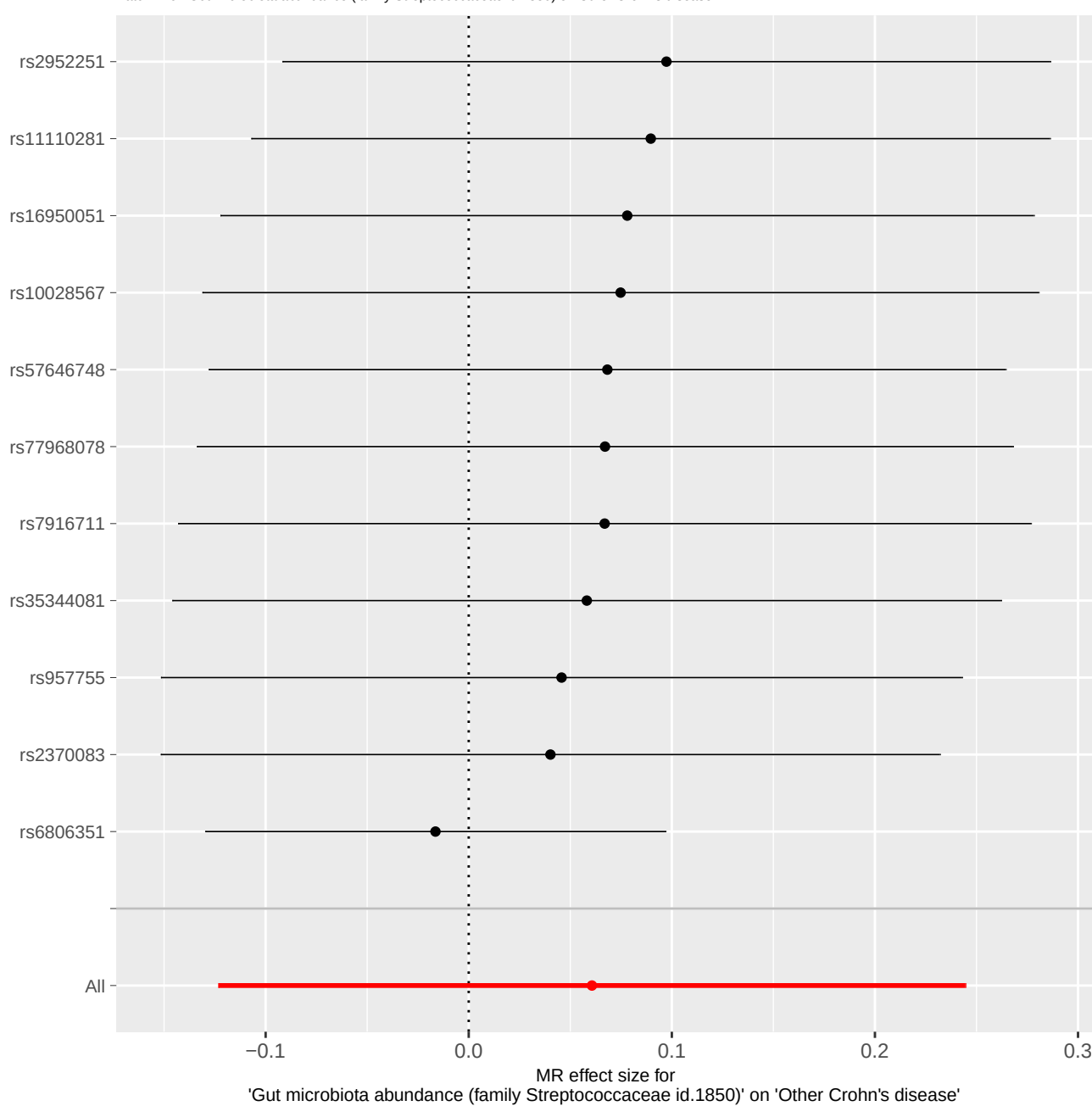


Batch 177 : Gut microbiota abundance (family Rikenellaceae id.967) on Other Crohn's disease



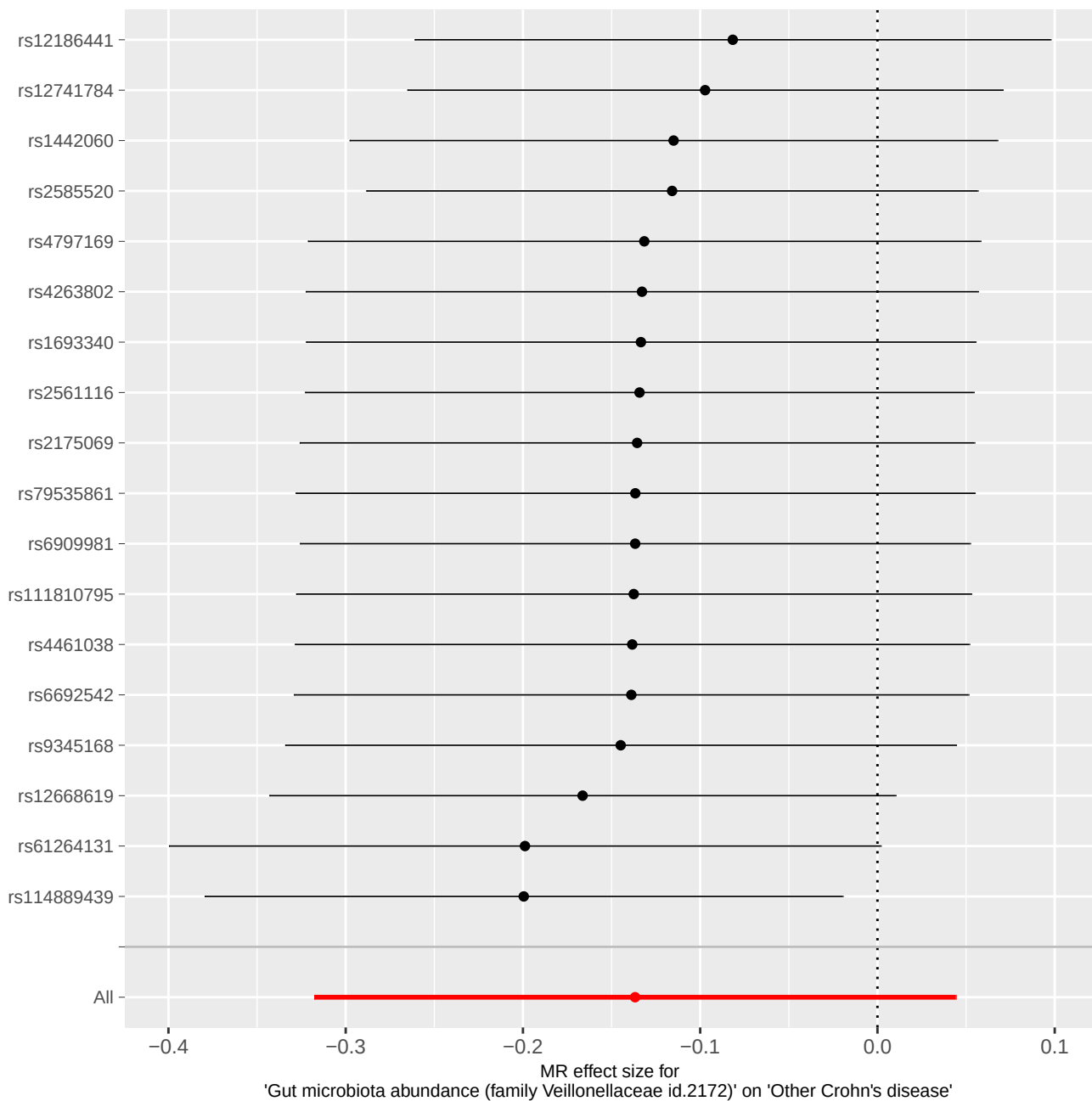
Batch 178 : Gut microbiota abundance (family Ruminococcaceae id.2050) on Other Crohn's disease

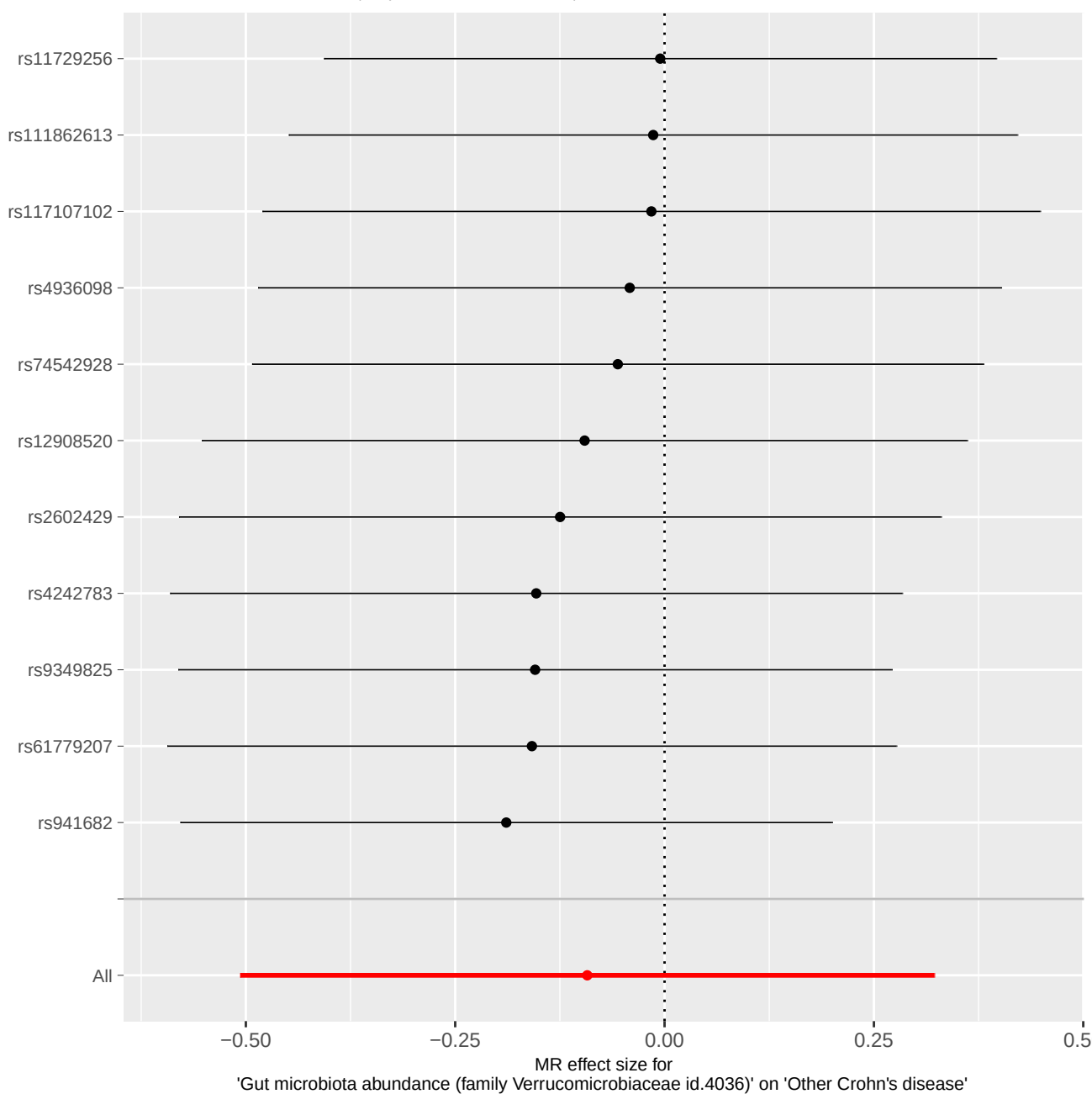


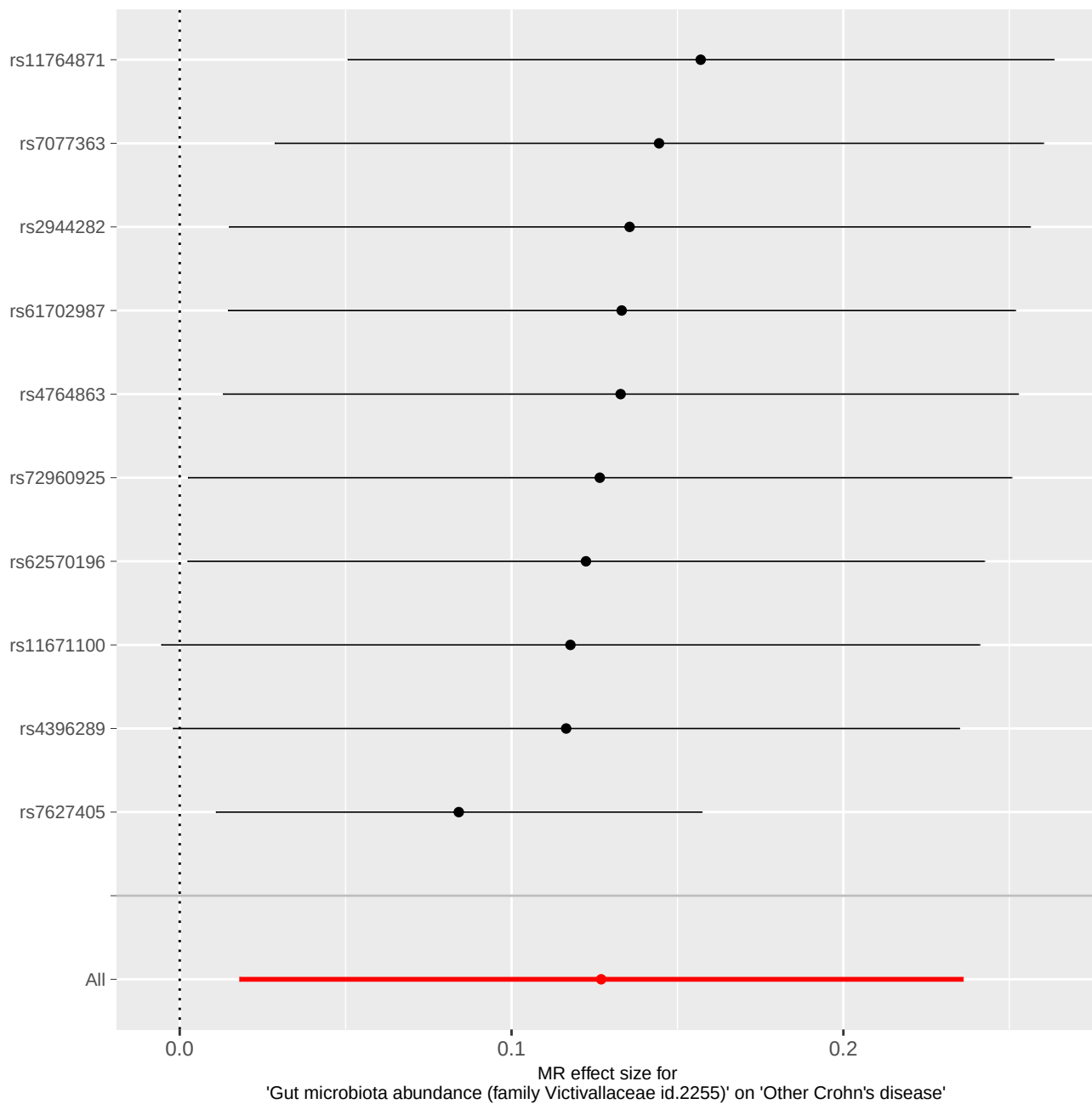


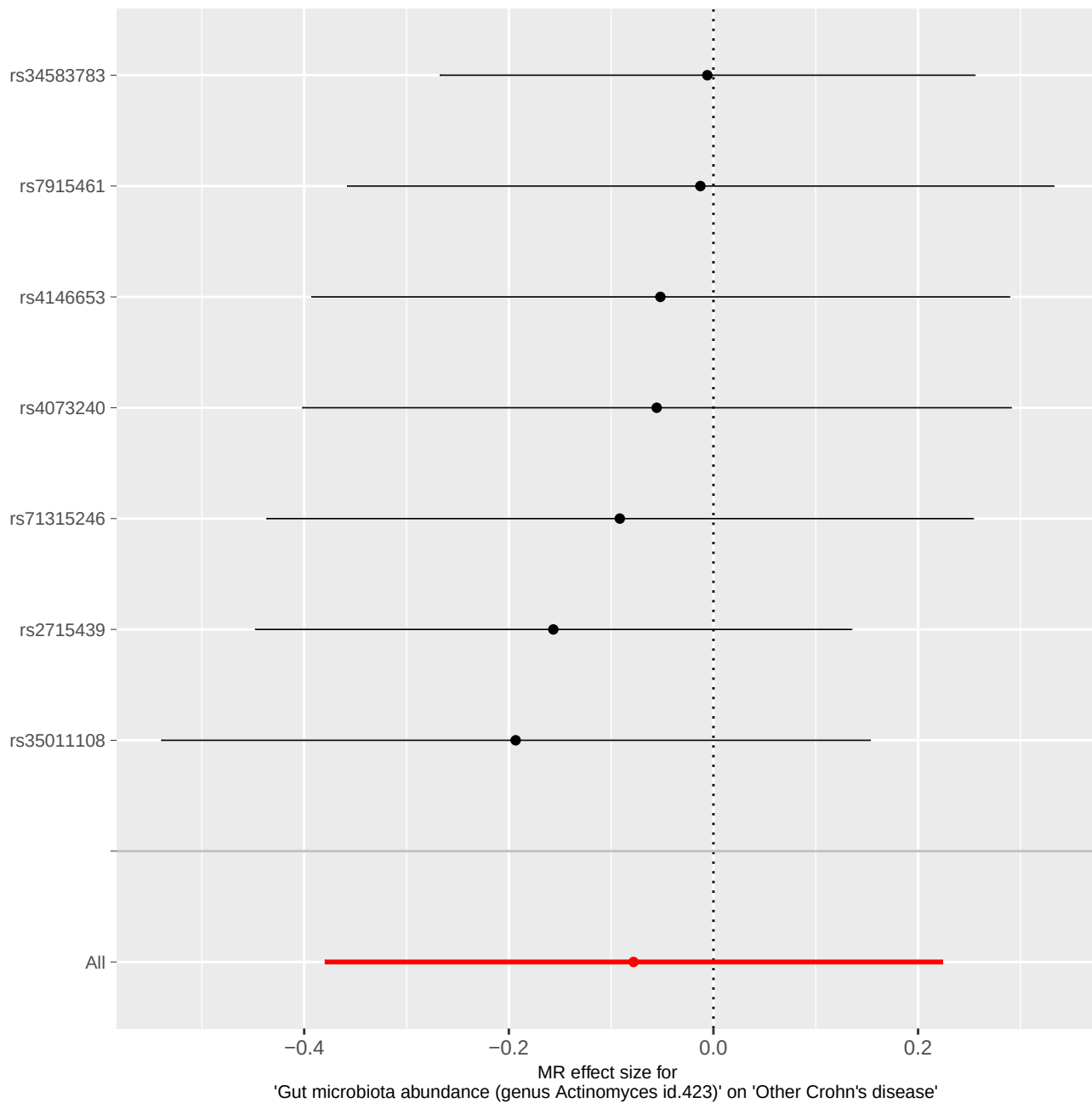
MR effect size for
'Gut microbiota abundance (family Streptococcaceae id.1850)' on 'Other Crohn's disease'

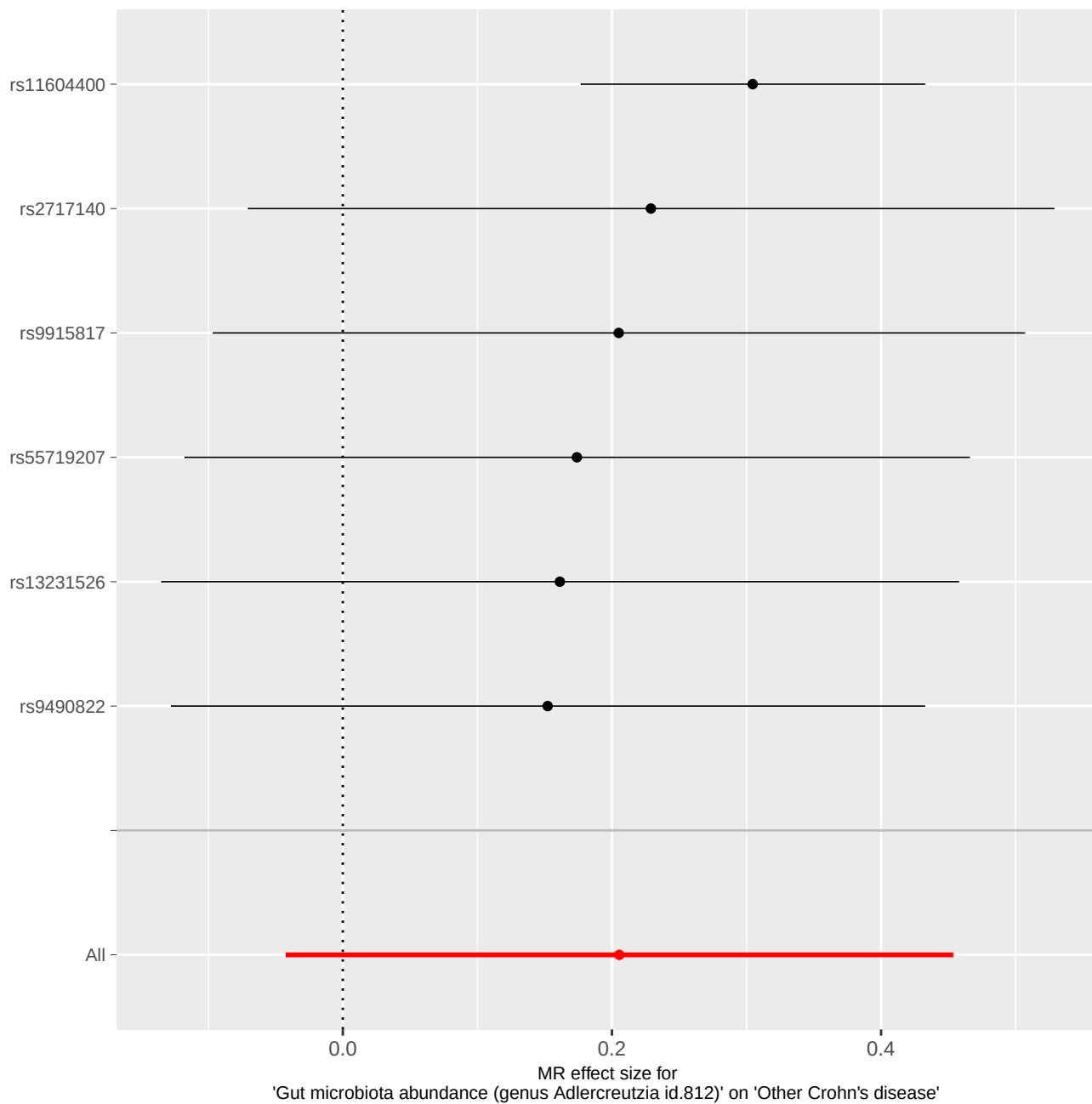
Batch 180 : Gut microbiota abundance (family Veillonellaceae id.2172) on Other Crohn's disease



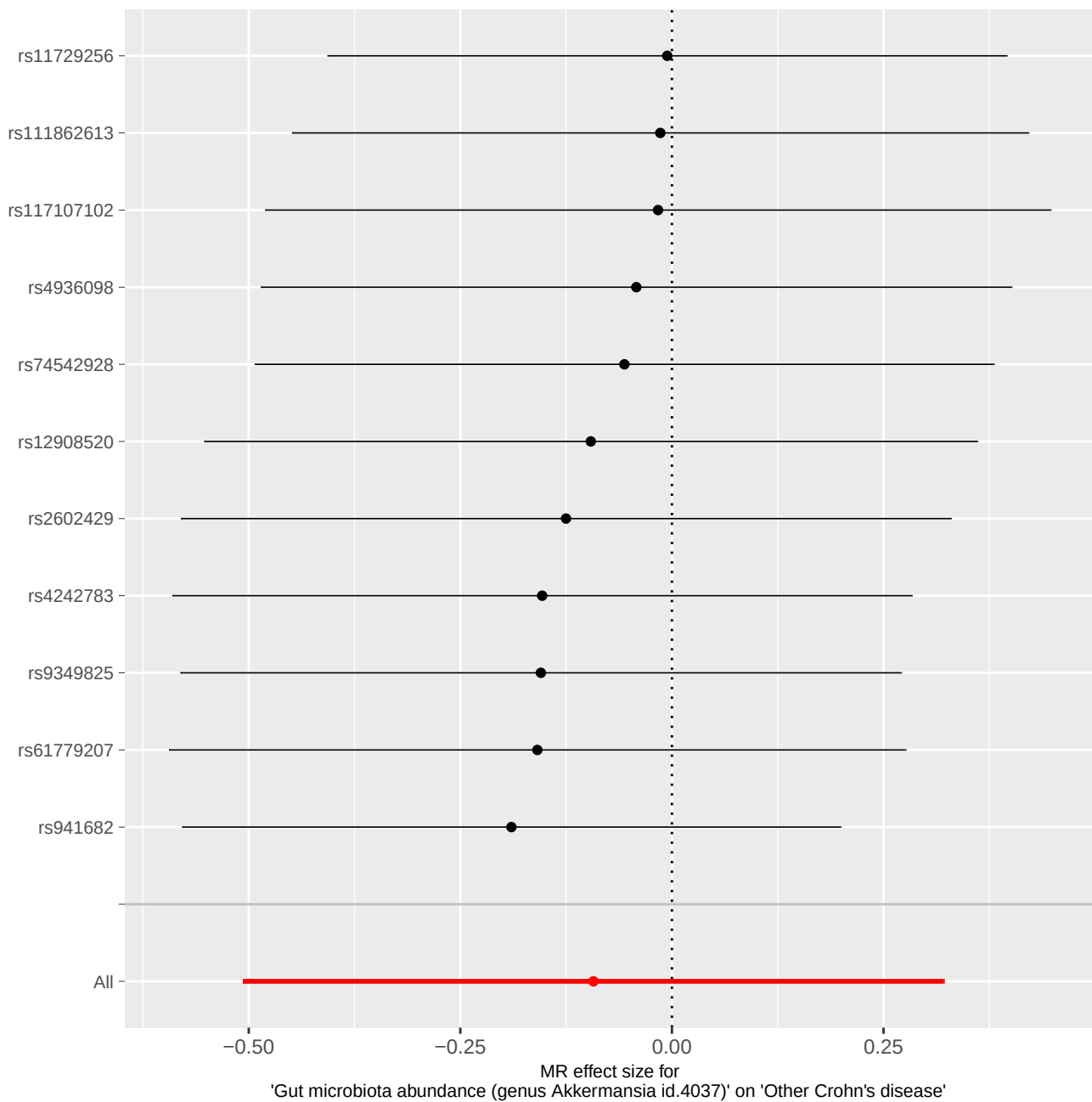




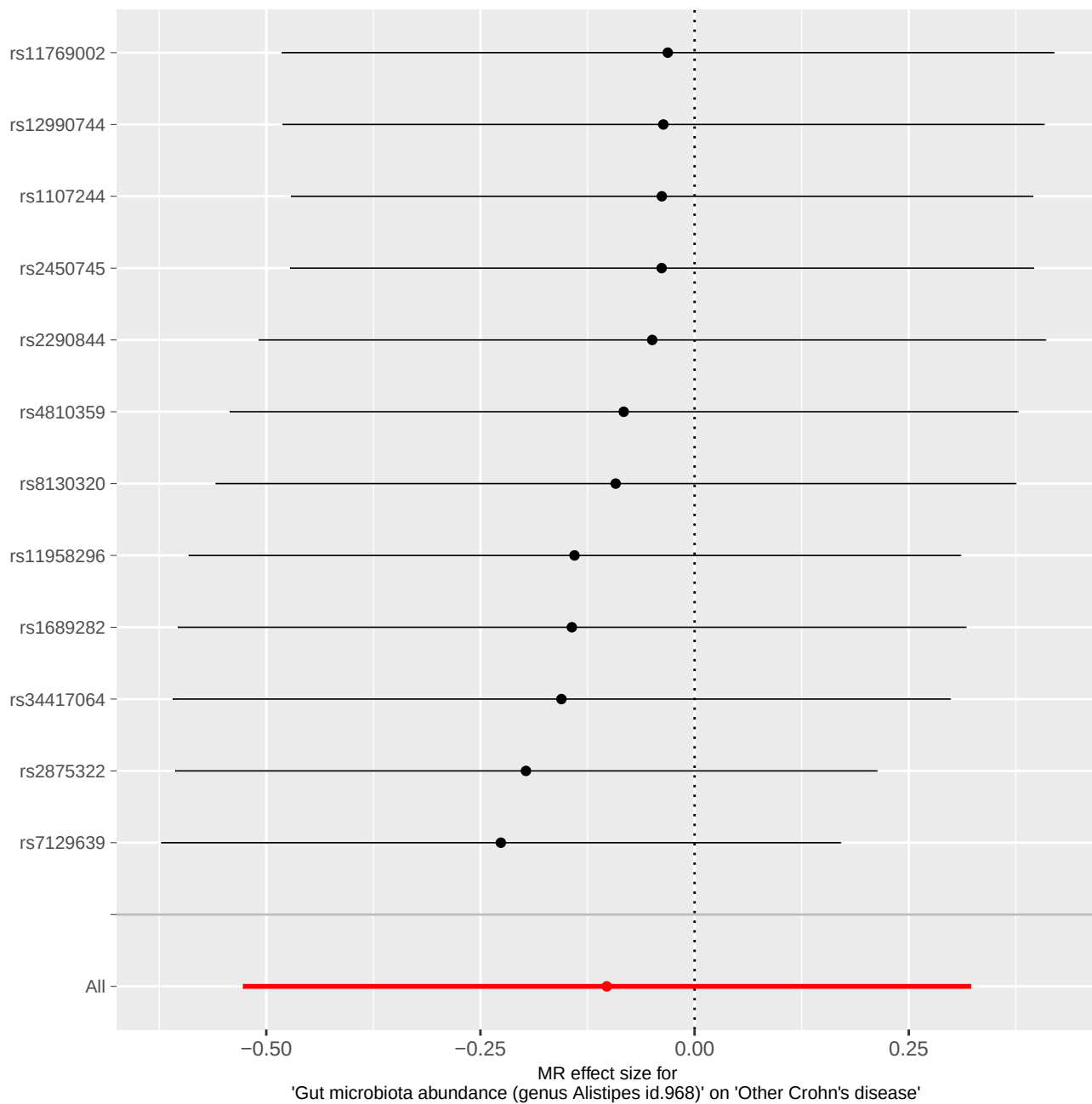


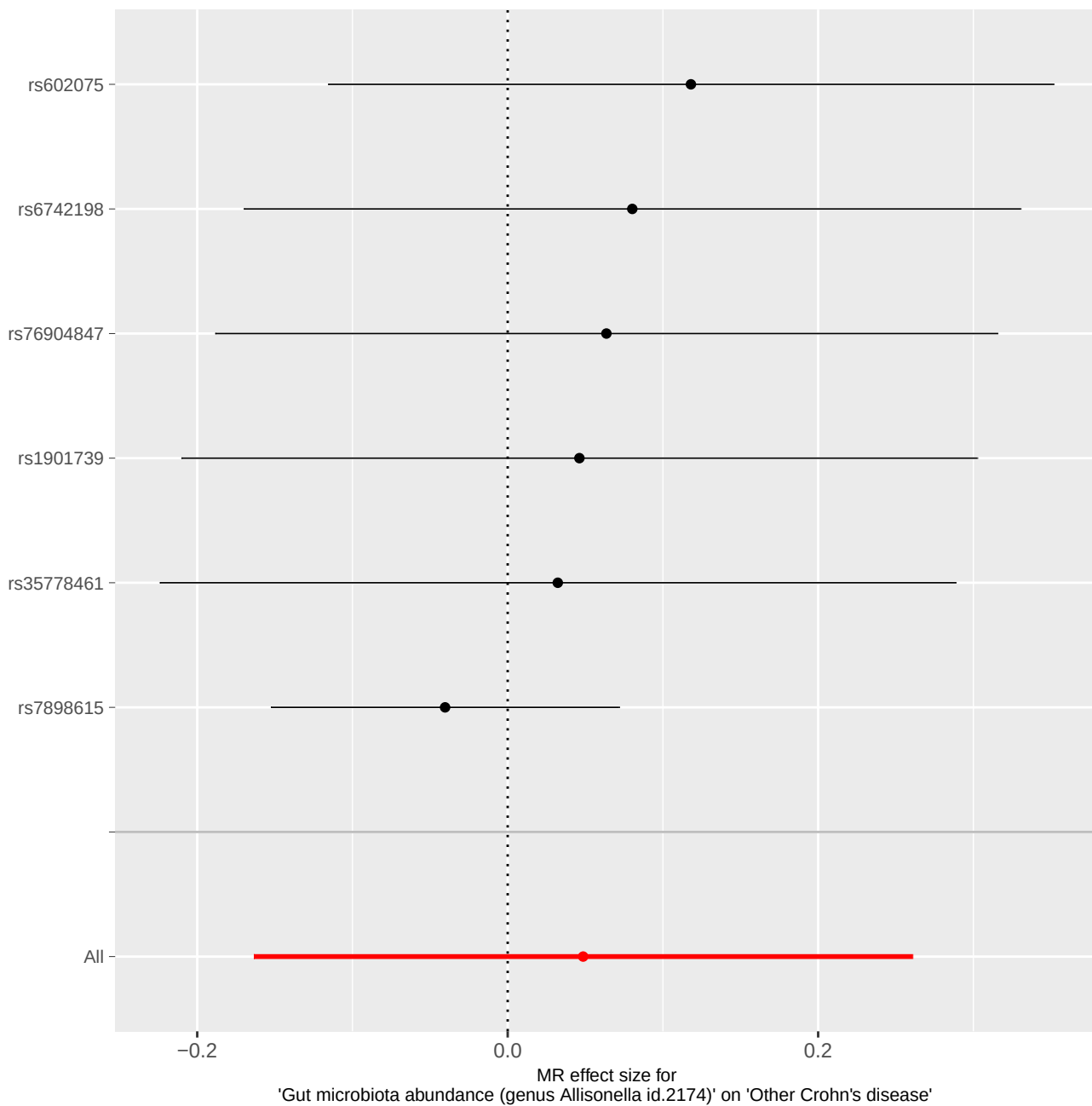


Batch 185 : Gut microbiota abundance (genus Akkermansia id.4037) on Other Crohn's disease

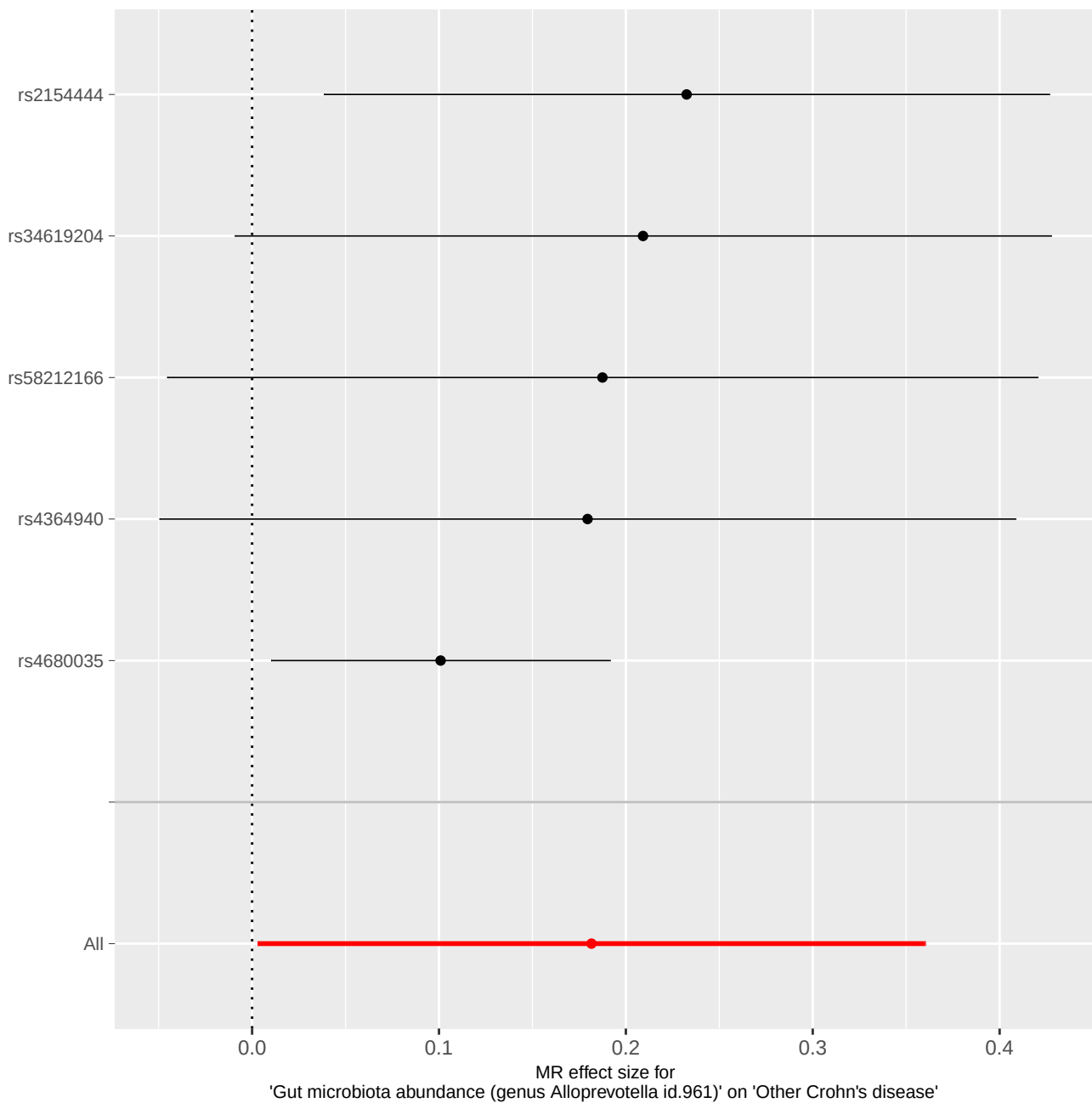


Batch 186 : Gut microbiota abundance (genus Alistipes id.968) on Other Crohn's disease

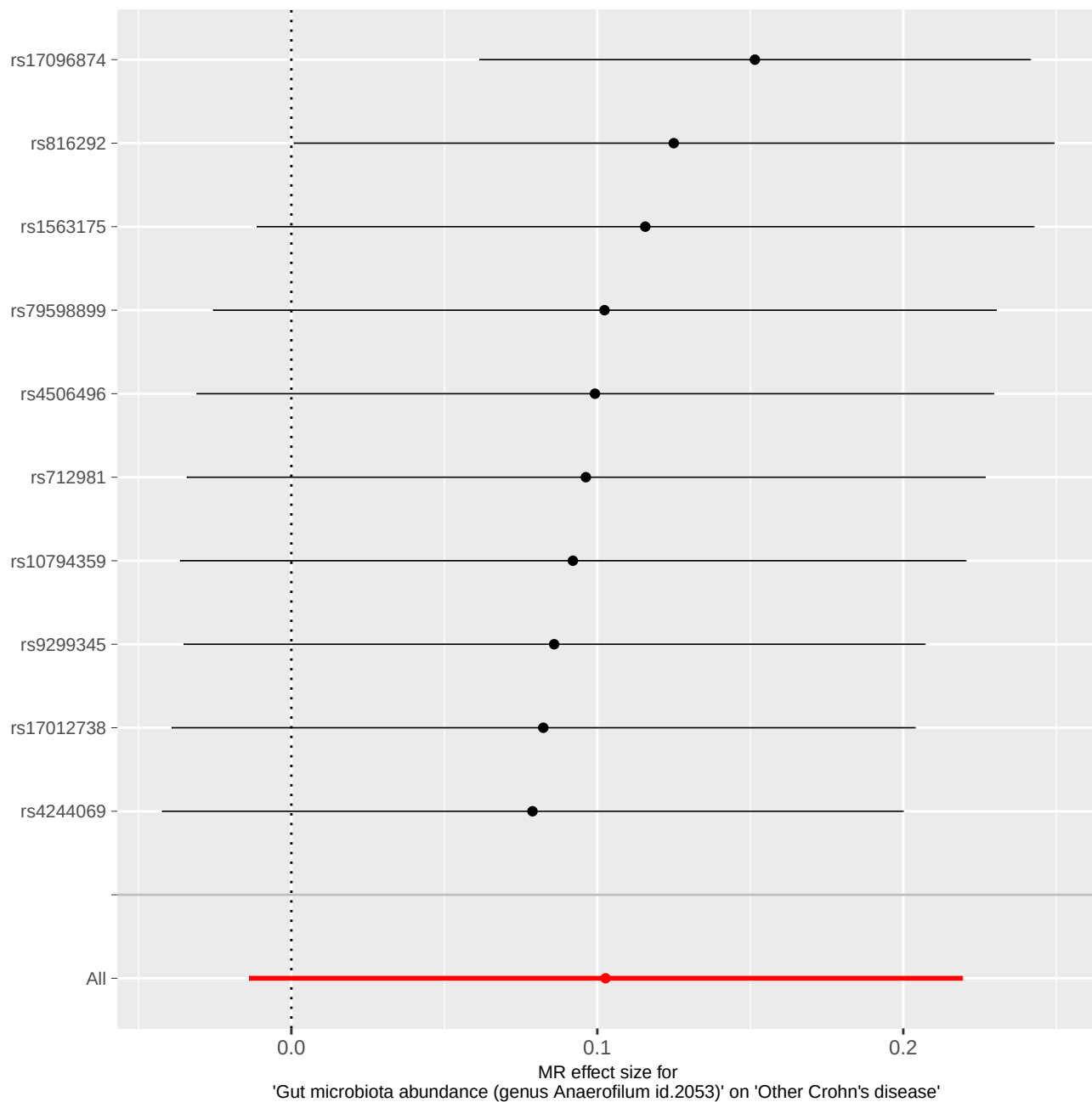




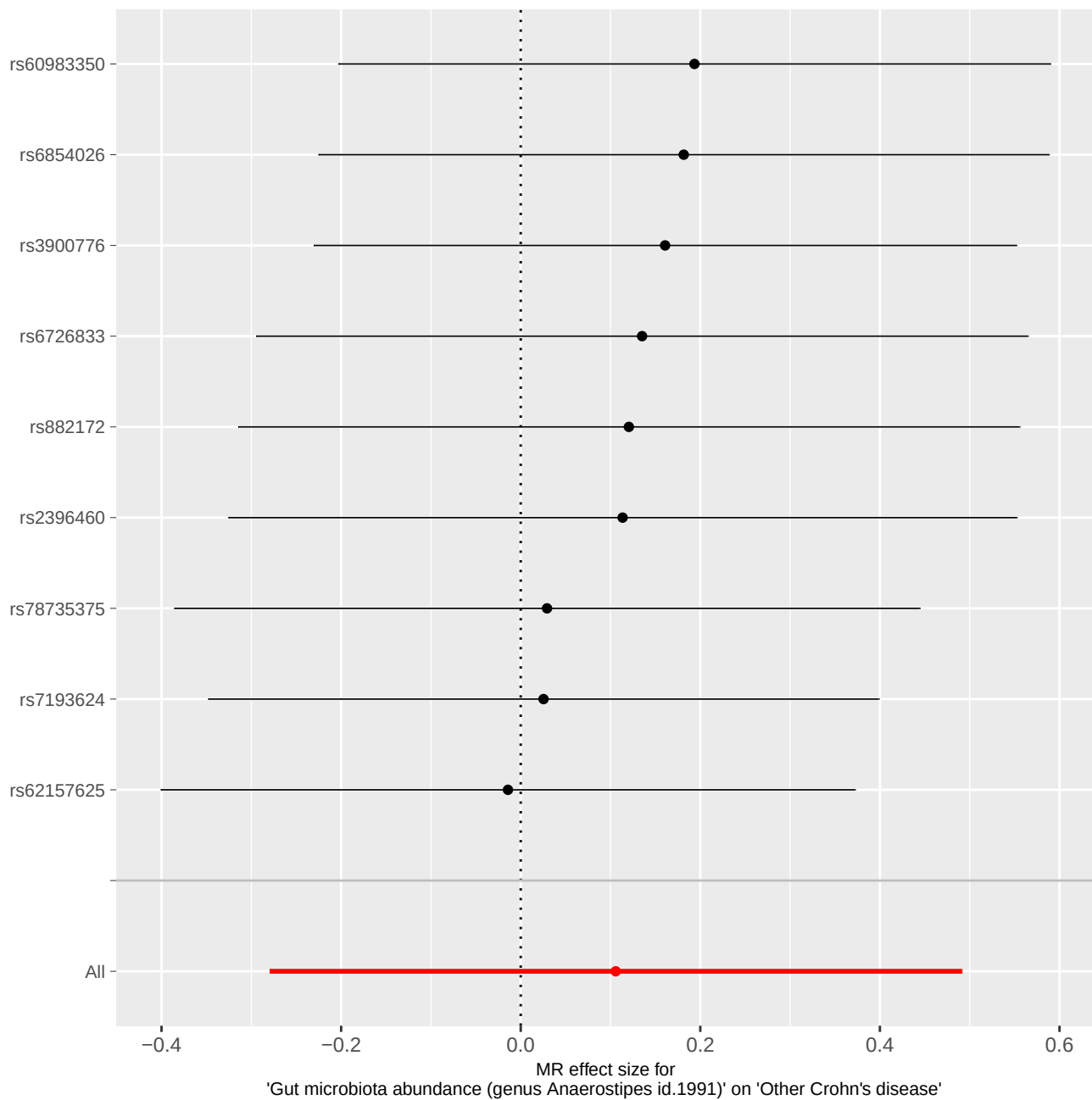
Batch 188 : Gut microbiota abundance (genus Alloprevotella id.961) on Other Crohn's disease

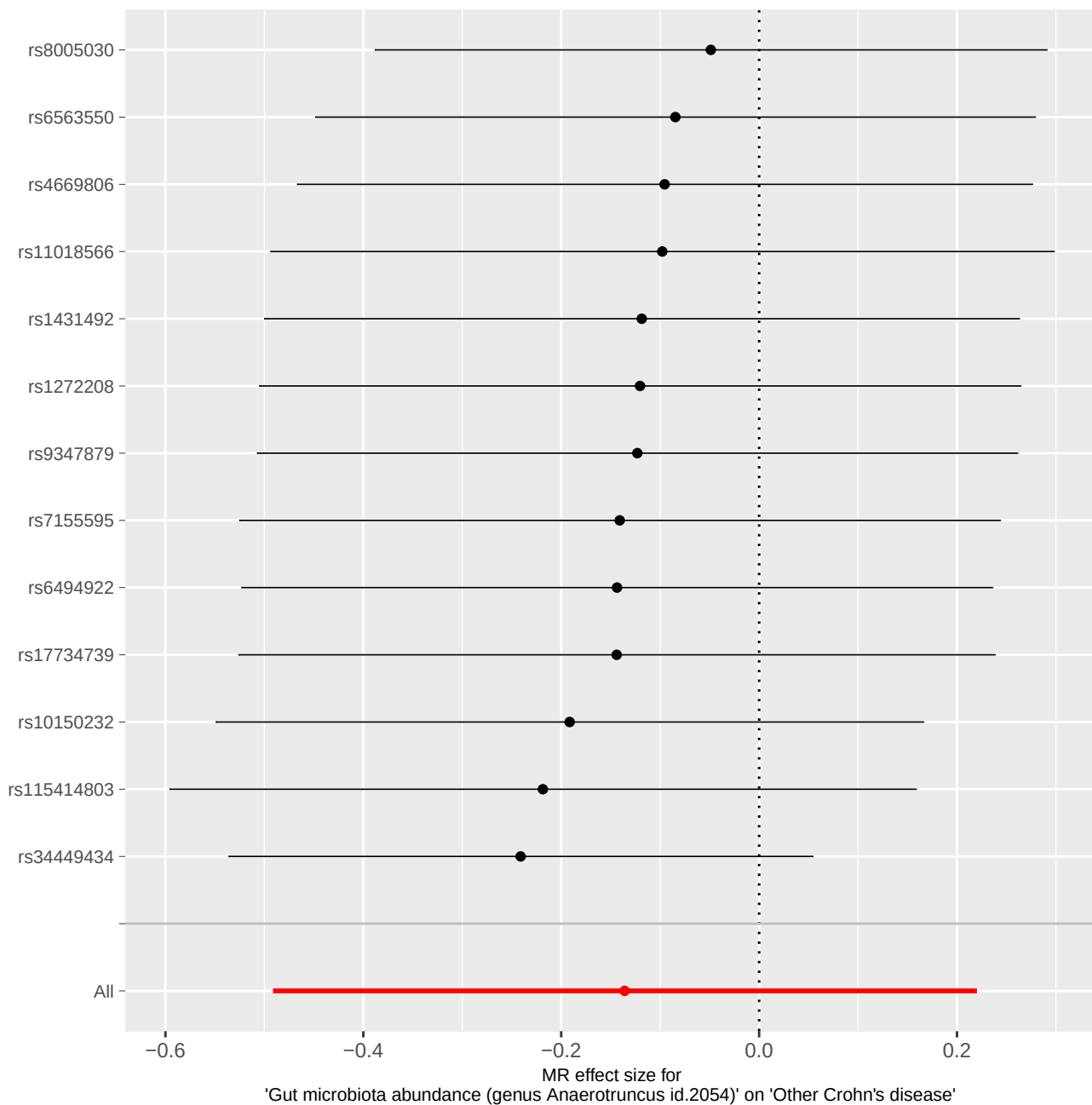


Batch 189 : Gut microbiota abundance (genus Anaerofilum id.2053) on Other Crohn's disease

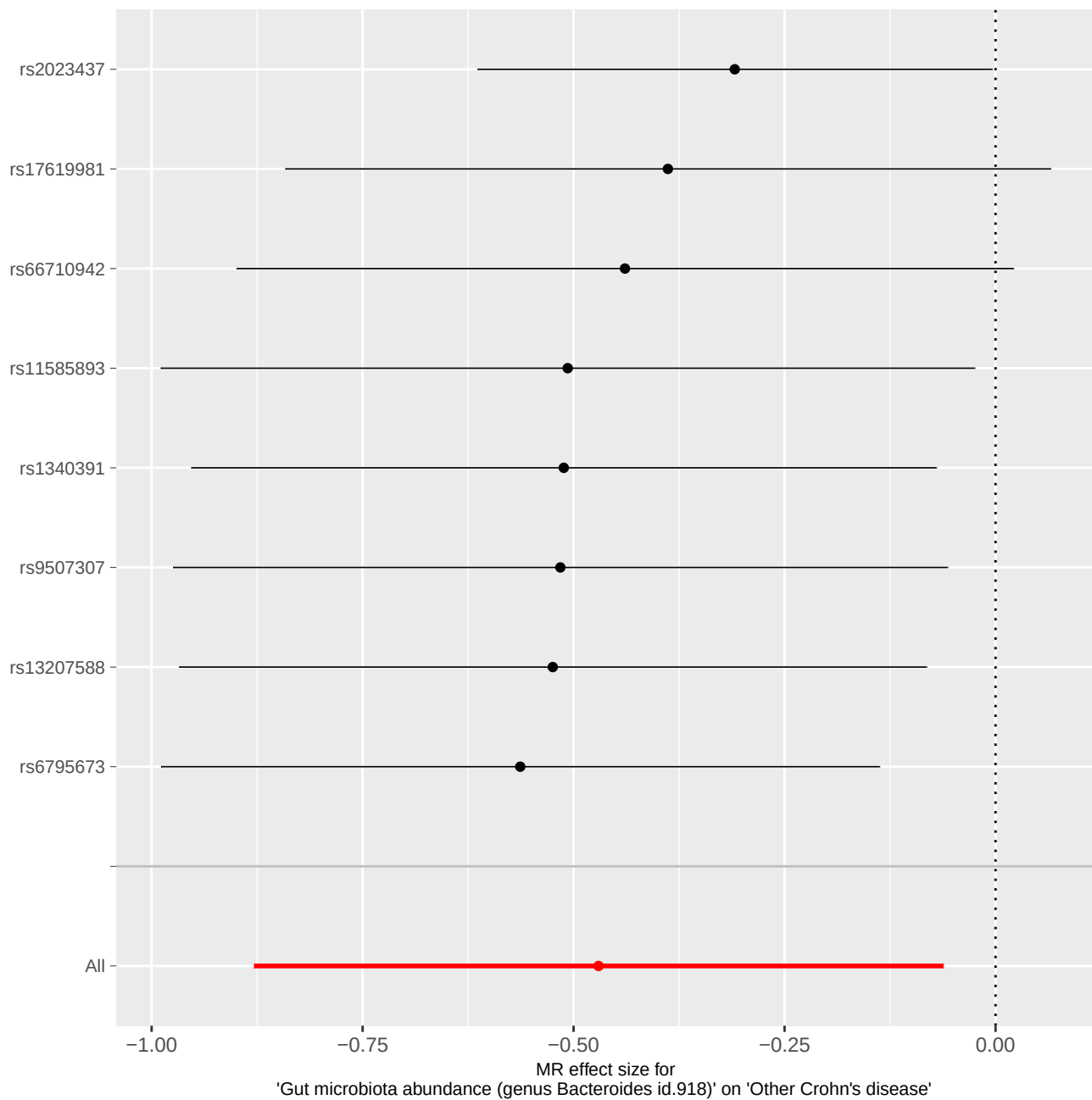


Batch 190 : Gut microbiota abundance (genus Anaerostipes id.1991) on Other Crohn's disease

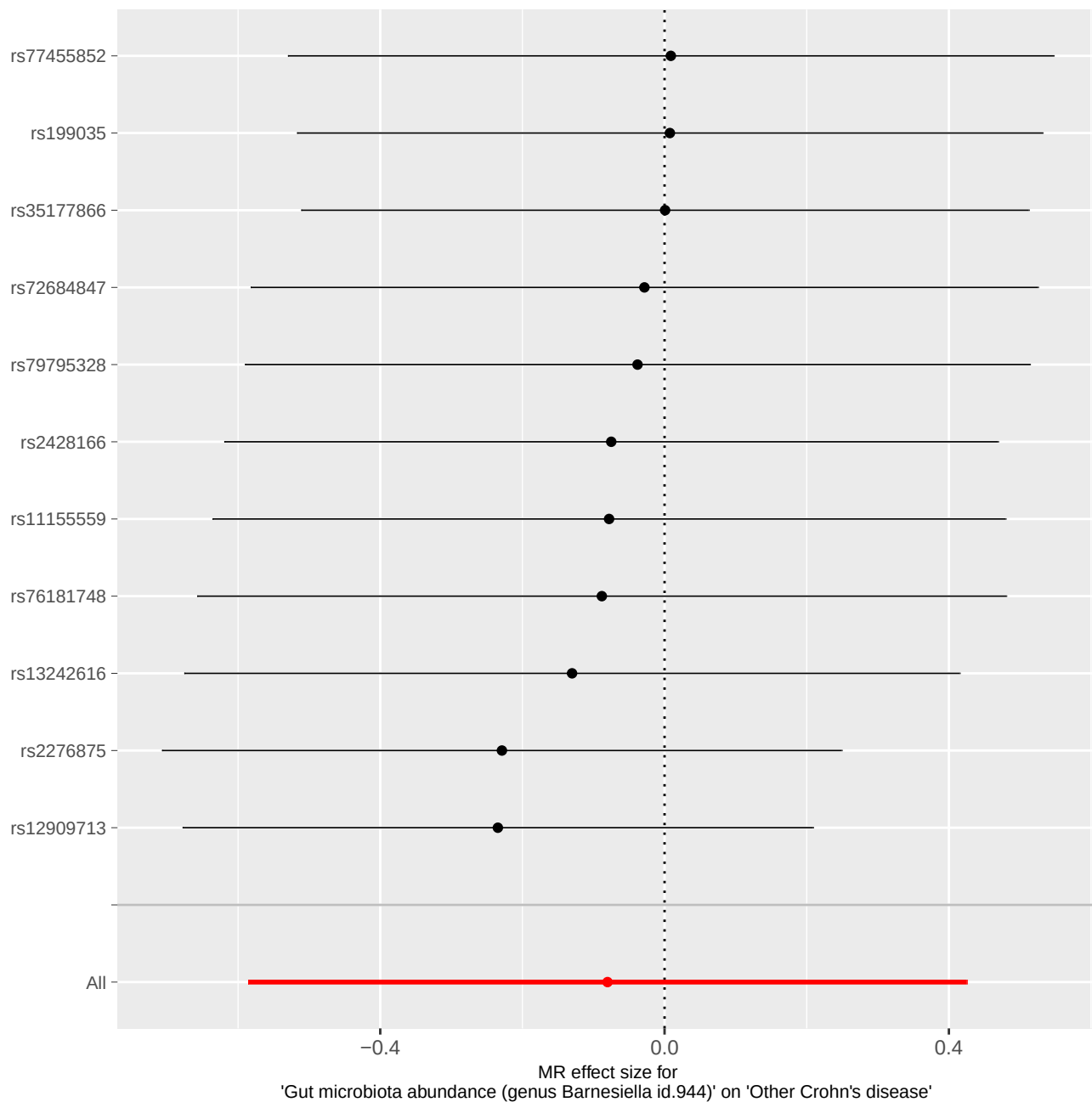


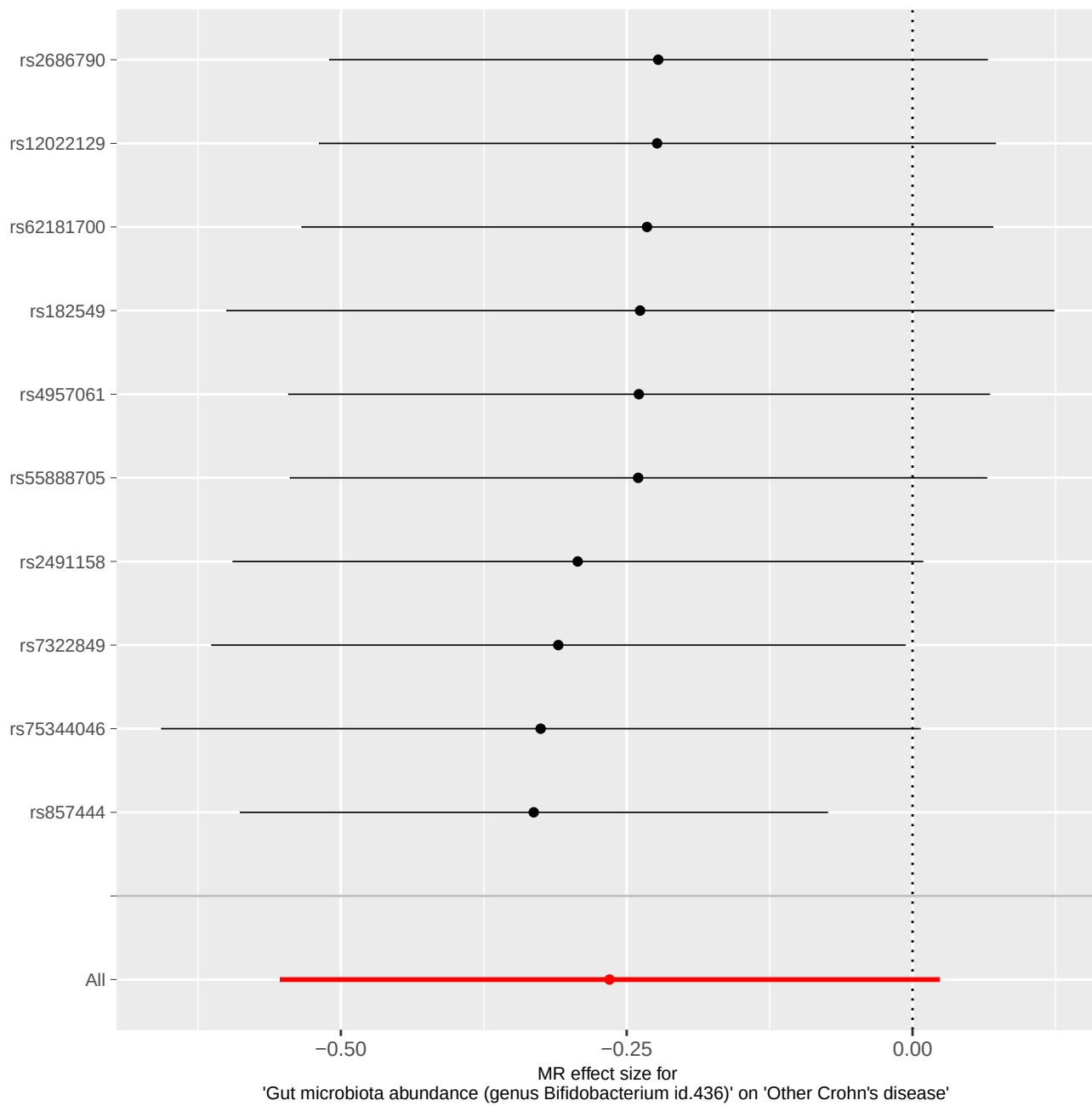


Batch 192 : Gut microbiota abundance (genus Bacteroides id.918) on Other Crohn's disease

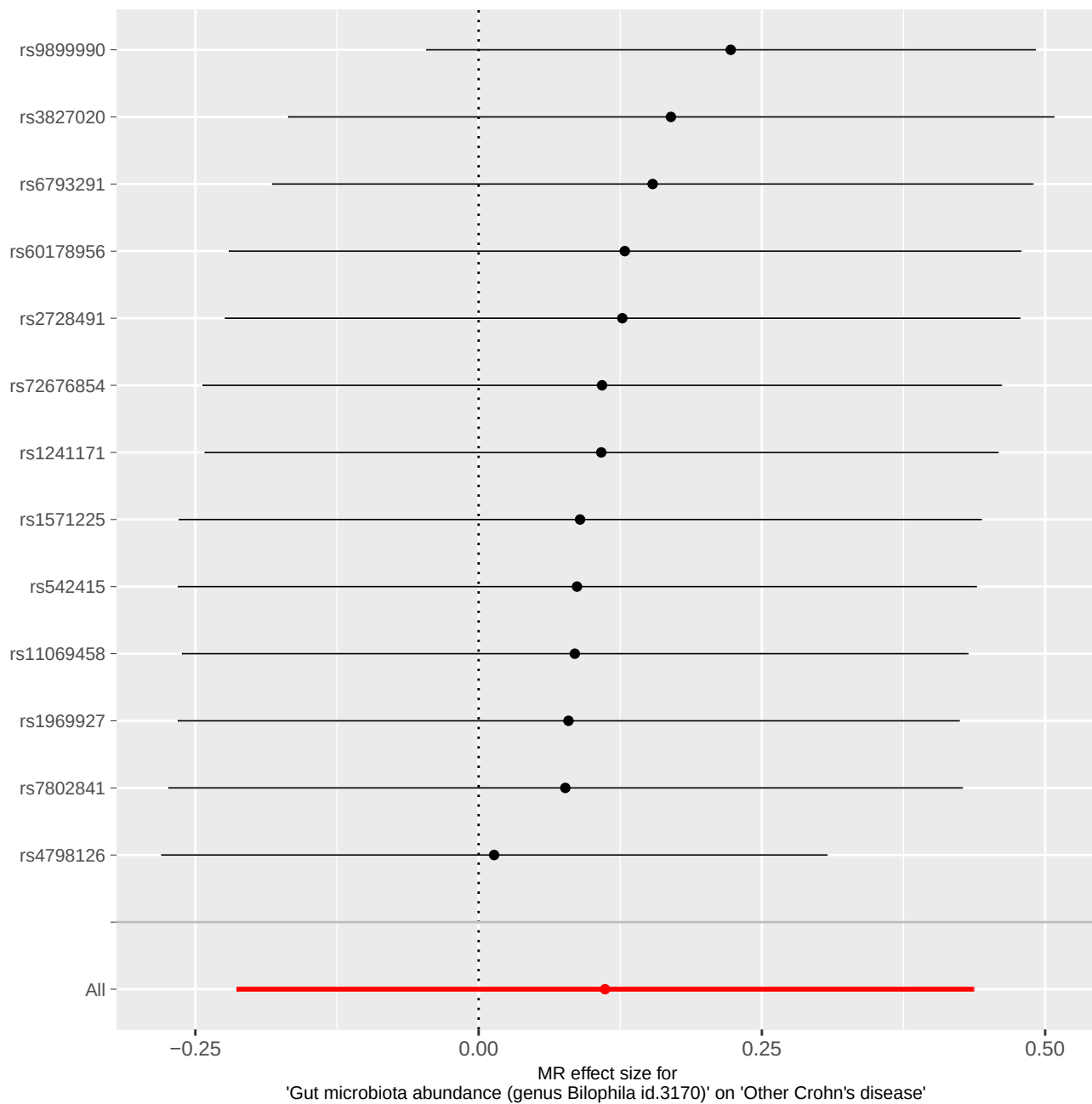


Batch 193 : Gut microbiota abundance (genus Barnesiella id.944) on Other Crohn's disease

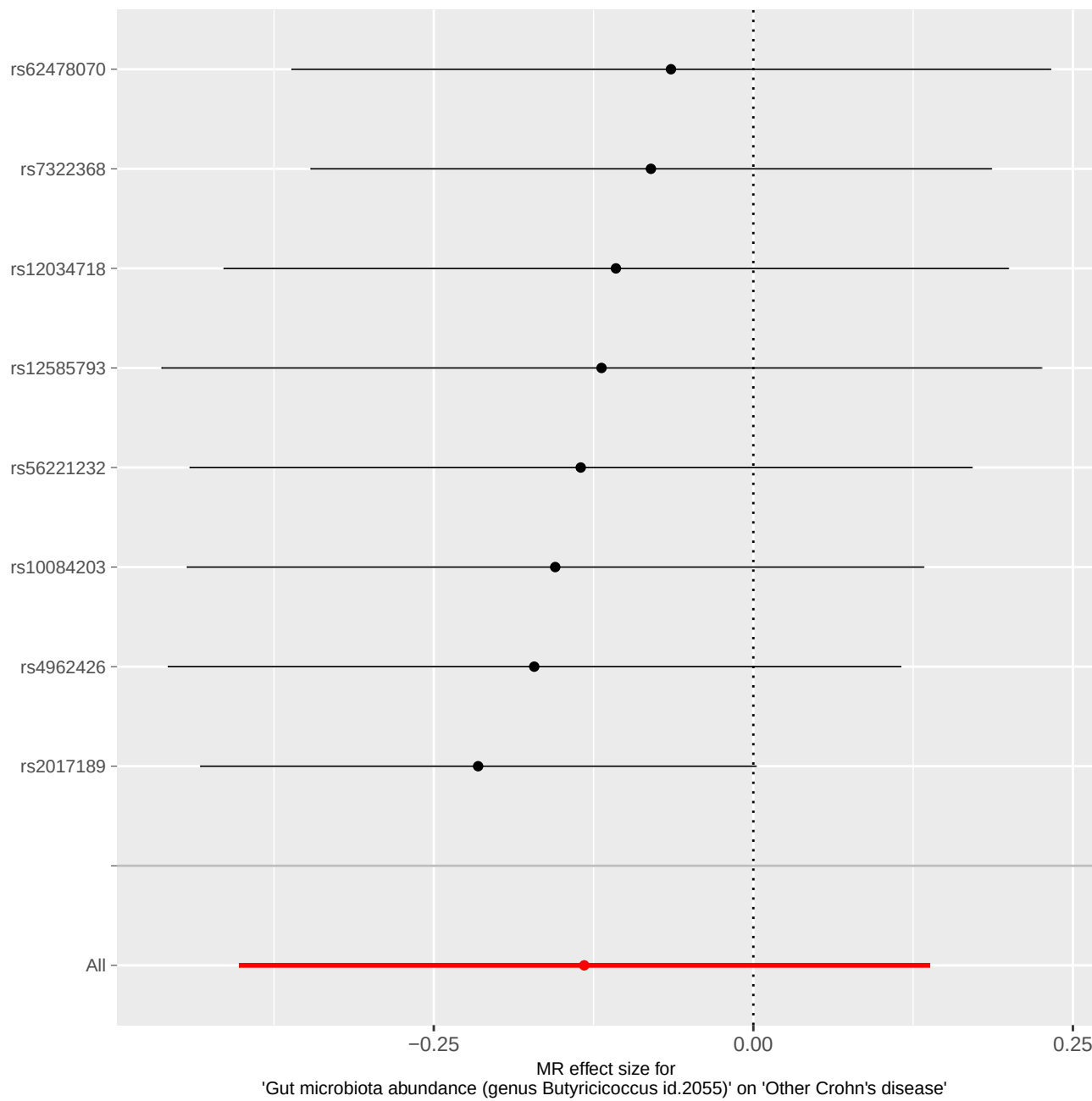


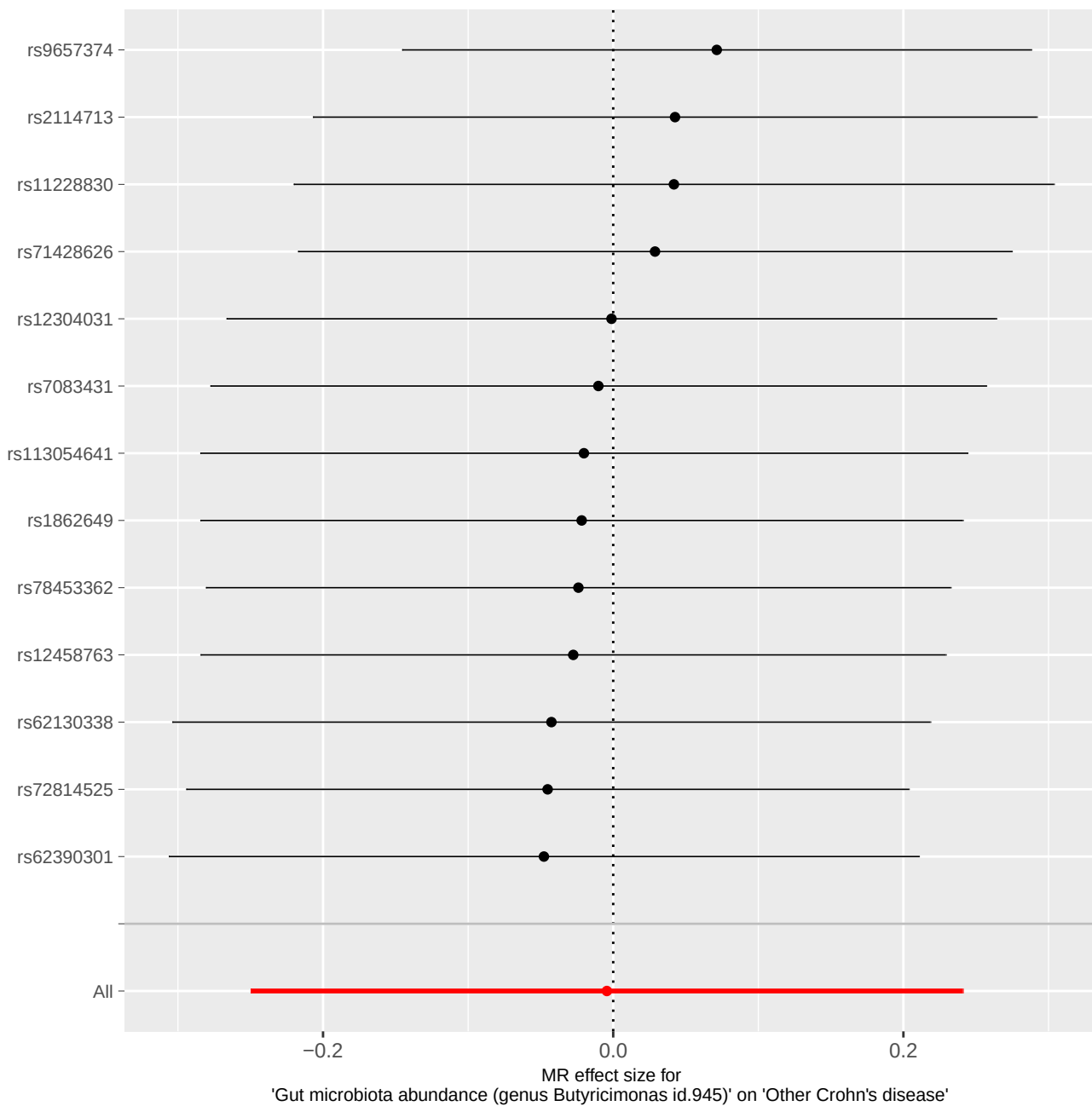


Batch 195 : Gut microbiota abundance (genus Bilophila id.3170) on Other Crohn's disease

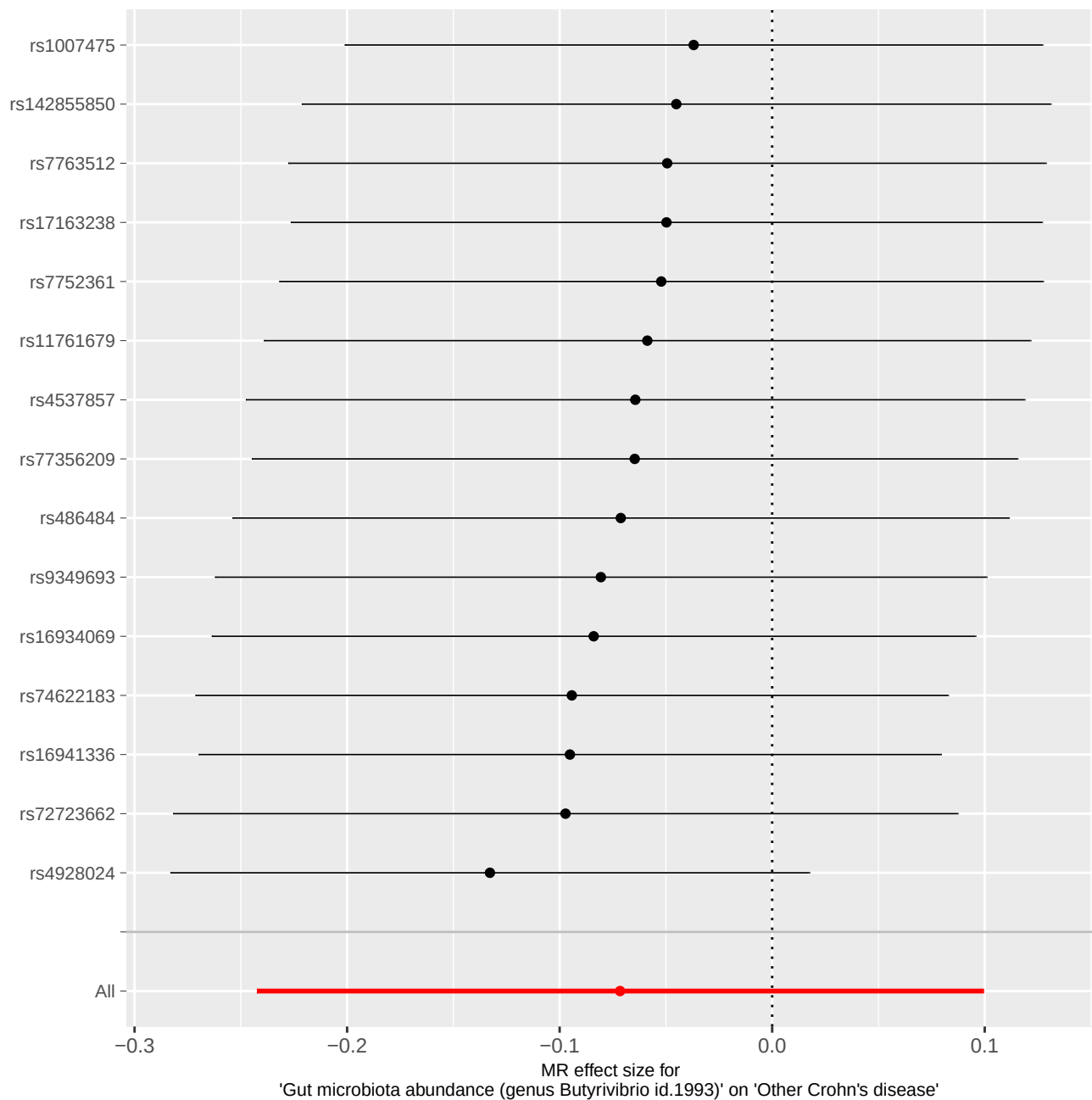


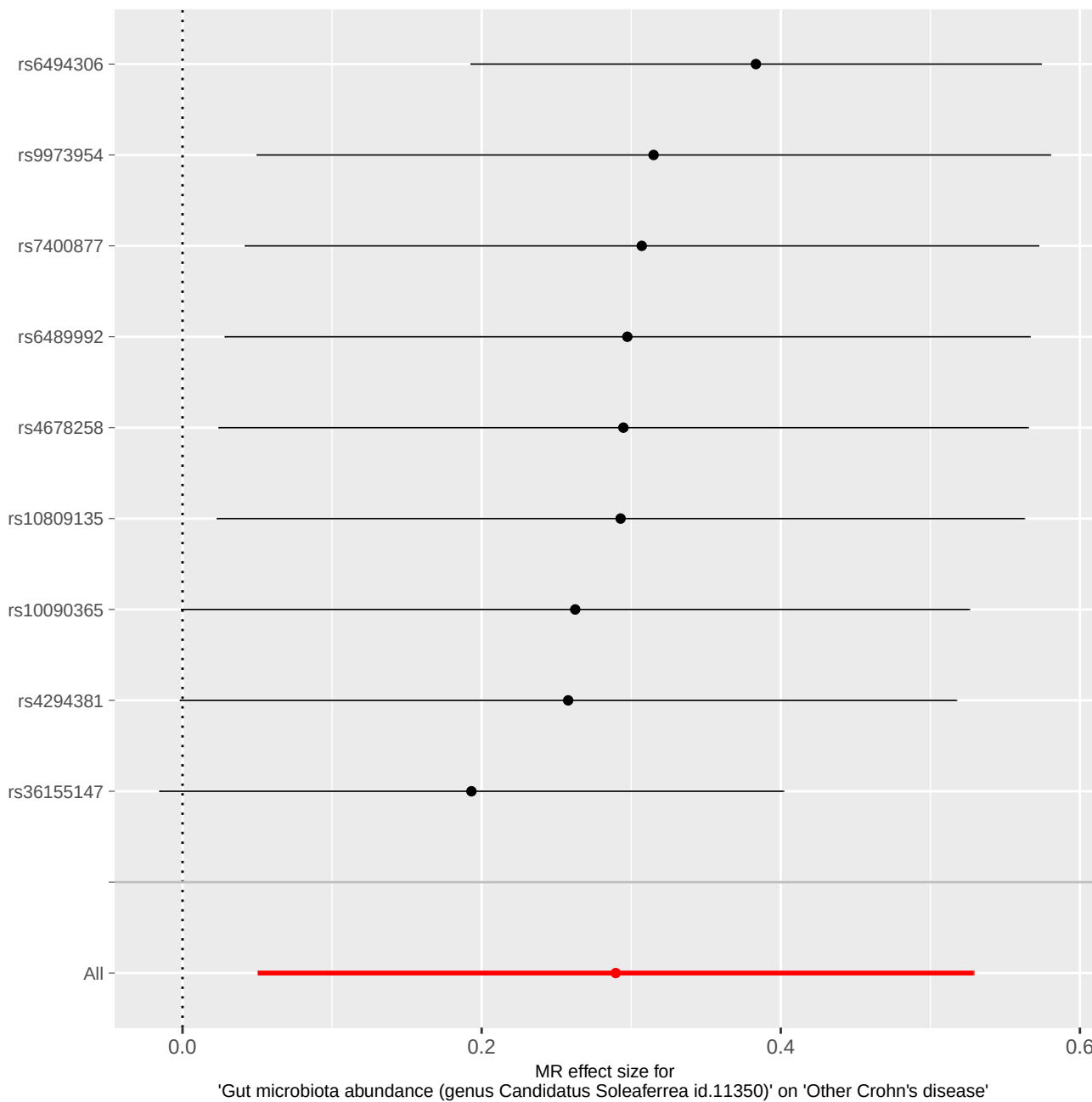
Batch 197 : Gut microbiota abundance (genus Butyricicoccus id.2055) on Other Crohn's disease

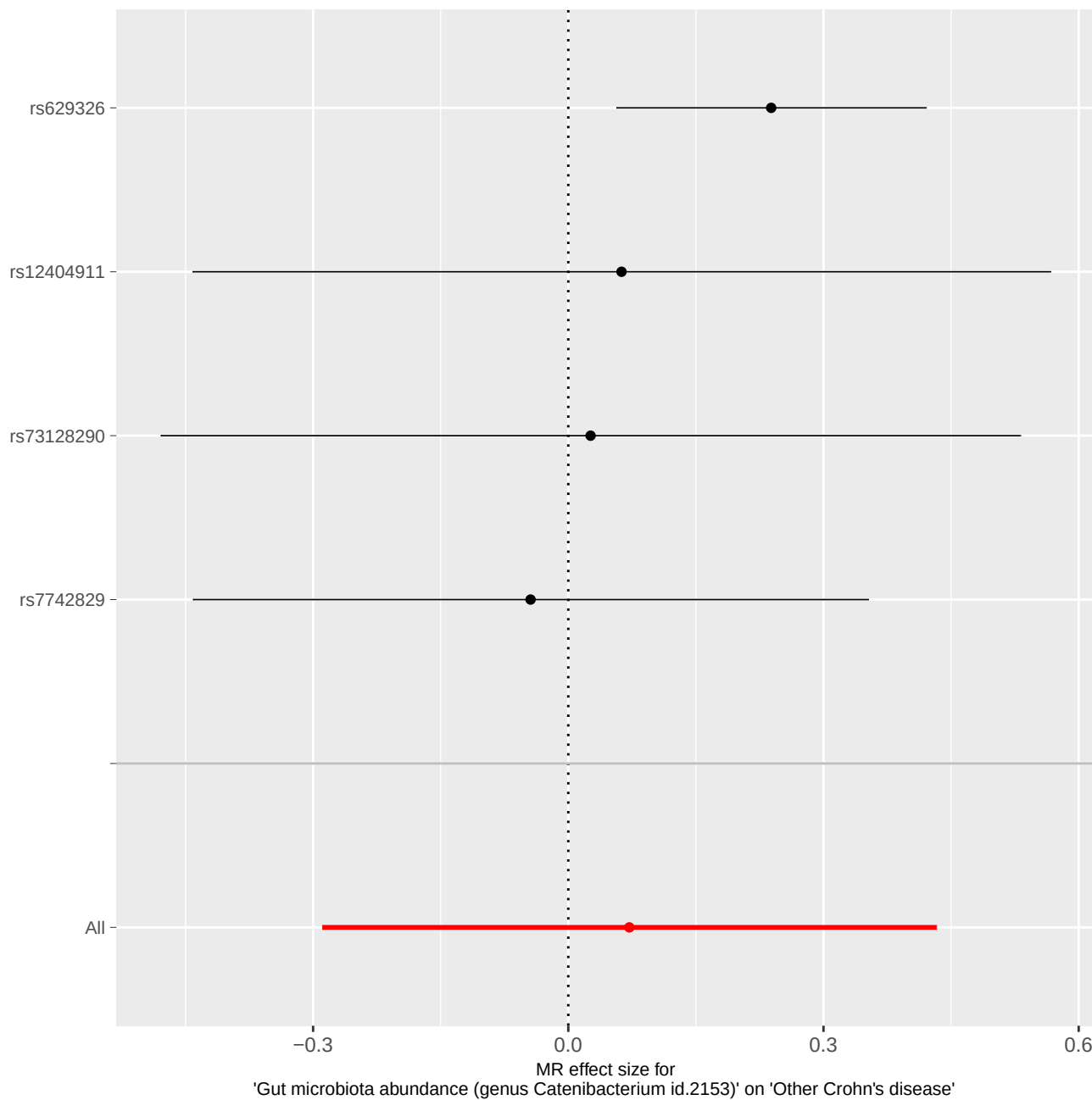


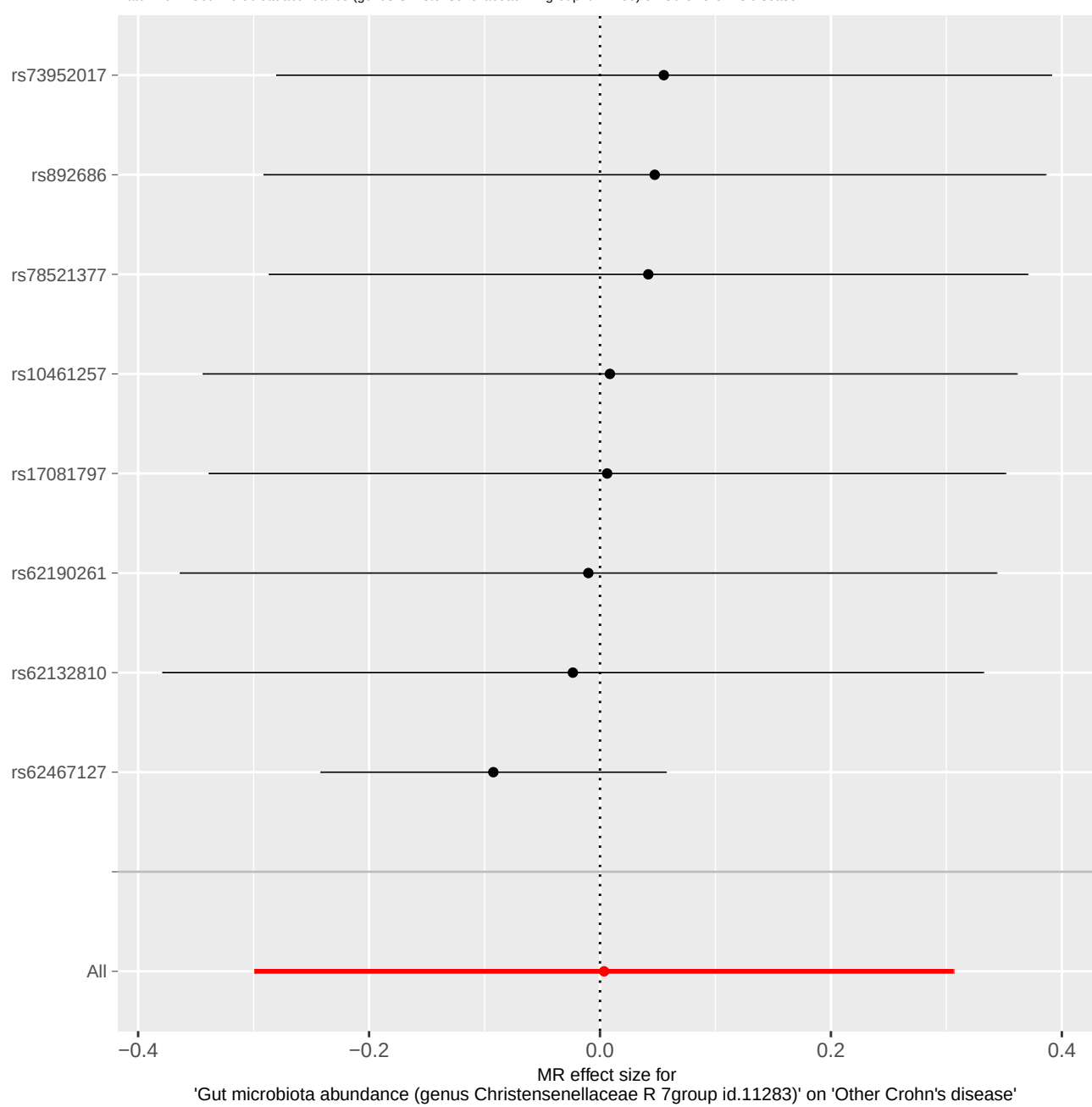


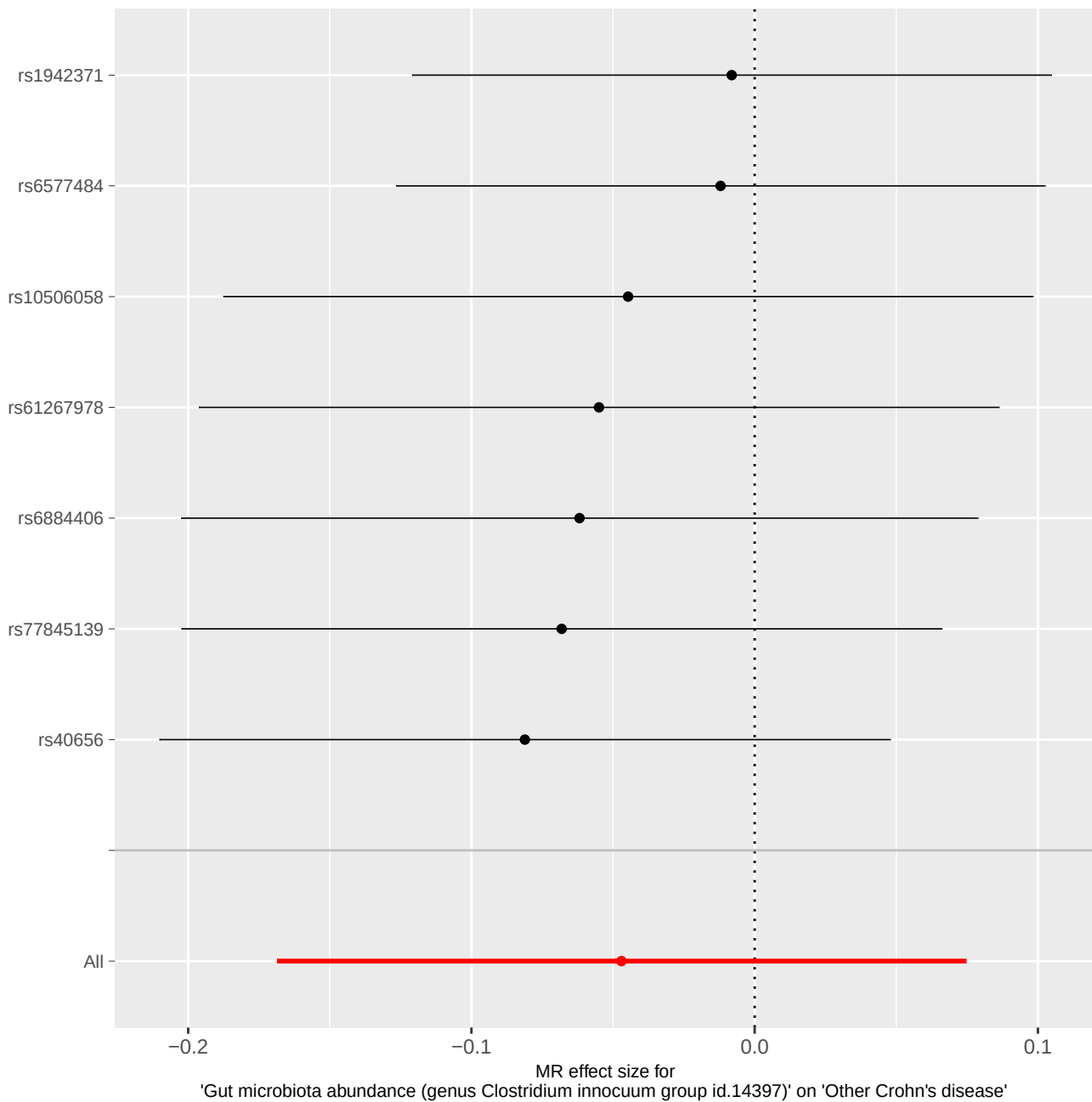
Batch 199 : Gut microbiota abundance (genus Butyrivibrio id.1993) on Other Crohn's disease

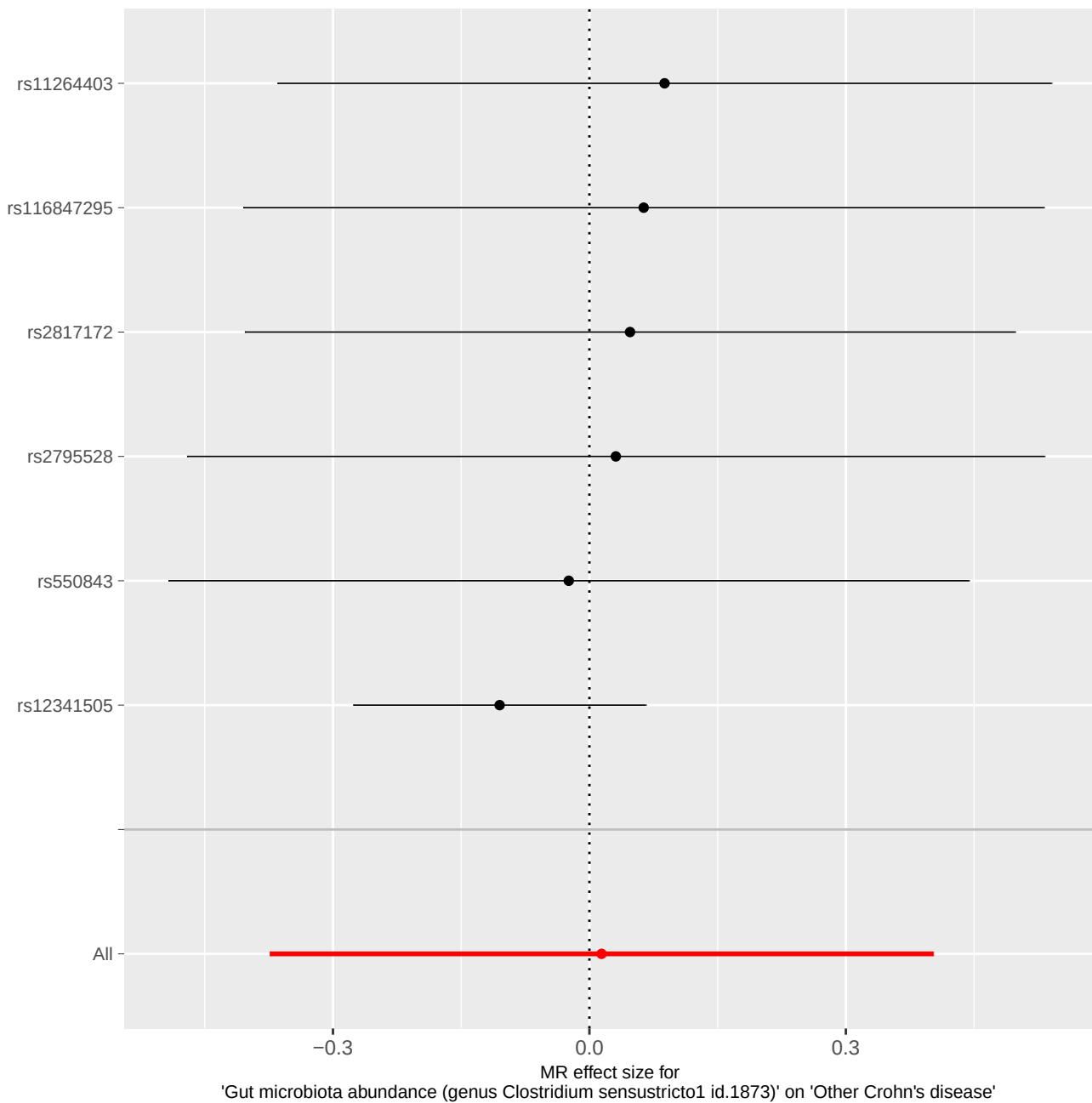


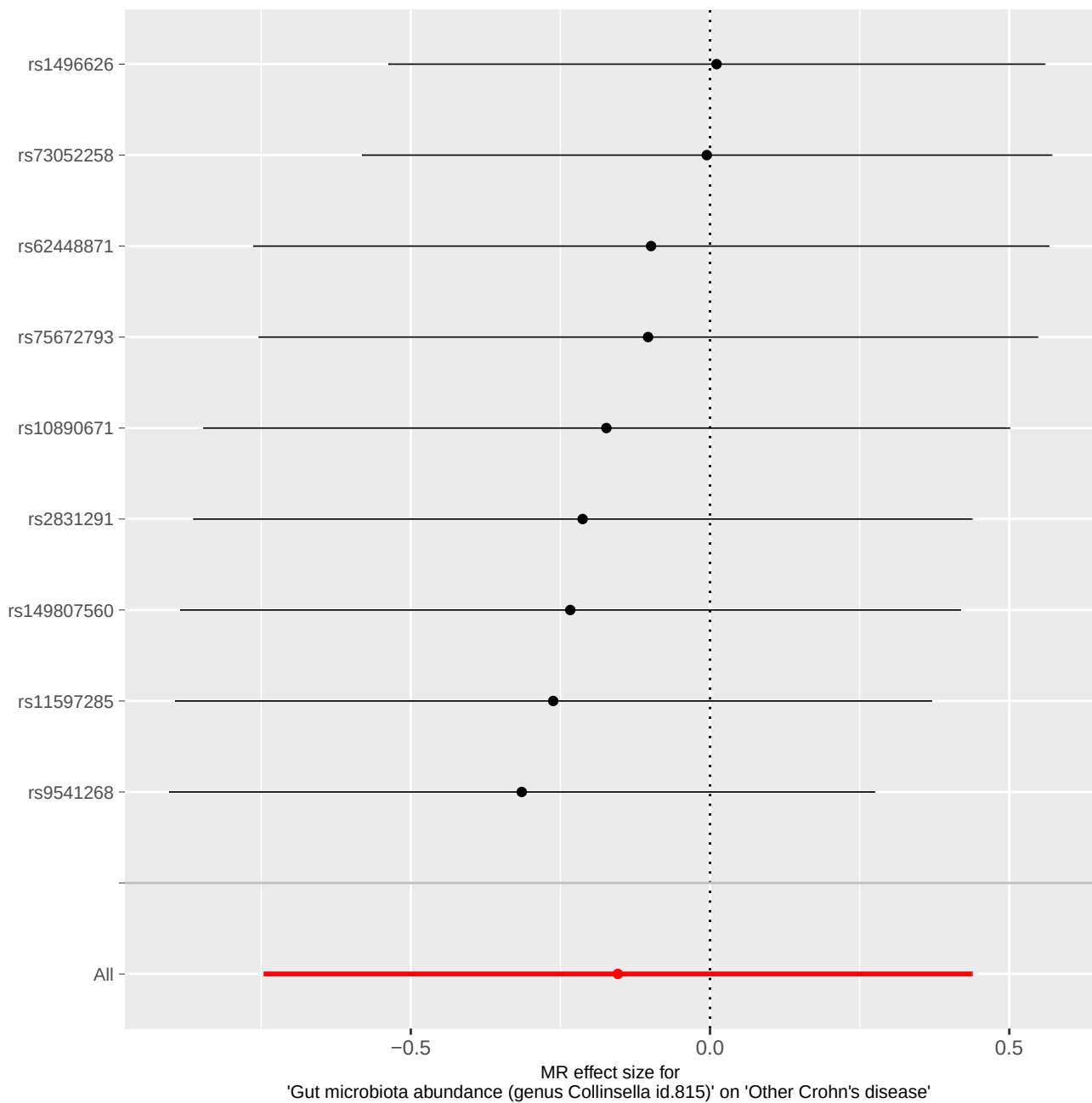


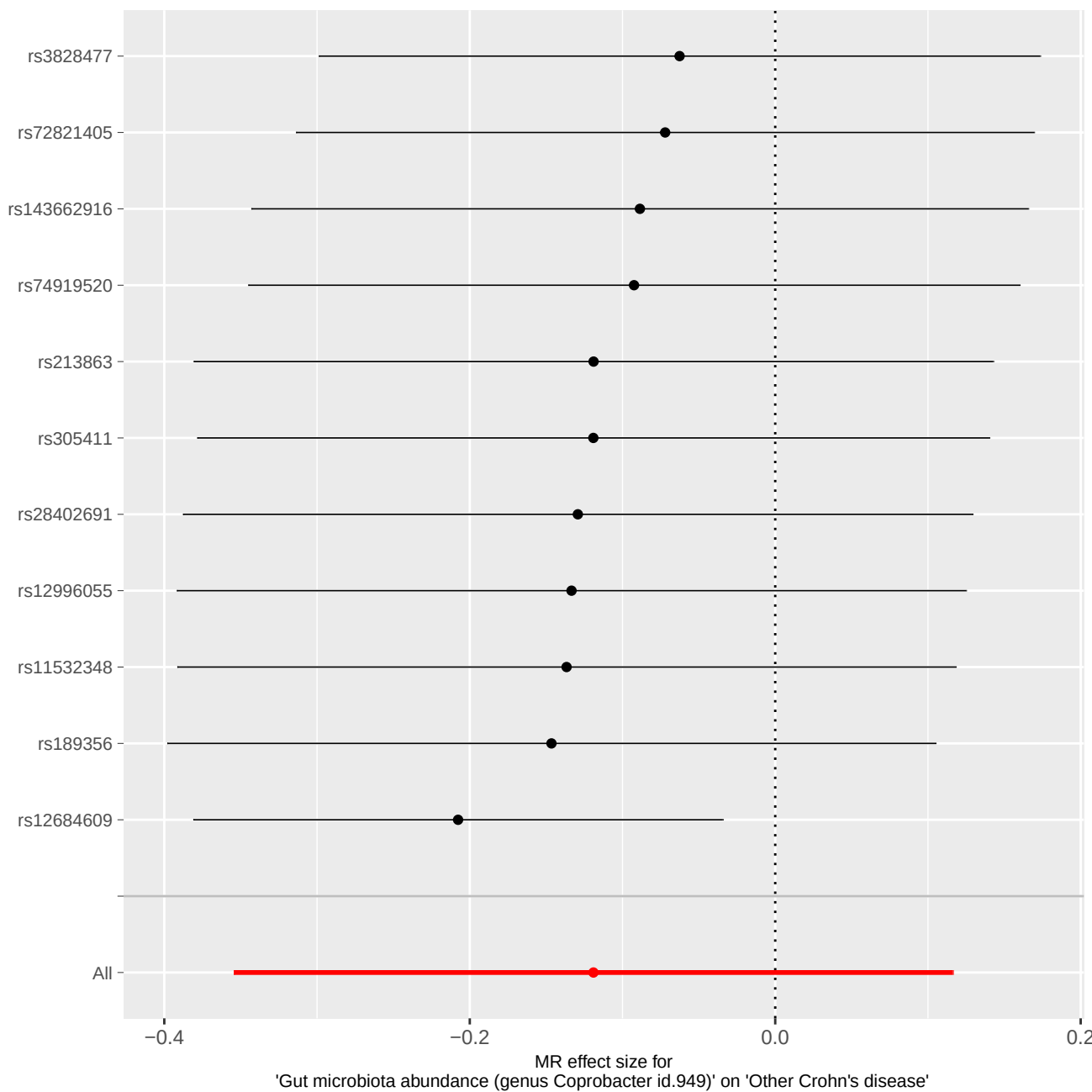


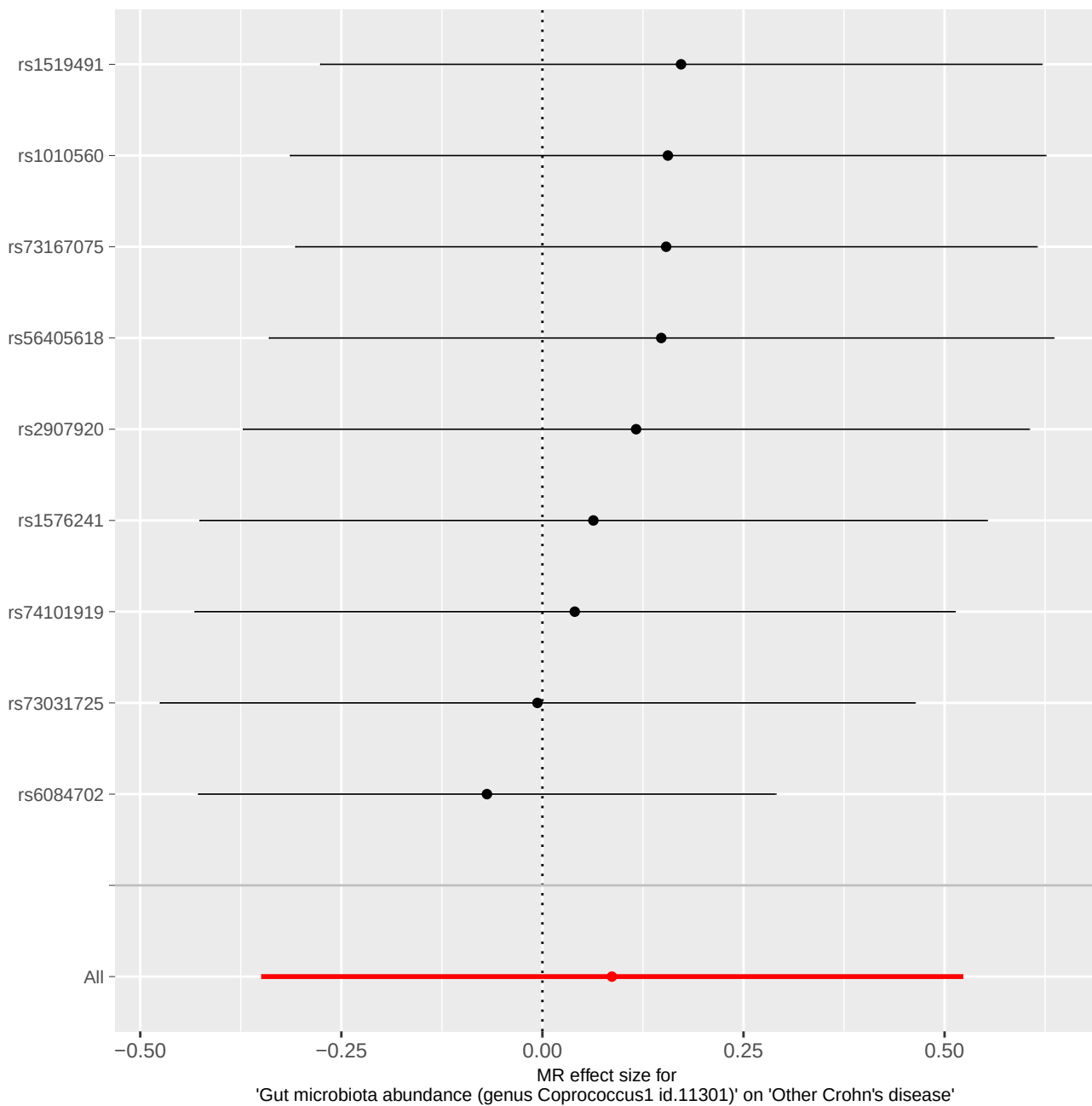


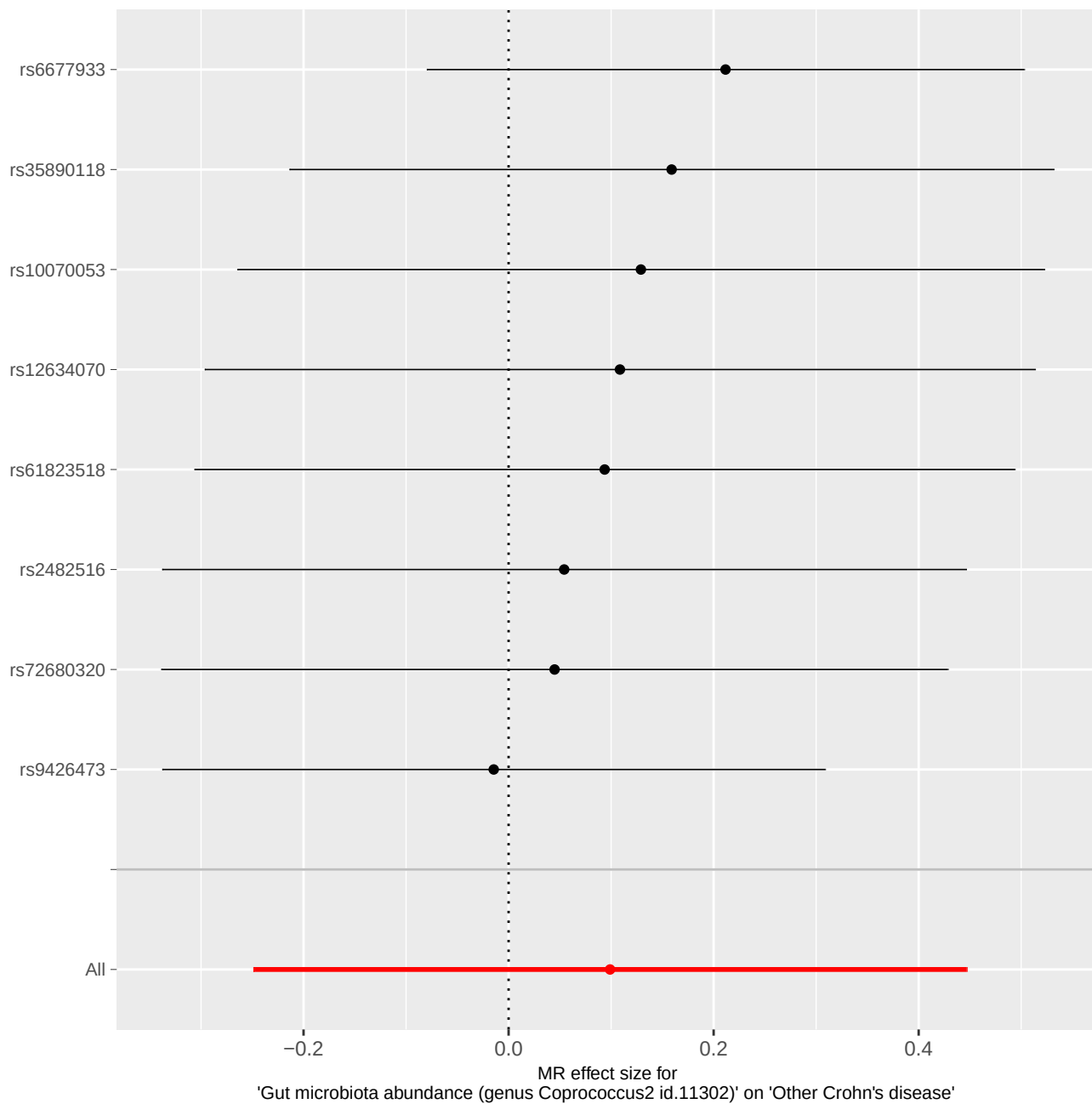


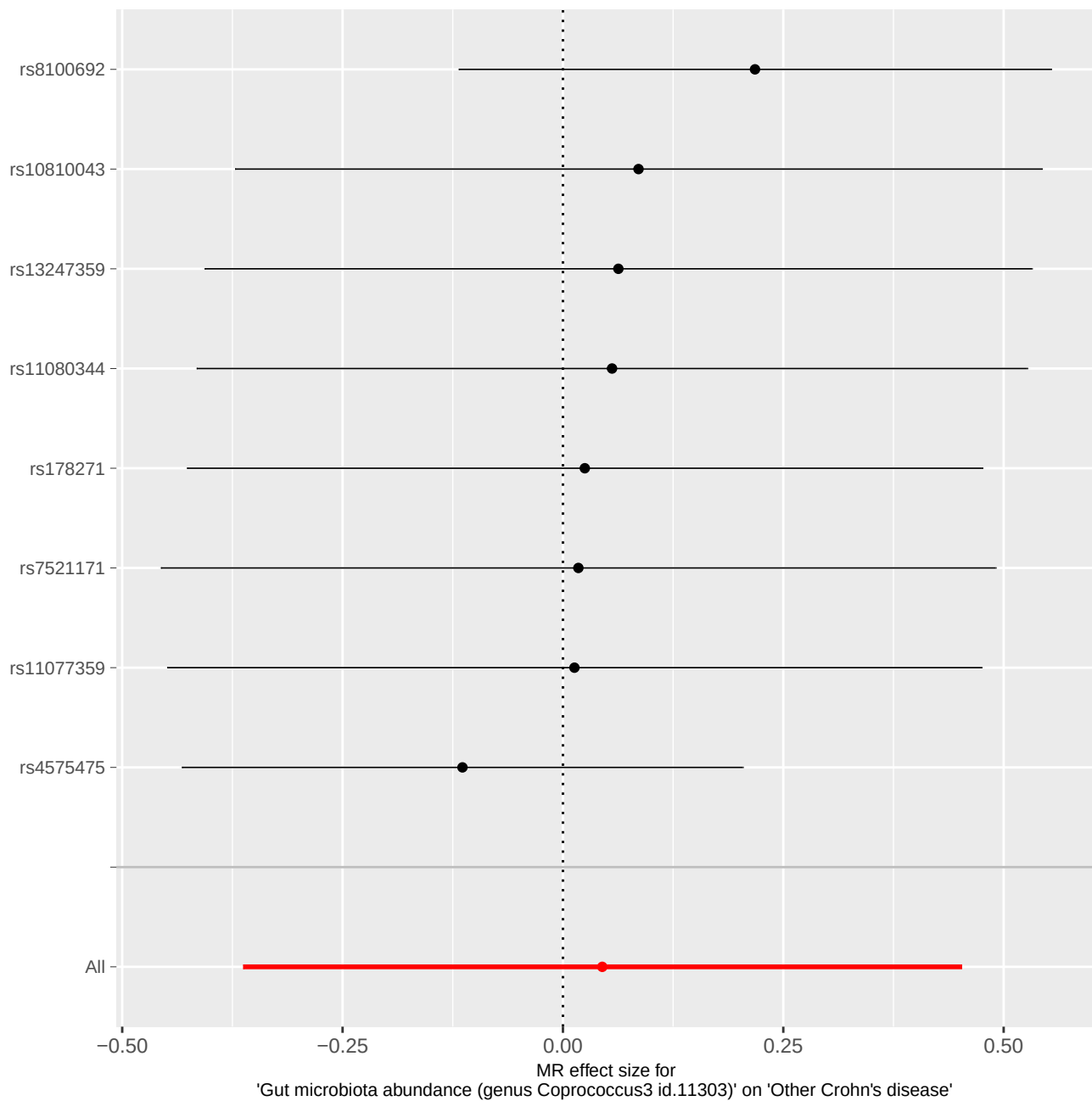


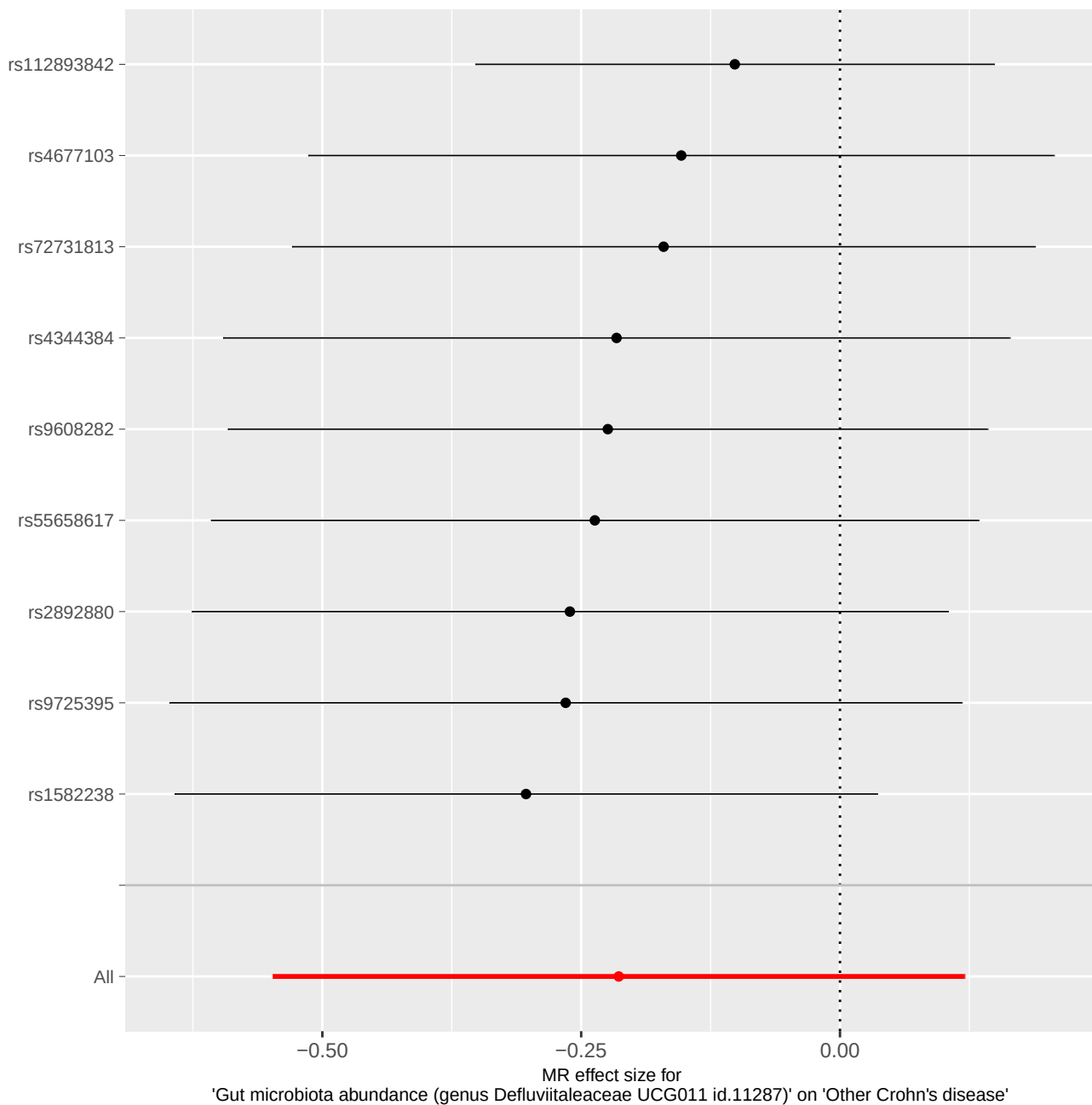


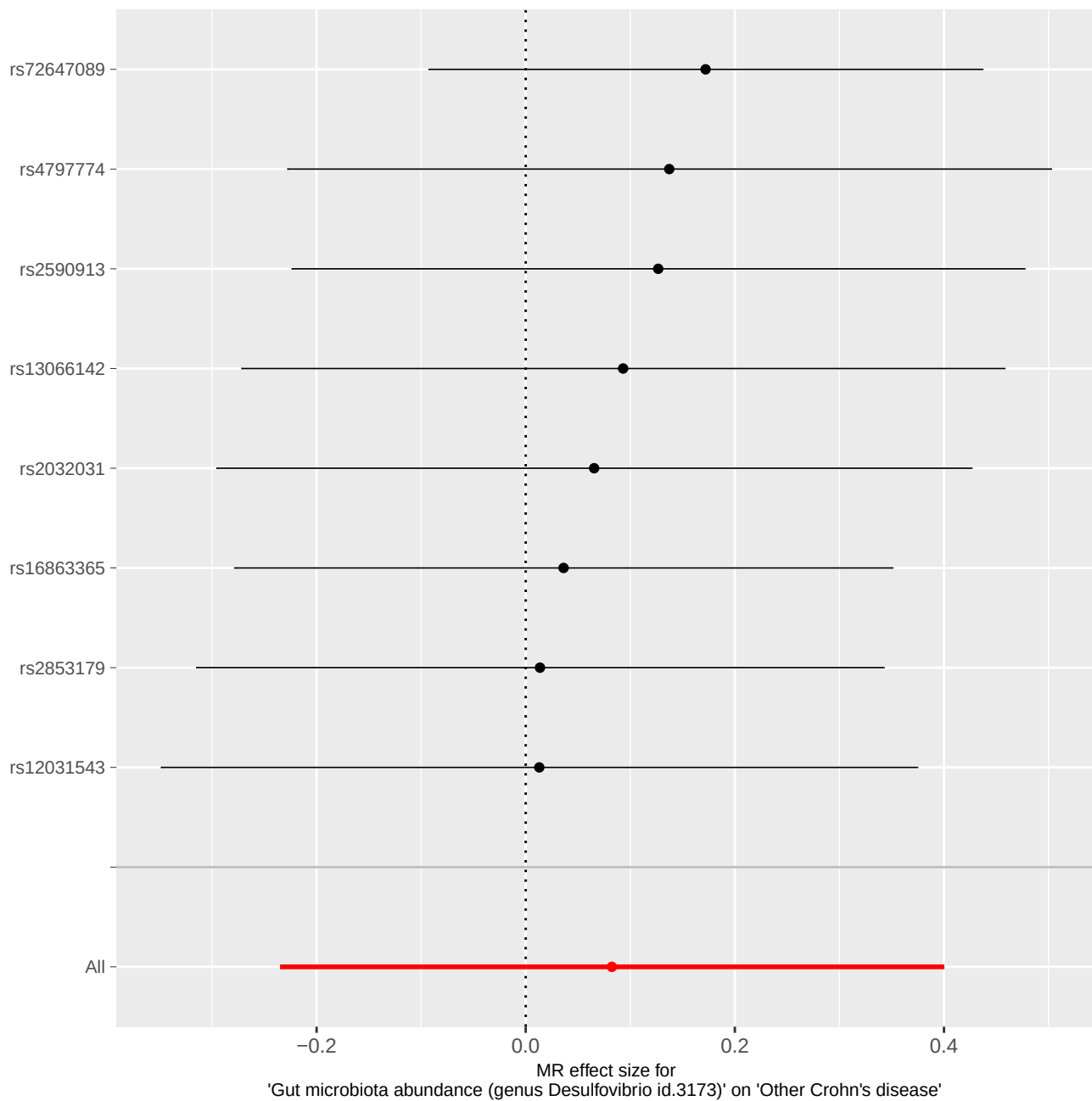




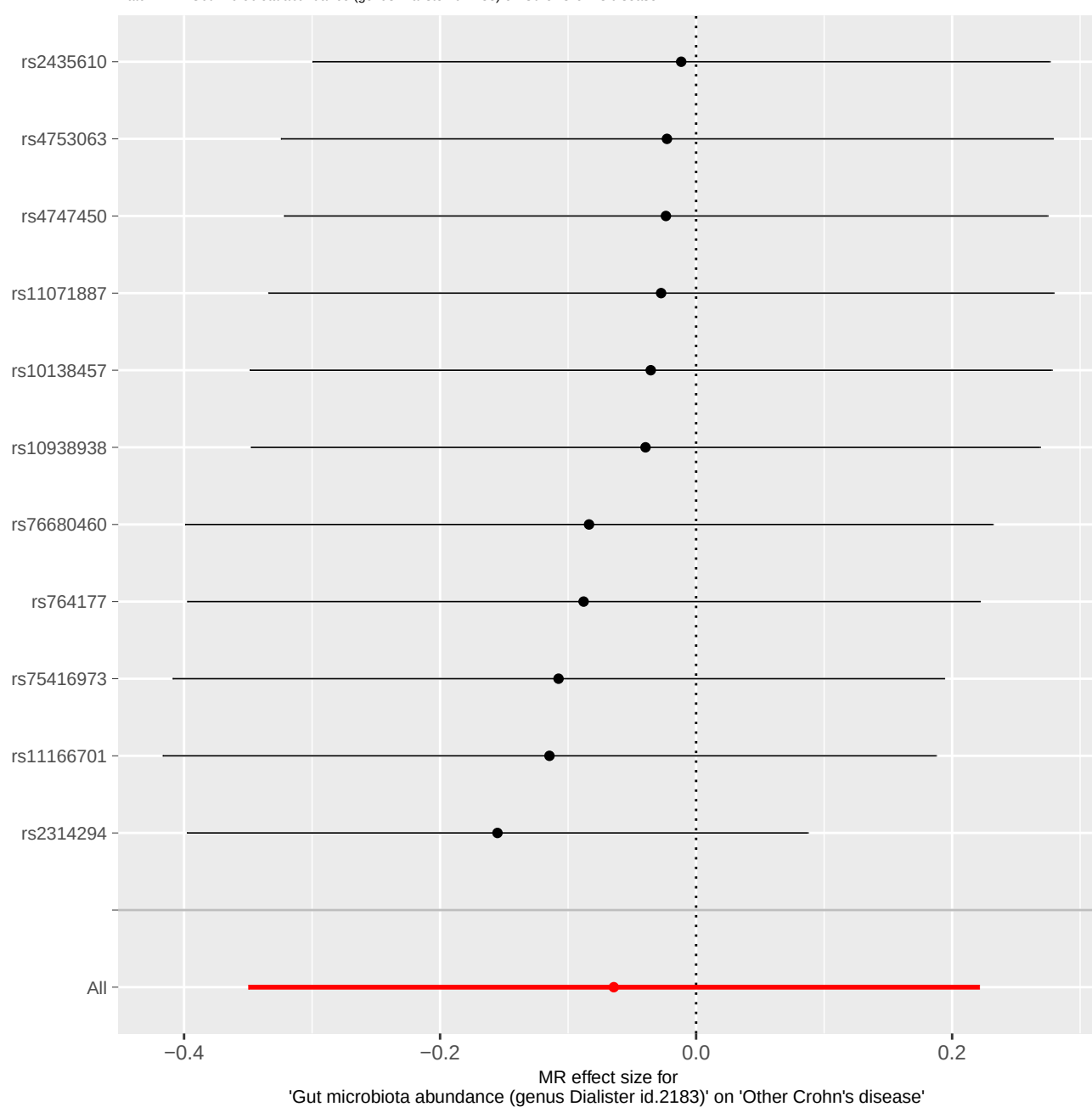


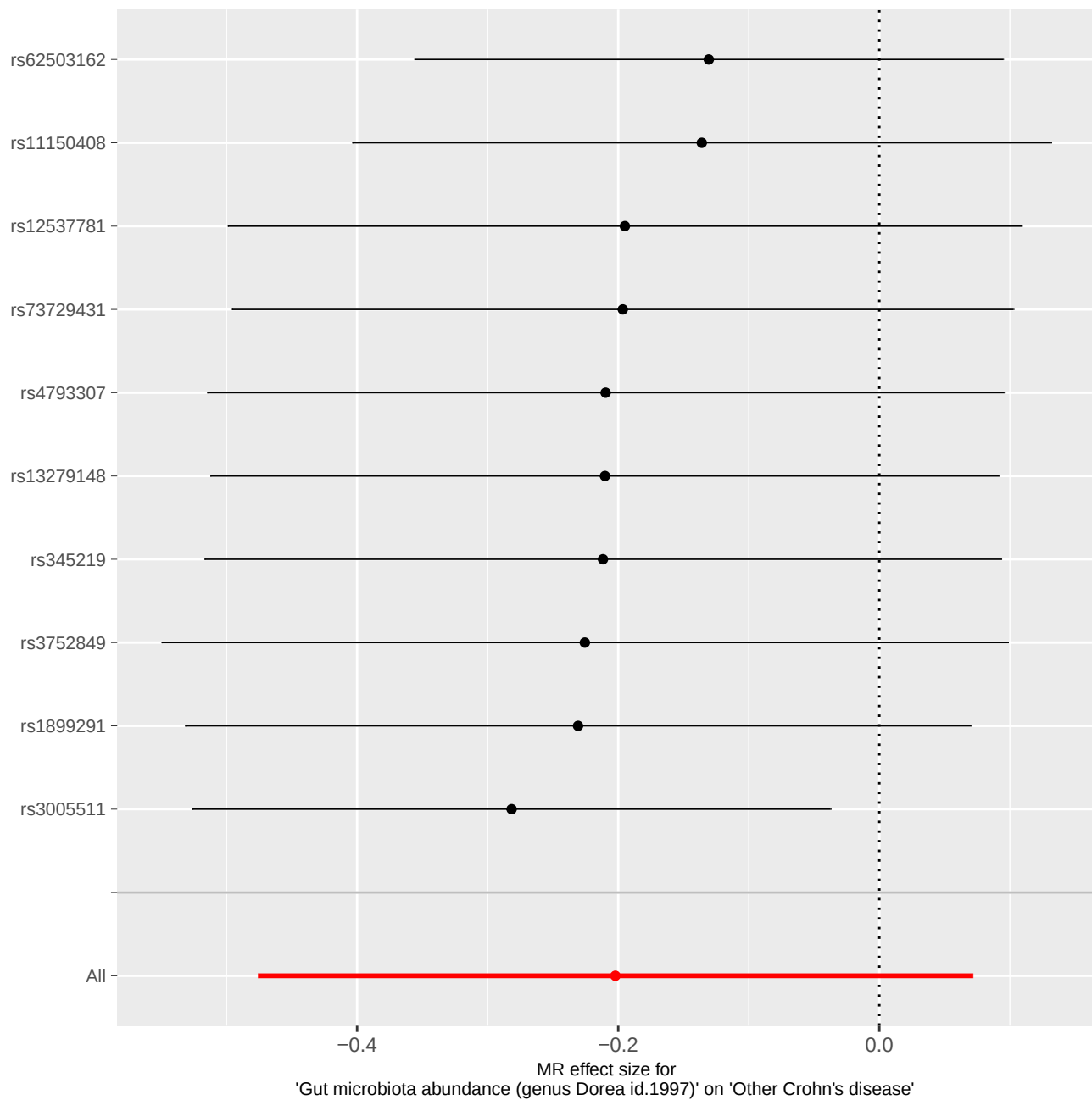


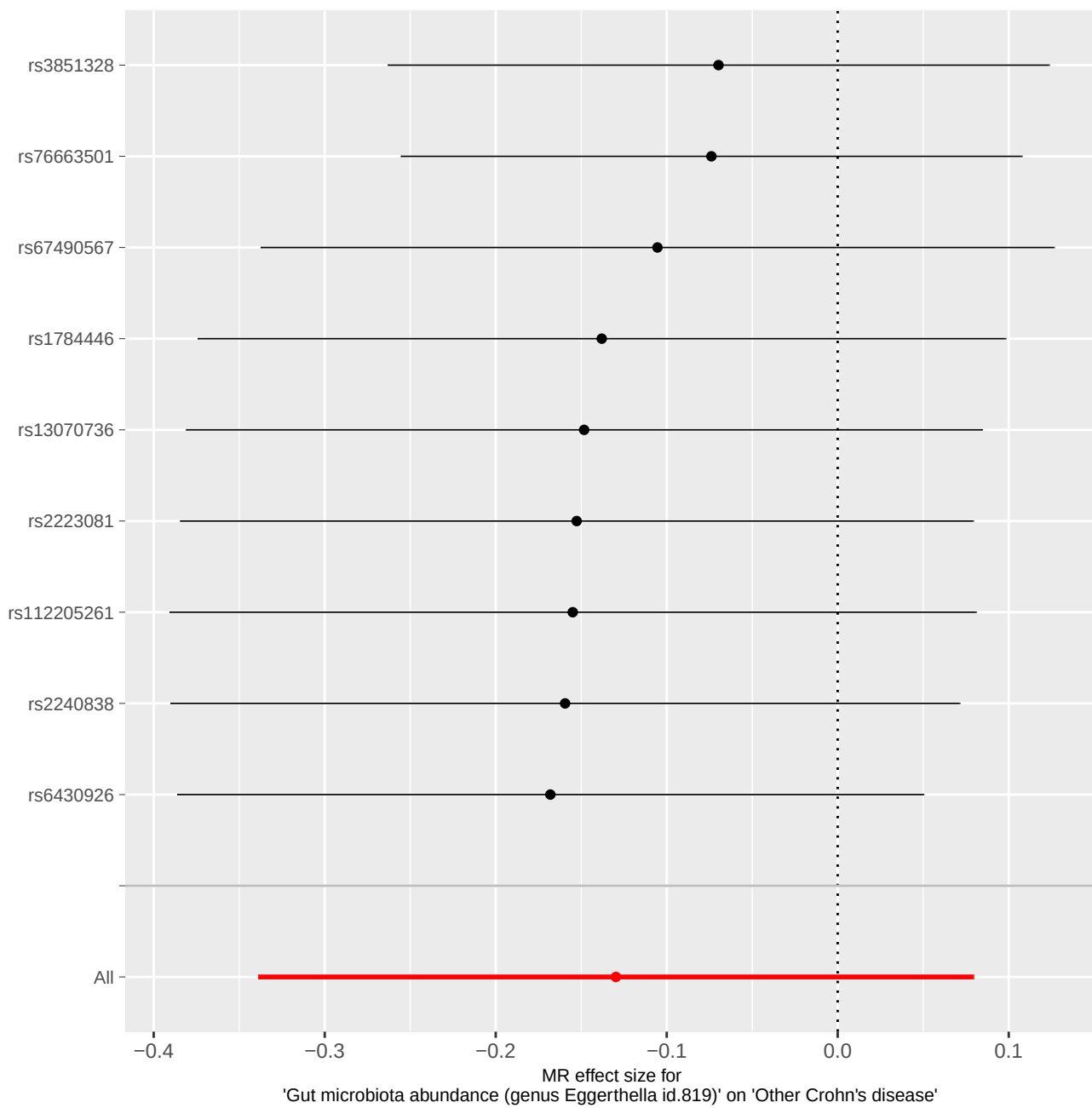


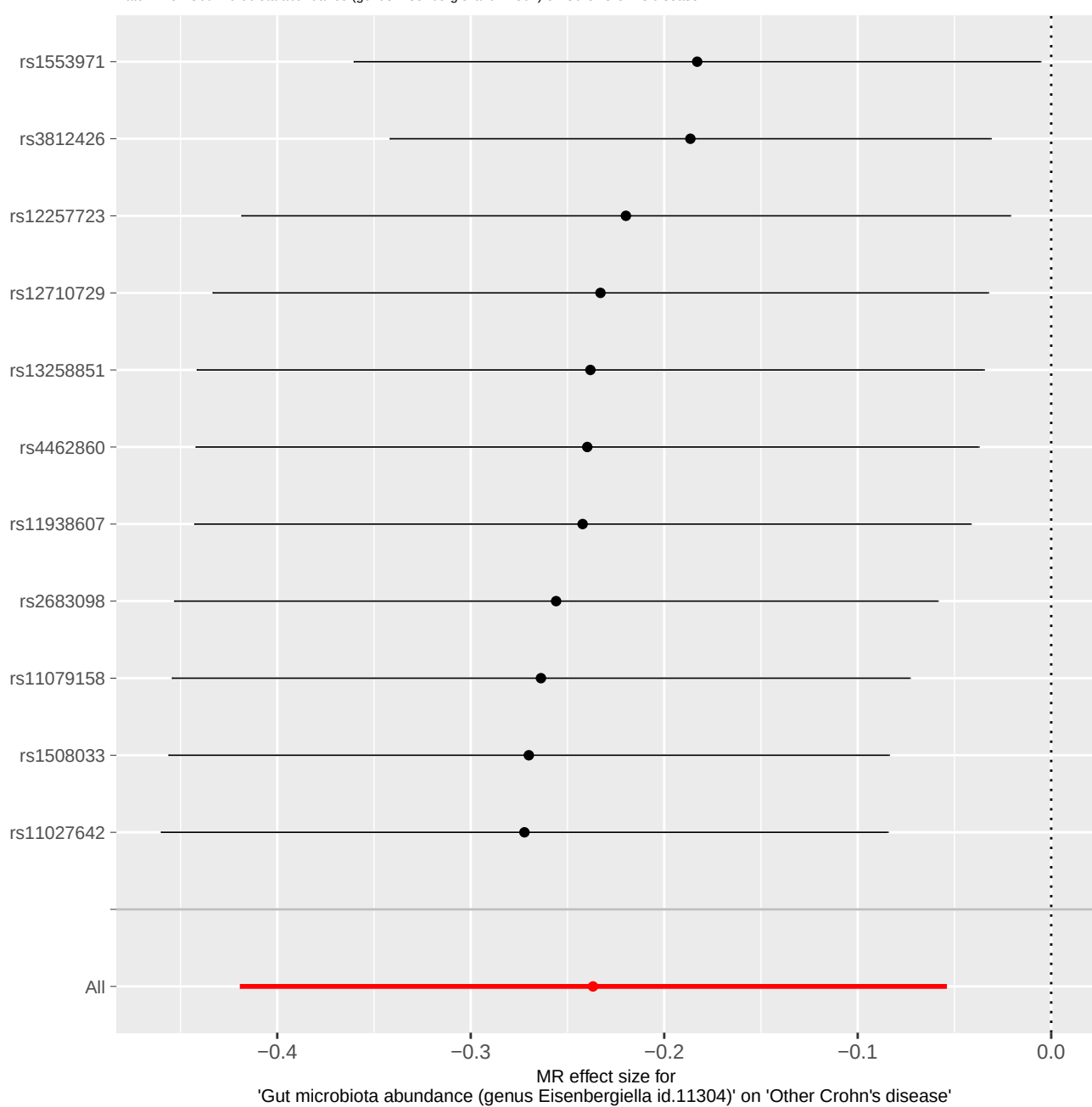


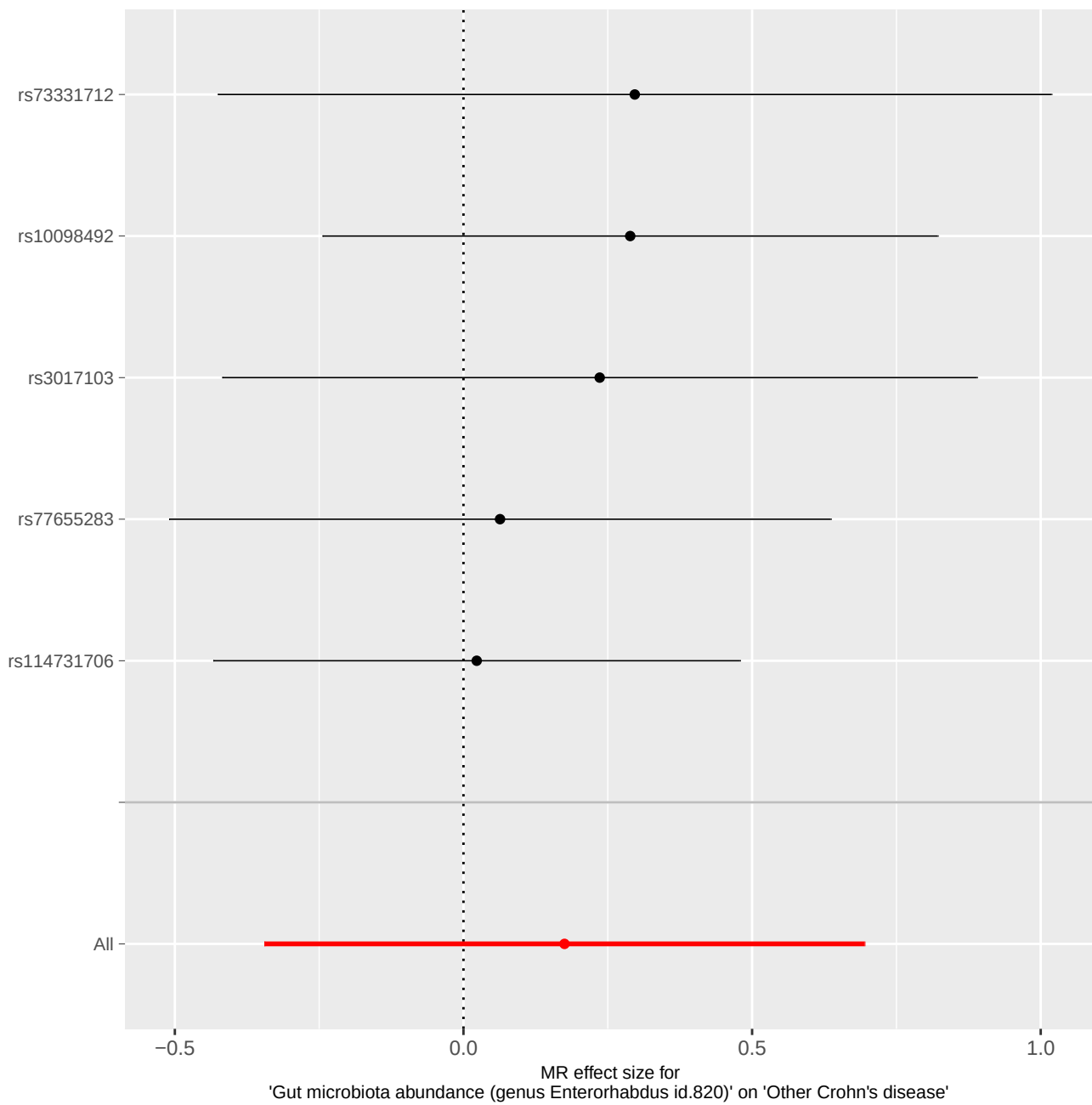
Batch 212 : Gut microbiota abundance (genus Dialister id.2183) on Other Crohn's disease

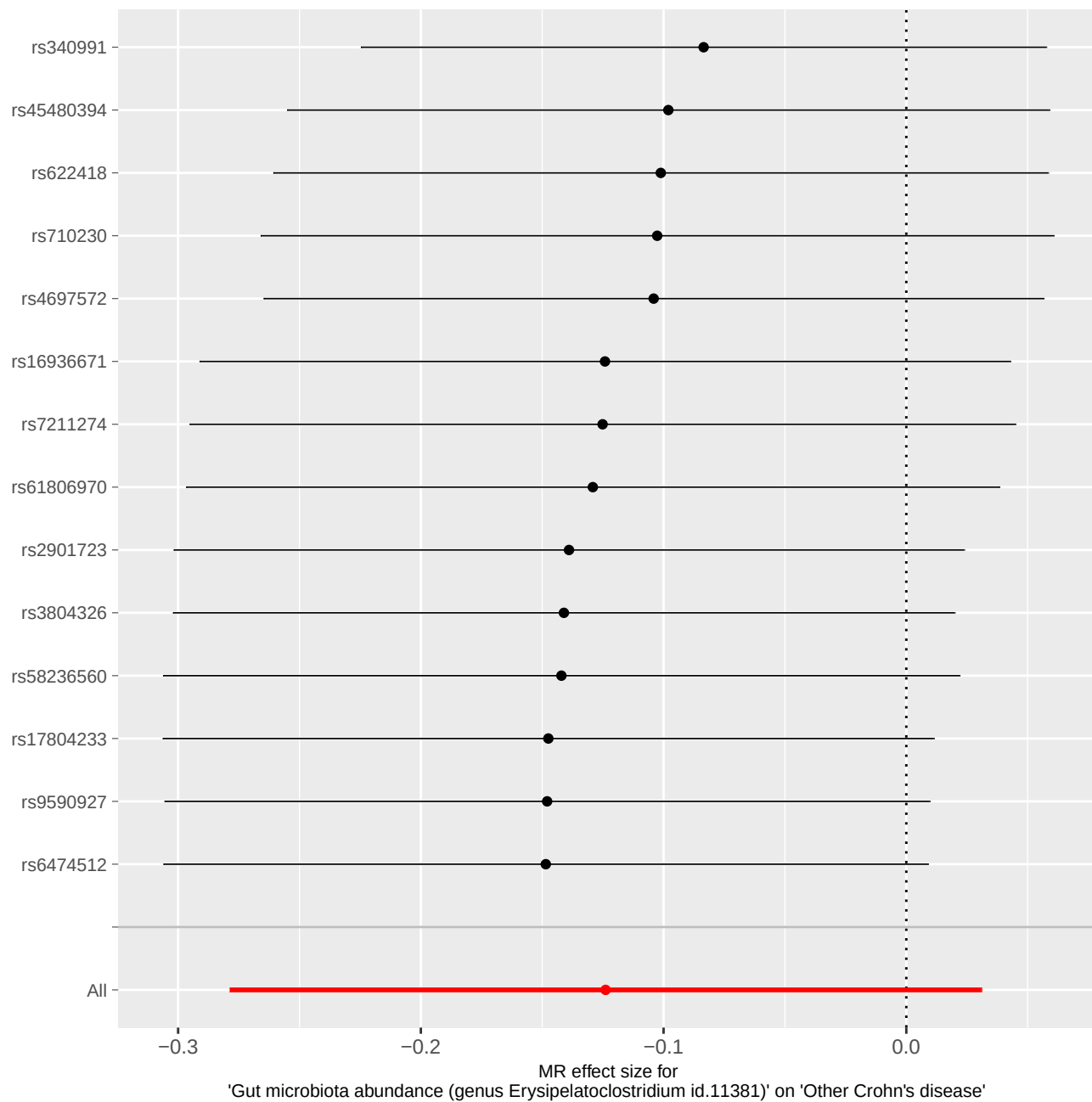


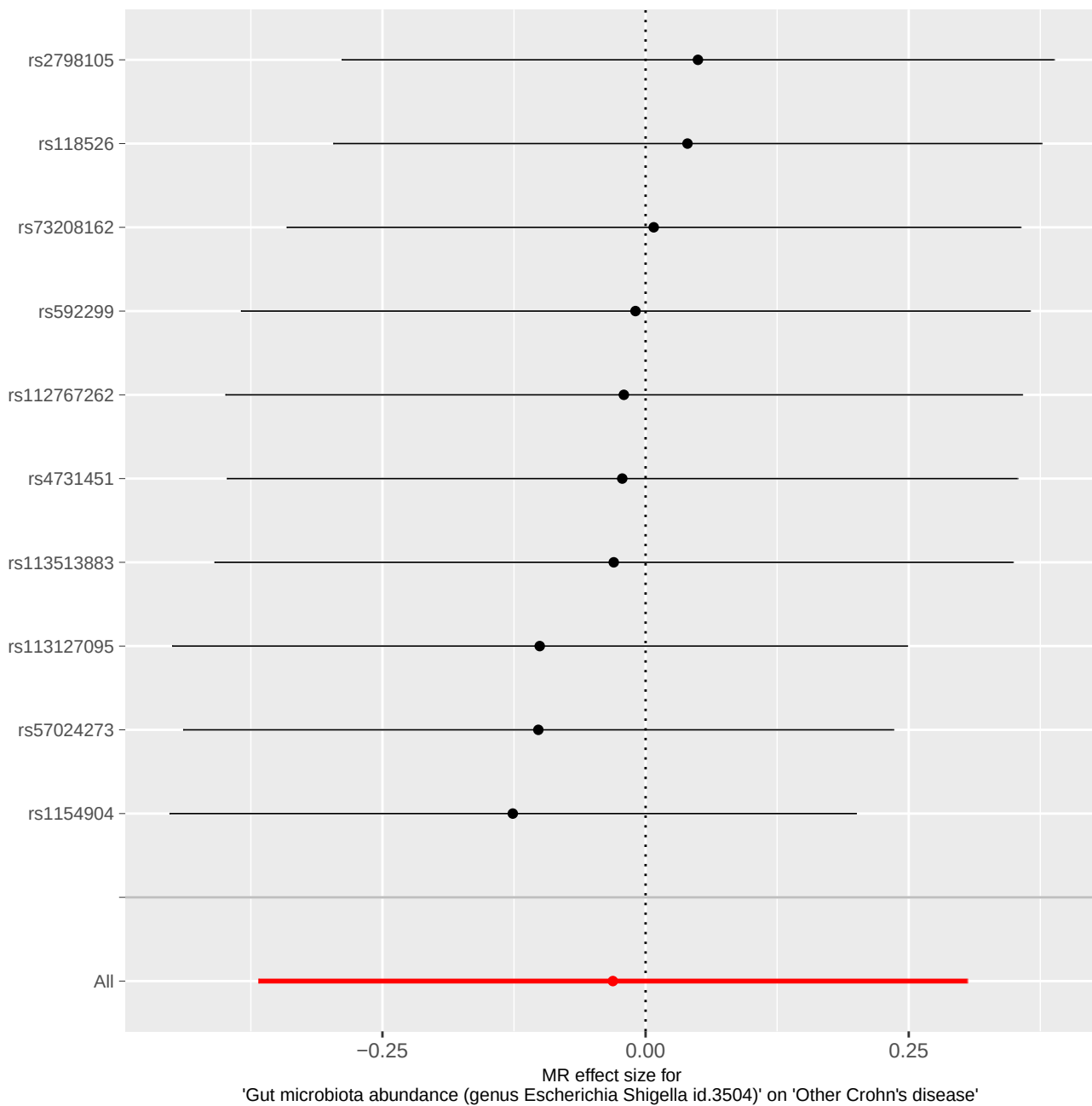


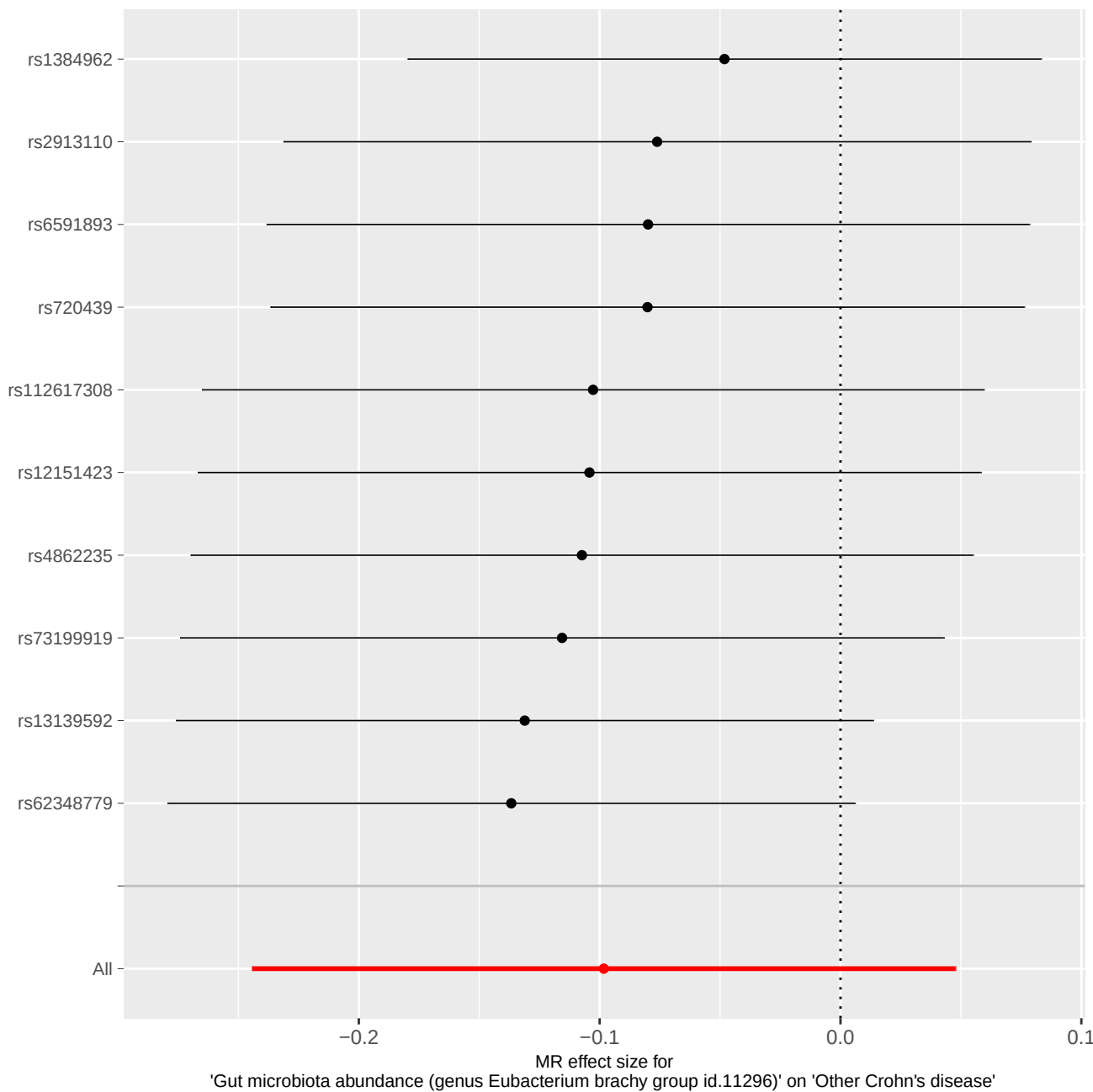






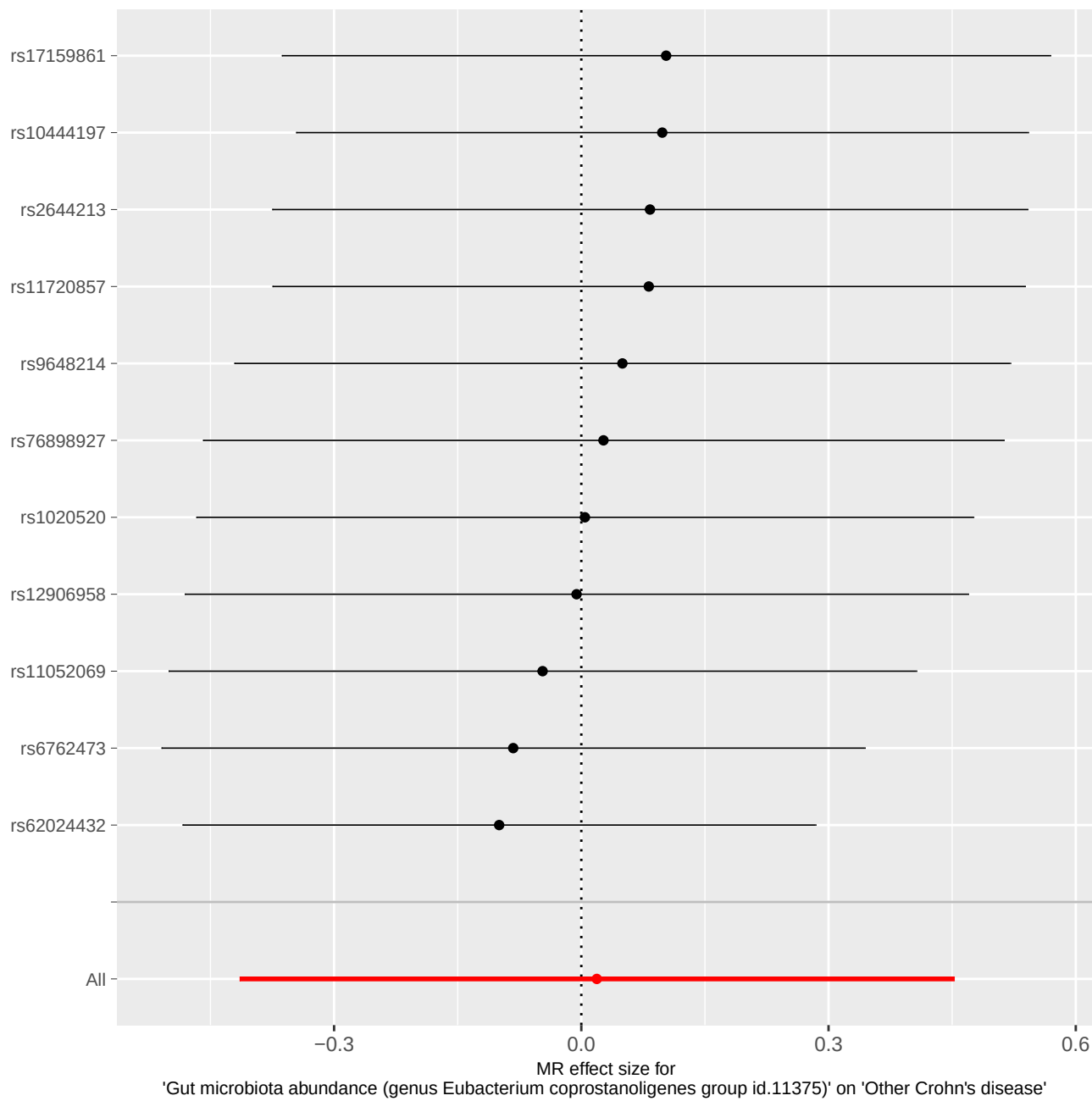


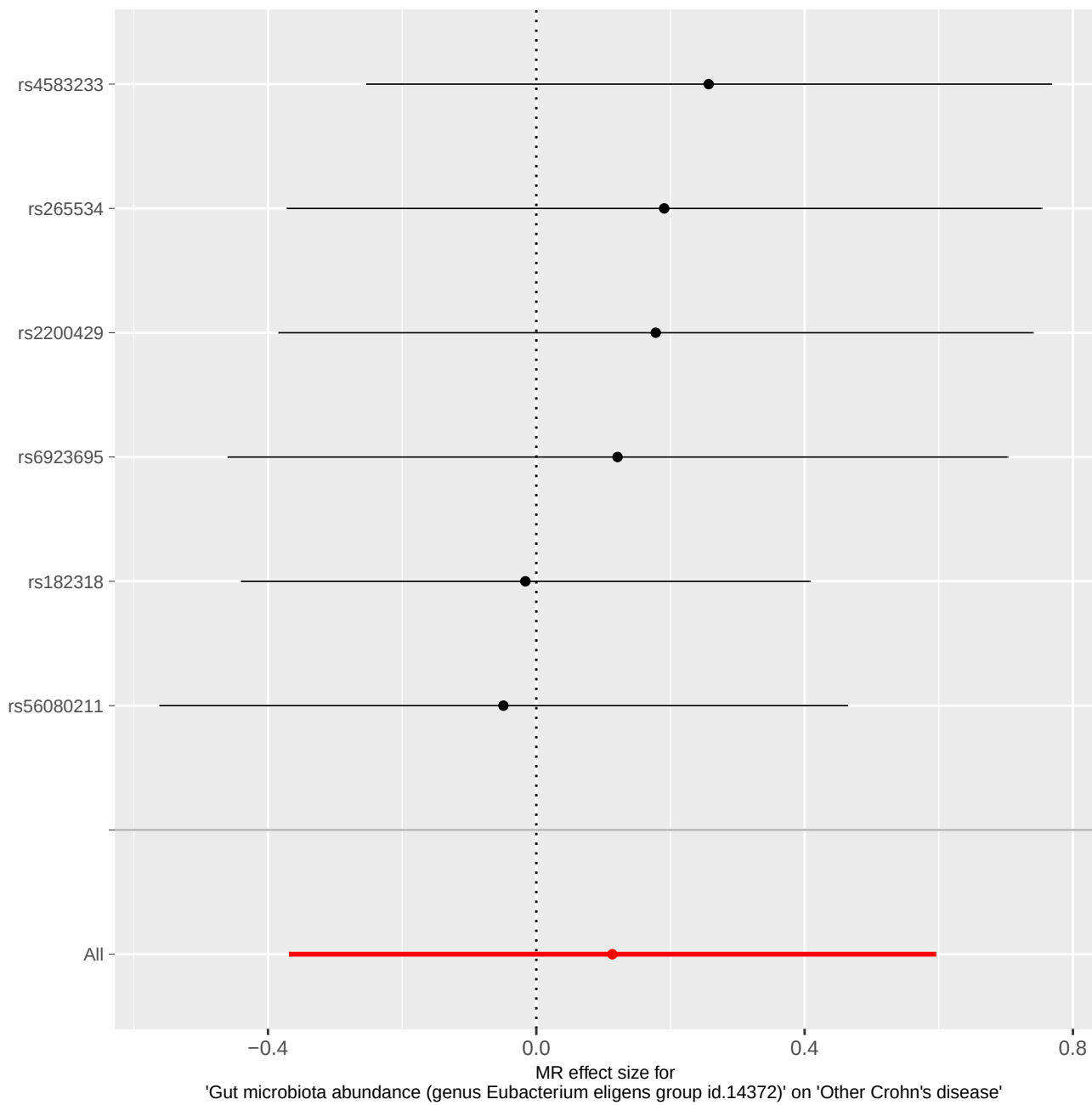




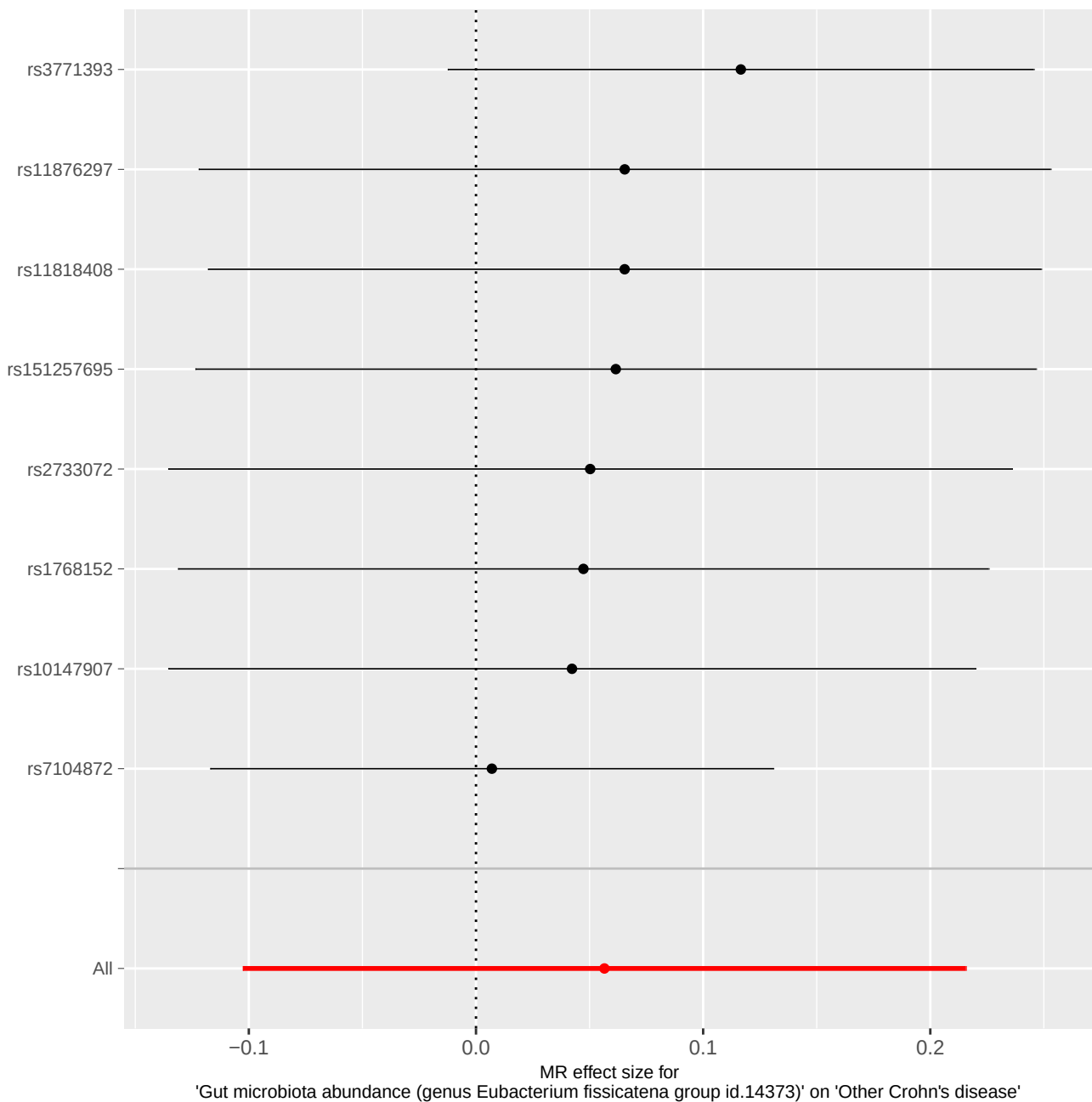
MR effect size for
'Gut microbiota abundance (genus Eubacterium brachy group id.11296)' on 'Other Crohn's disease'

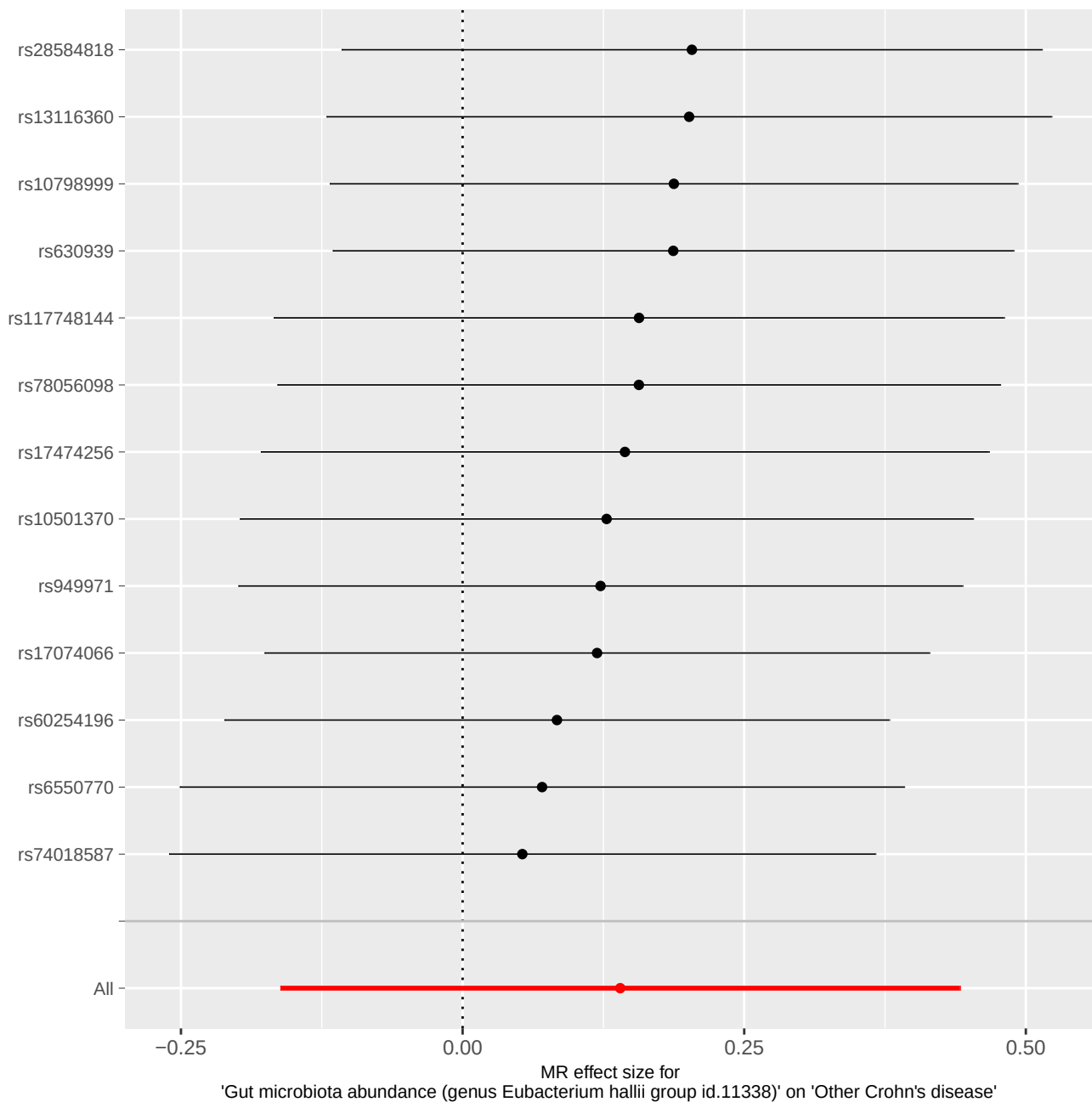
Batch 221 : Gut microbiota abundance (genus Eubacterium coprostanoligenes group id.11375) on Other Crohn's disease

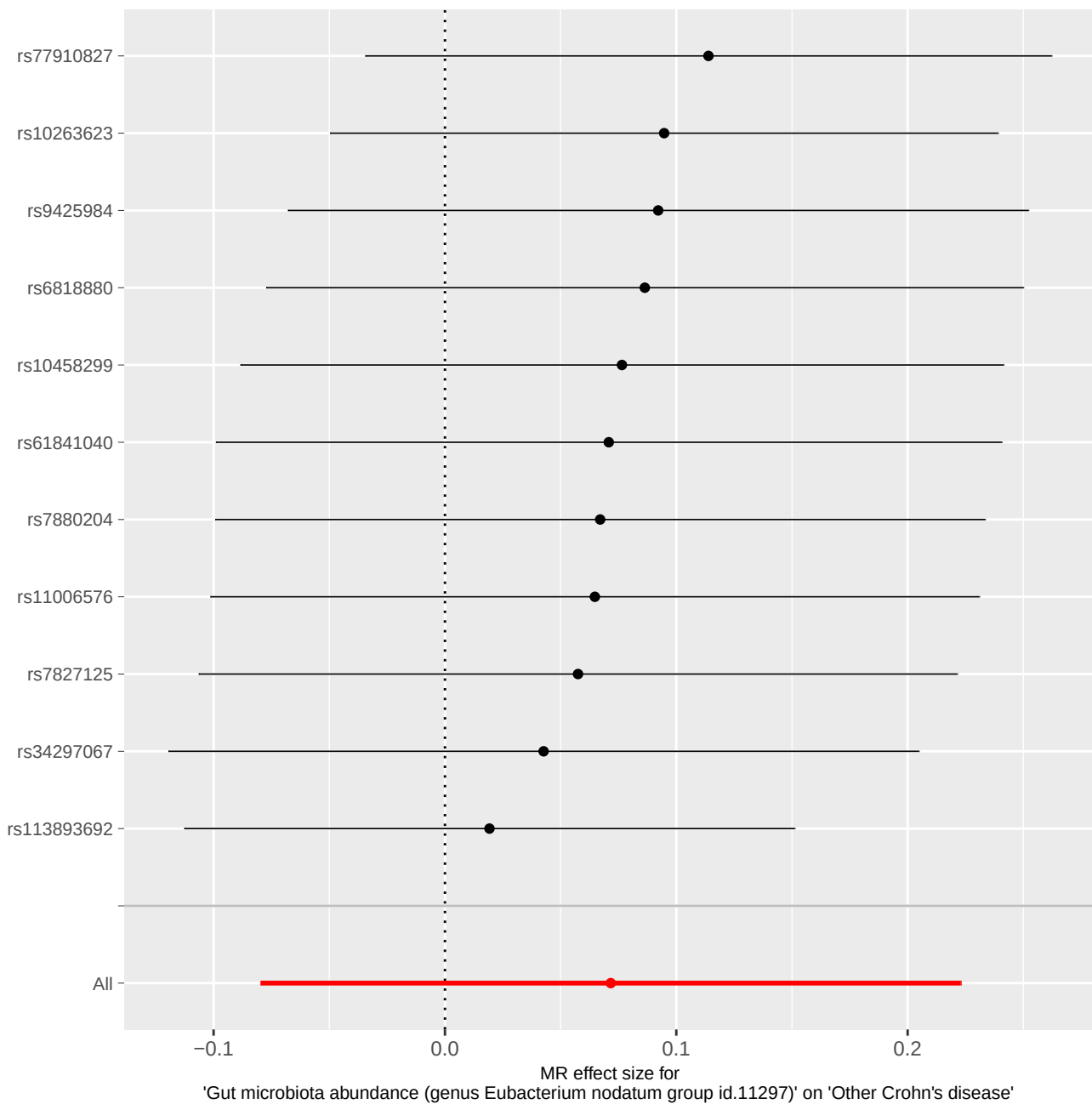


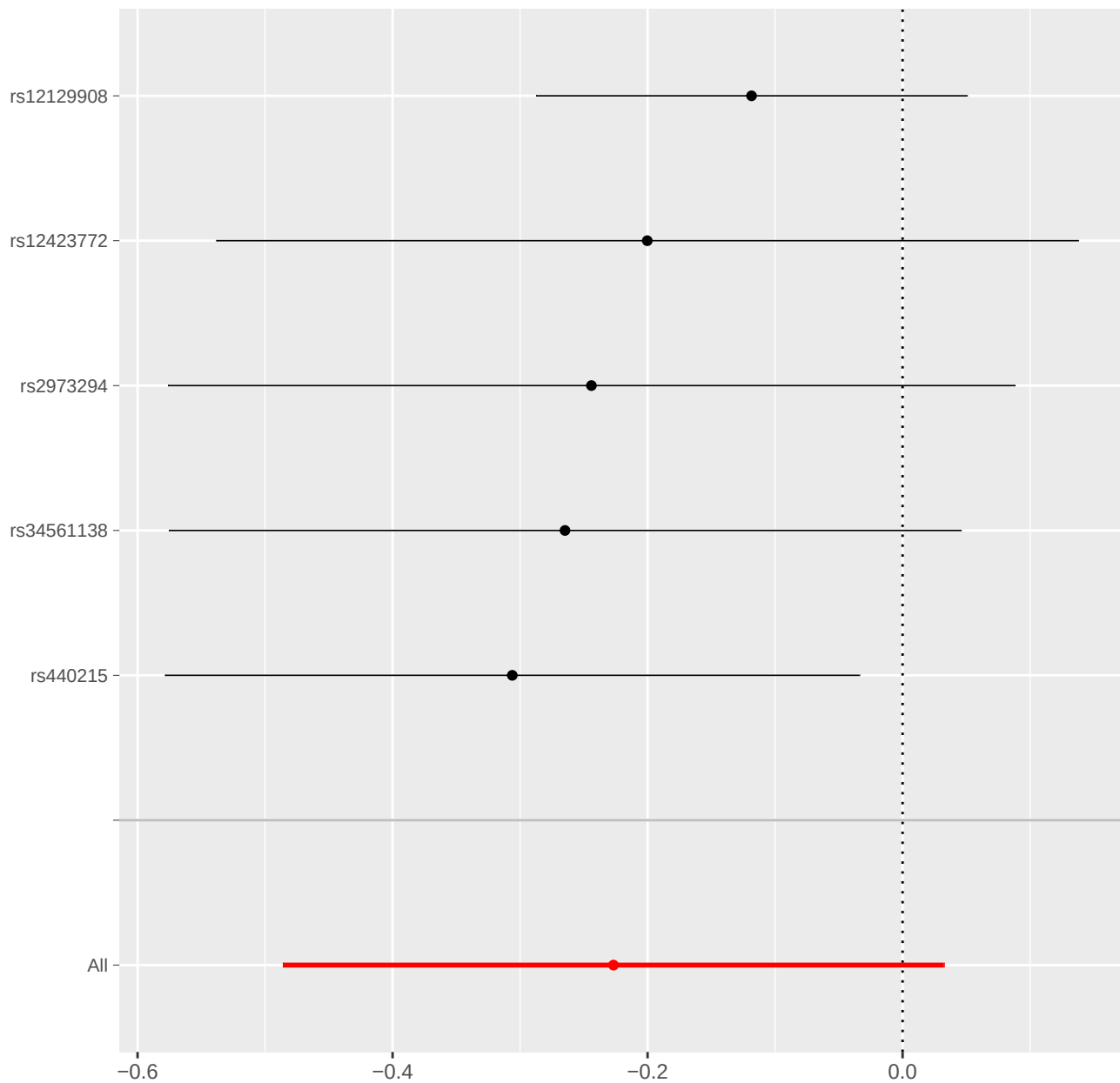


Batch 223 : Gut microbiota abundance (genus Eubacterium fissicatena group id.14373) on Other Crohn's disease

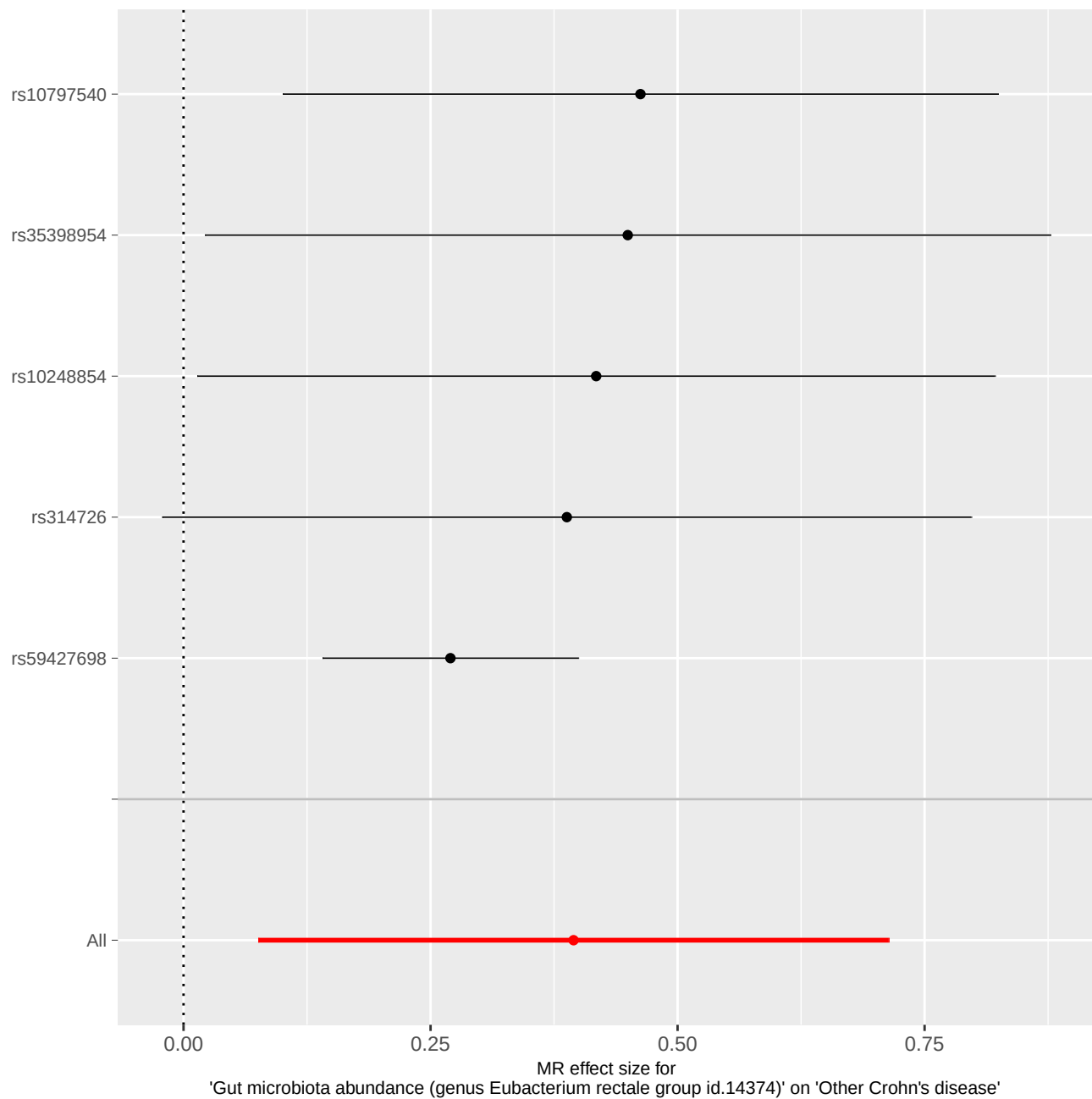


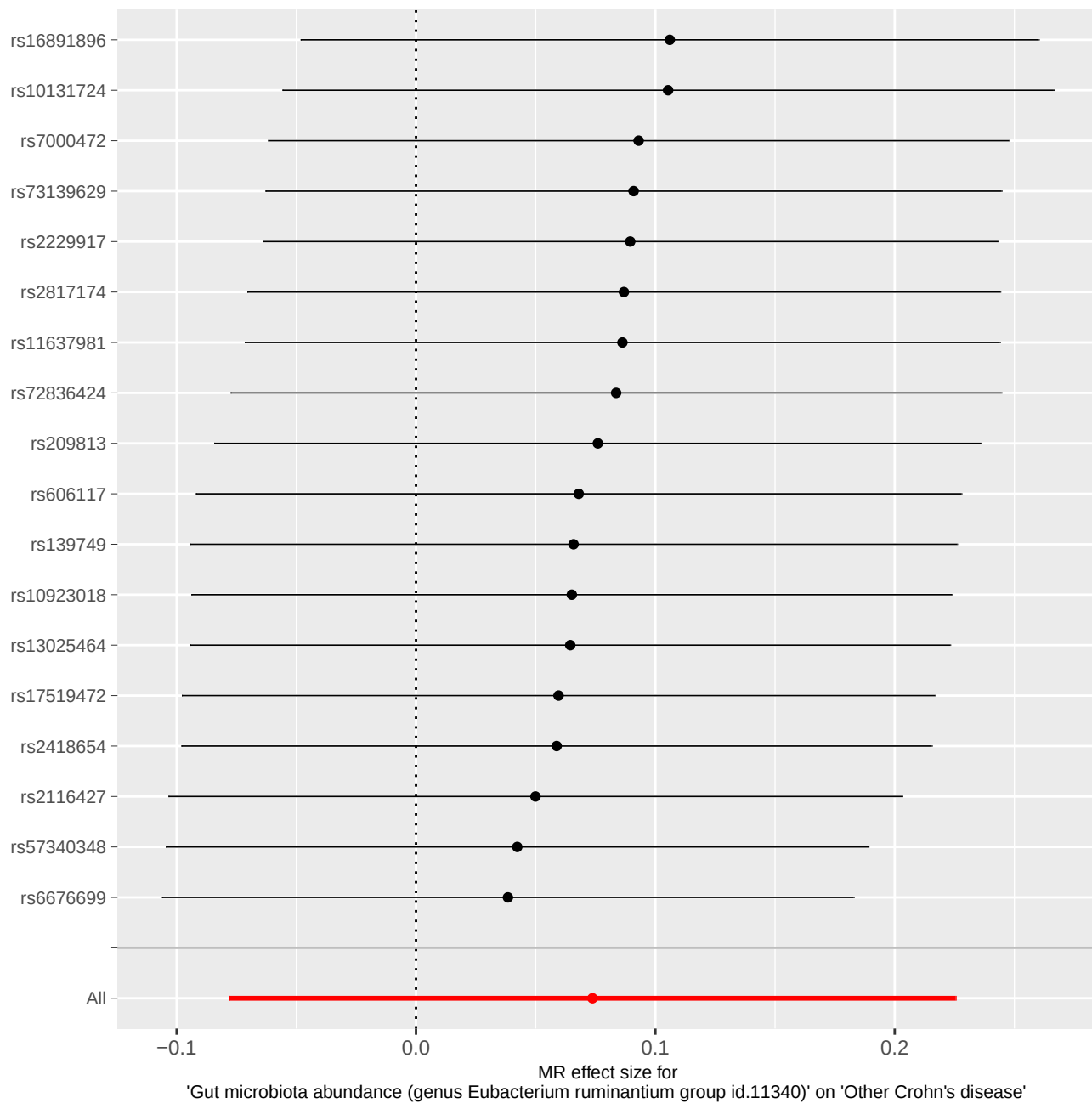


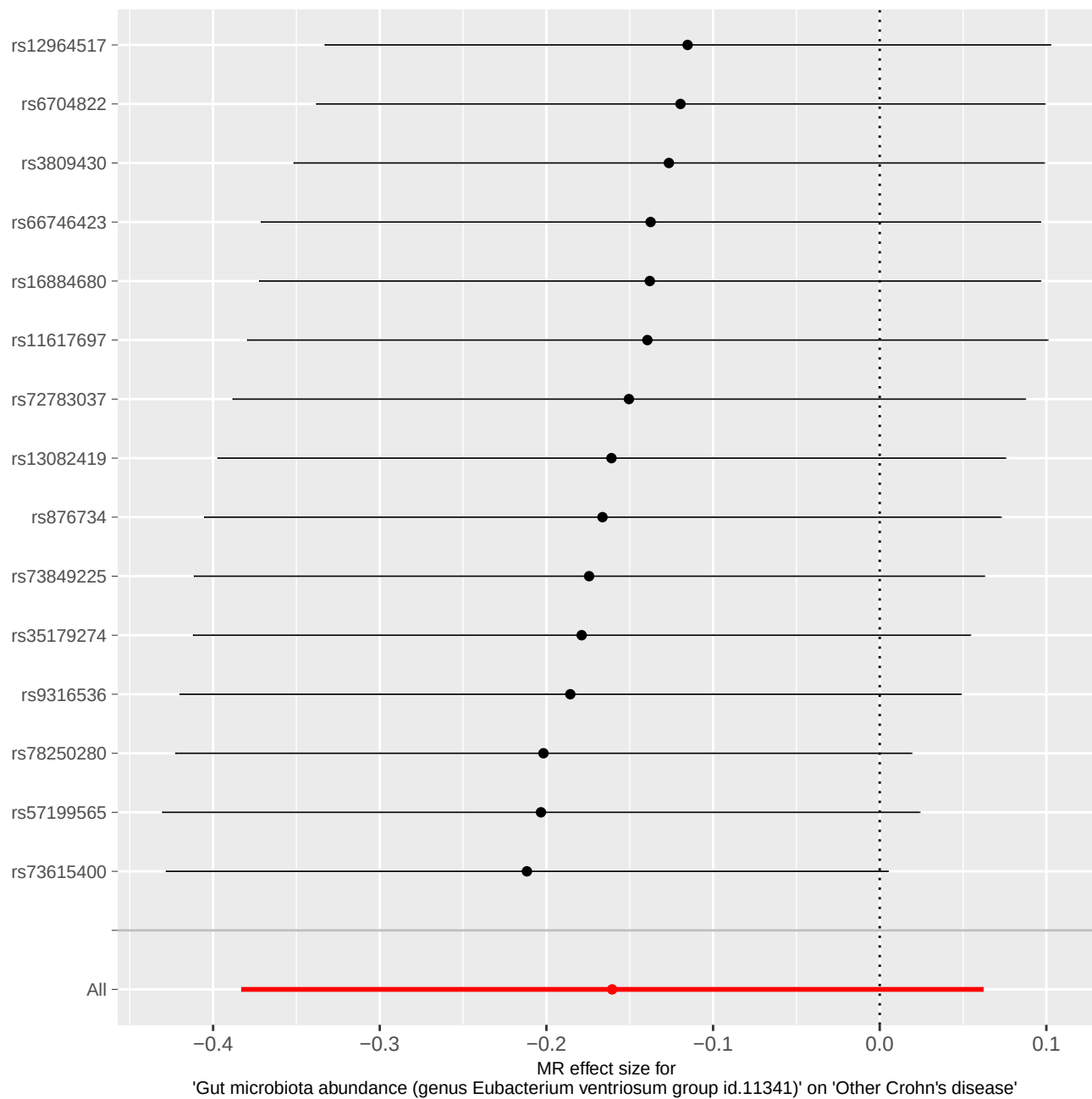


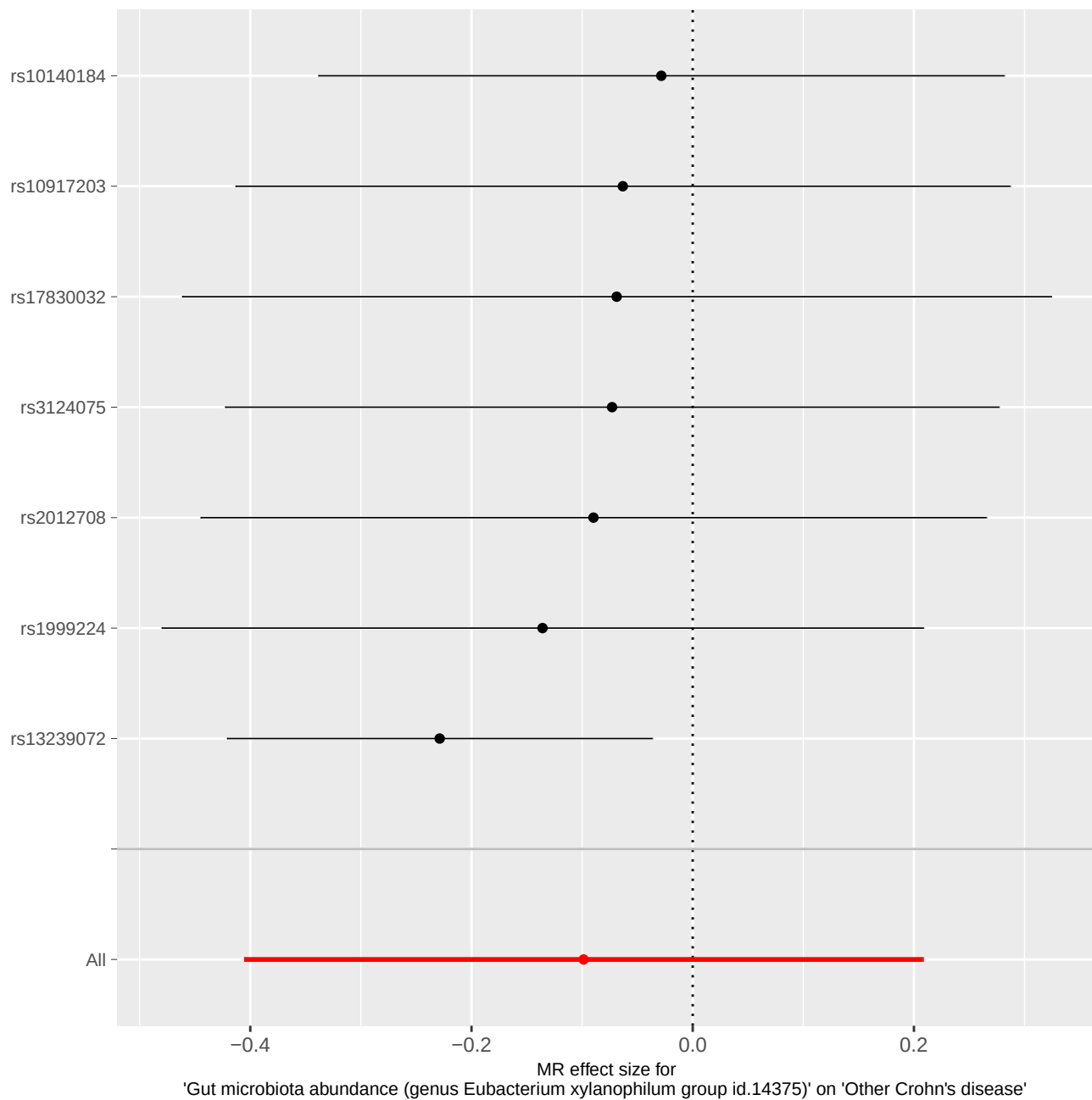


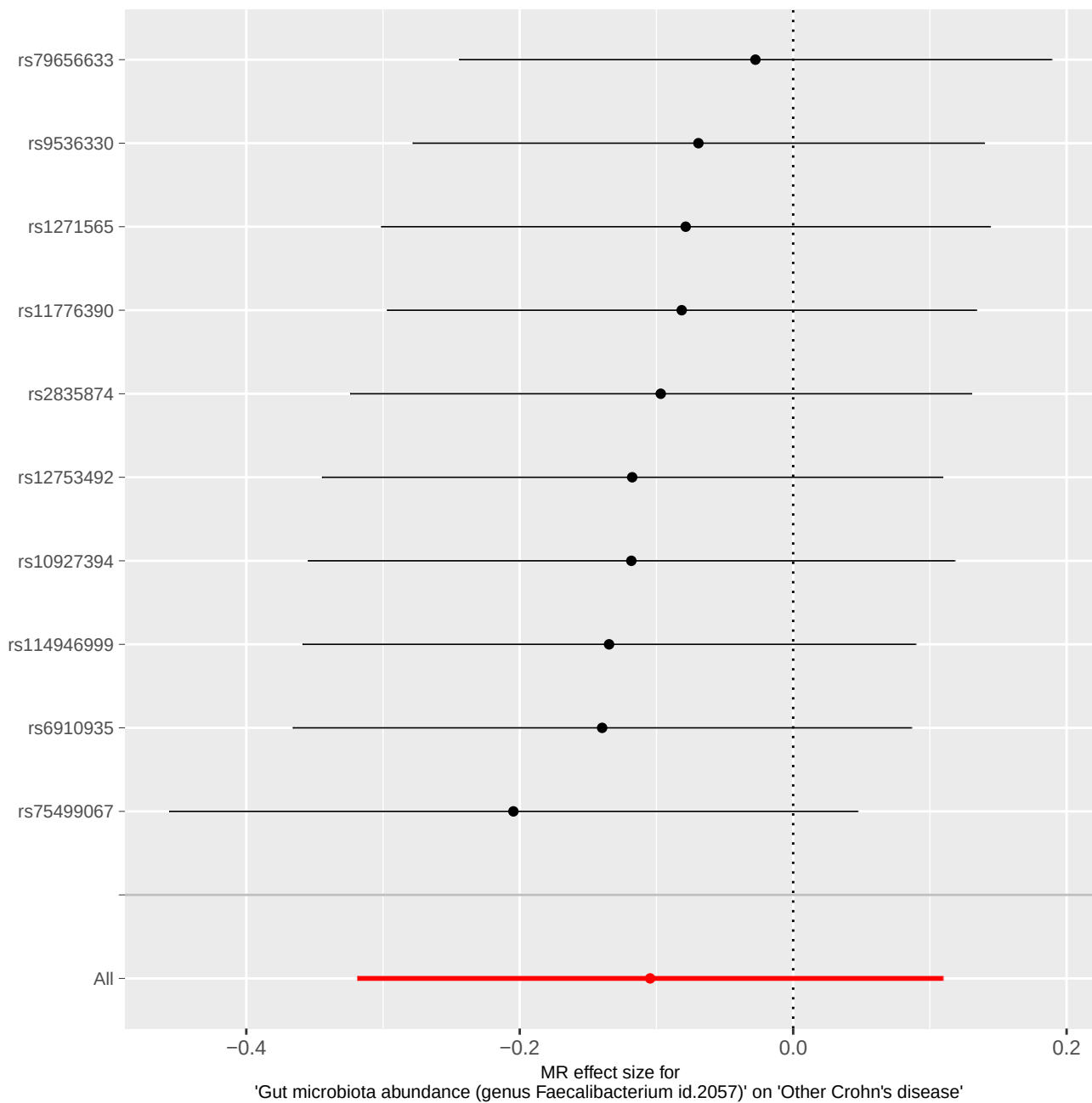
MR effect size for
'Gut microbiota abundance (genus Eubacterium oxidoreducens group id.11339)' on 'Other Crohn's disease'

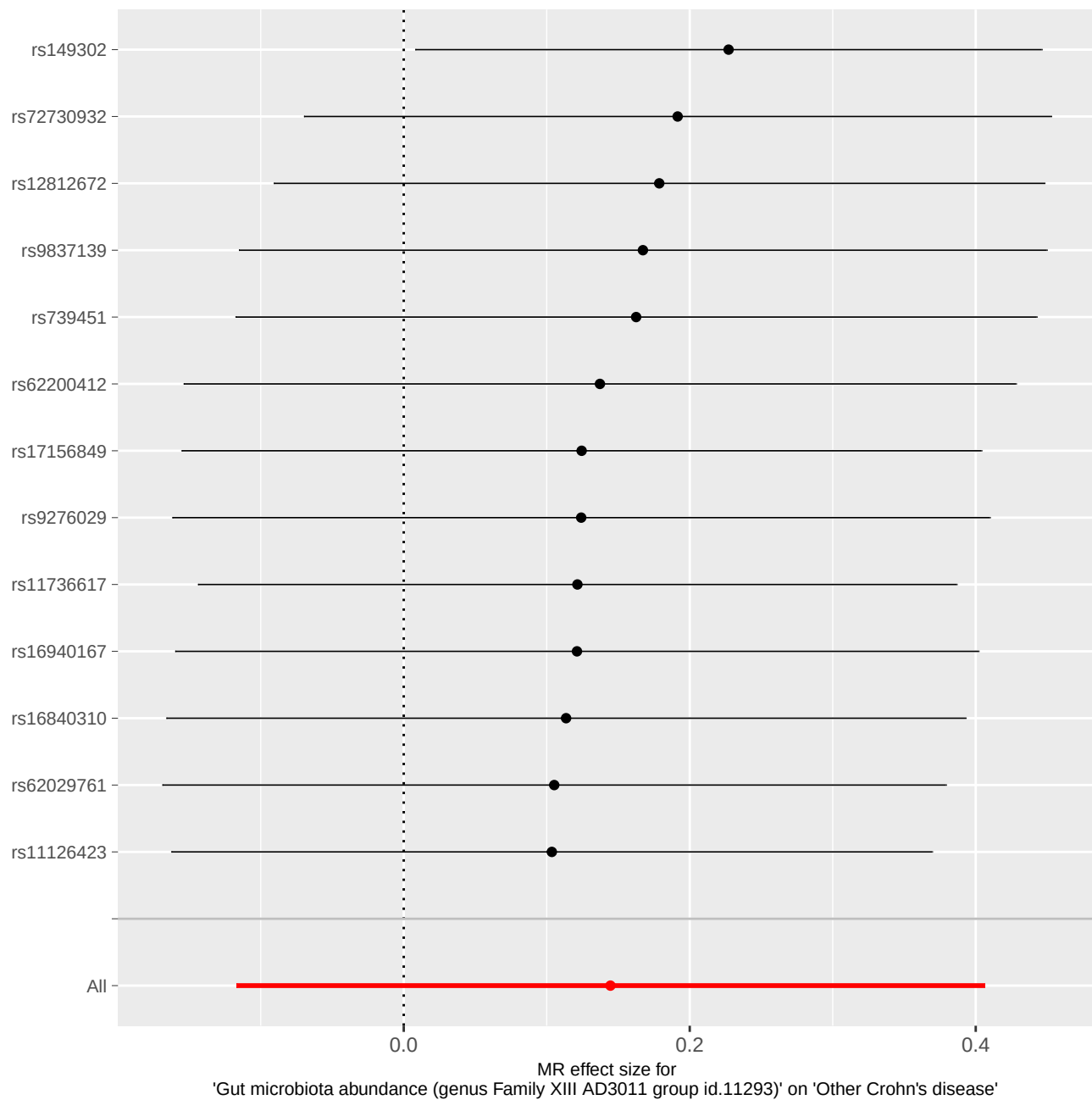


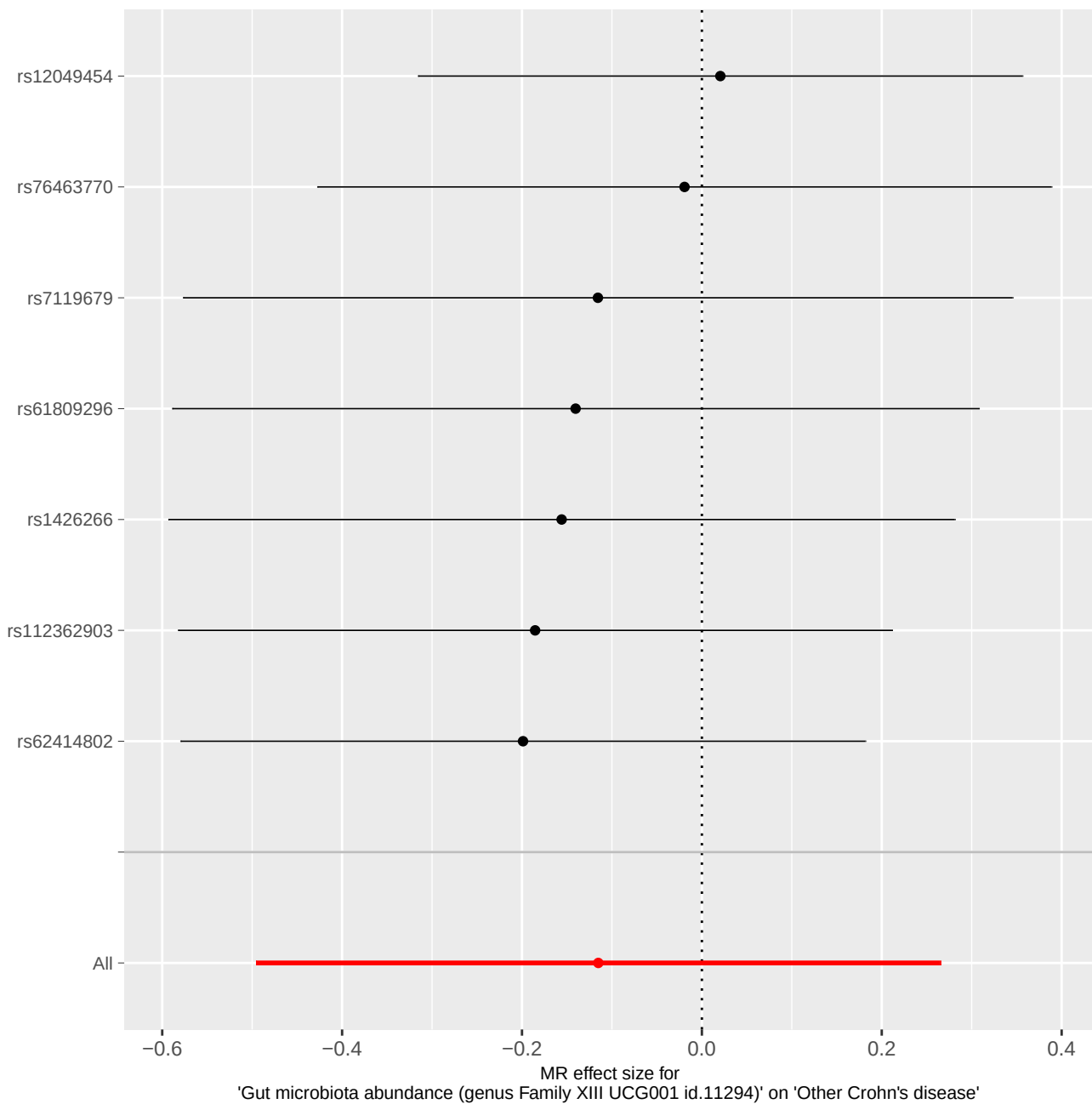


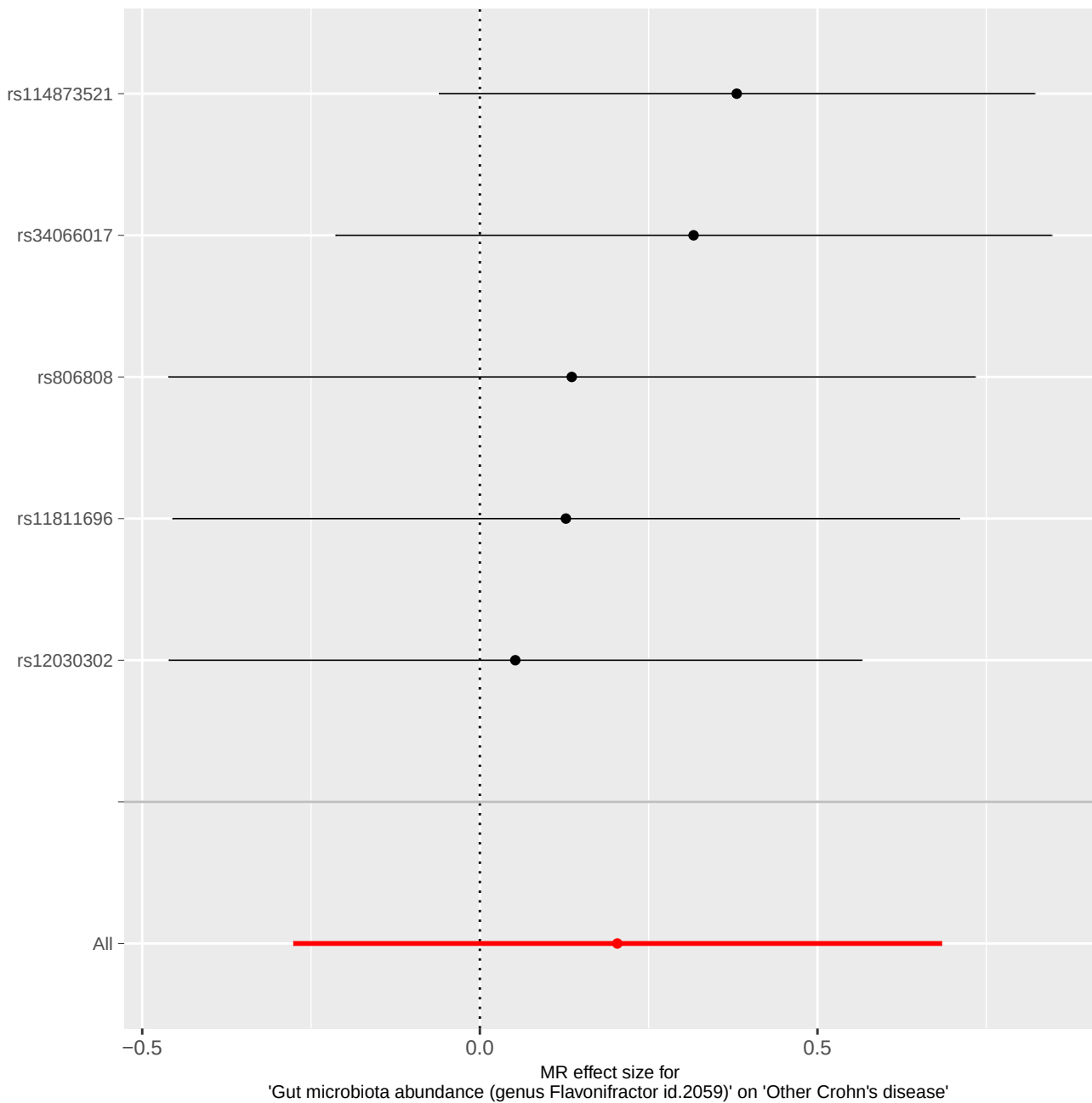




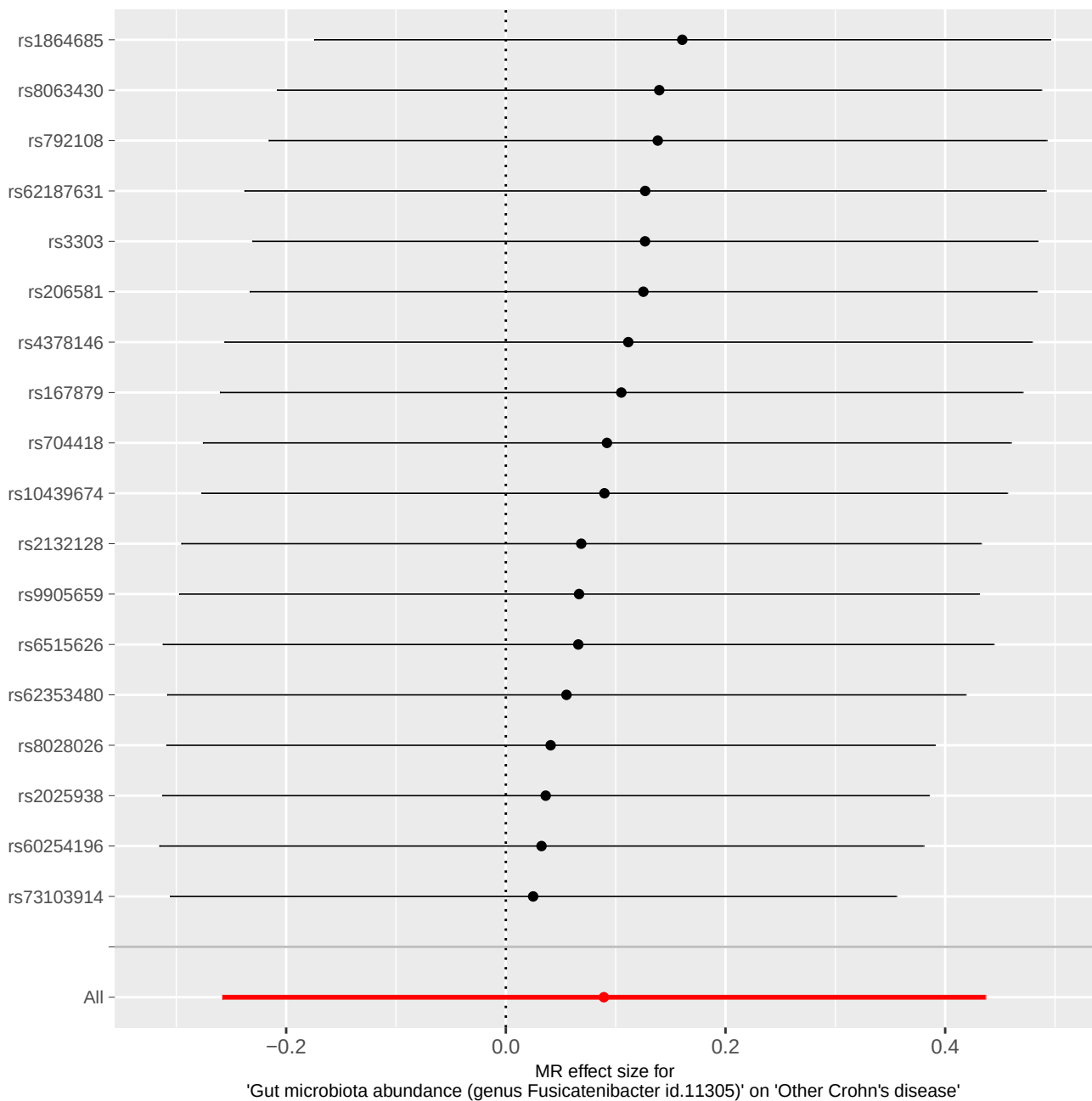


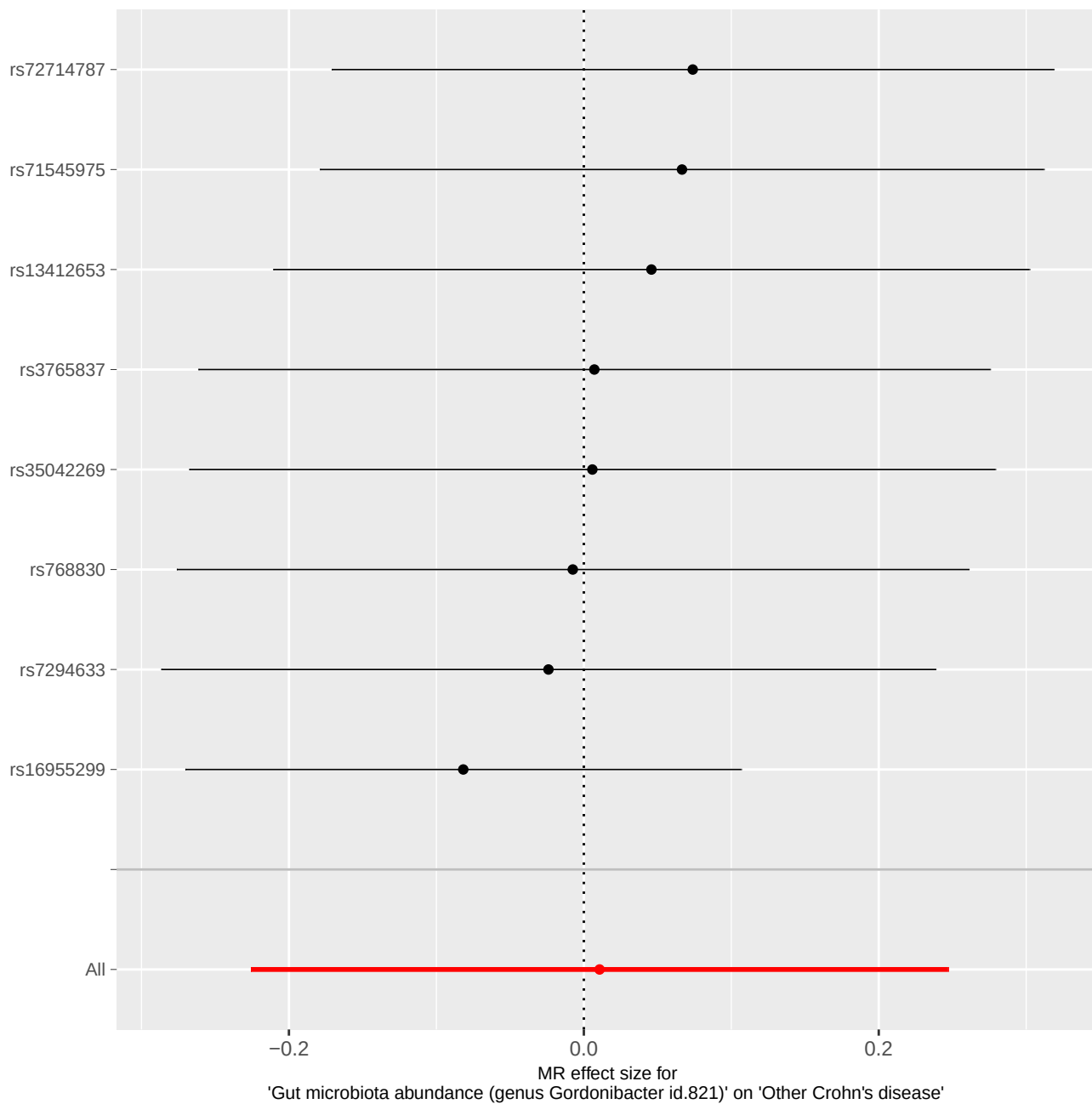


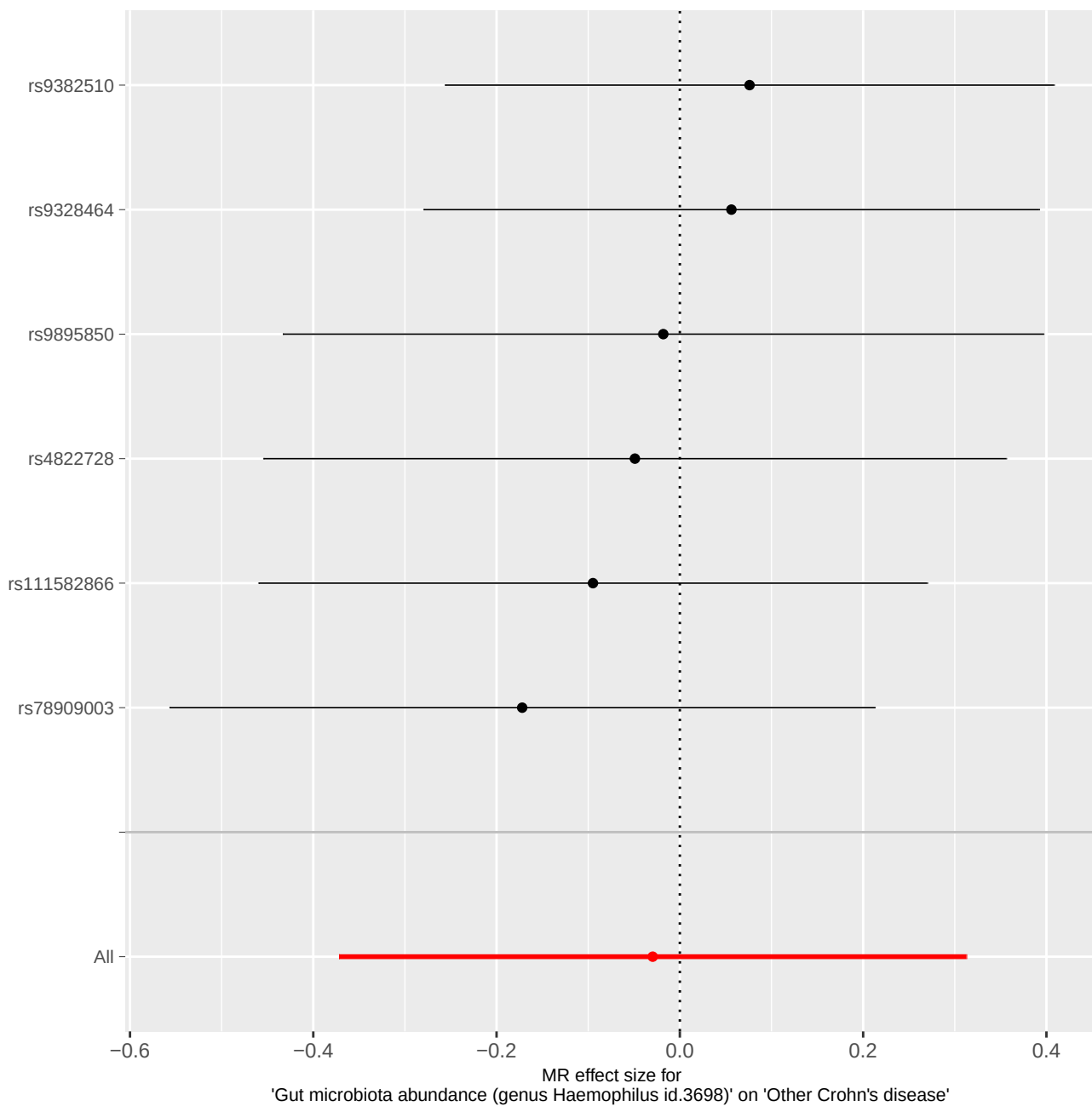


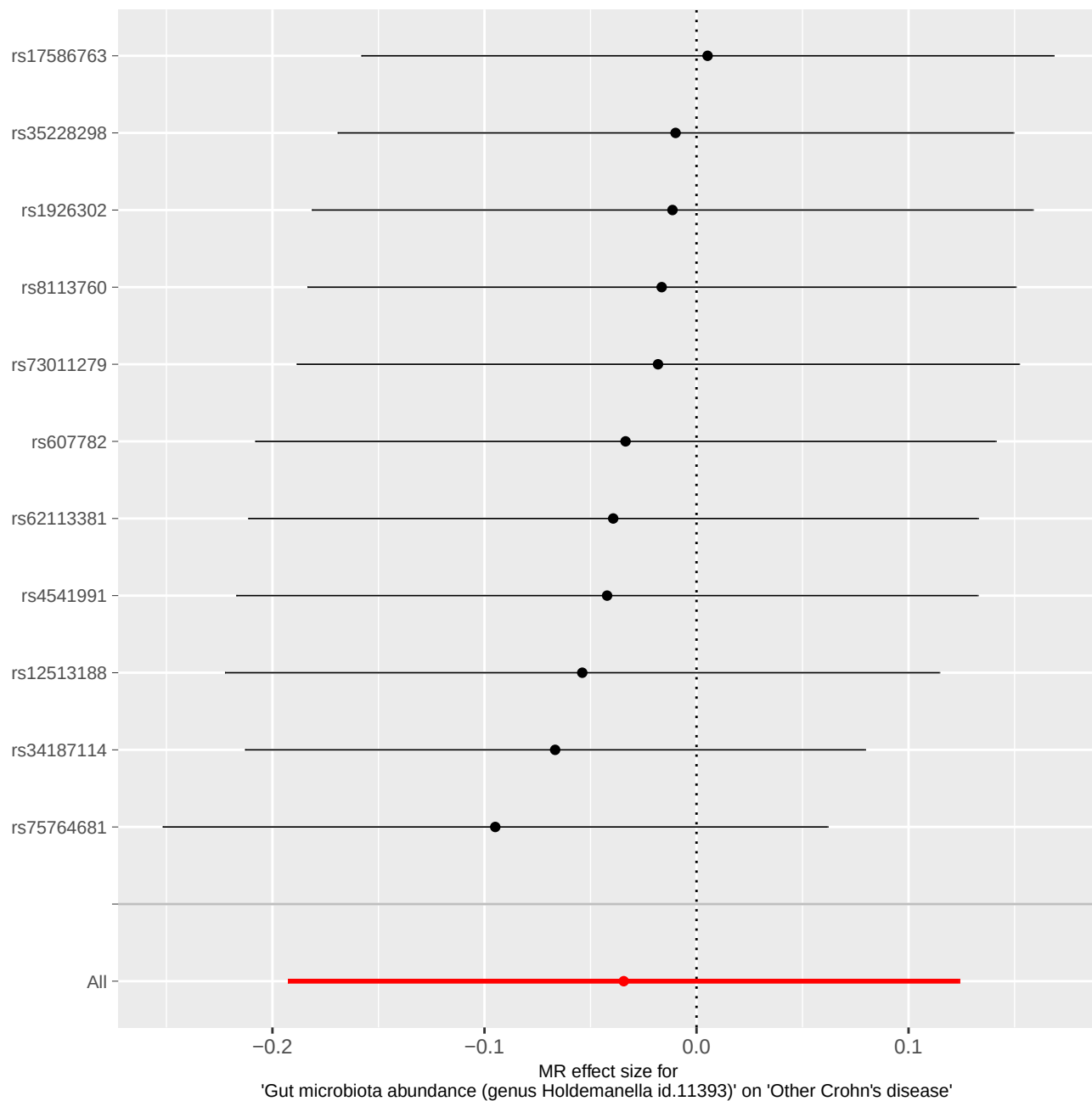


Batch 235 : Gut microbiota abundance (genus Fusicatenibacter id.11305) on Other Crohn's disease

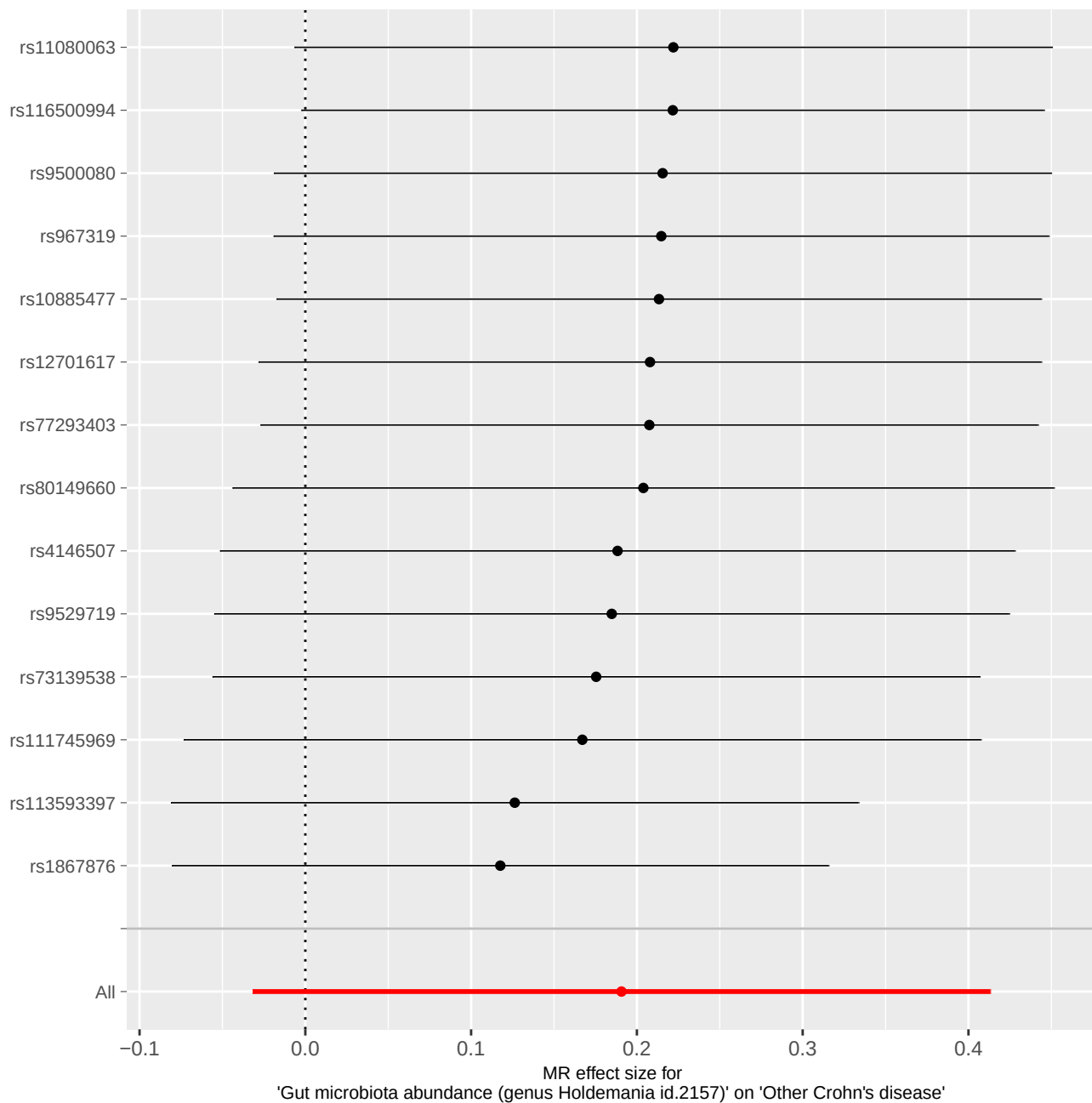


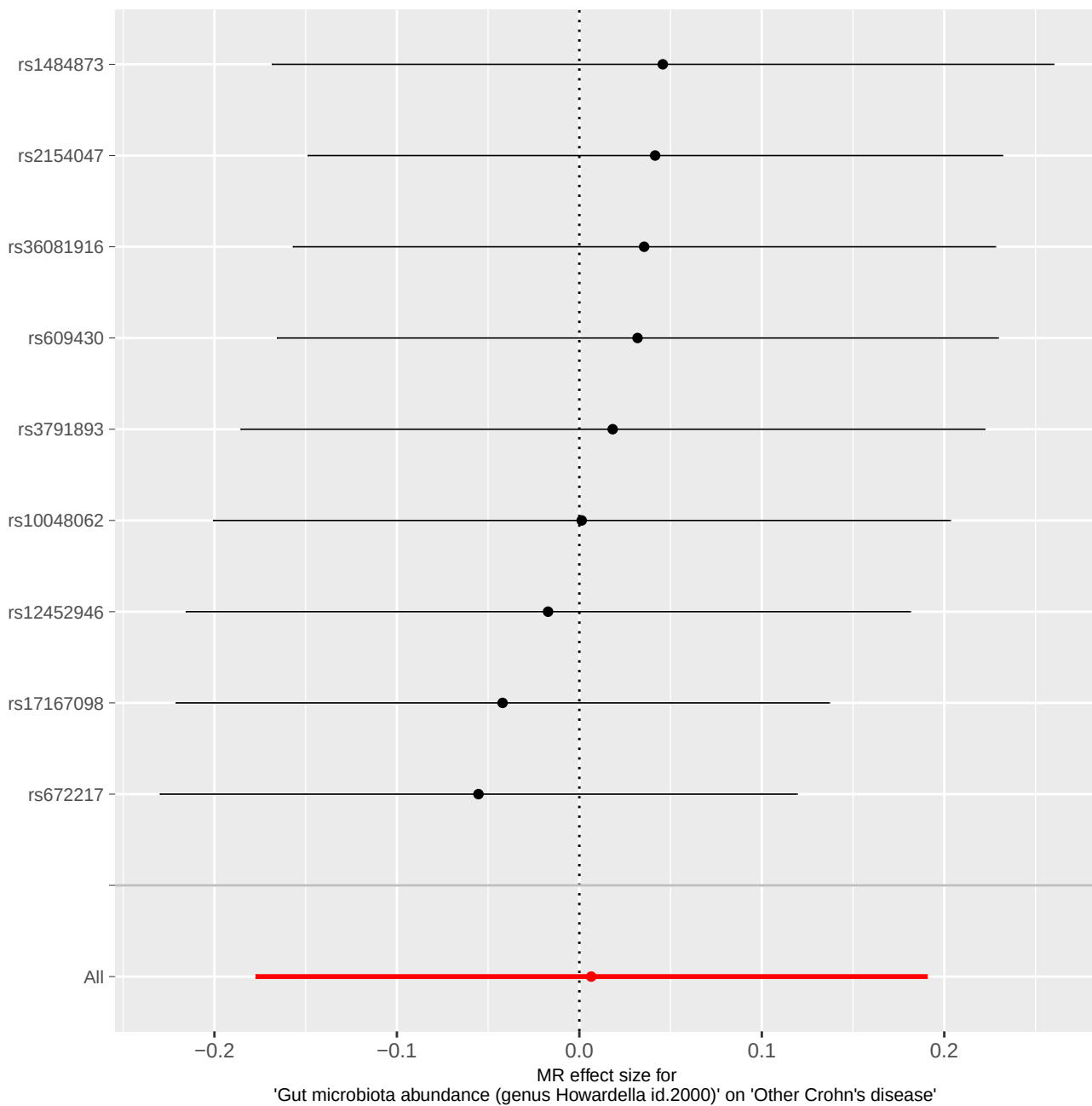


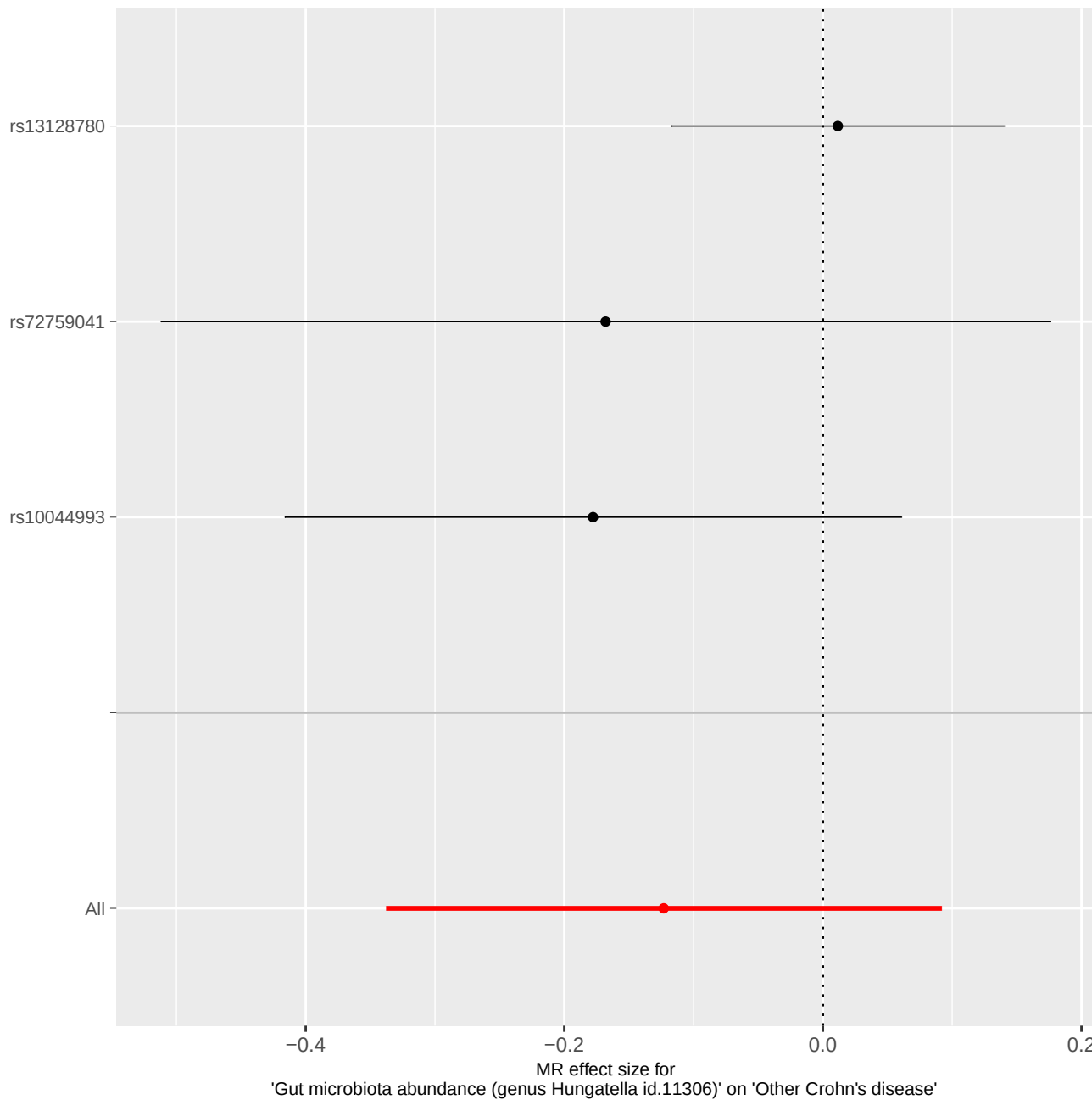


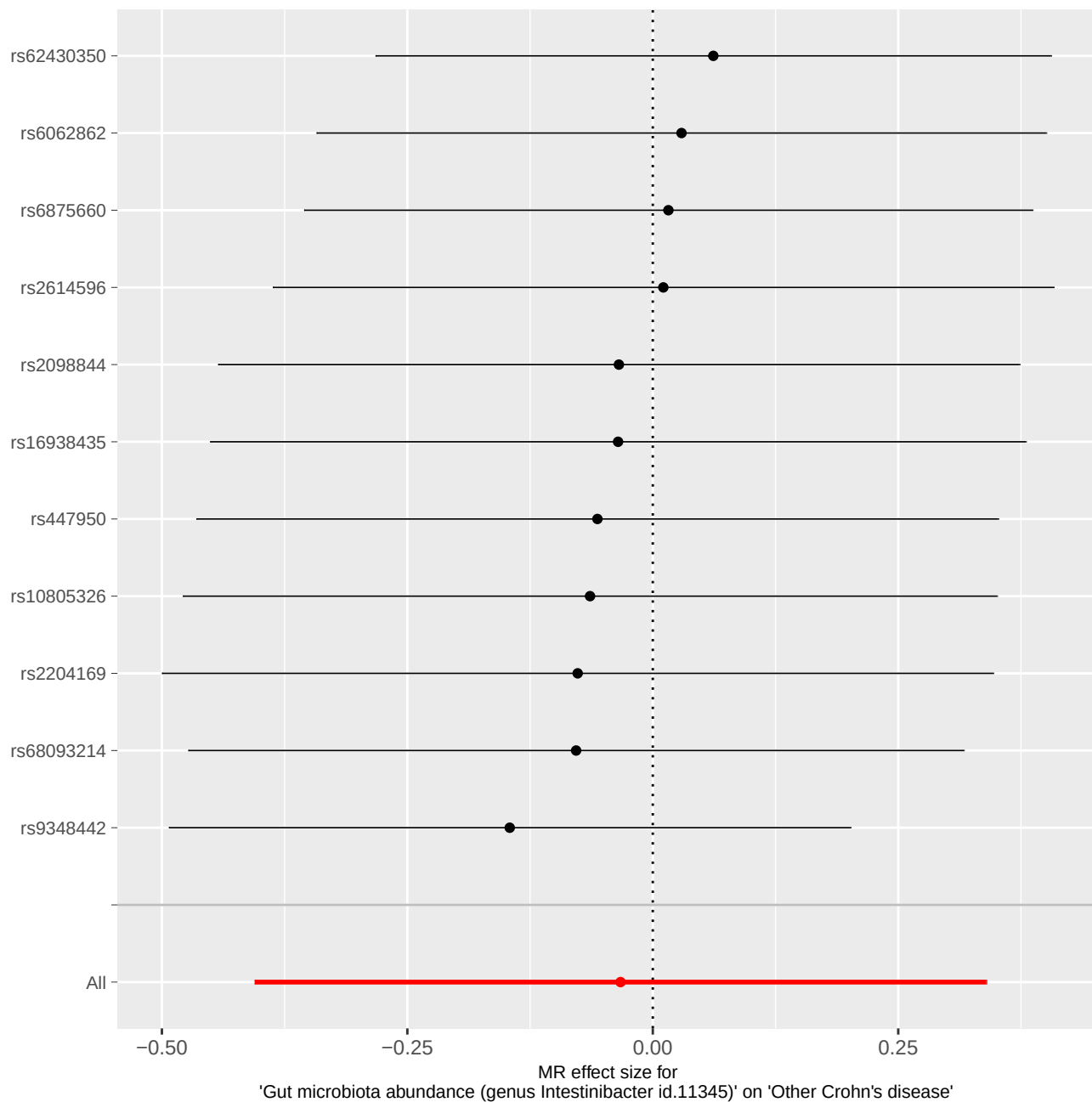


Batch 239 : Gut microbiota abundance (genus Holdemania id.2157) on Other Crohn's disease

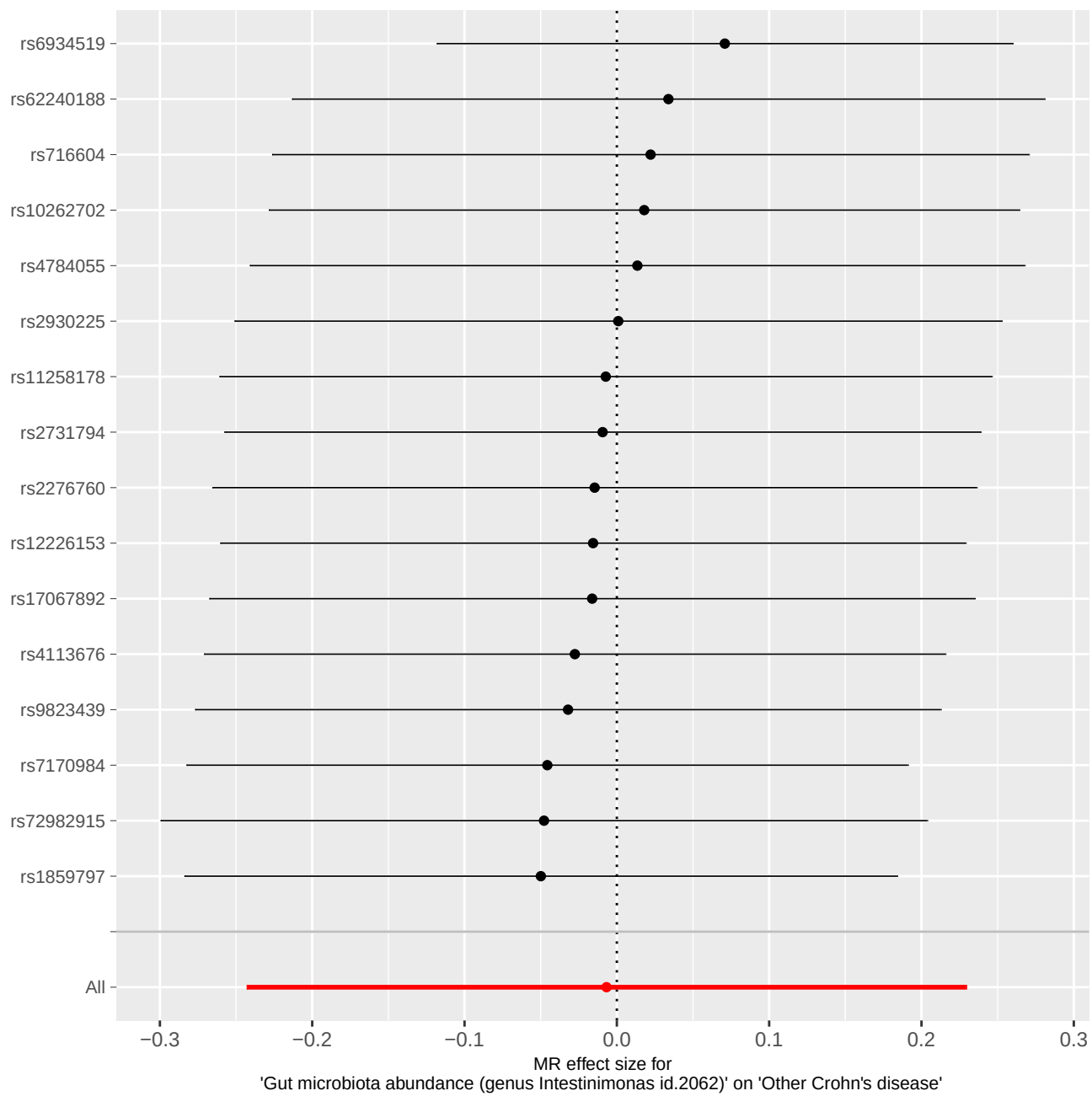


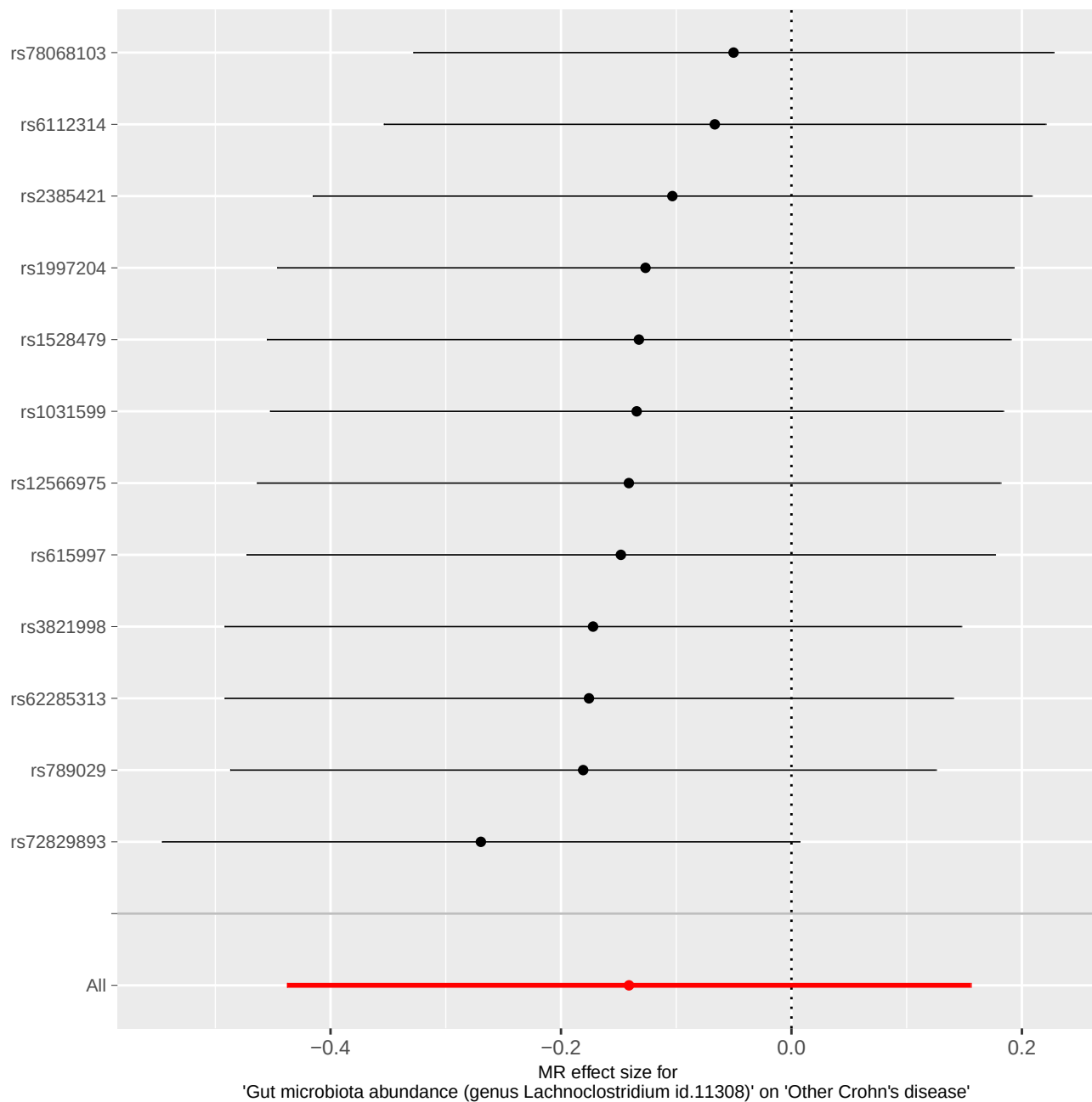


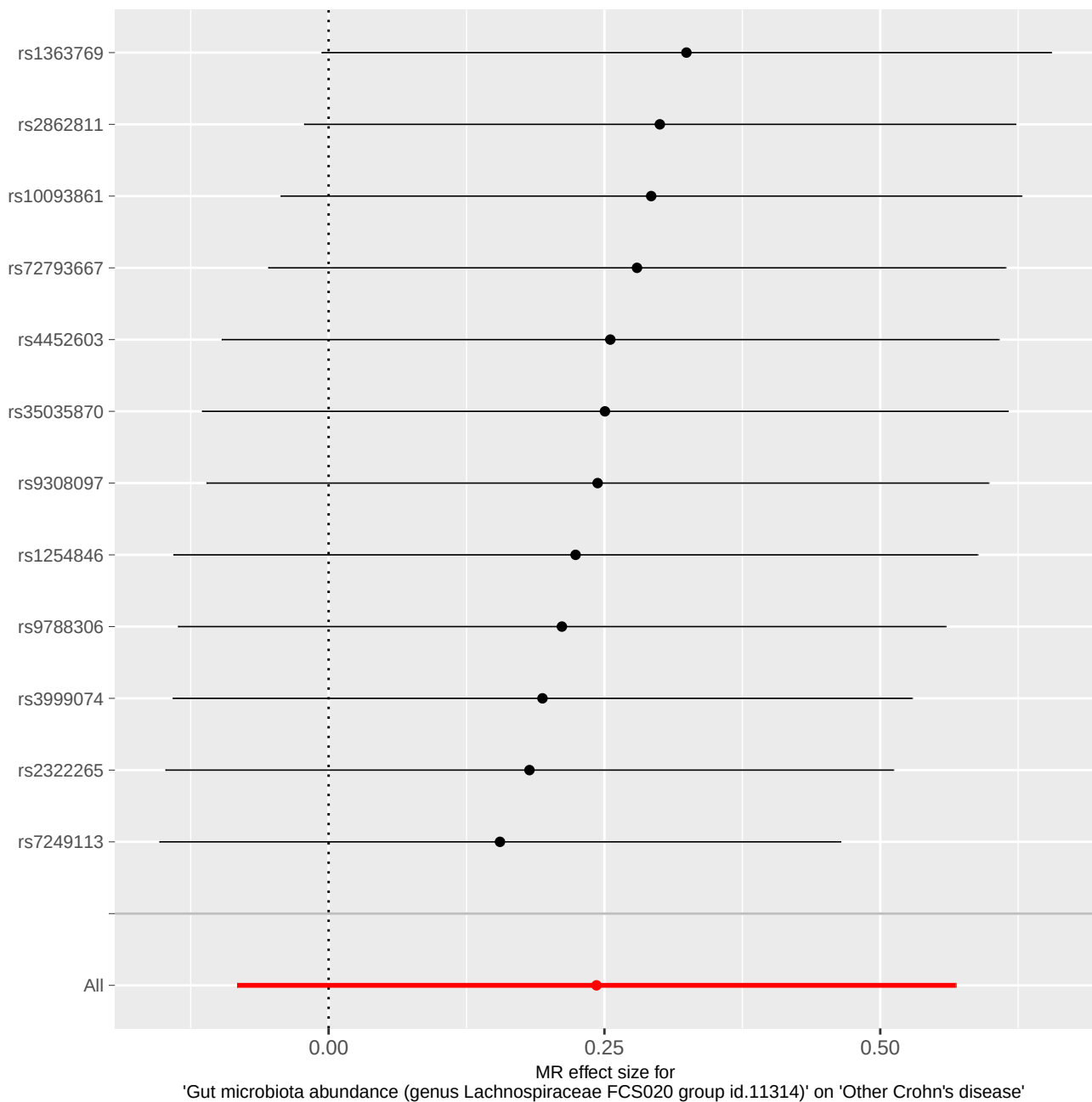


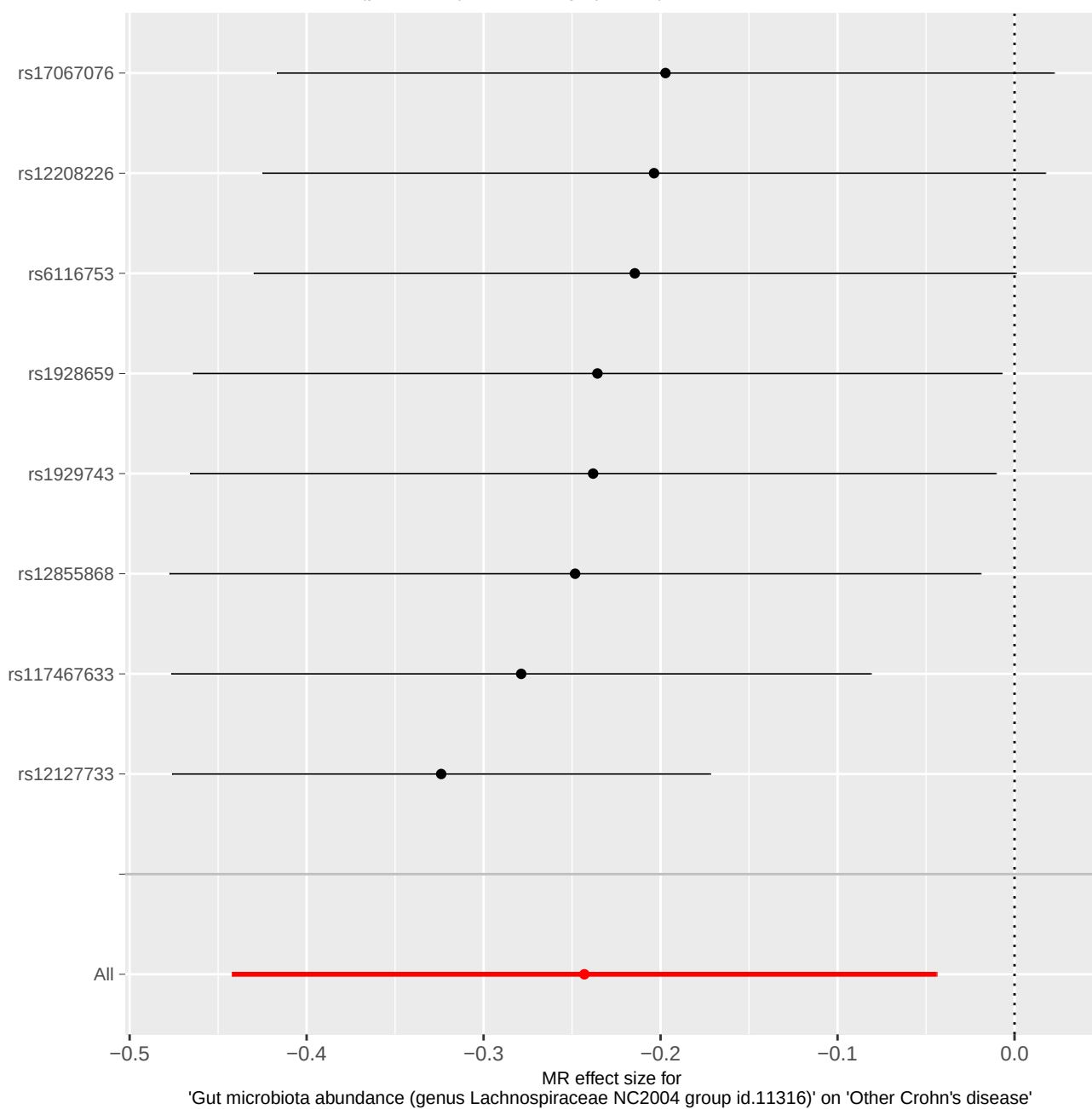


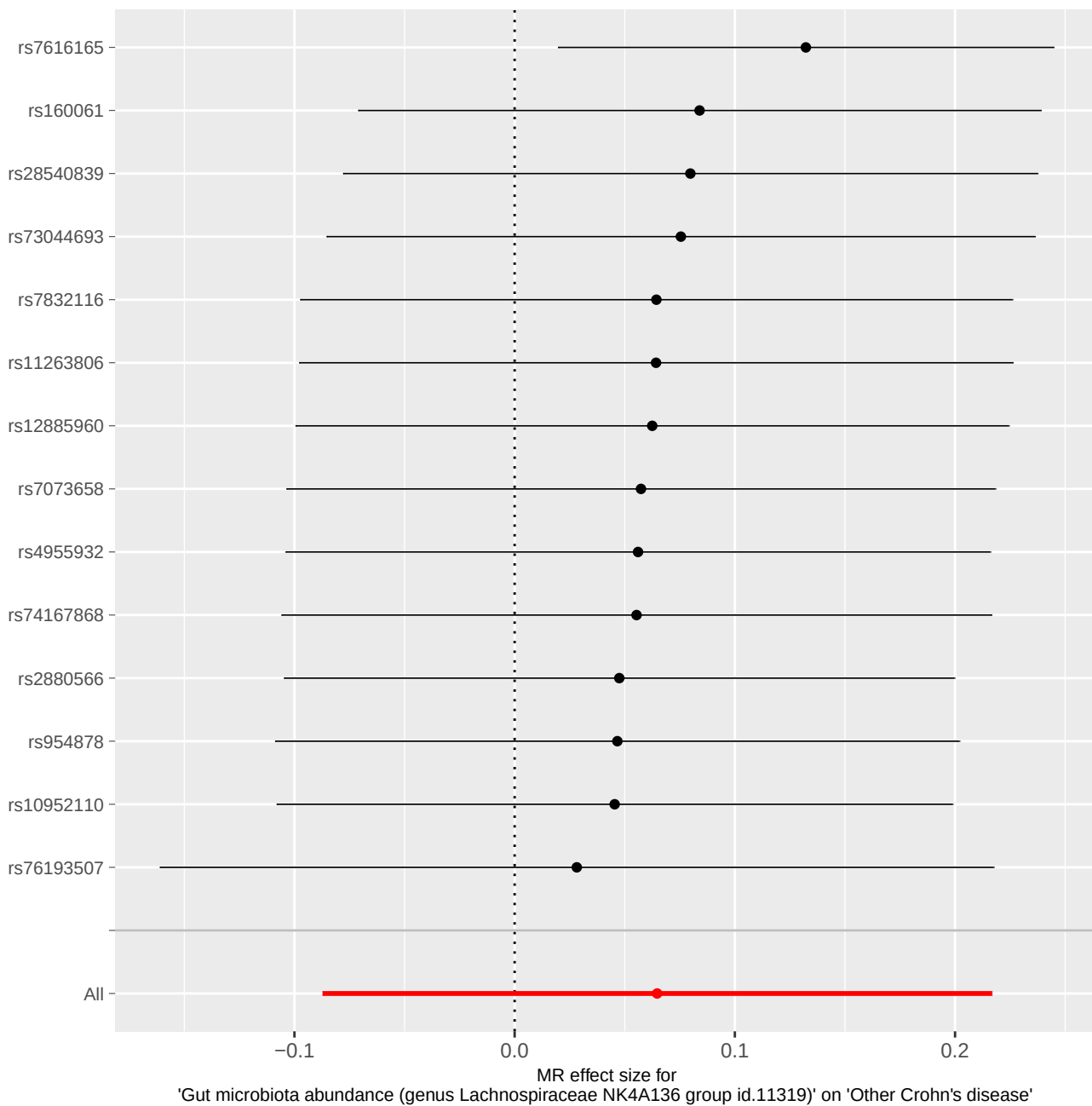
Batch 243 : Gut microbiota abundance (genus Intestinimonas id.2062) on Other Crohn's disease



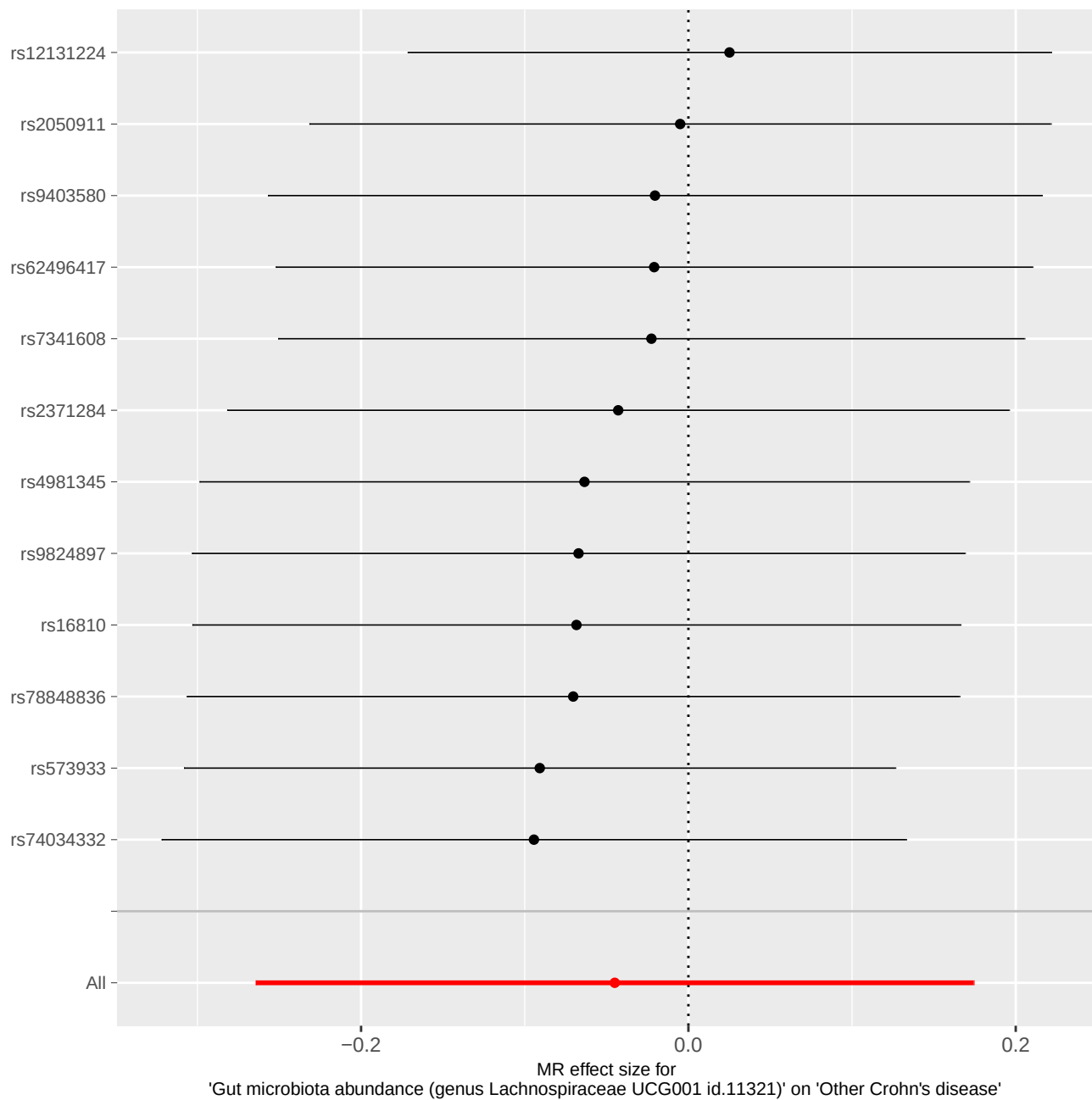


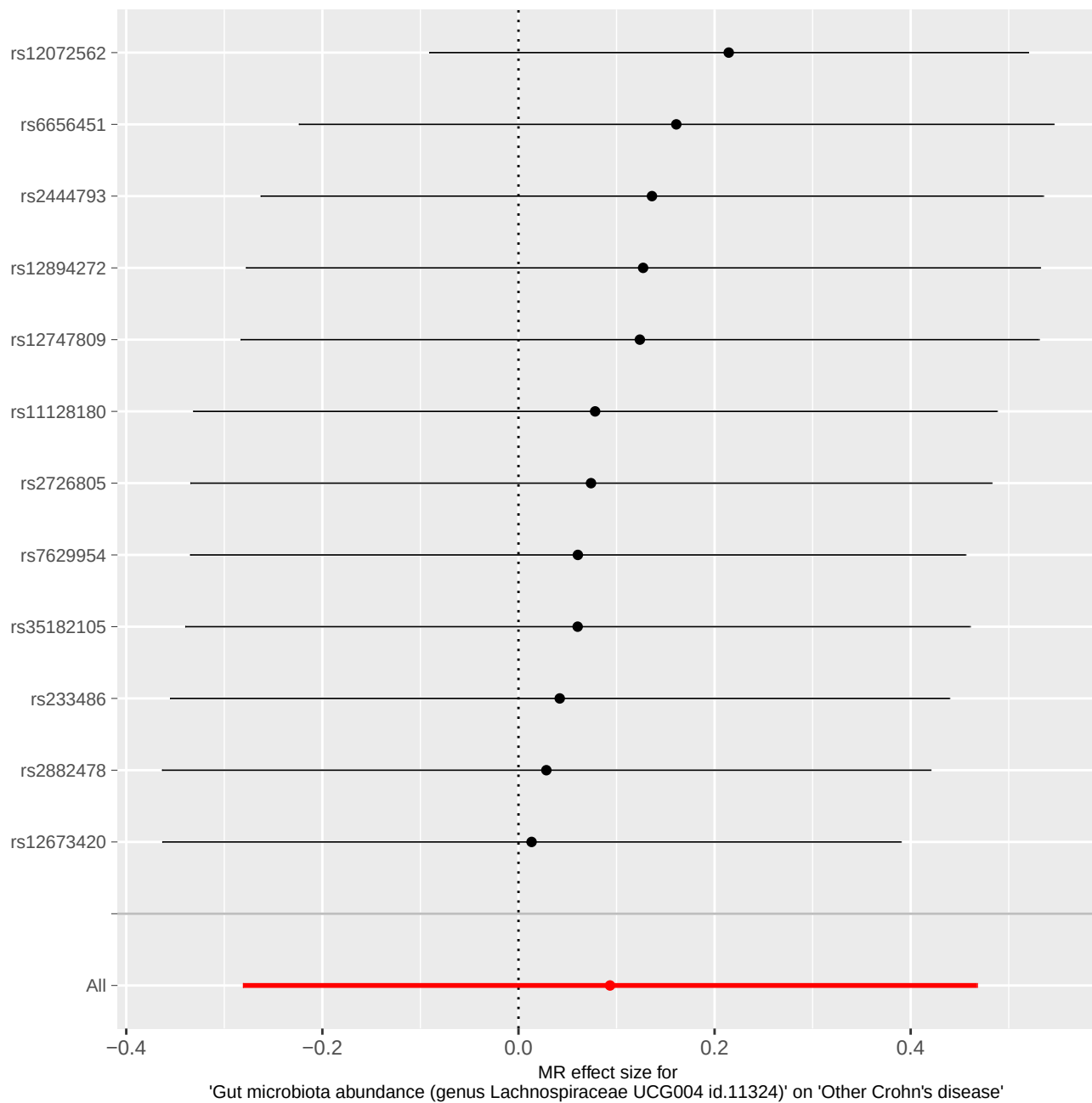


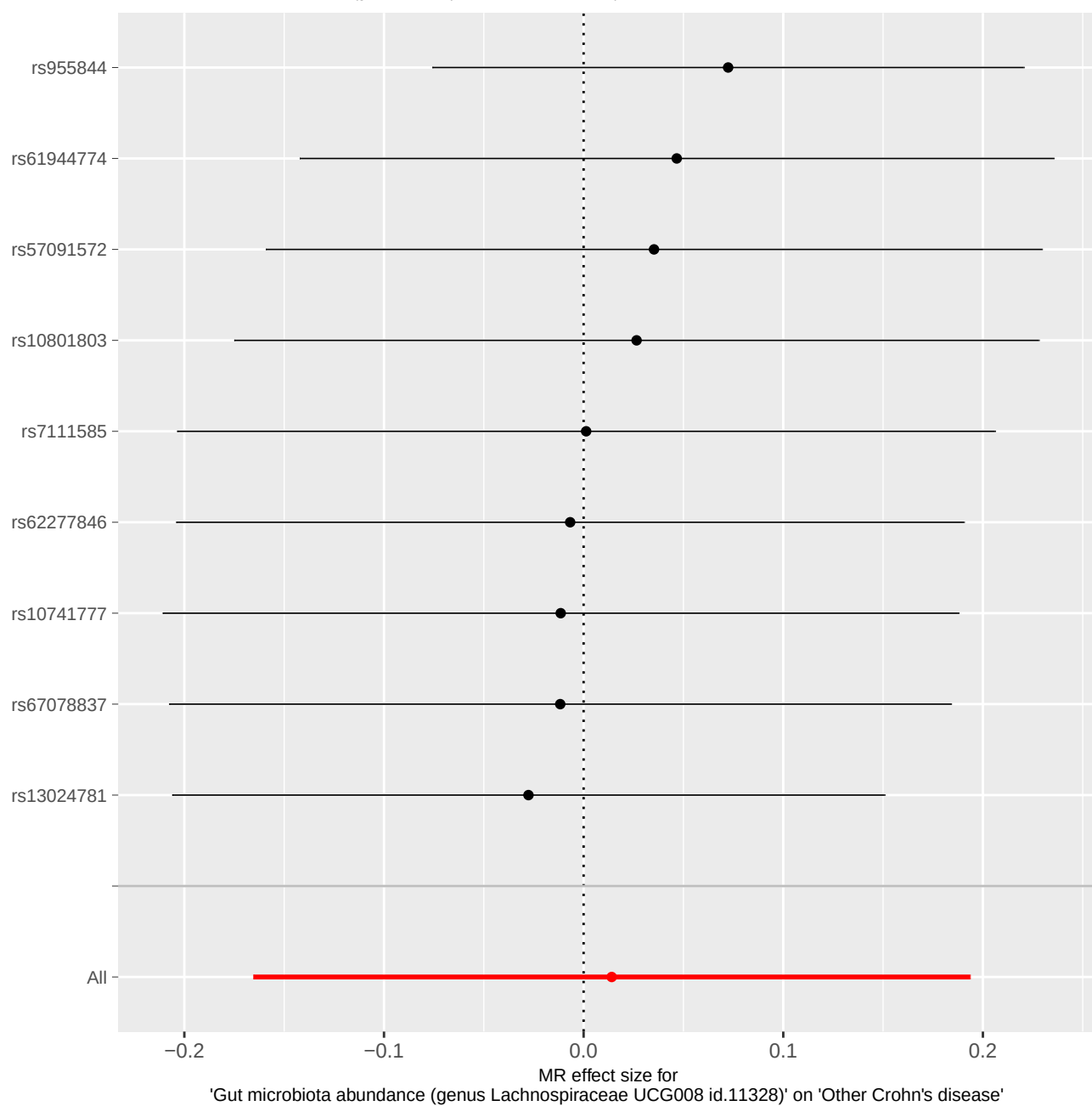


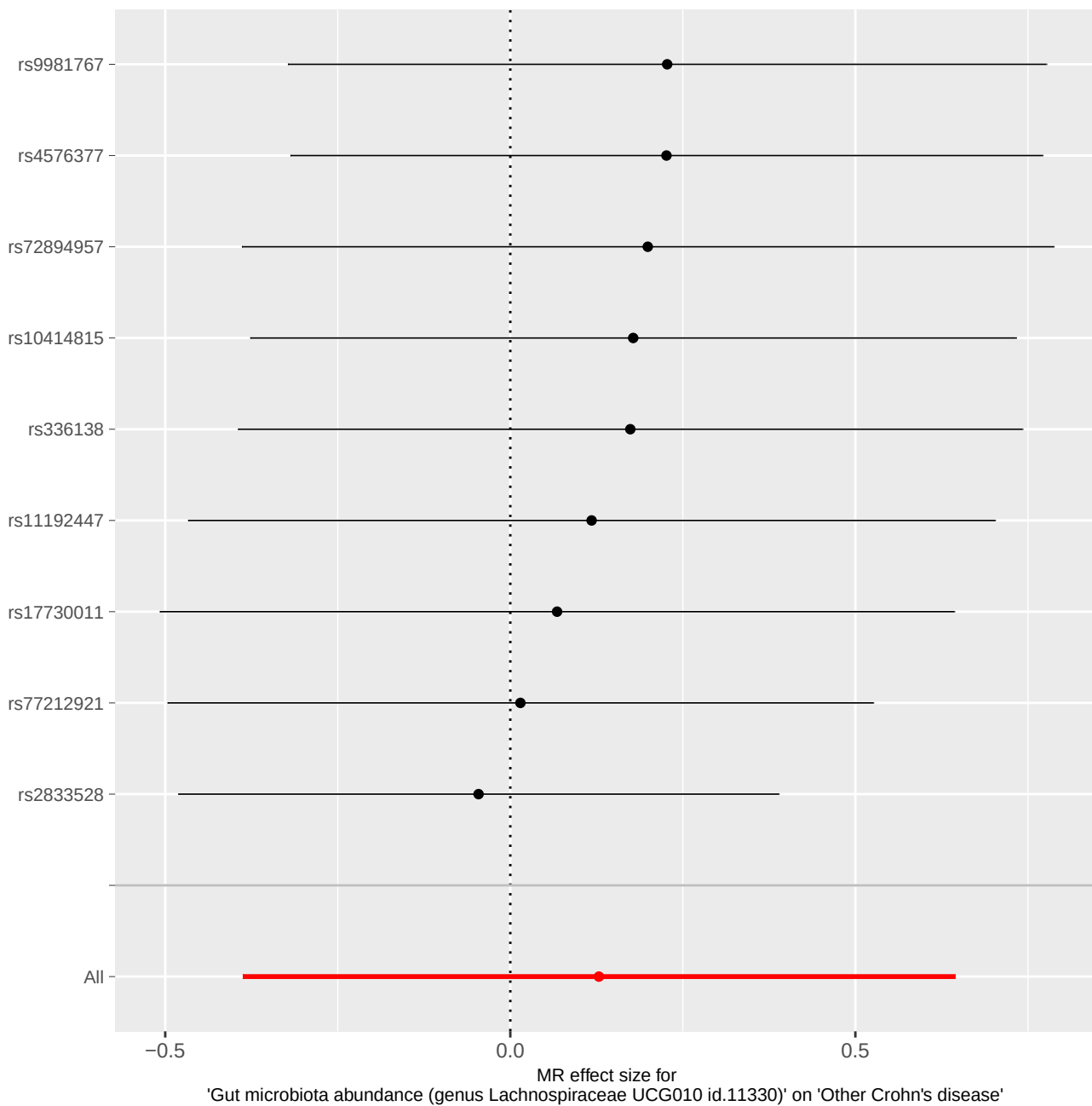


MR effect size for
'Gut microbiota abundance (genus Lachnospiraceae NK4A136 group id.11319)' on 'Other Crohn's disease'

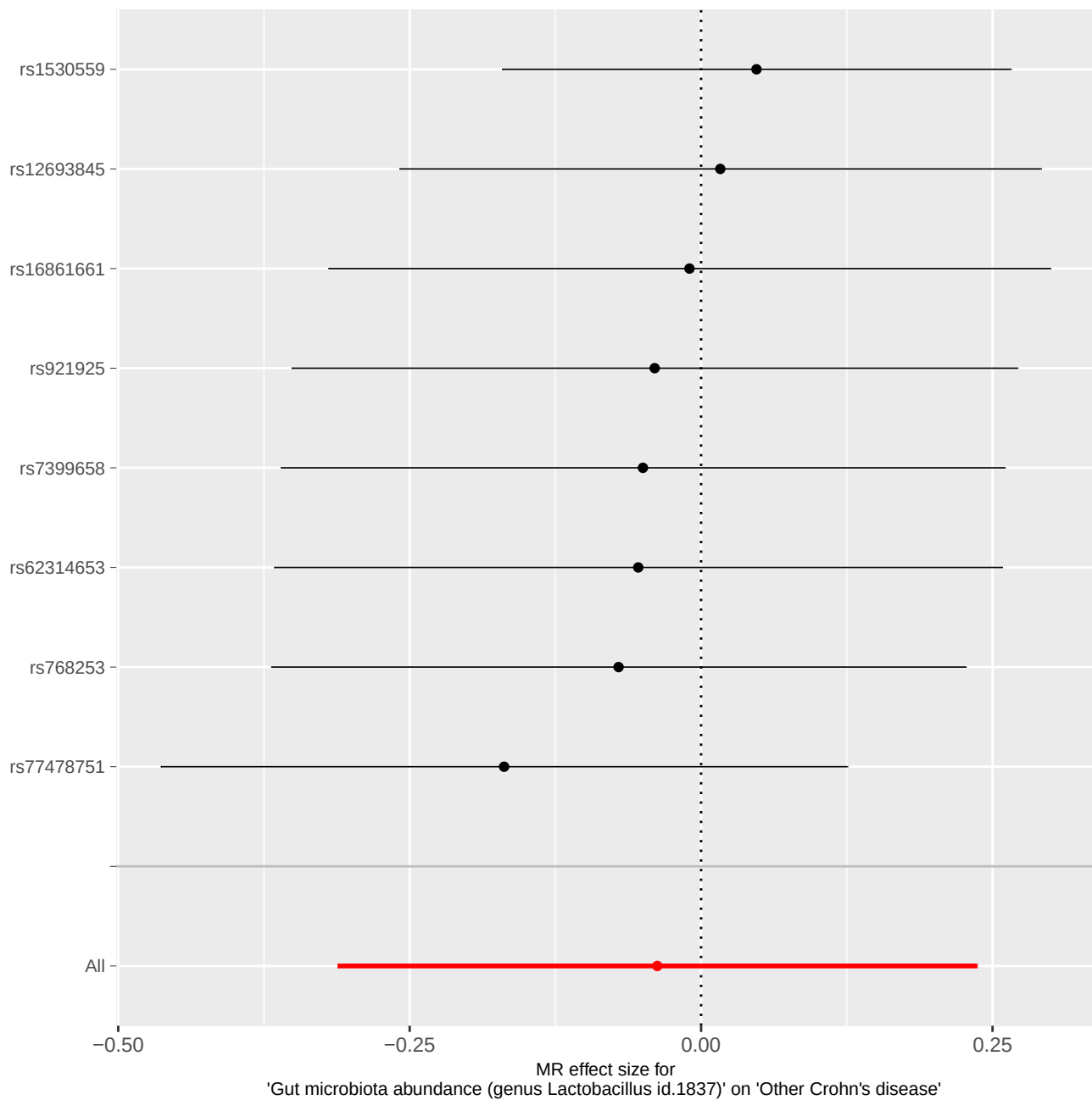




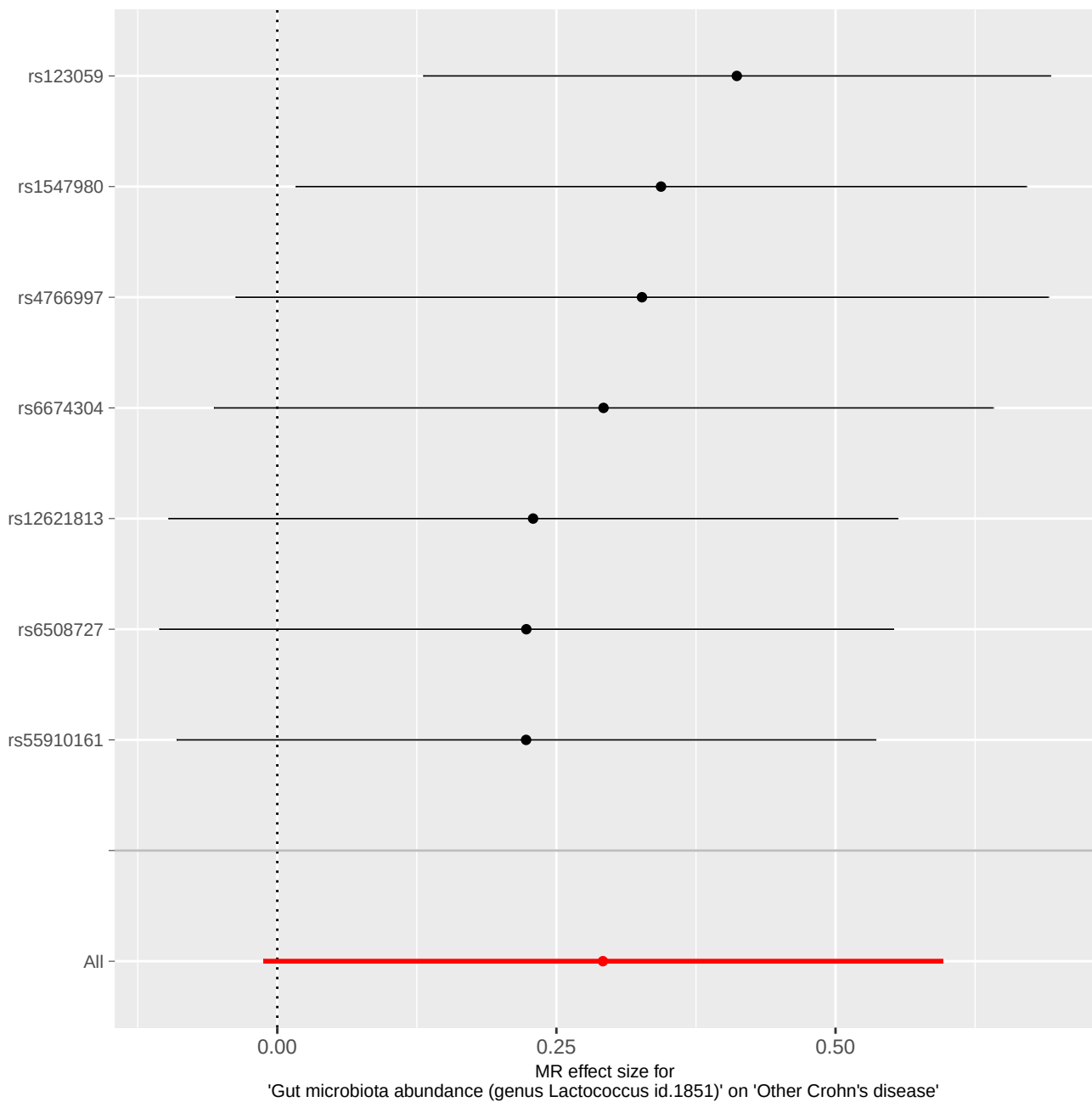


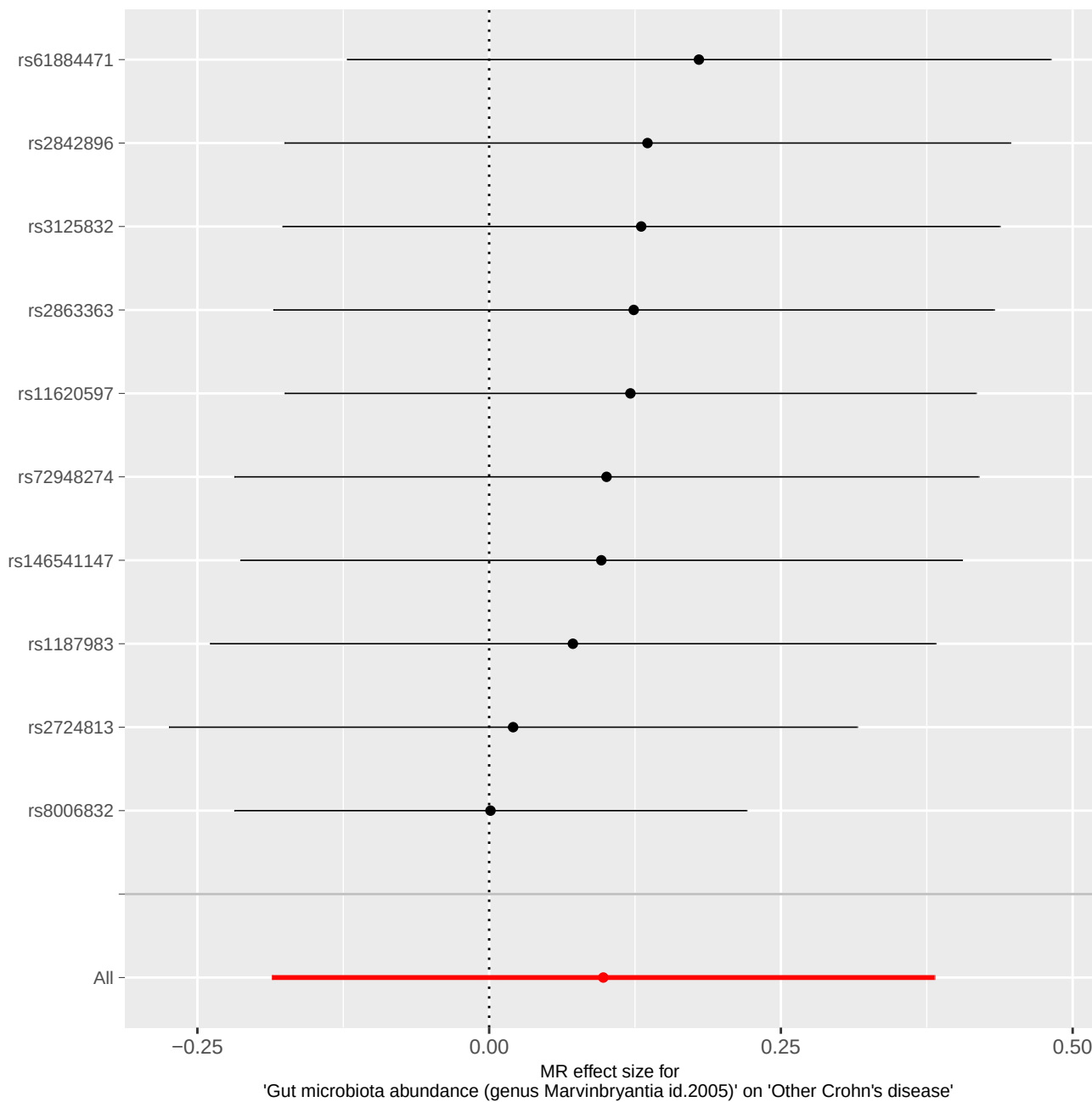


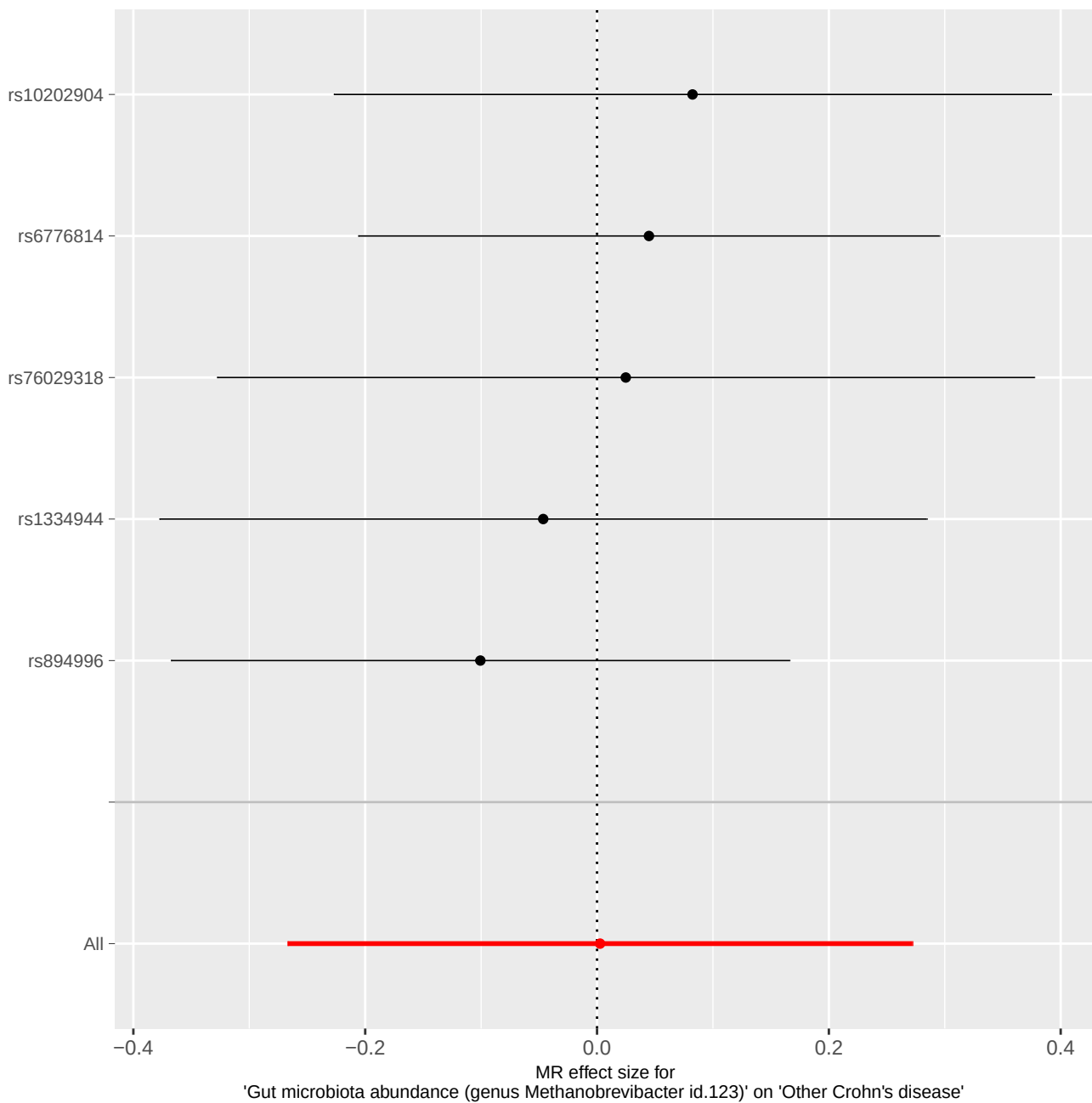
Batch 254 : Gut microbiota abundance (genus Lactobacillus id.1837) on Other Crohn's disease

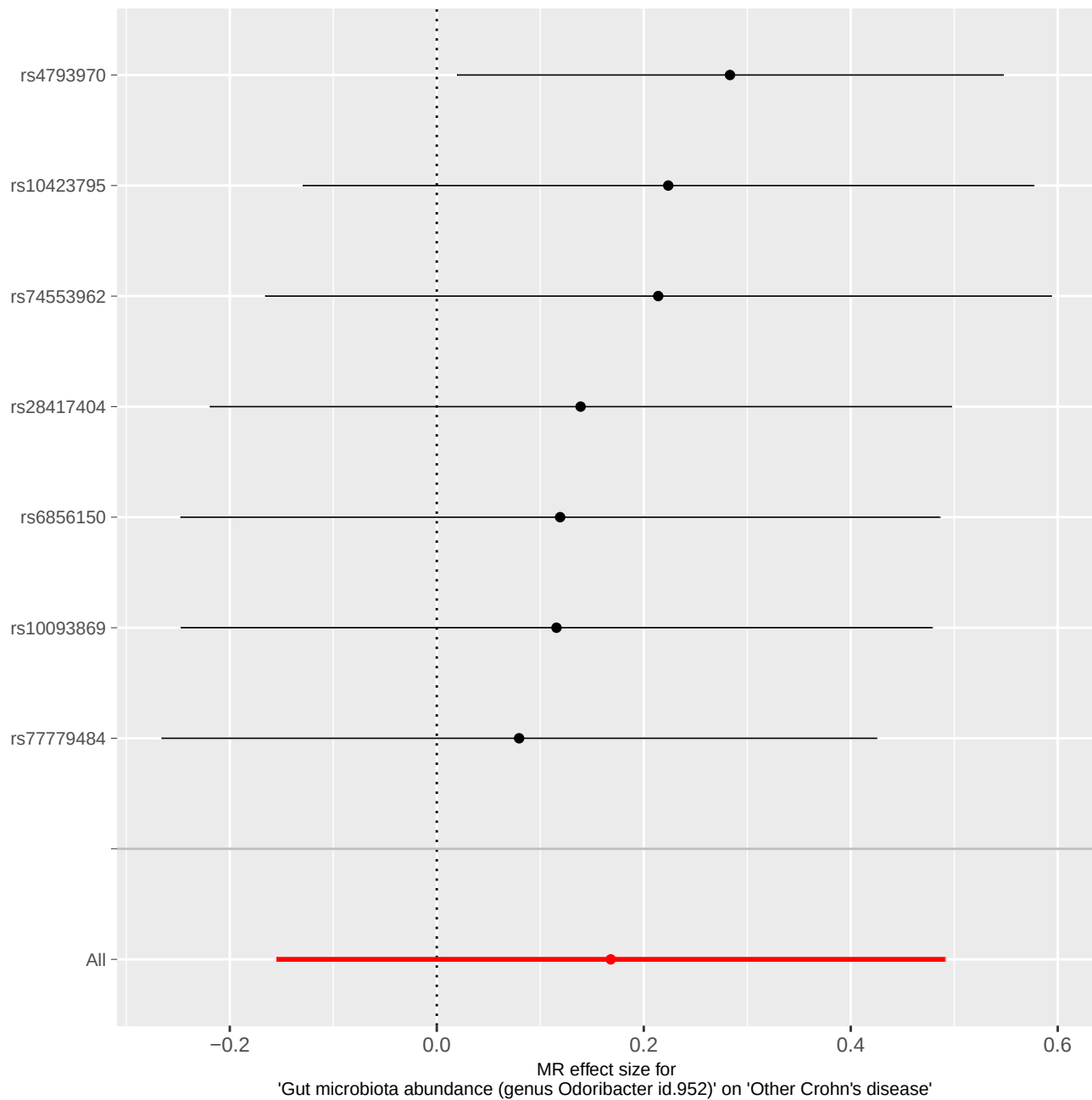


Batch 255 : Gut microbiota abundance (genus Lactococcus id.1851) on Other Crohn's disease

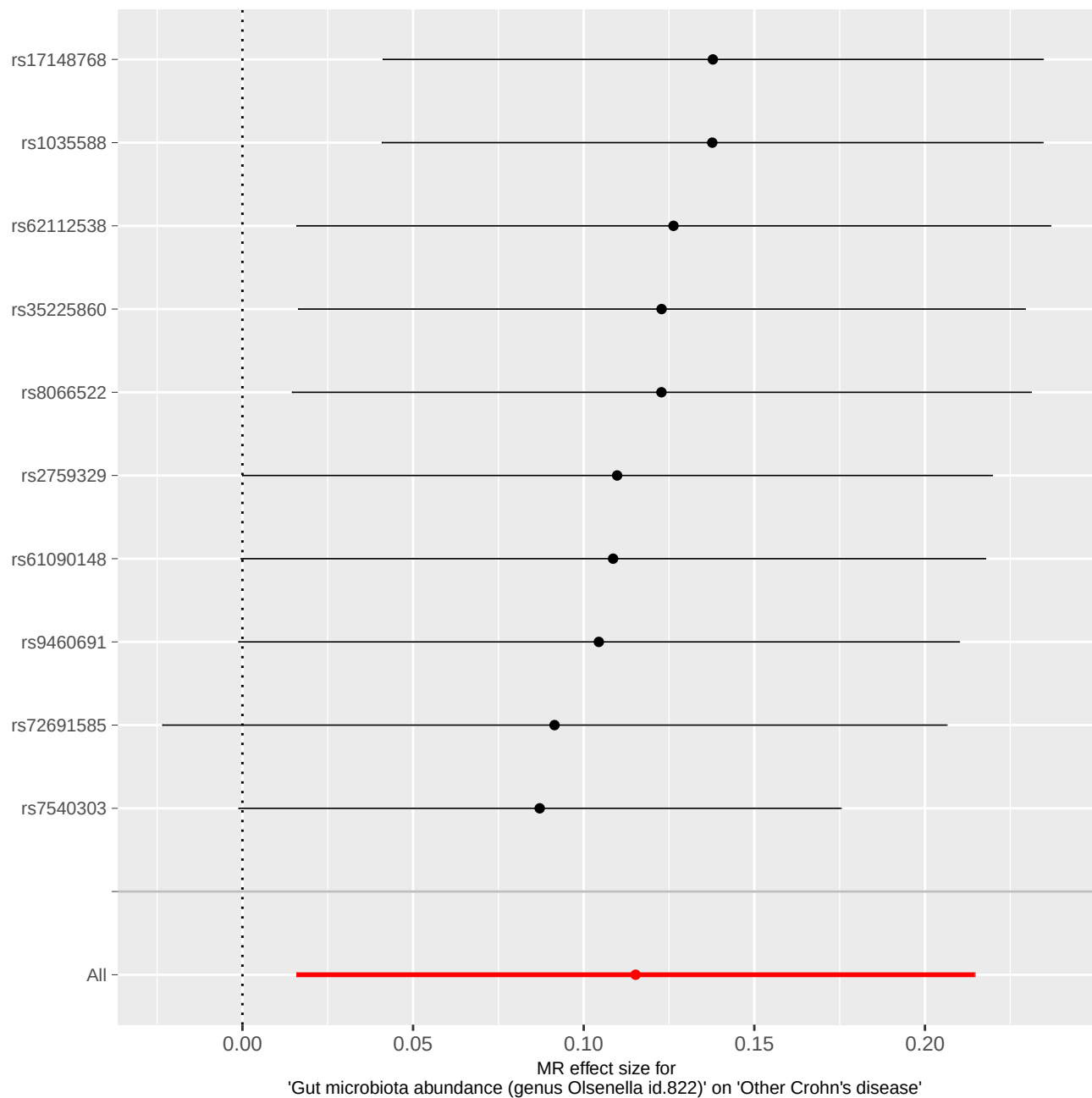




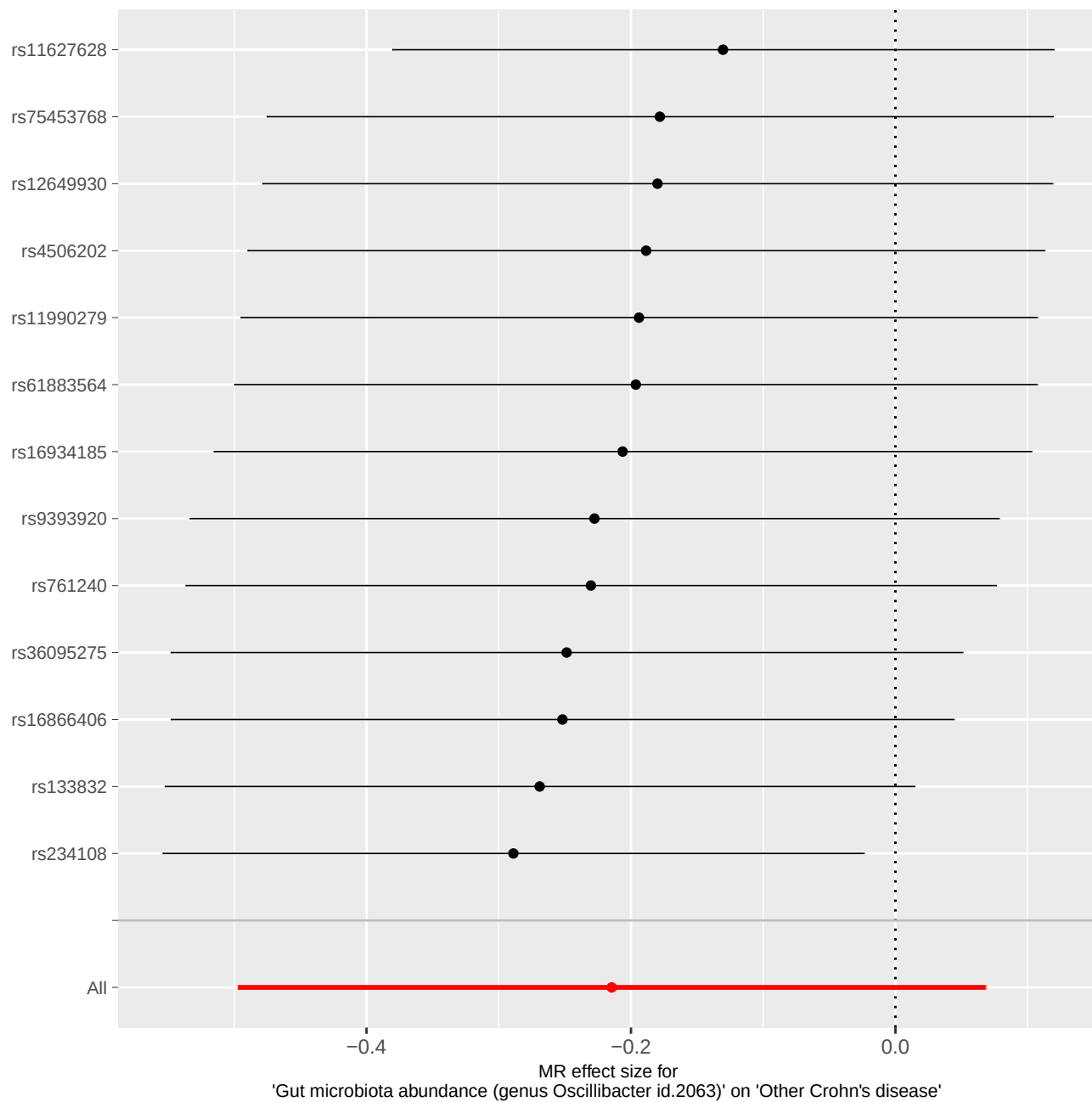




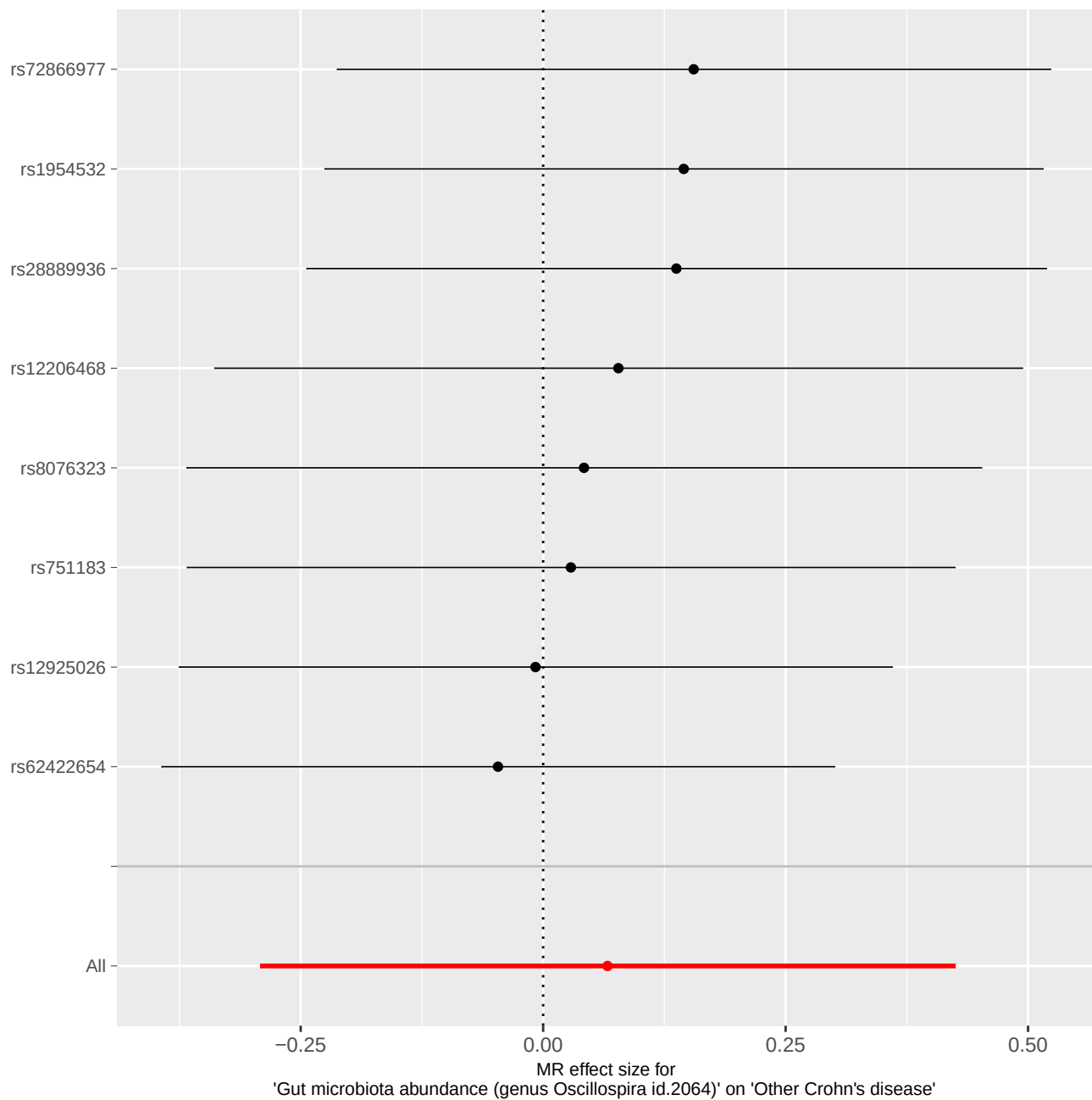
Batch 259 : Gut microbiota abundance (genus Olsenella id.822) on Other Crohn's disease



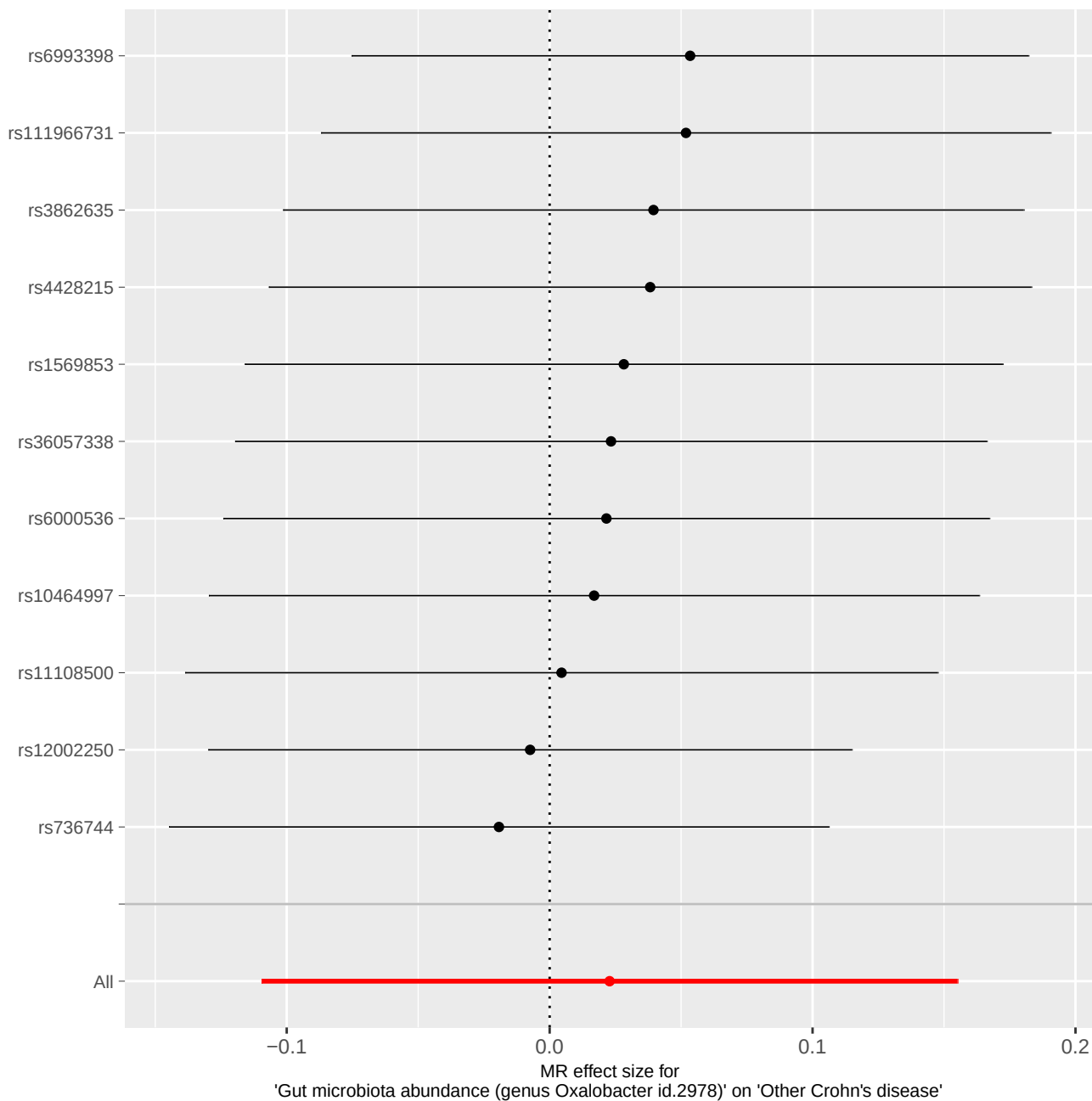
Batch 260 : Gut microbiota abundance (genus Oscillibacter id.2063) on Other Crohn's disease

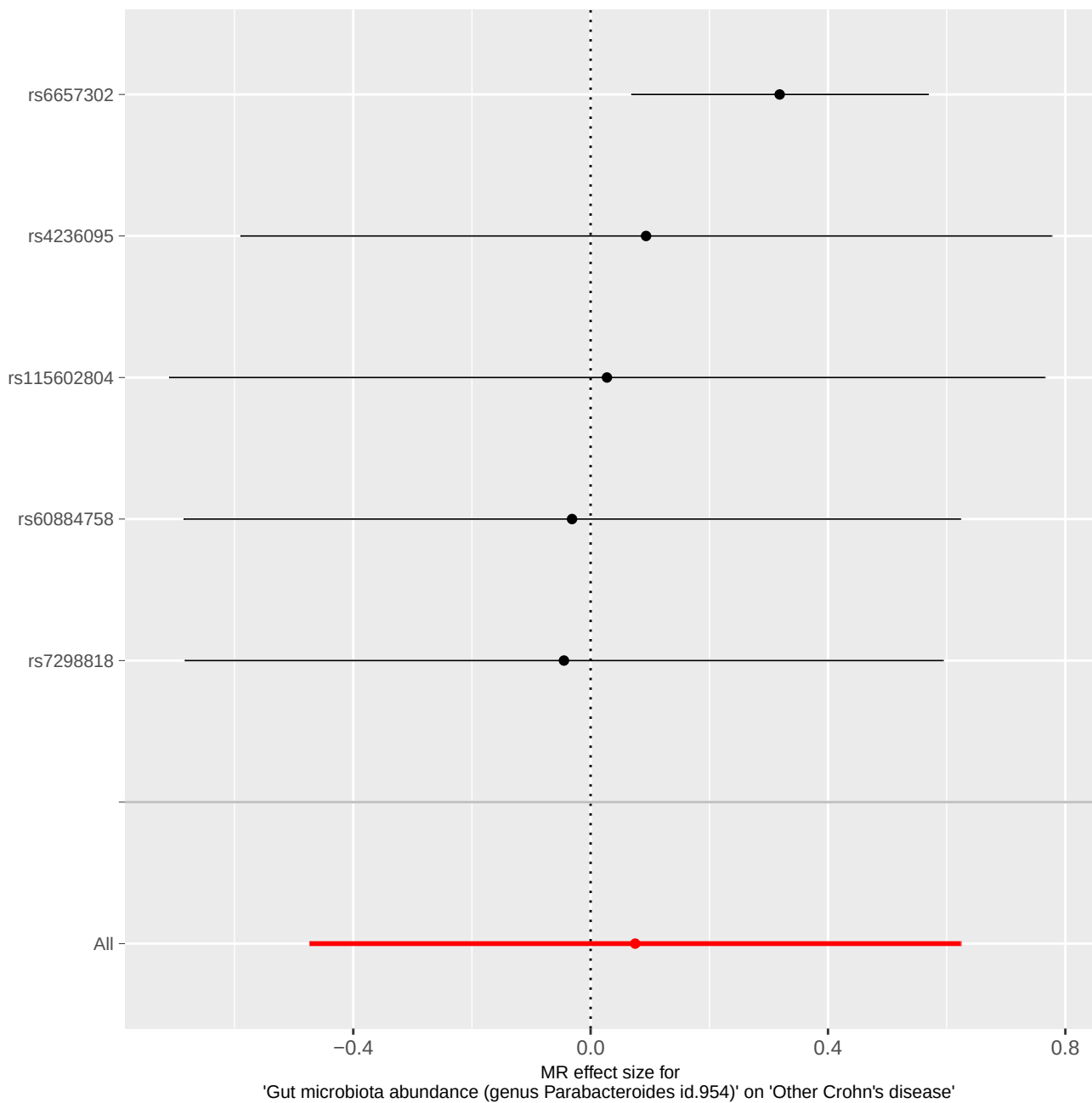


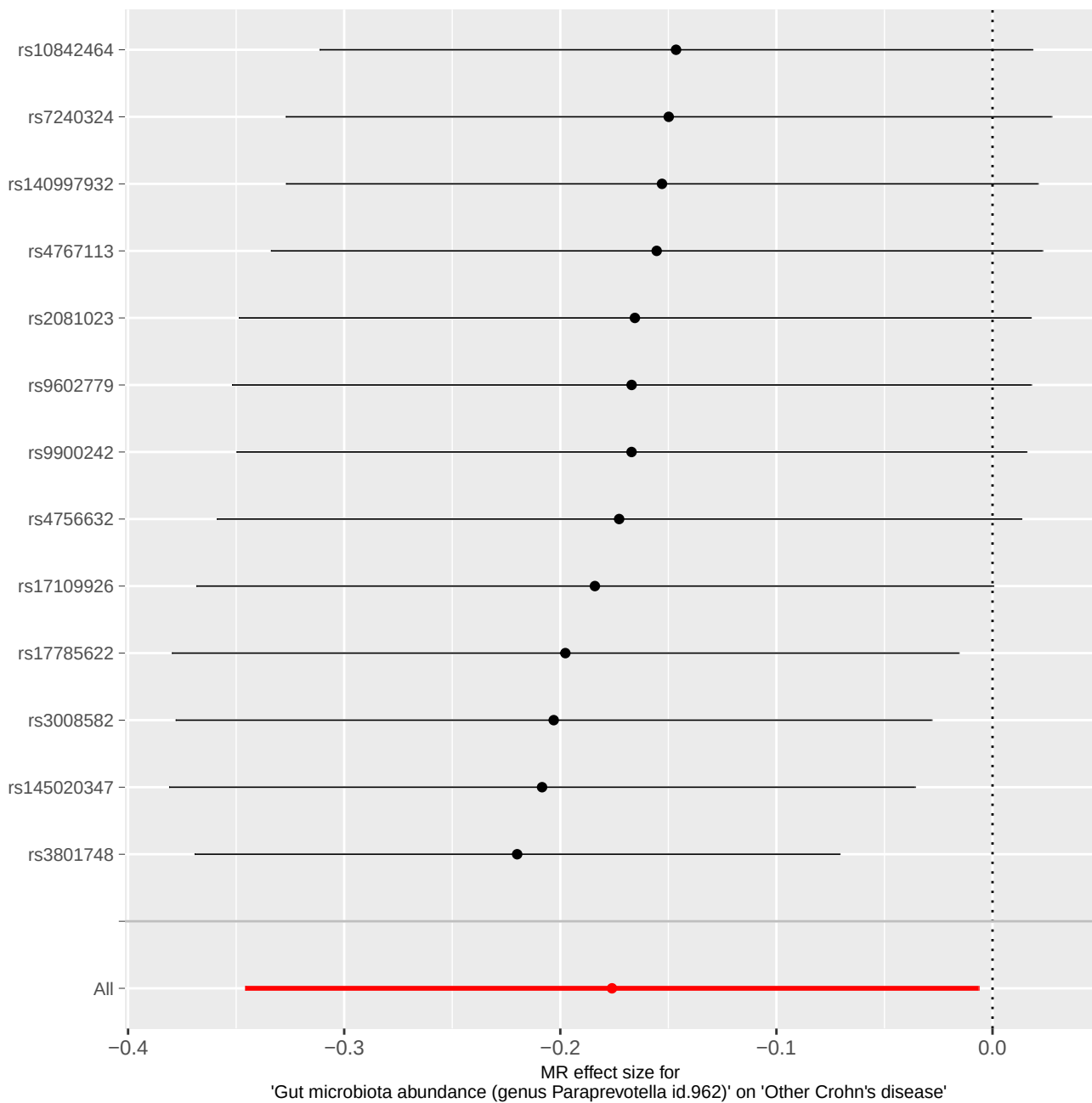
Batch 261 : Gut microbiota abundance (genus Oscillospira id.2064) on Other Crohn's disease



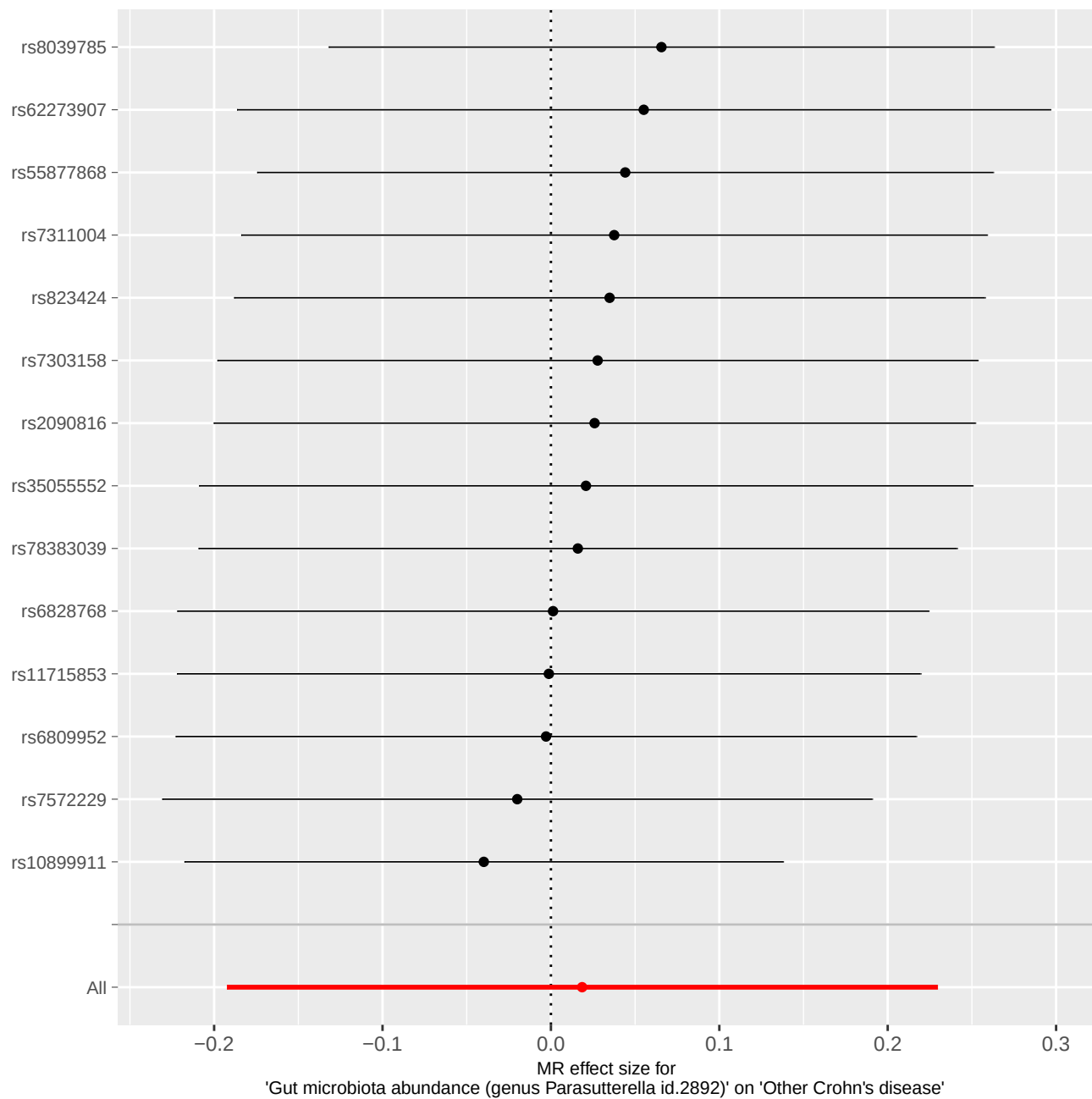
Batch 262 : Gut microbiota abundance (genus Oxalobacter id.2978) on Other Crohn's disease



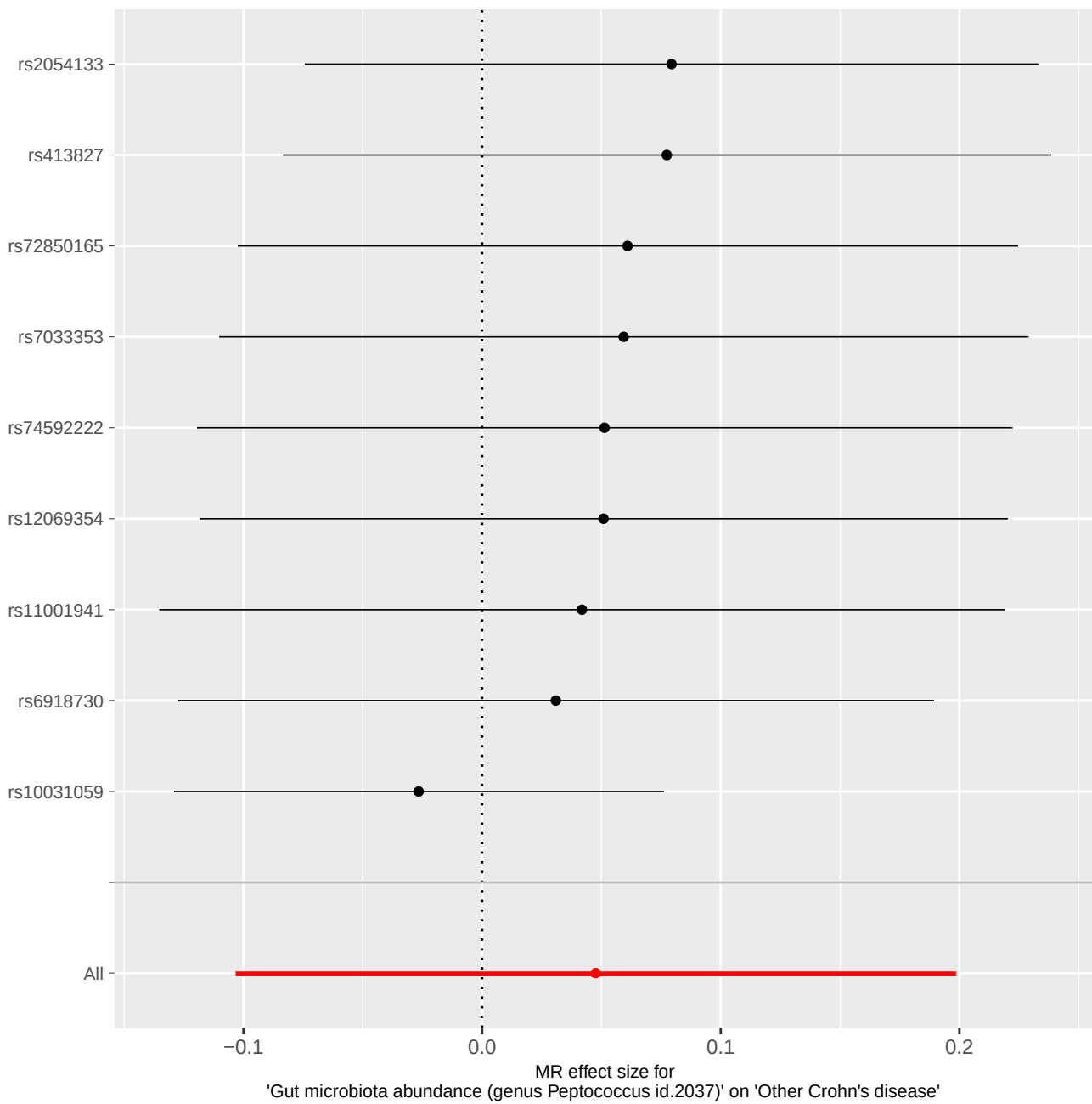


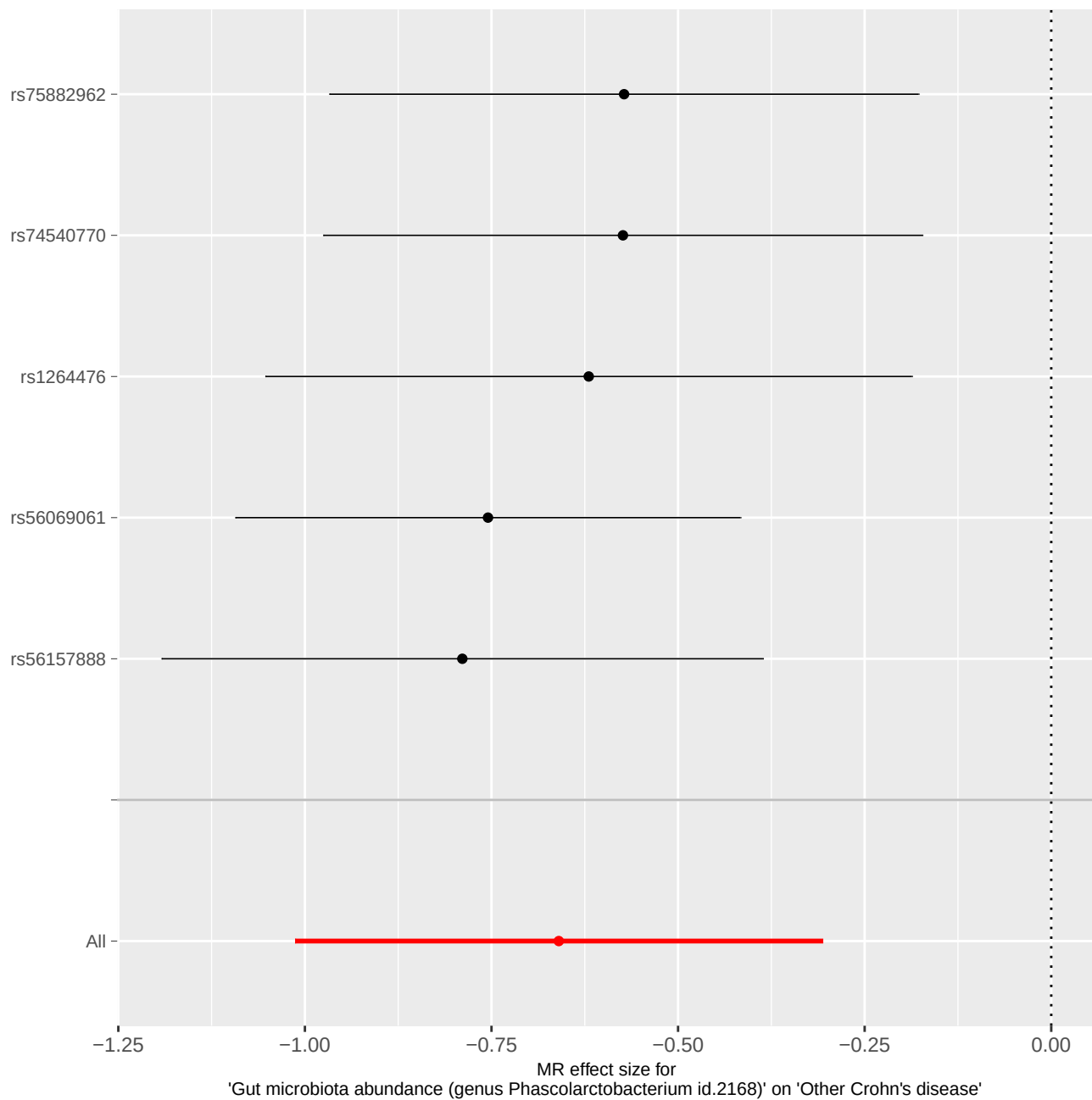


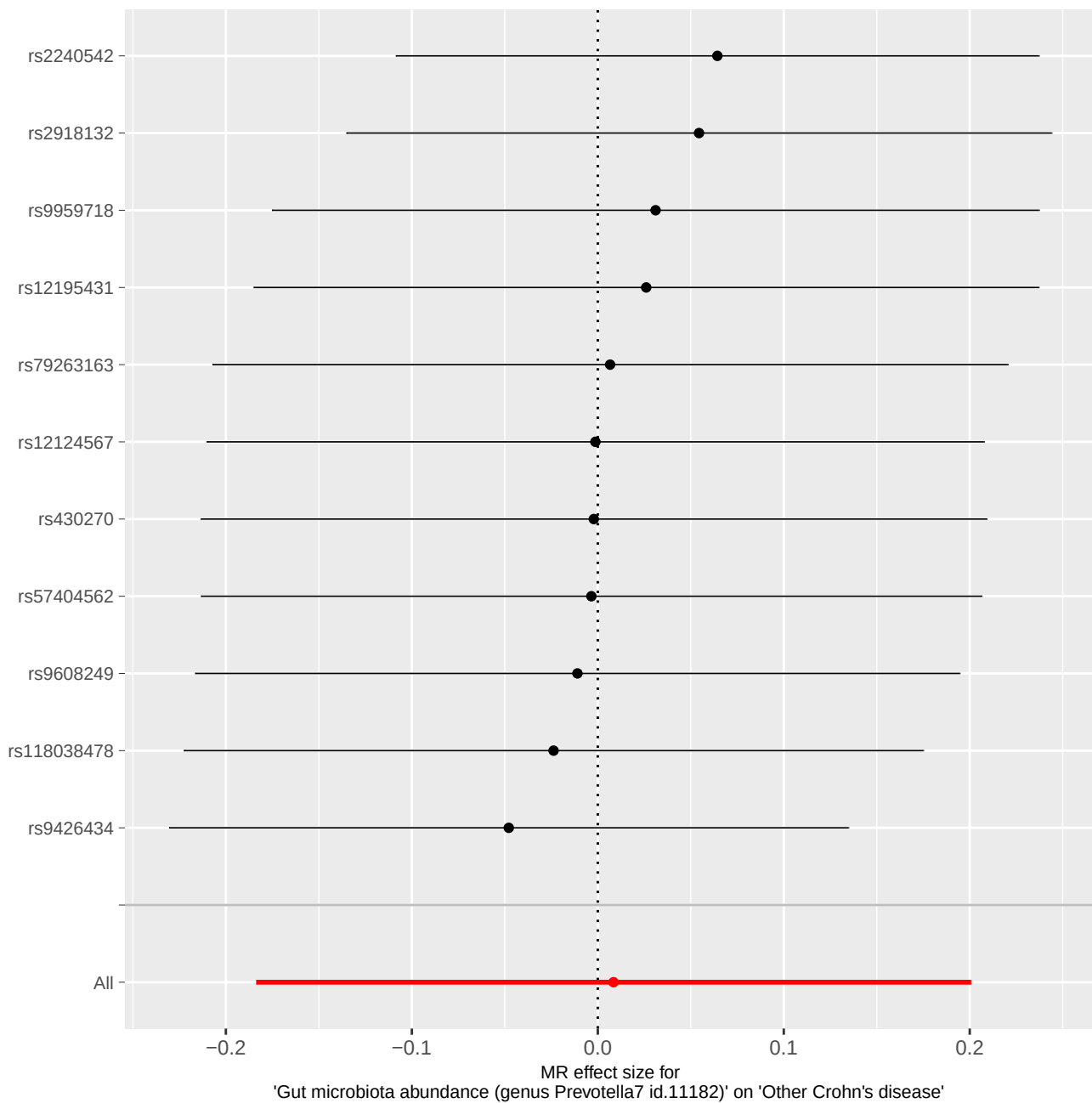
Batch 265 : Gut microbiota abundance (genus Parasutterella id.2892) on Other Crohn's disease



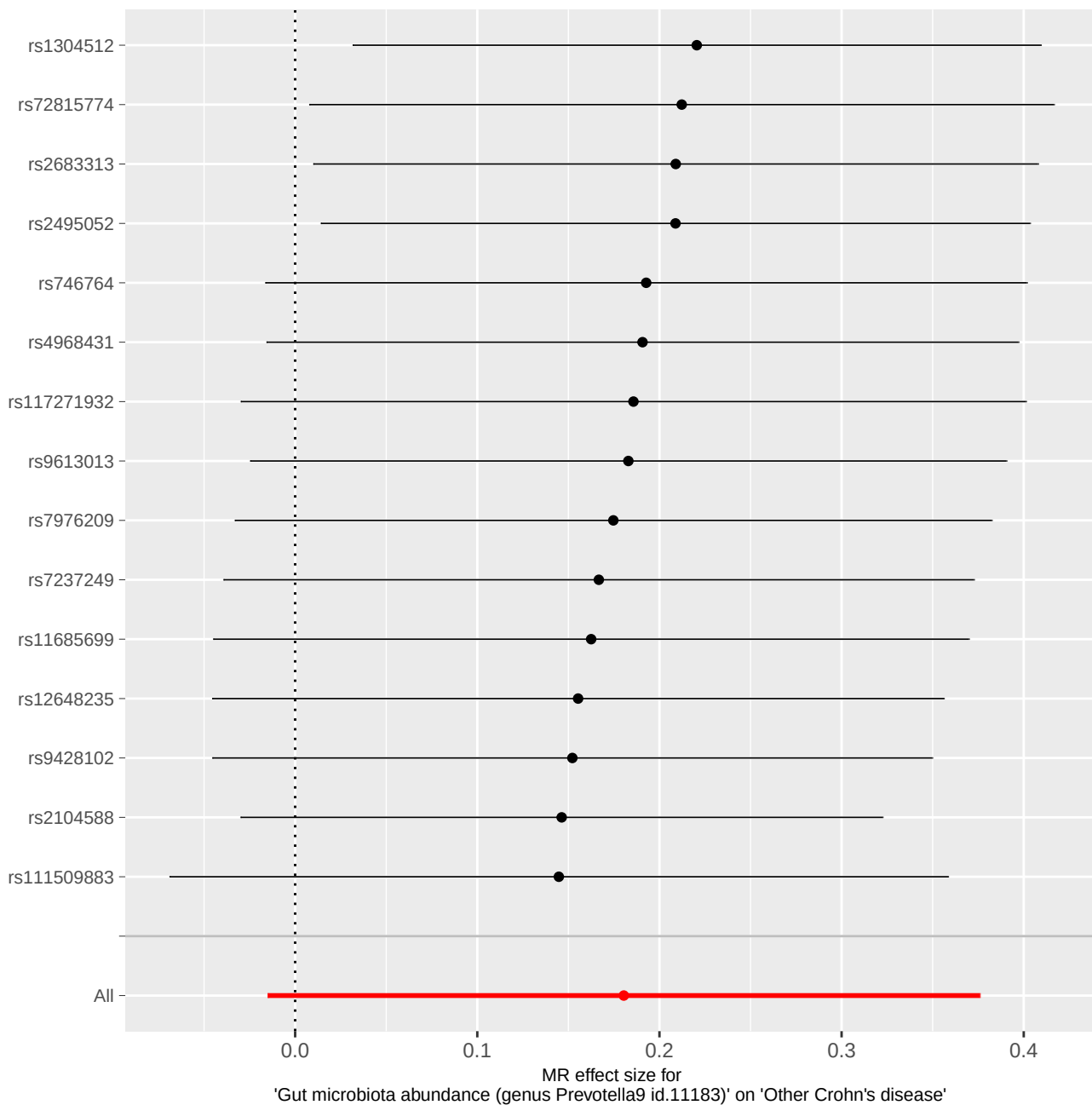
Batch 266 : Gut microbiota abundance (genus Peptococcus id.2037) on Other Crohn's disease

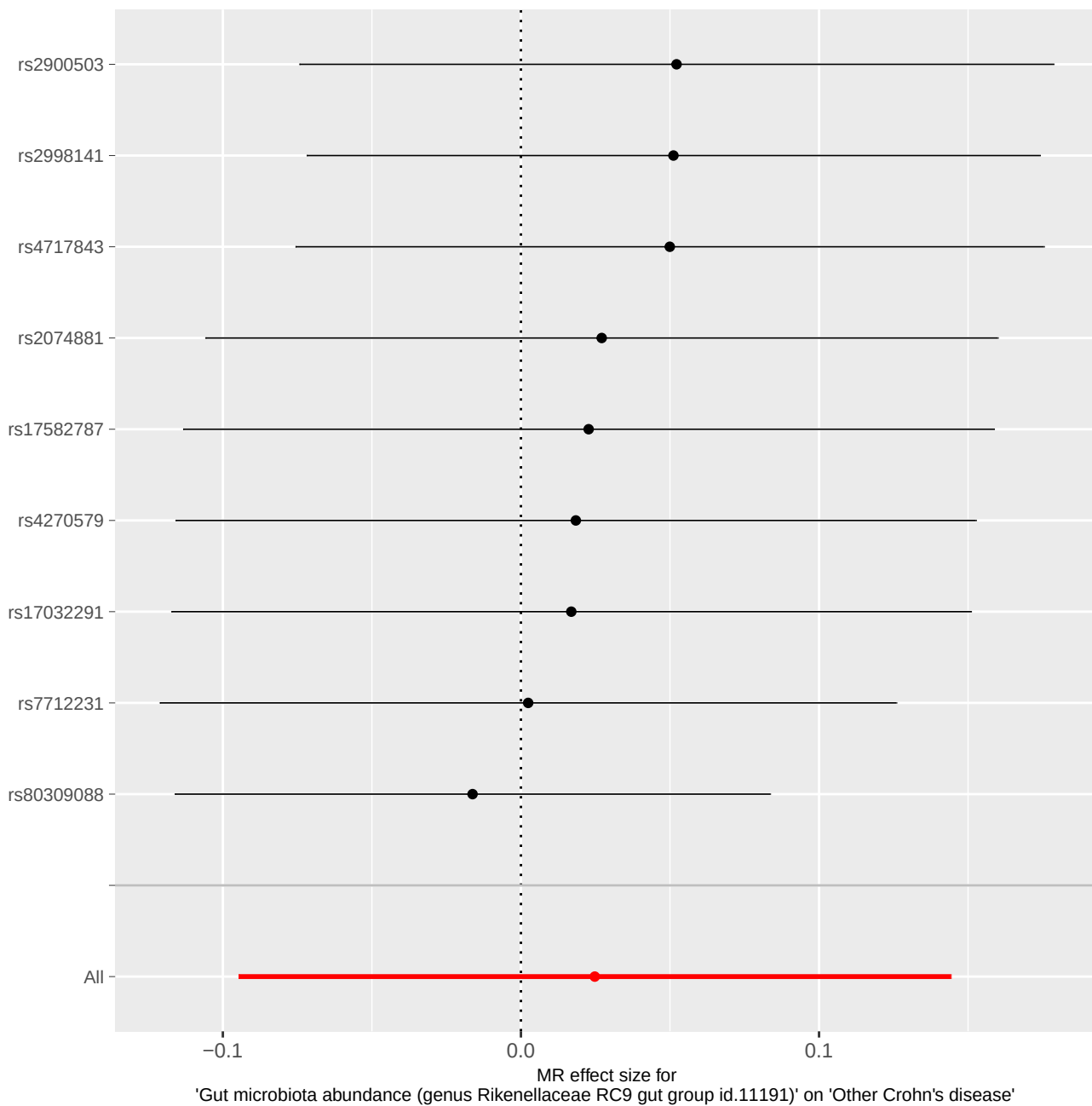


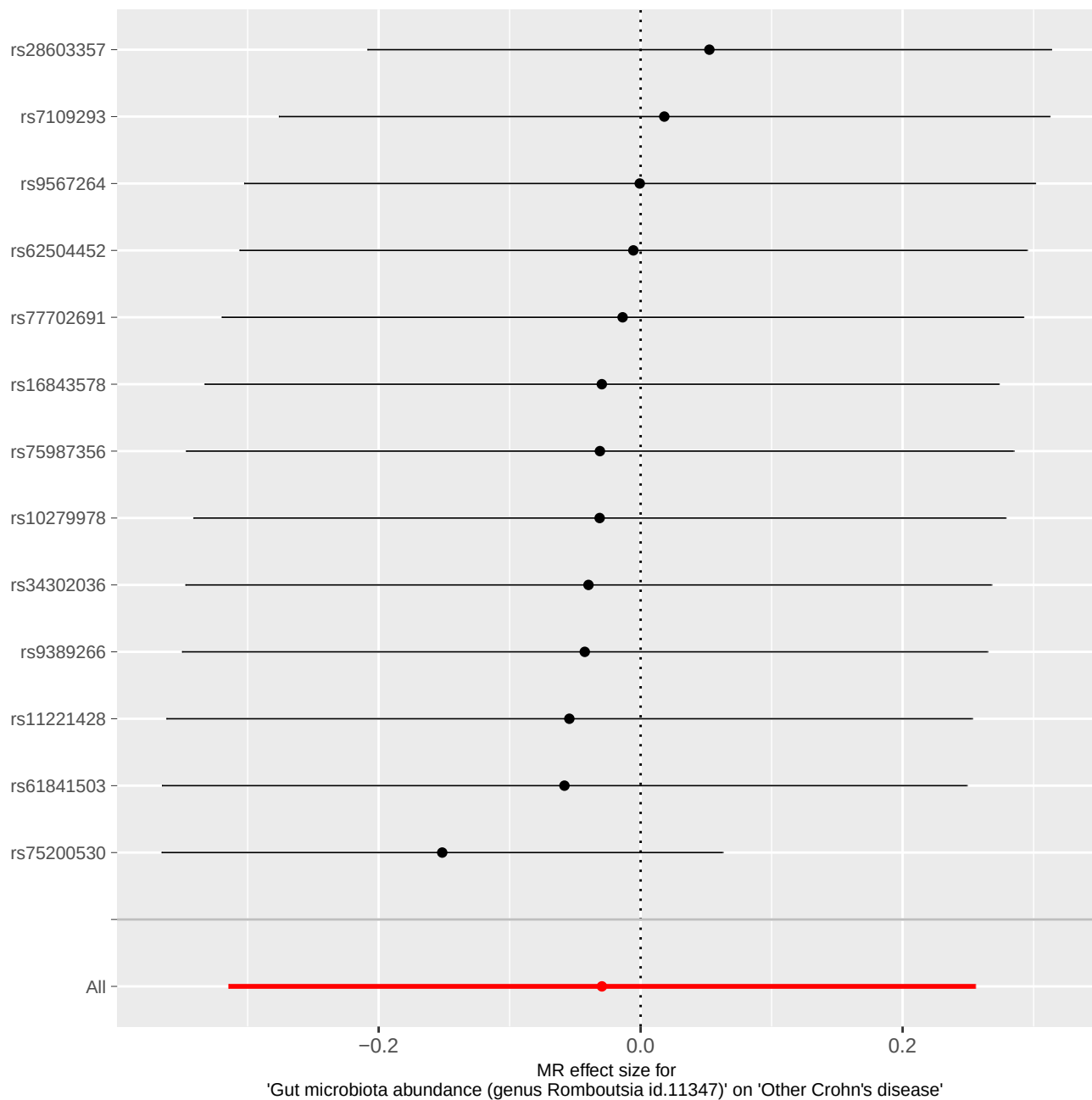


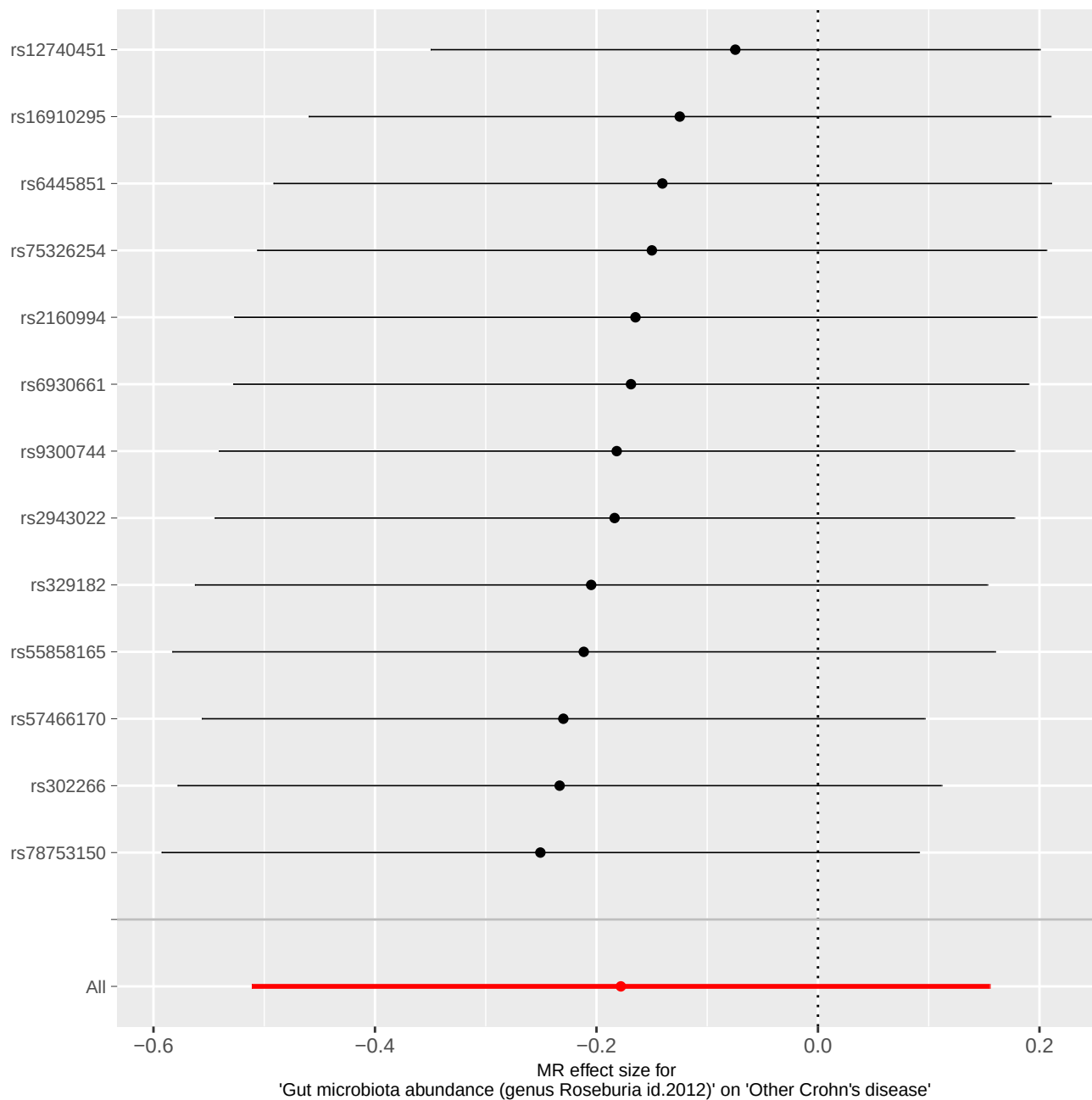


Batch 269 : Gut microbiota abundance (genus Prevotella9 id.11183) on Other Crohn's disease

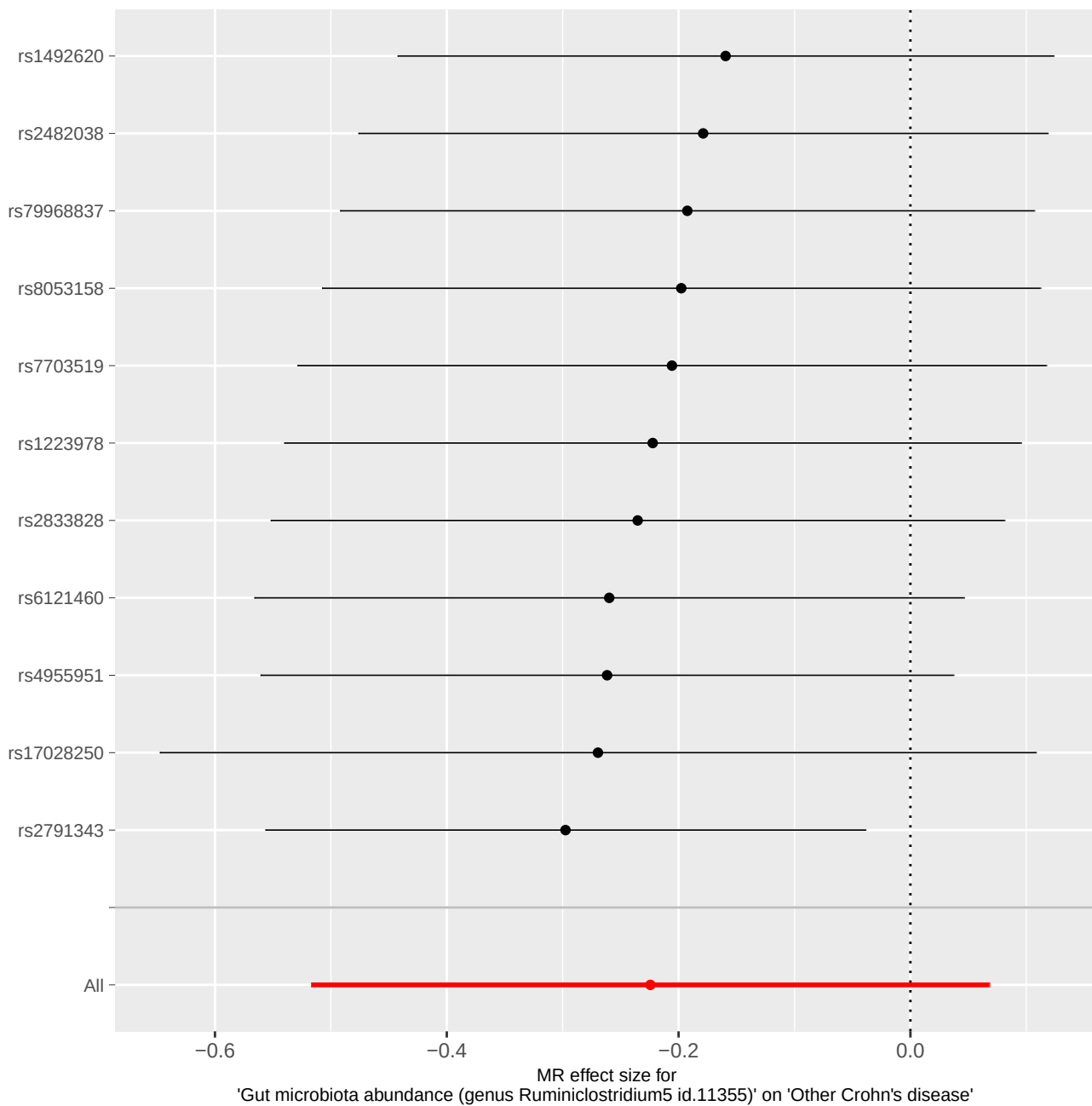


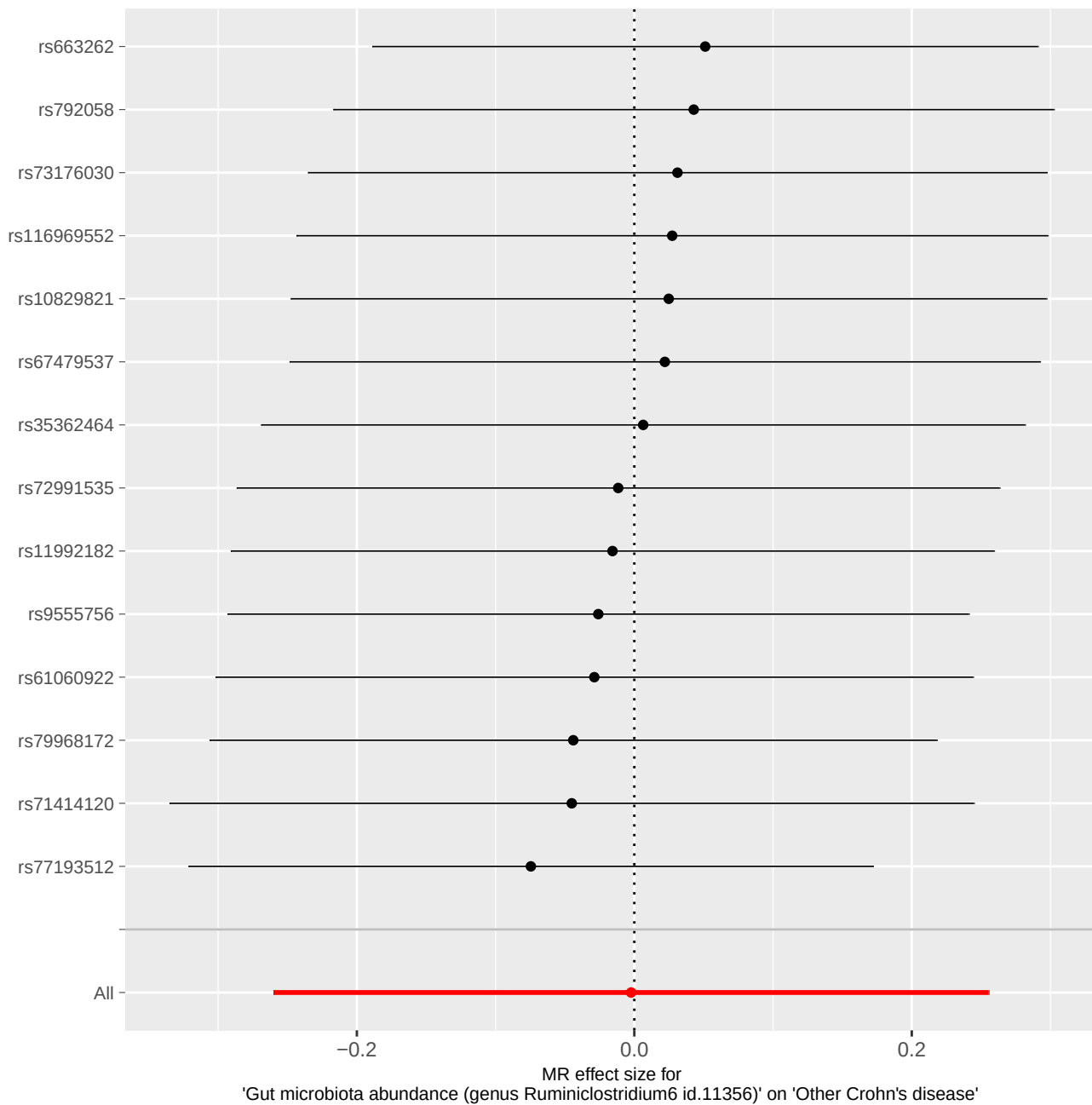


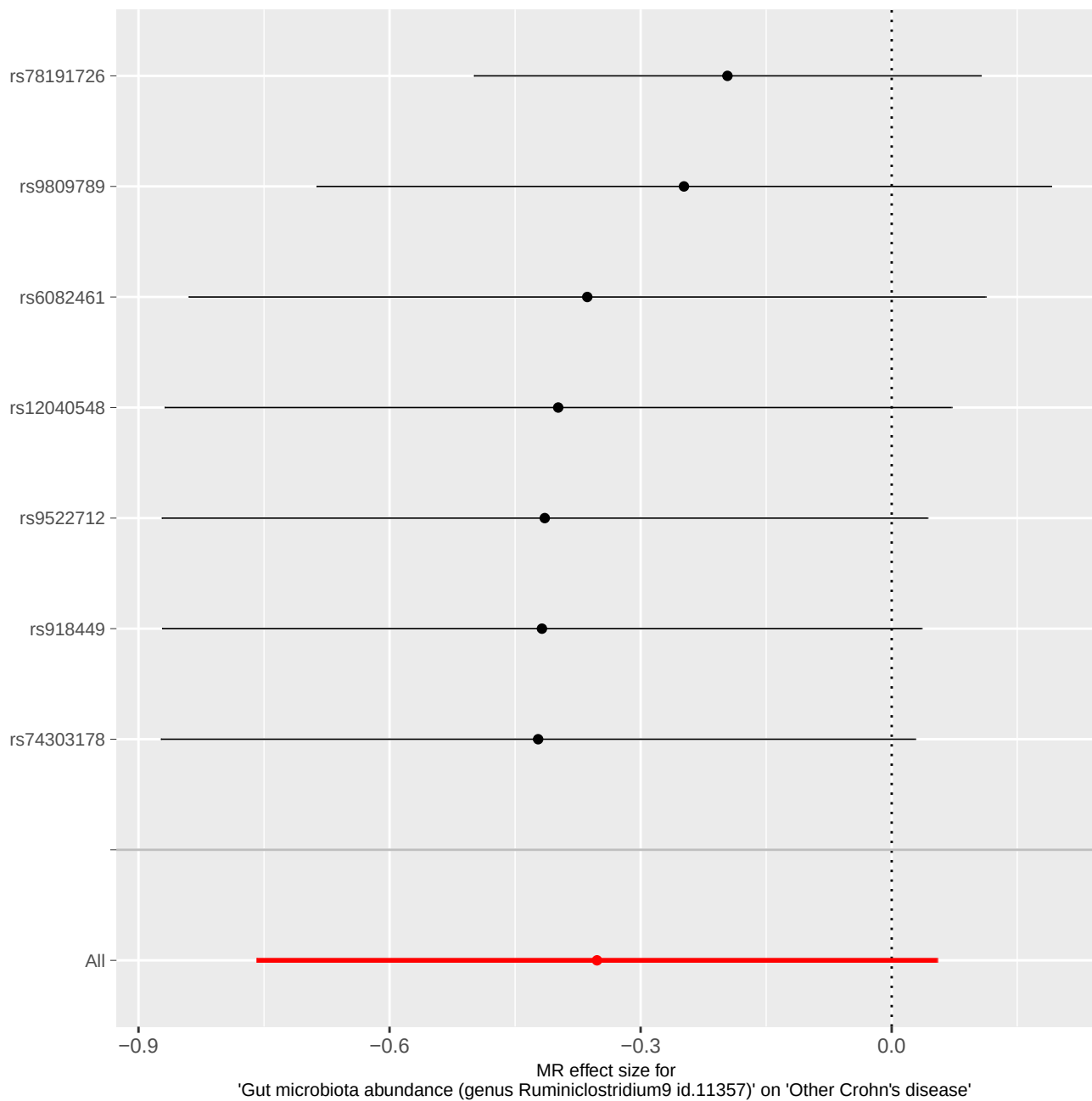


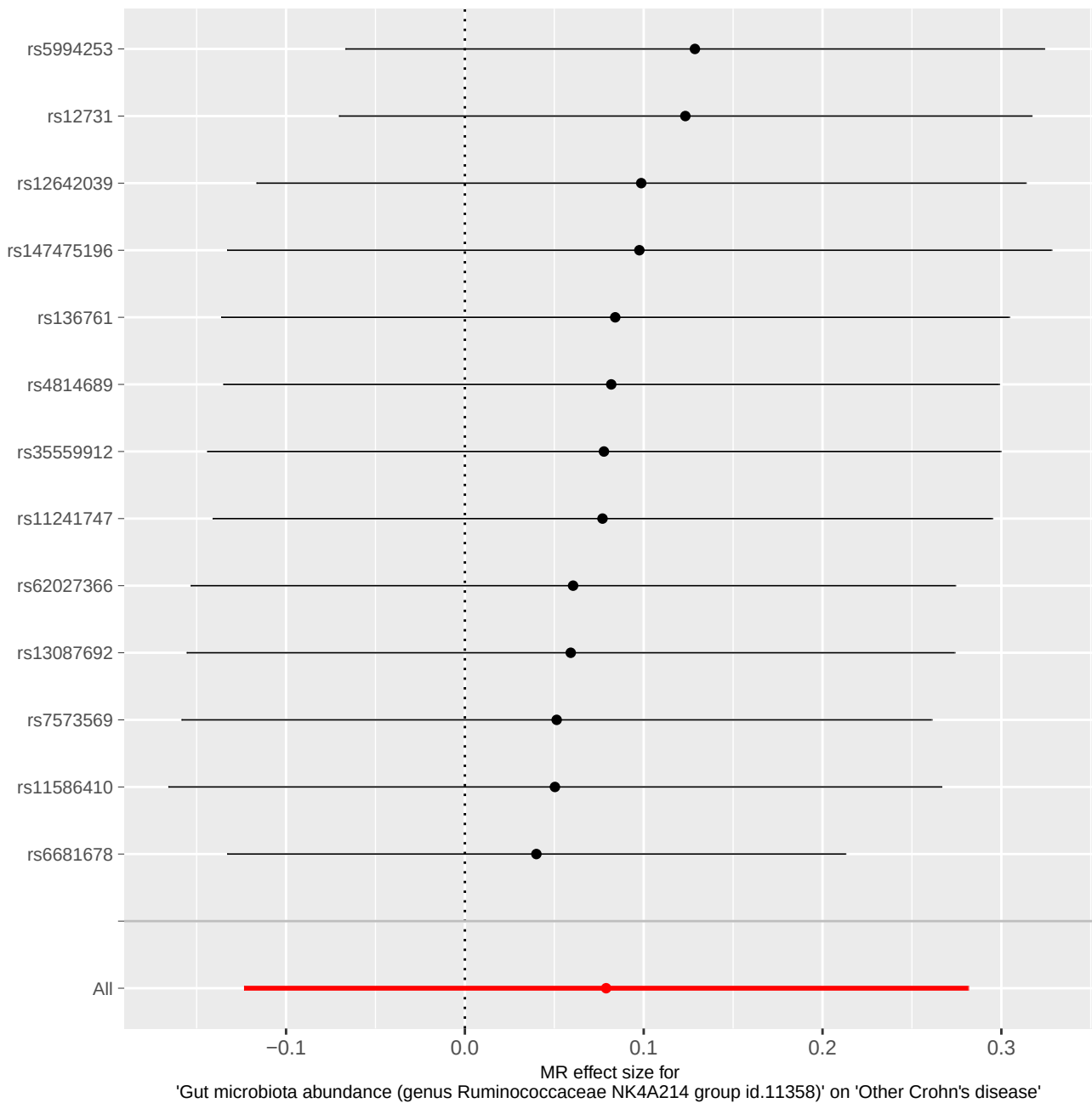


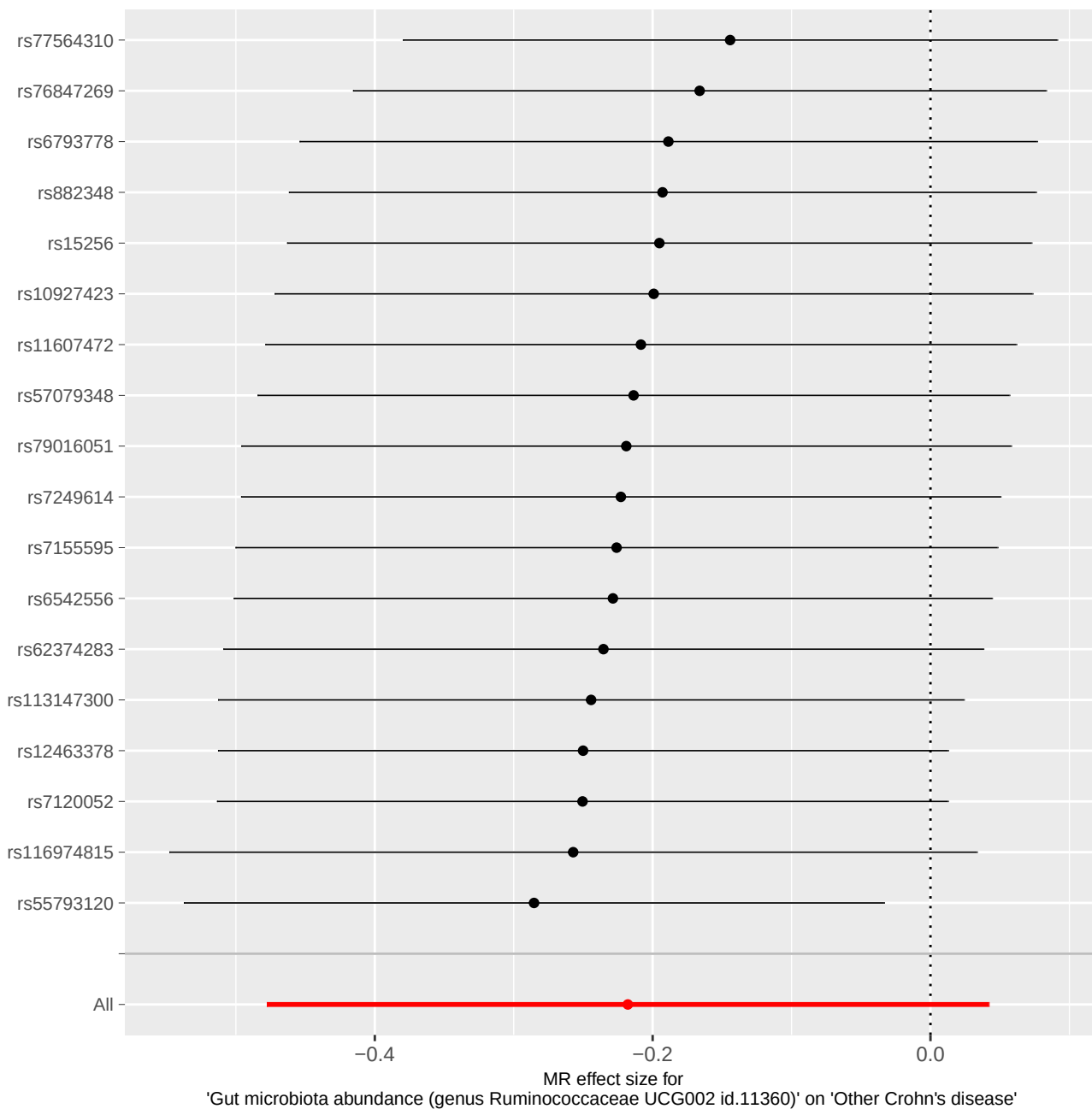
Batch 273 : Gut microbiota abundance (genus Ruminiclostridium5 id.11355) on Other Crohn's disease

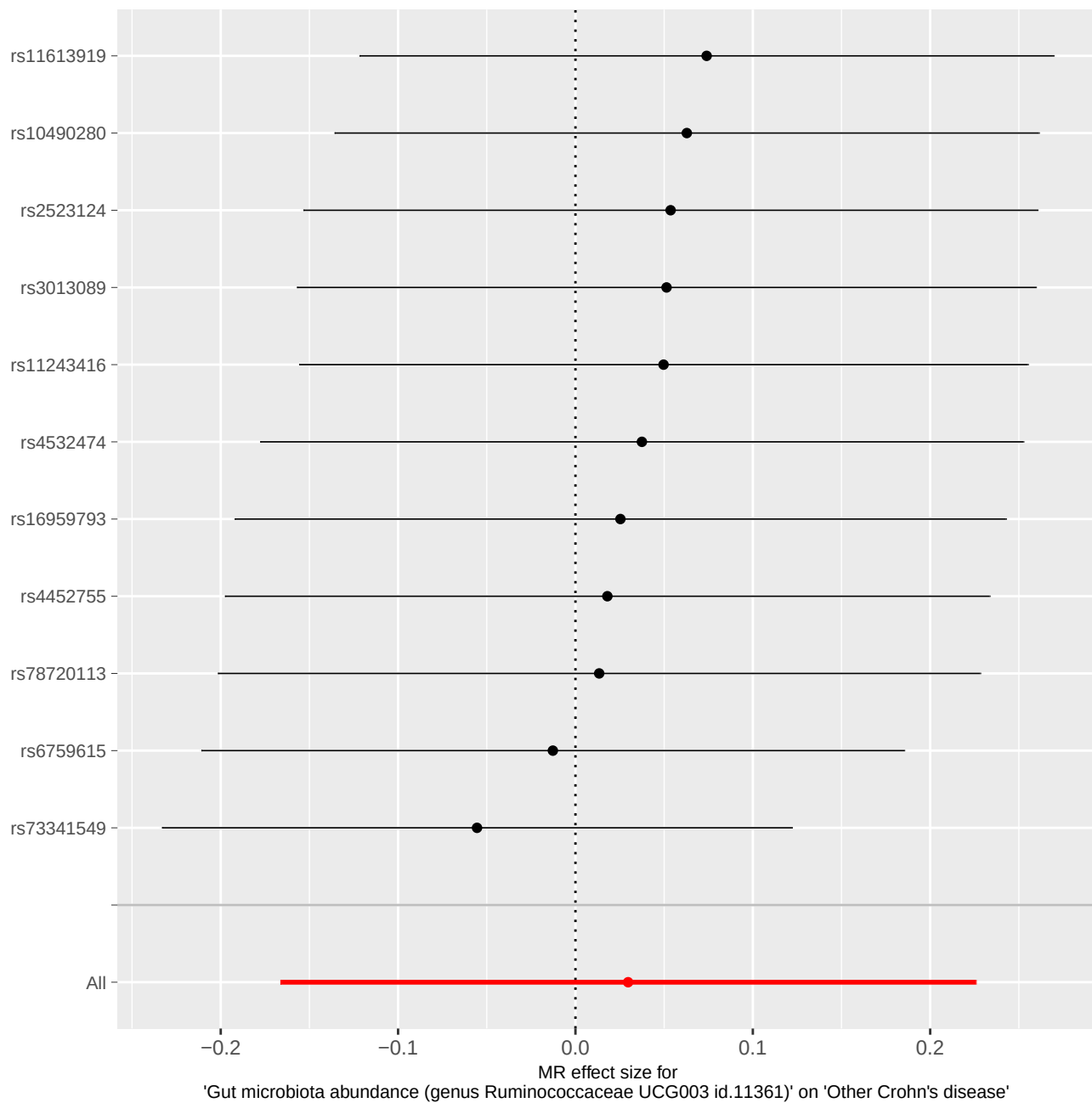


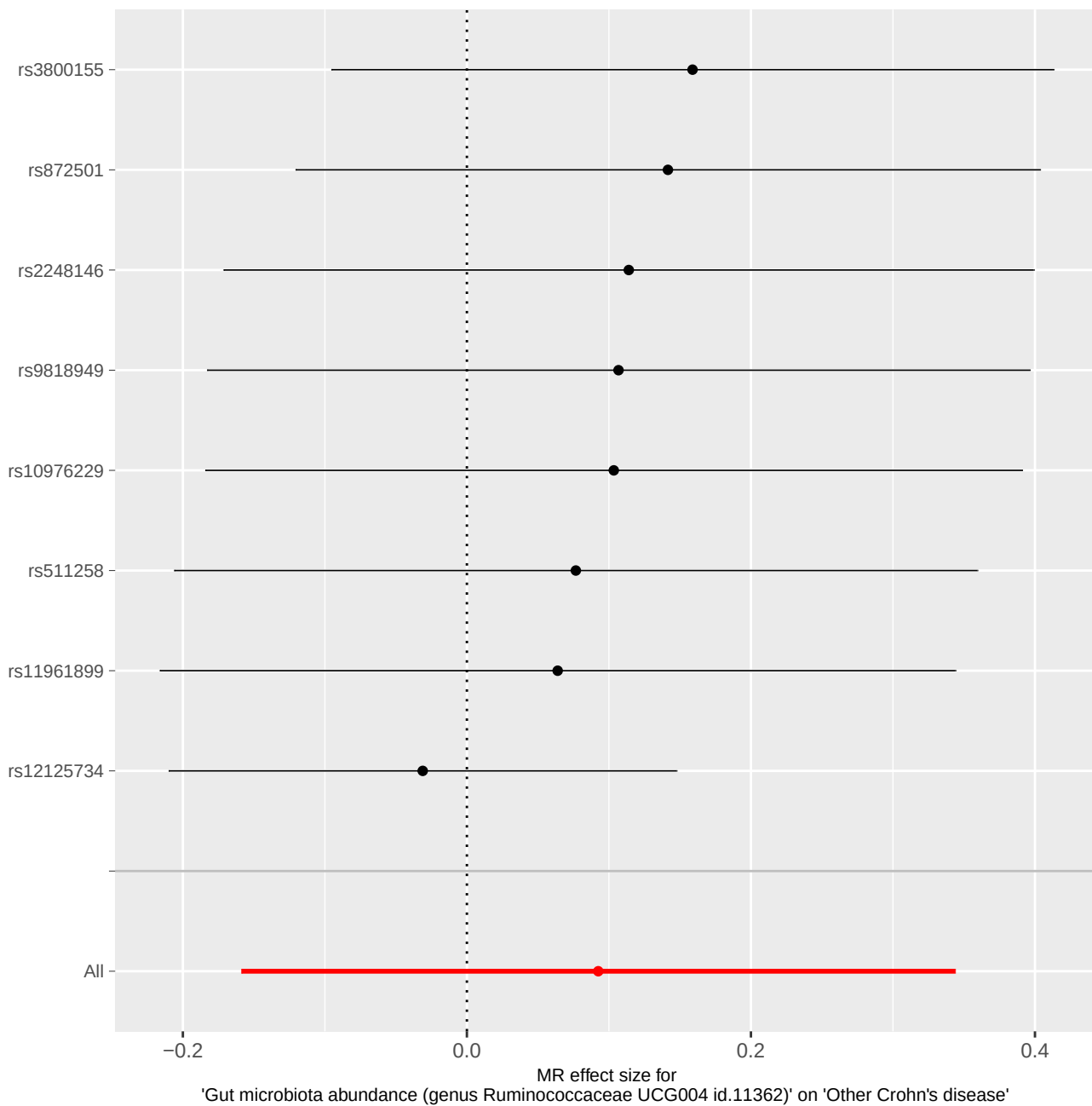


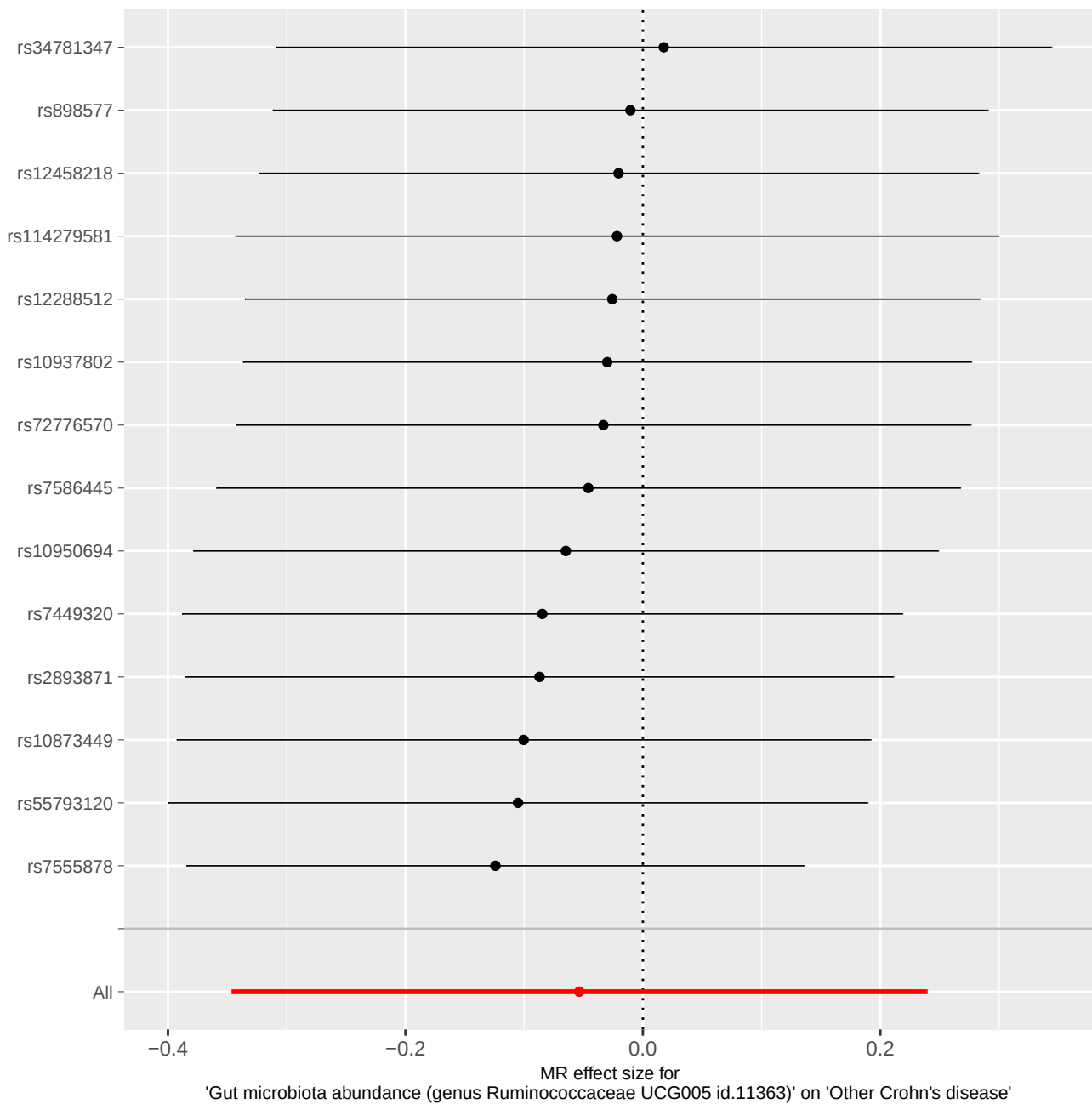


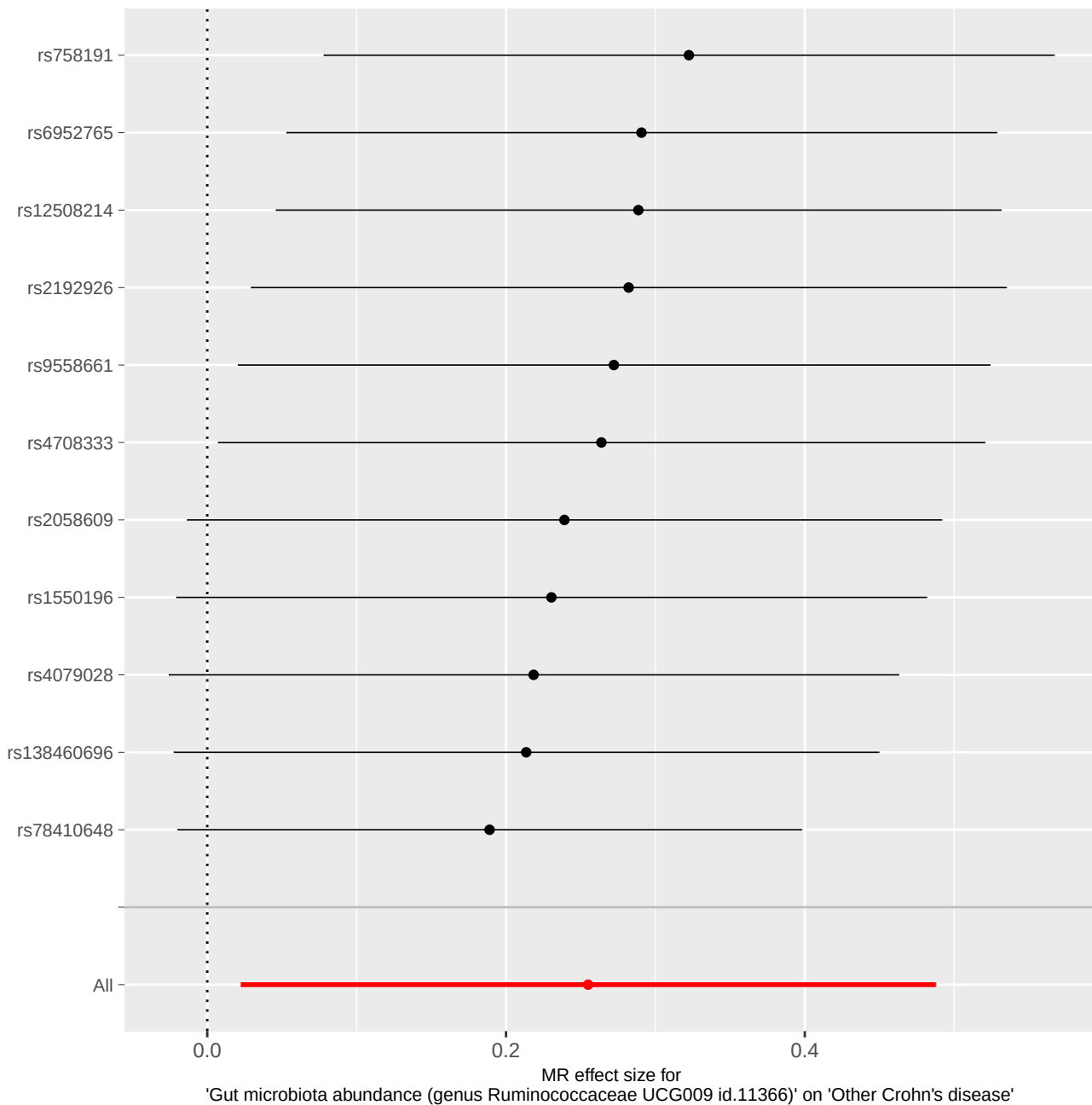


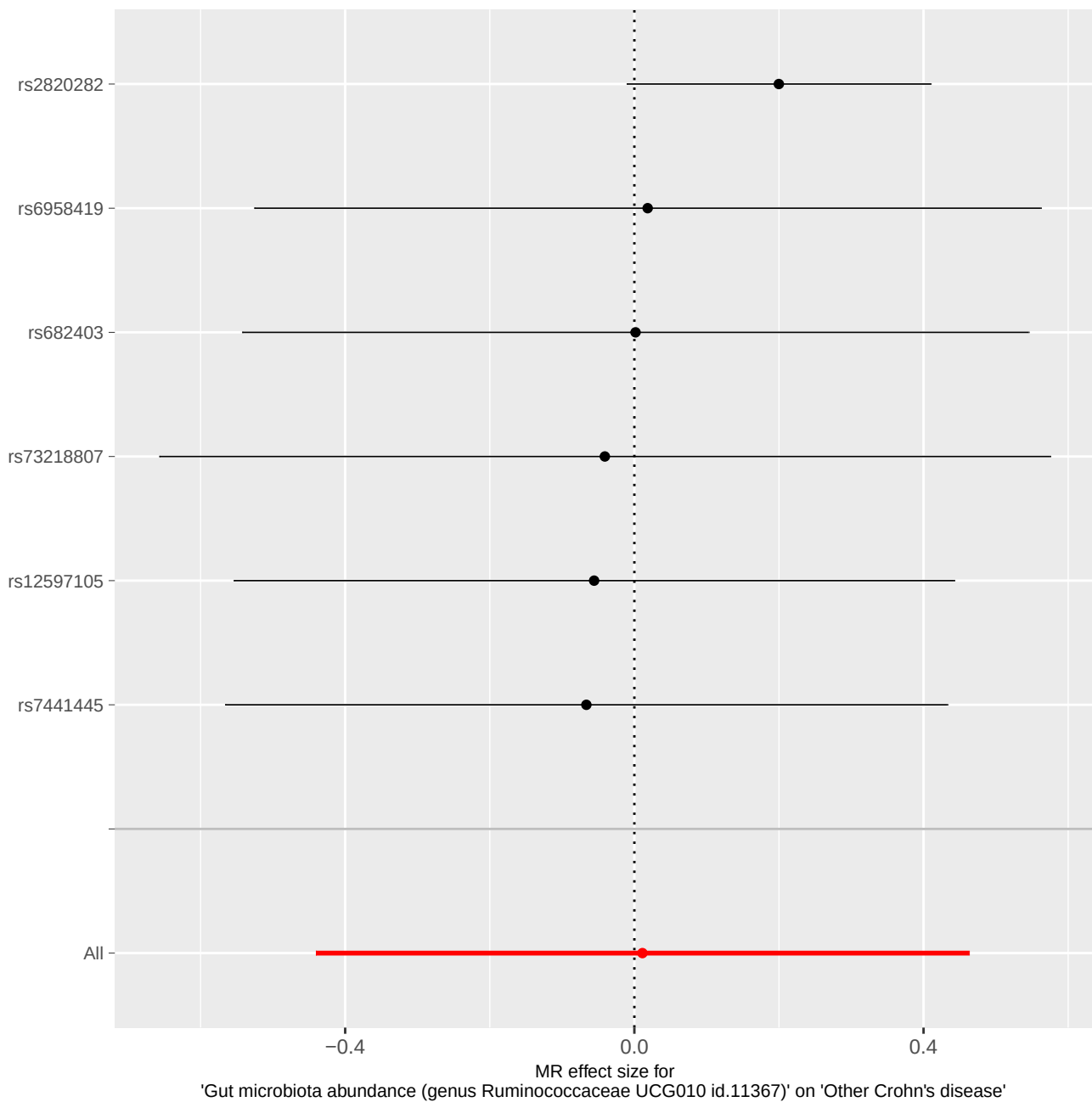


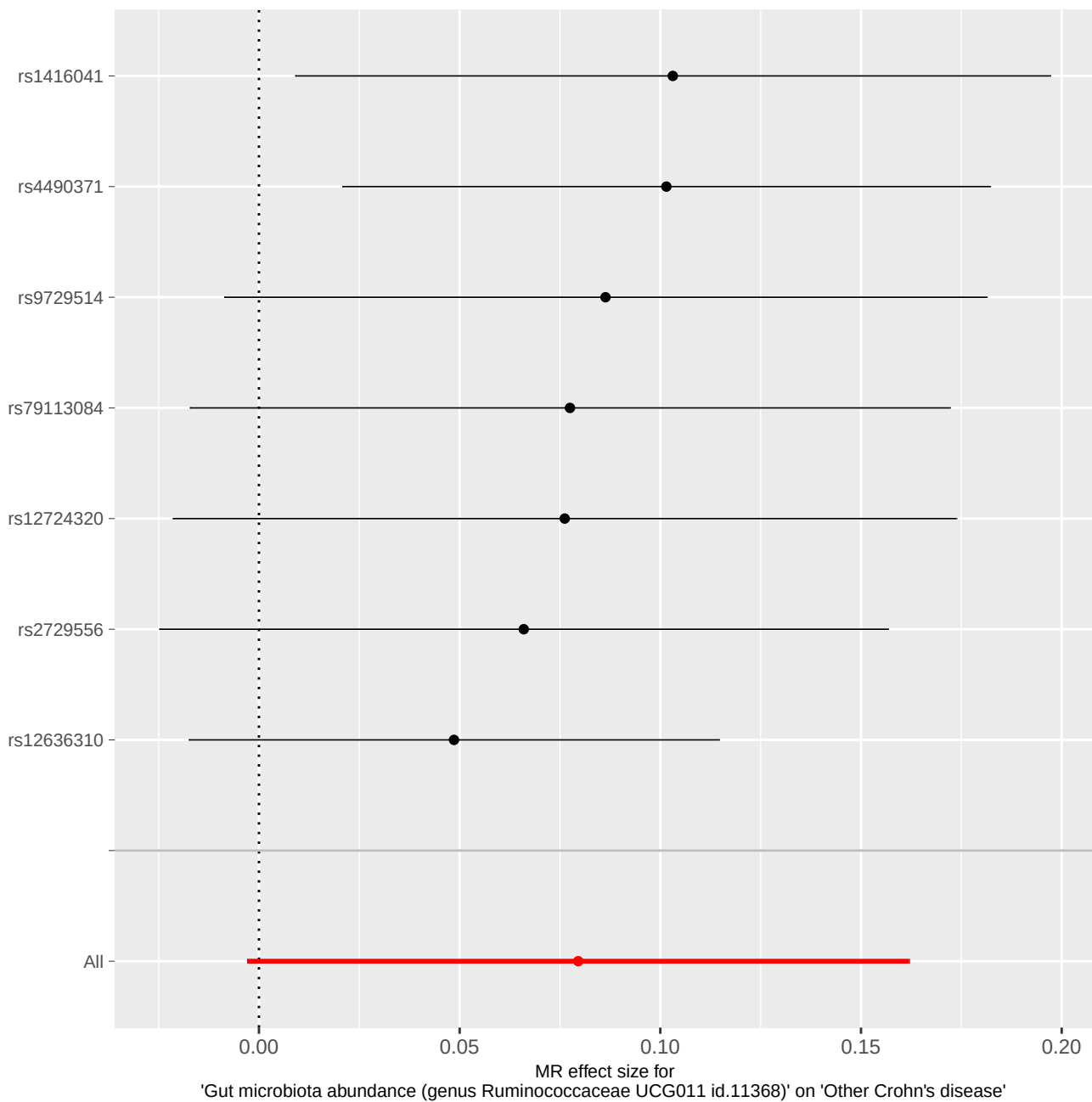


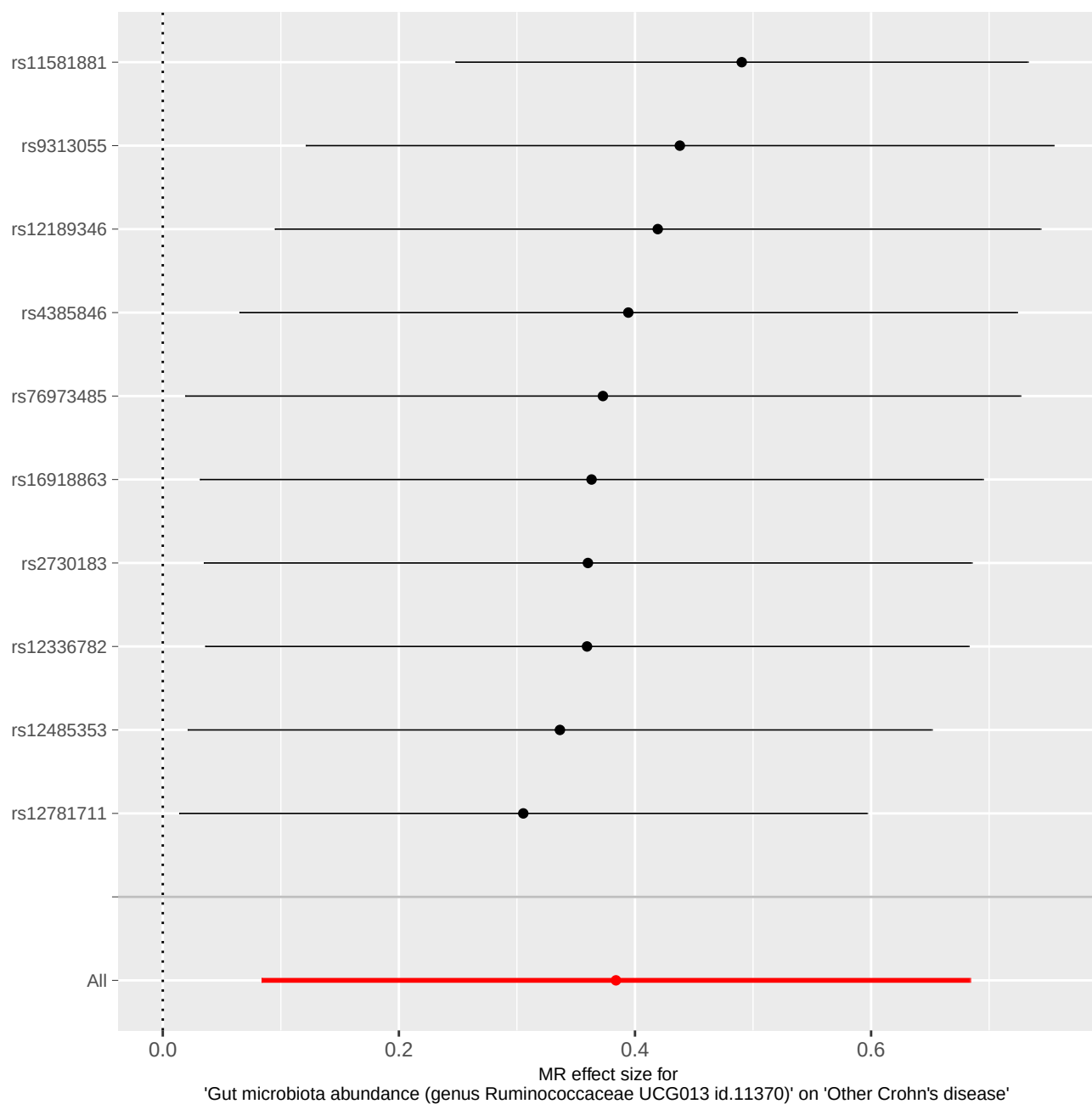


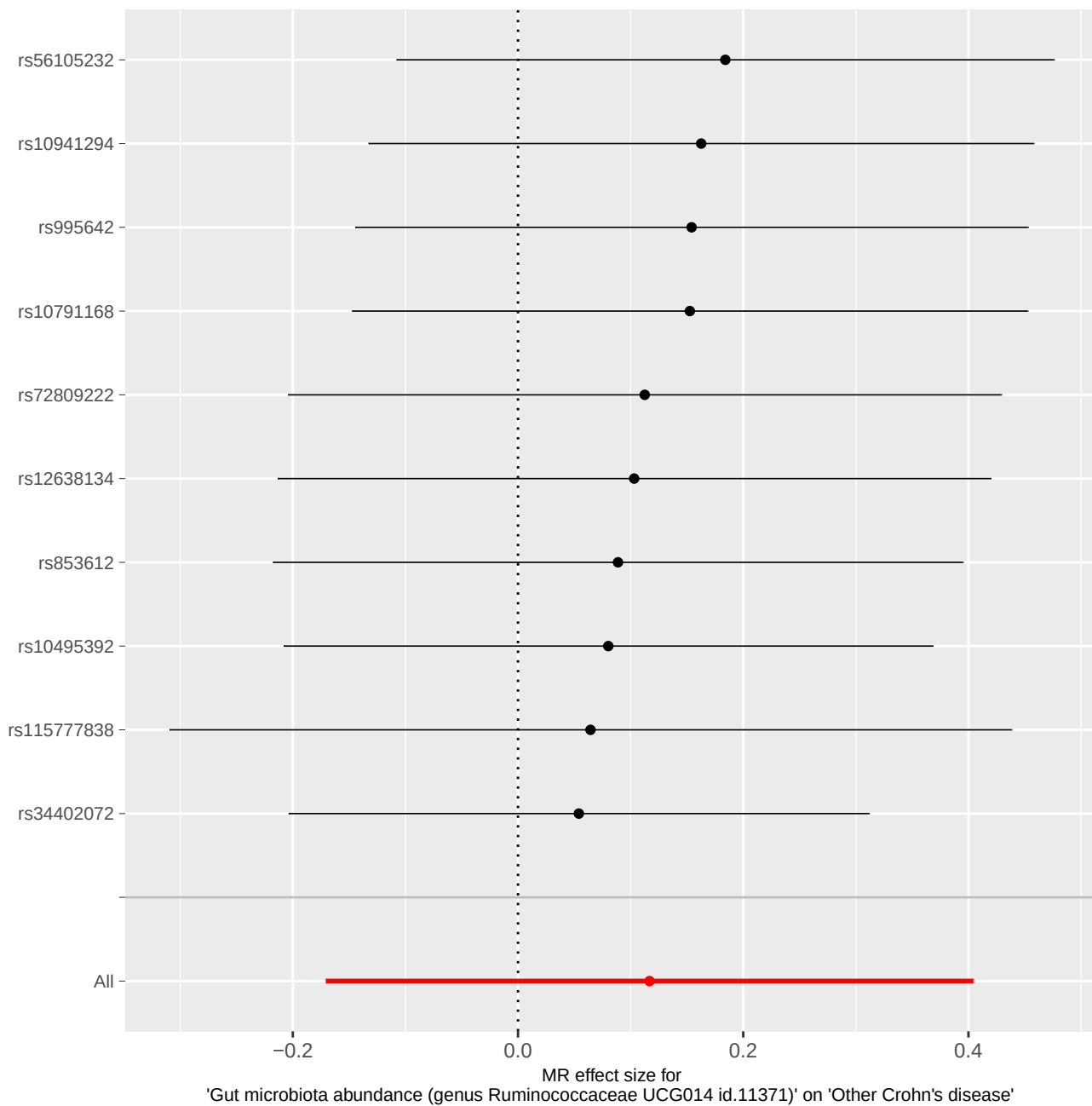


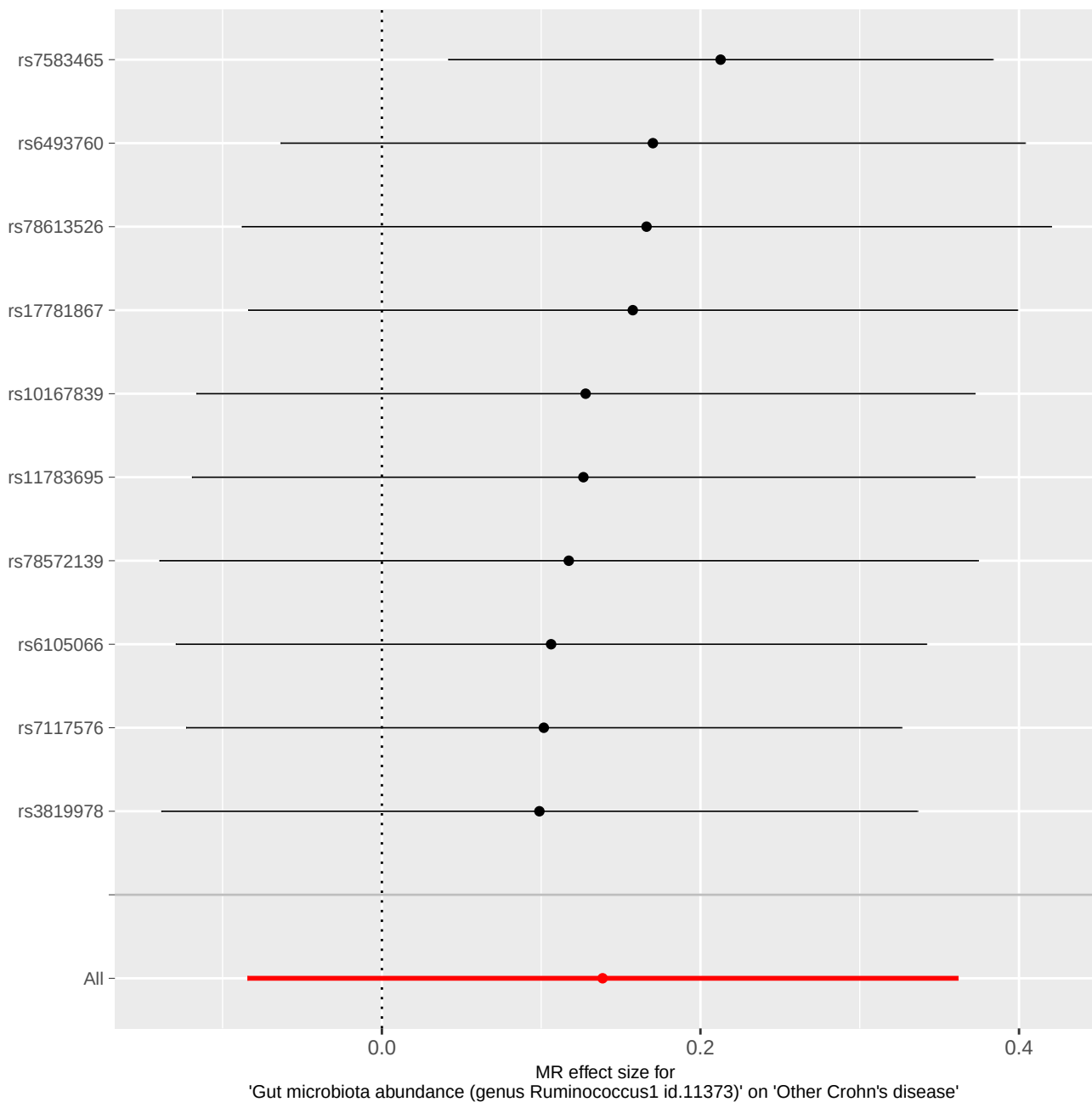




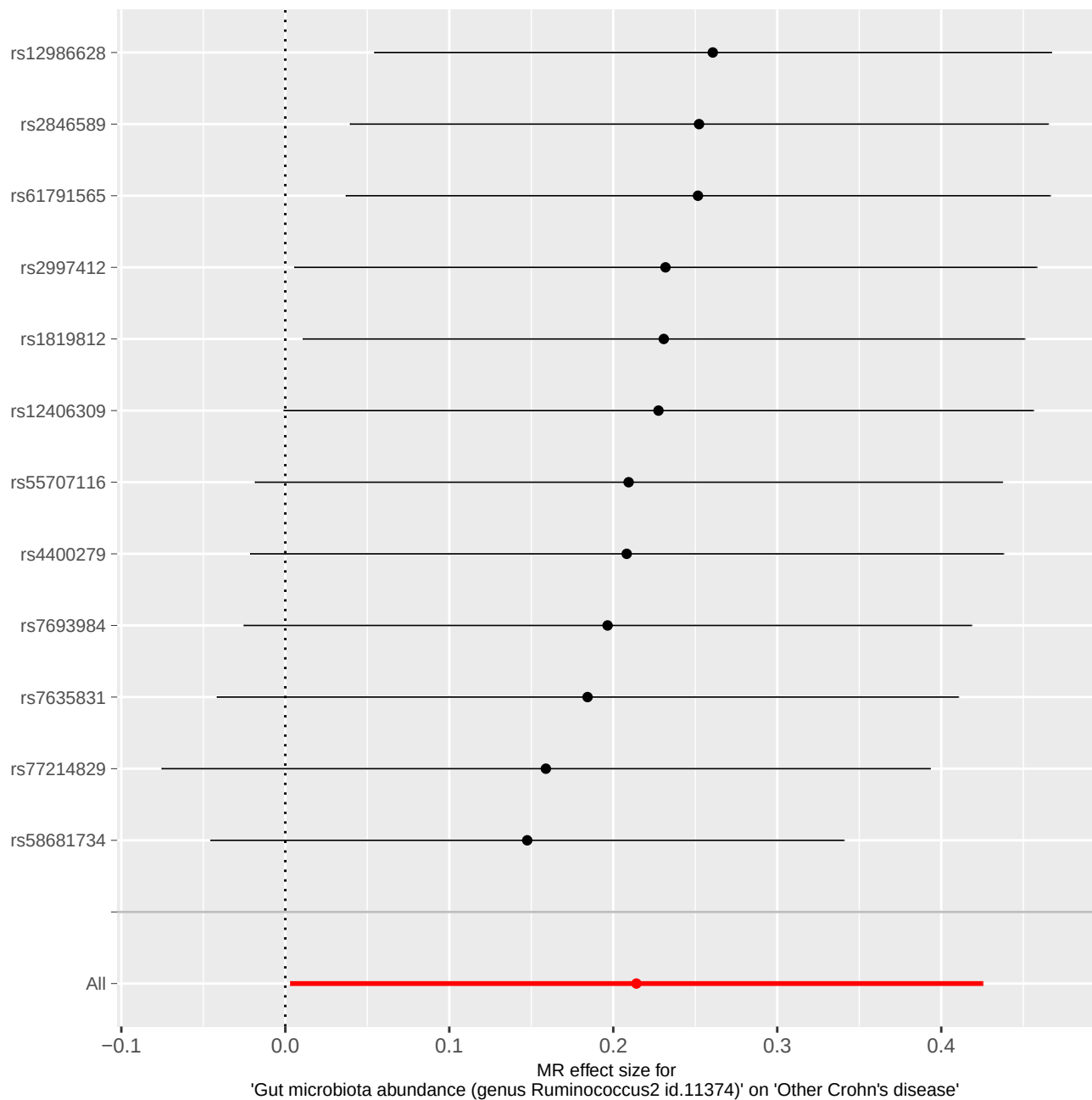


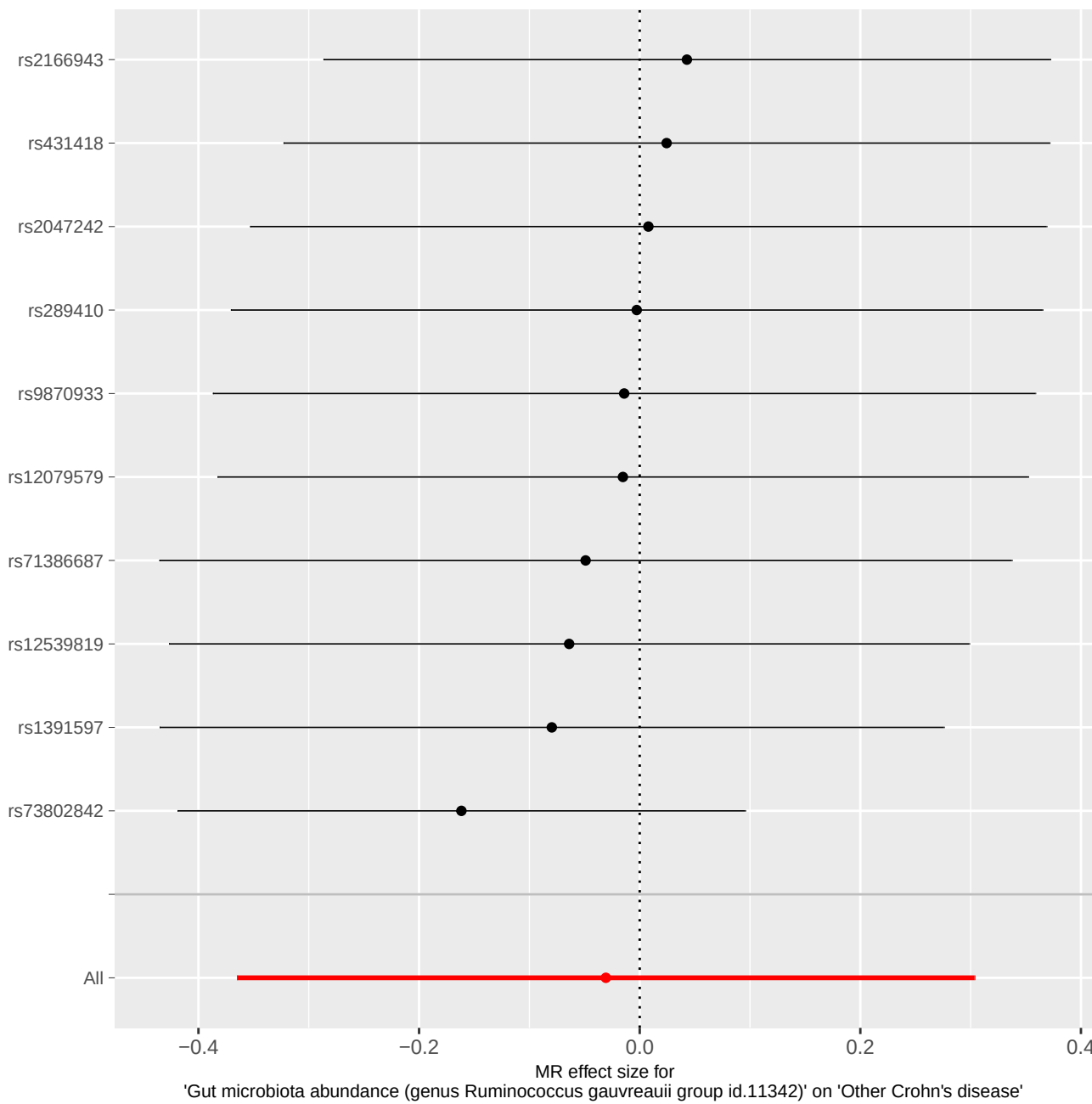


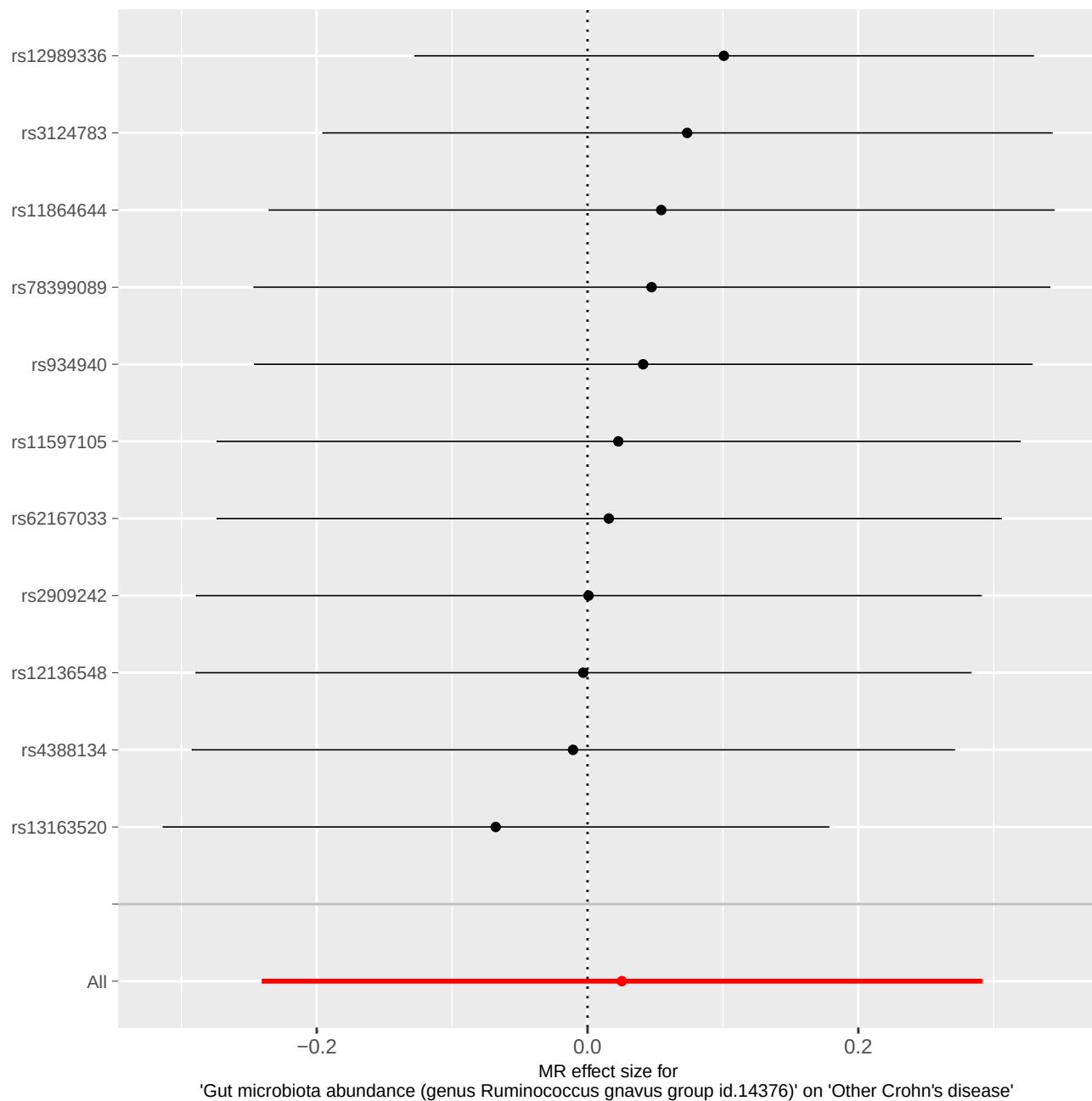


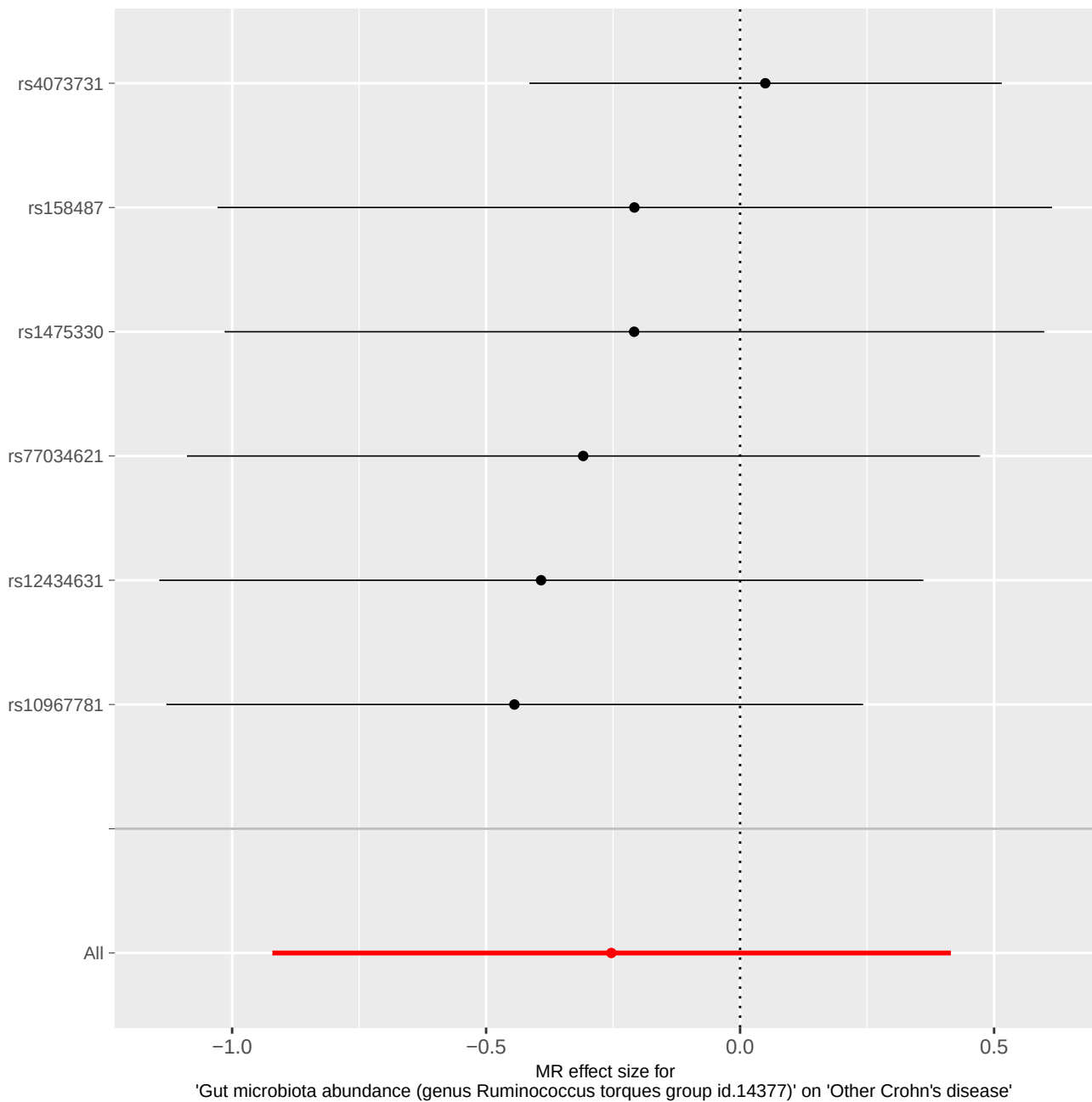


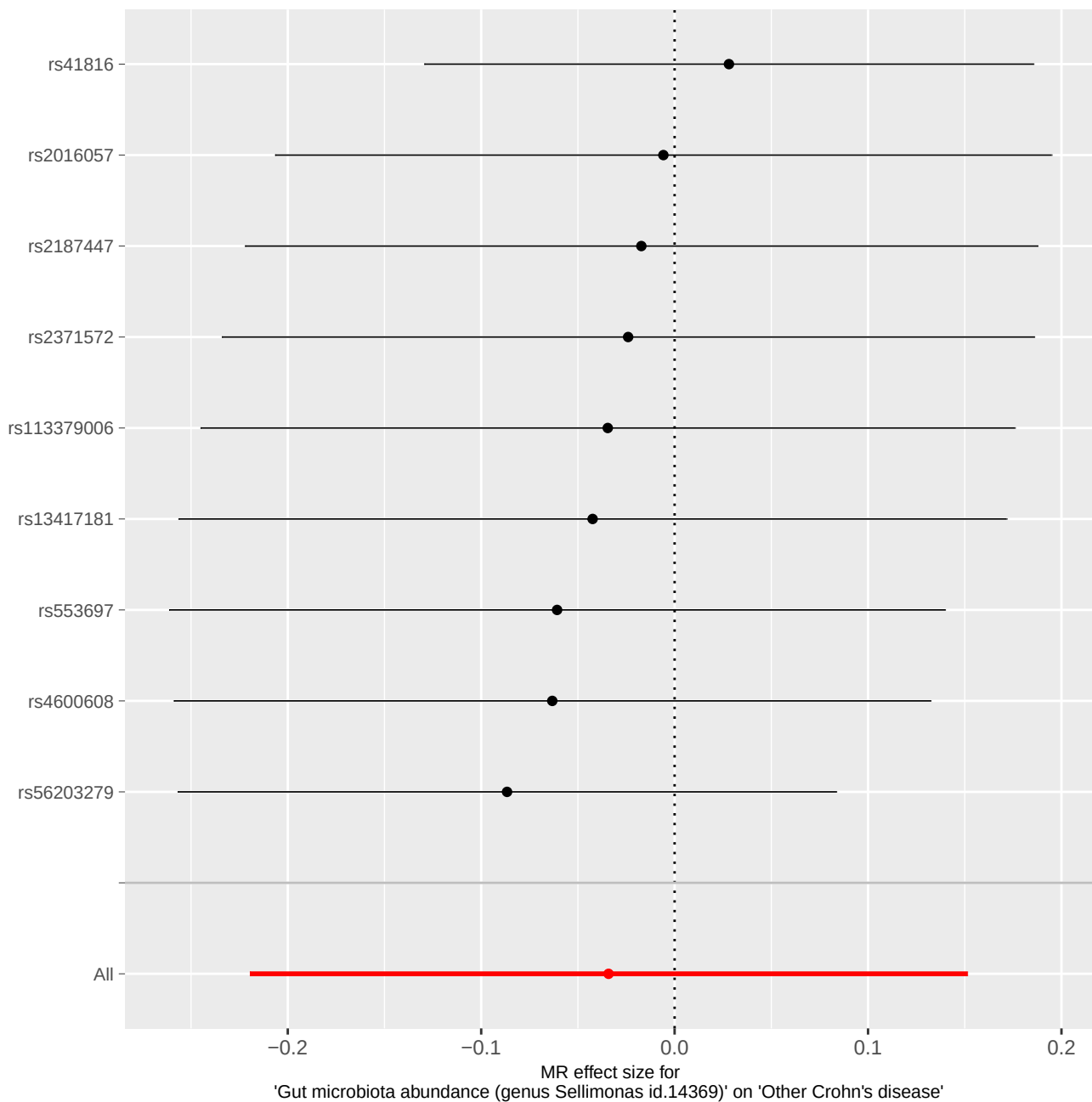
Batch 287 : Gut microbiota abundance (genus Ruminococcus2 id.11374) on Other Crohn's disease

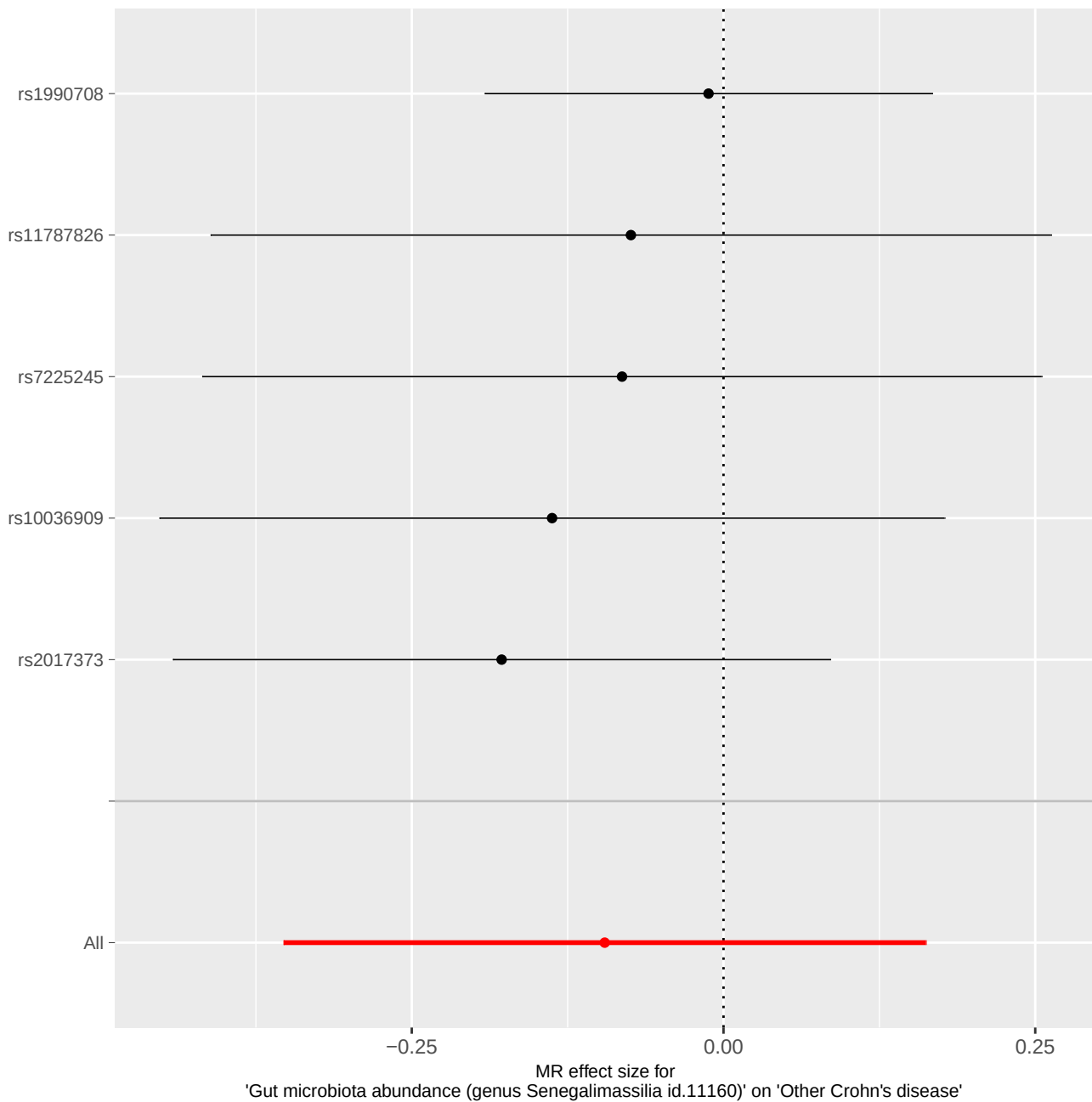




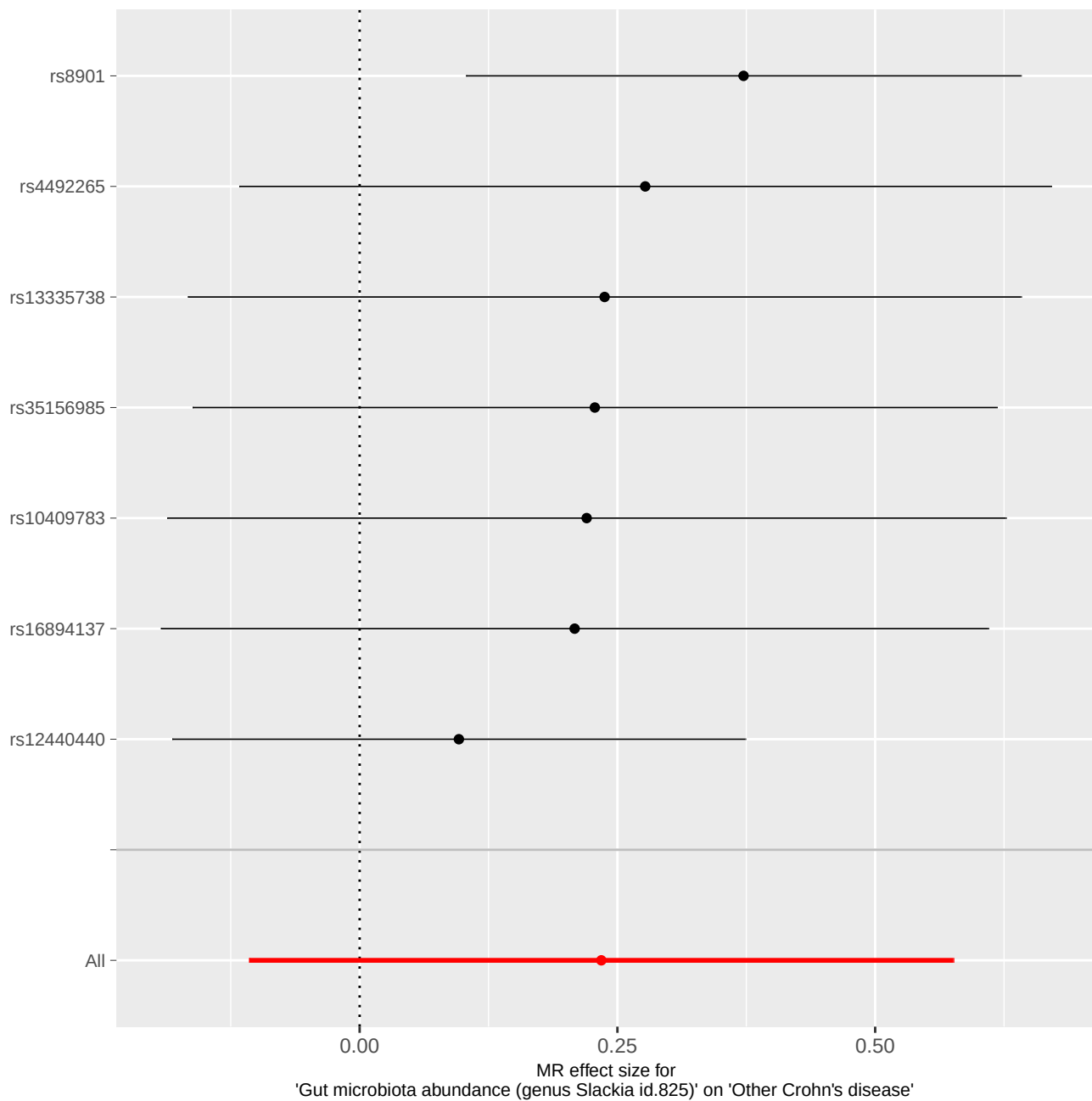


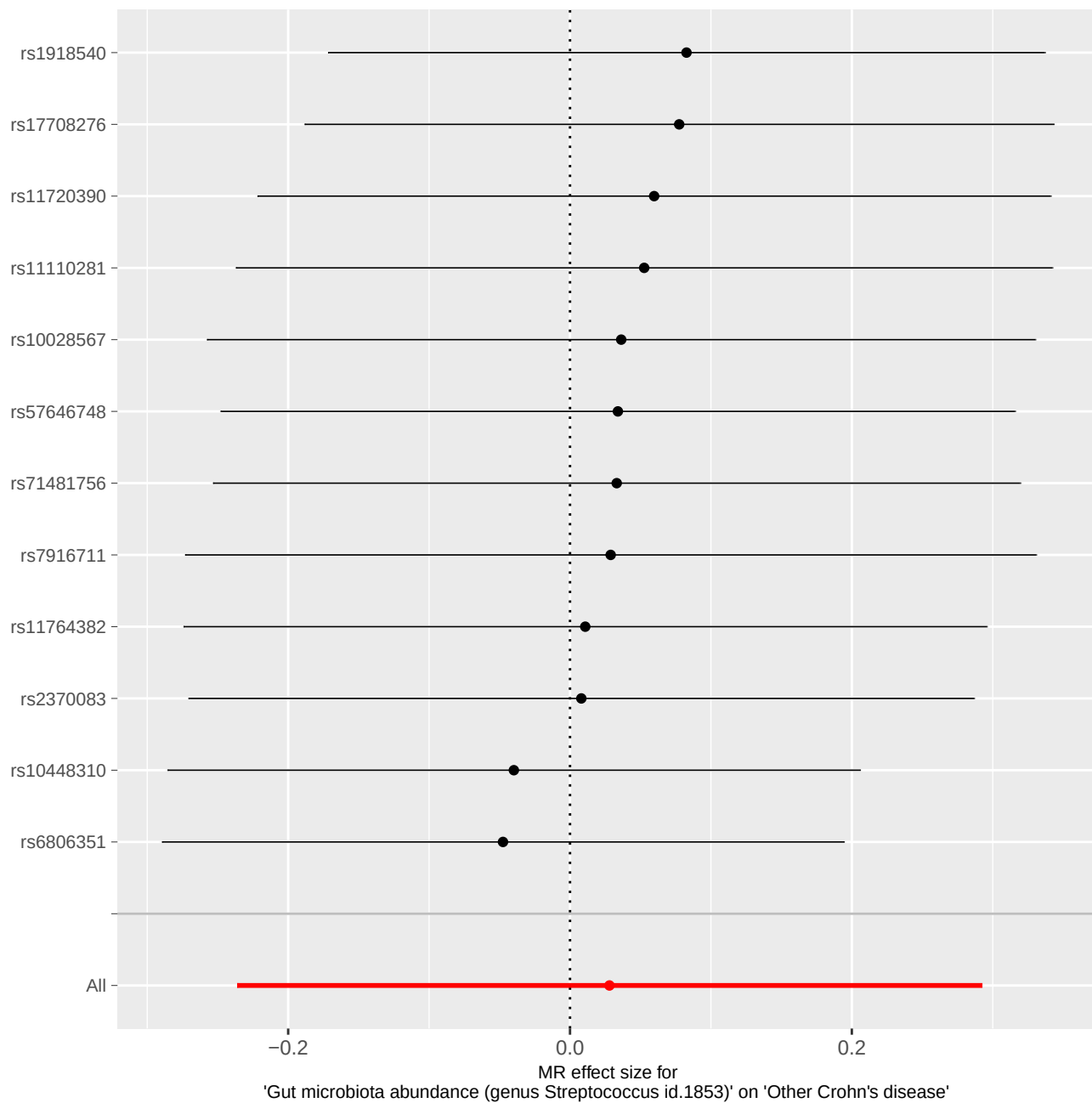


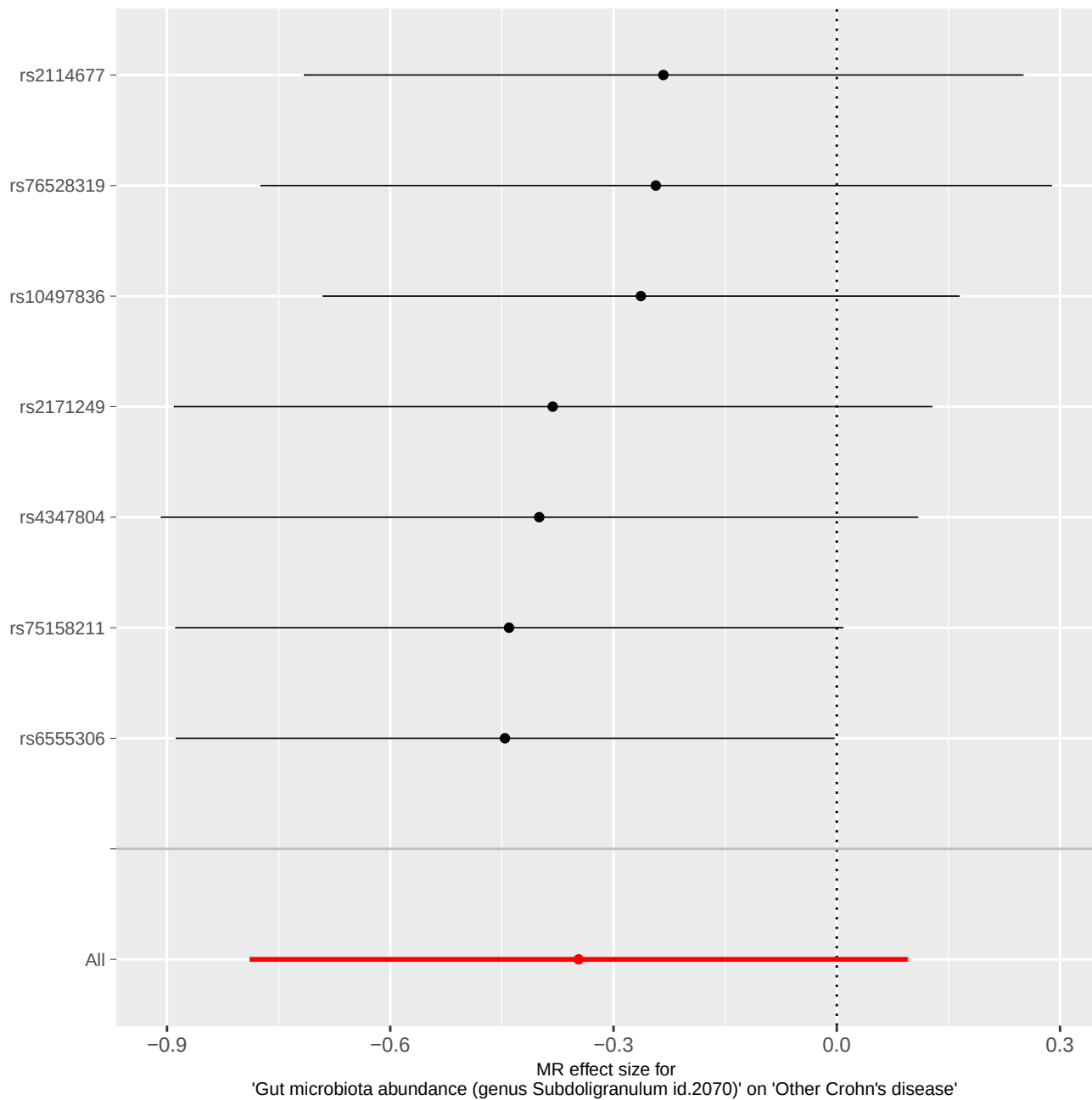




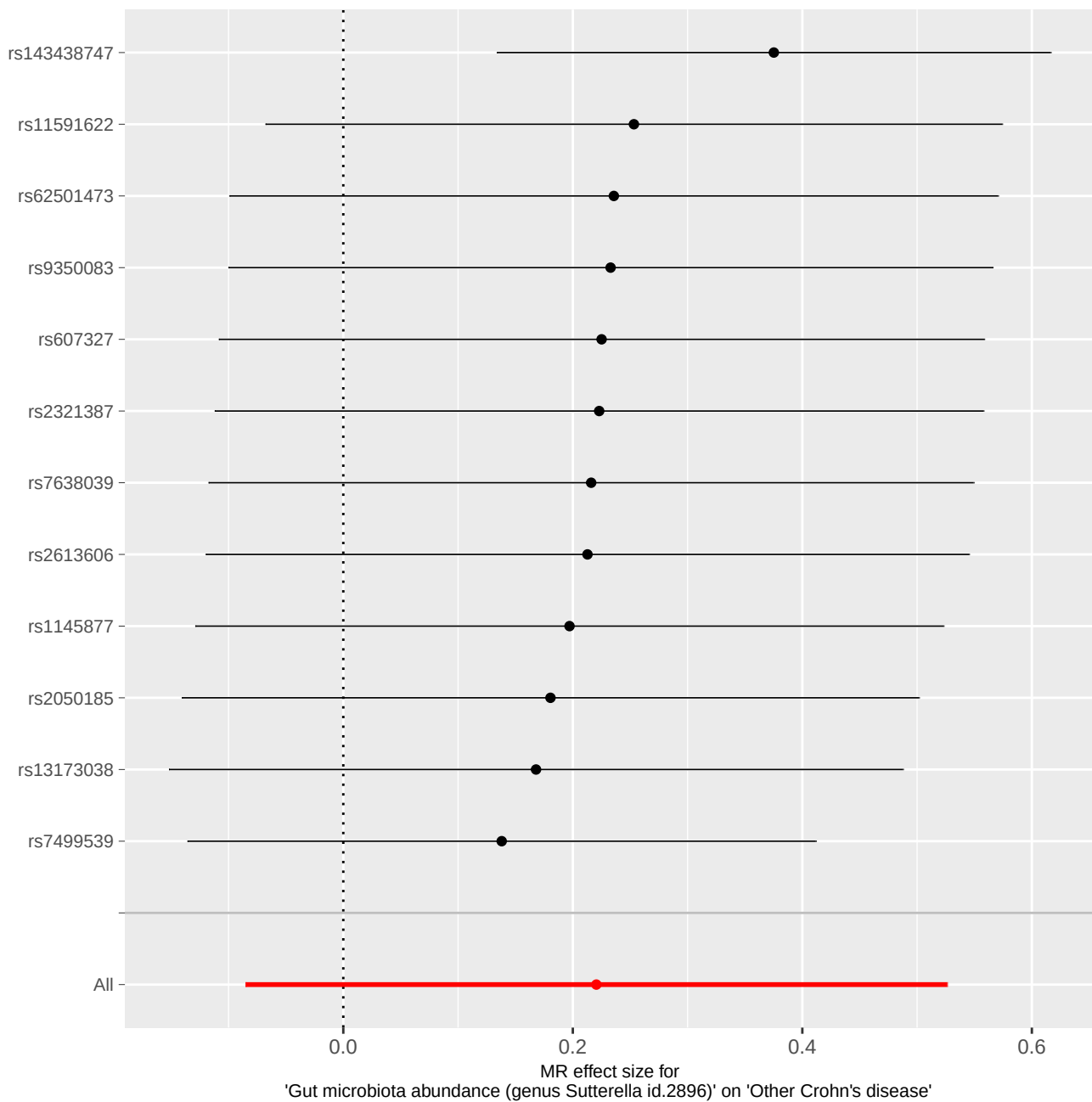
Batch 293 : Gut microbiota abundance (genus Slackia id.825) on Other Crohn's disease

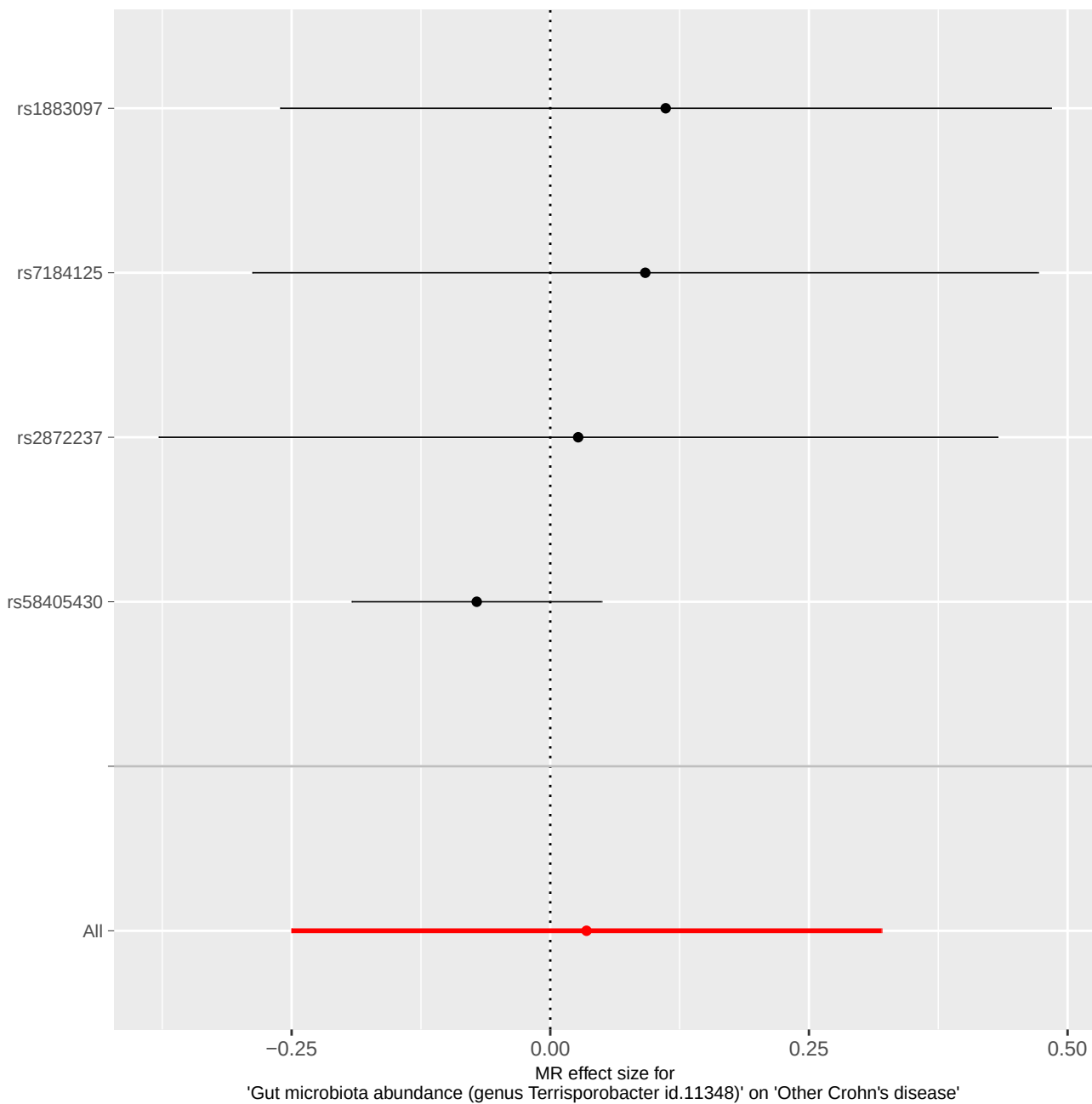




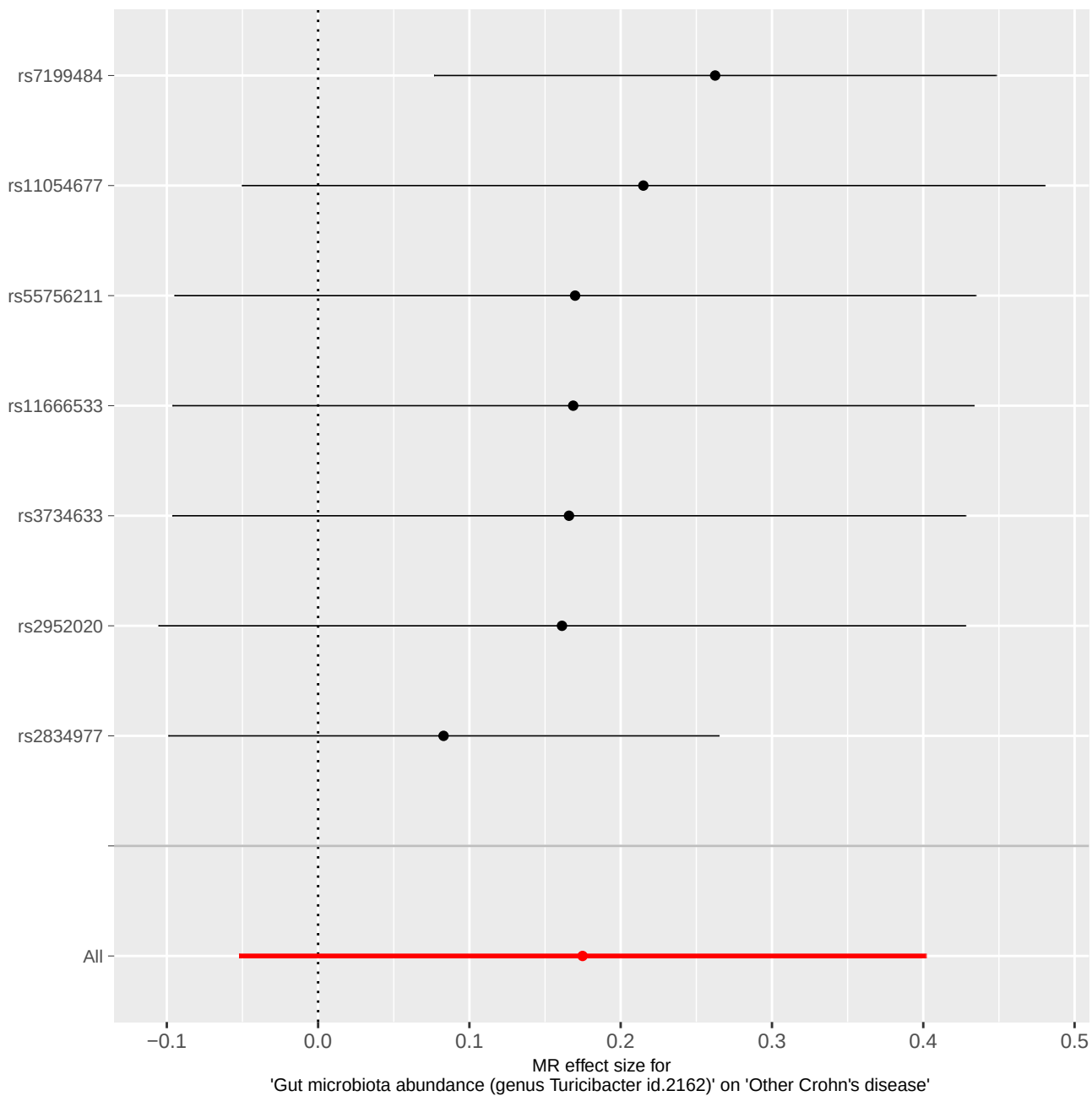


Batch 296 : Gut microbiota abundance (genus Sutterella id.2896) on Other Crohn's disease

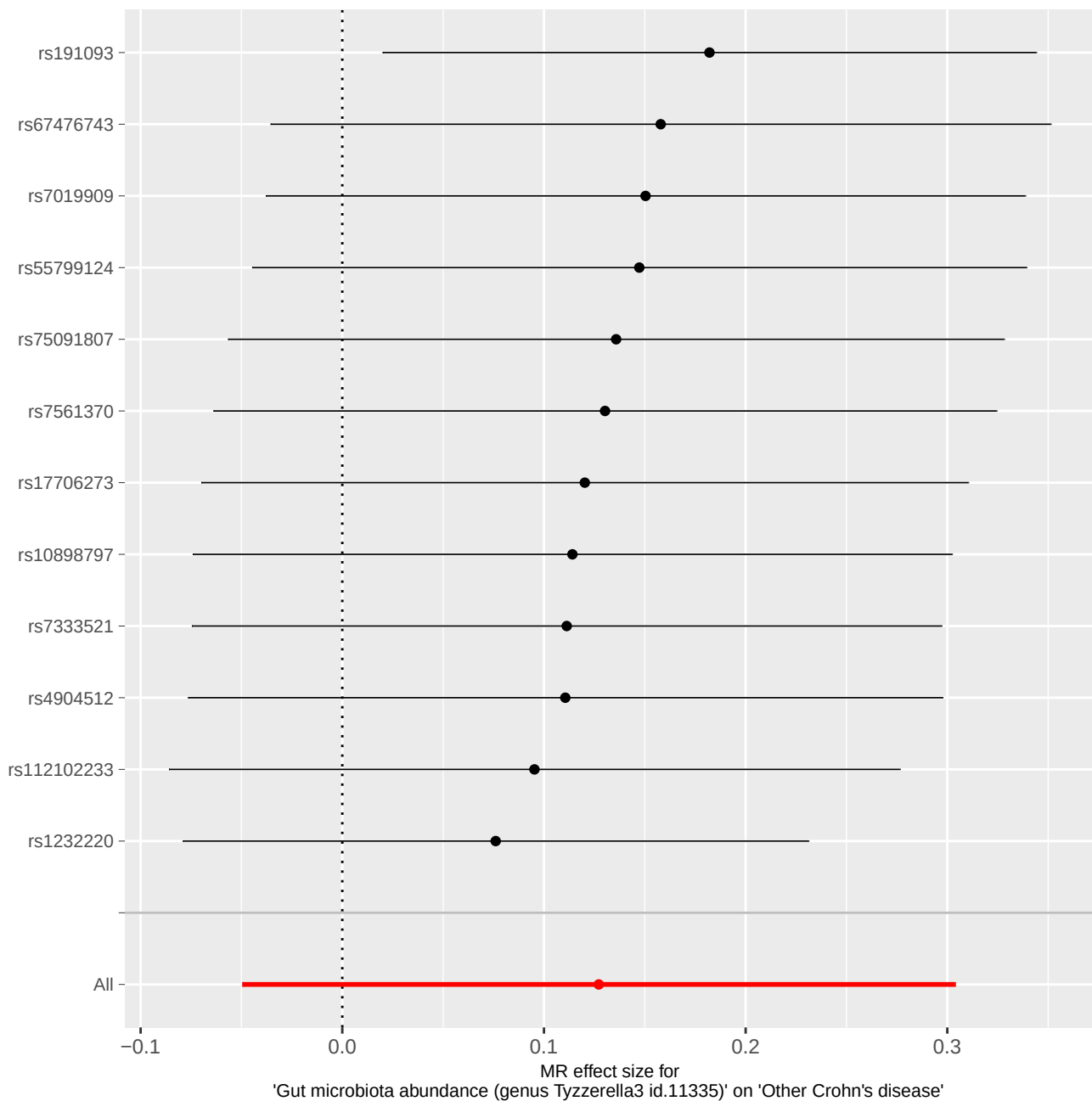


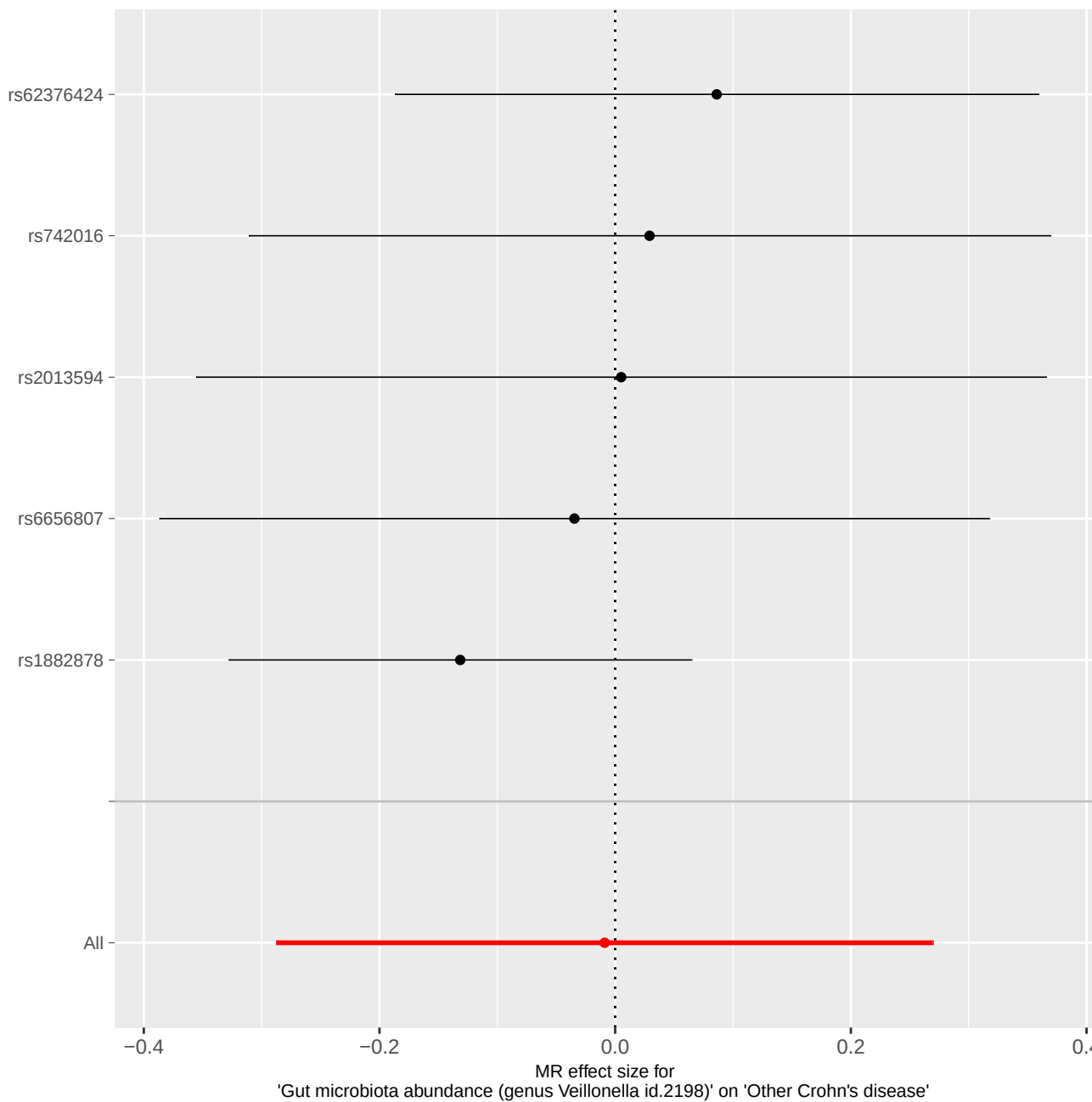


Batch 298 : Gut microbiota abundance (genus Turicibacter id.2162) on Other Crohn's disease

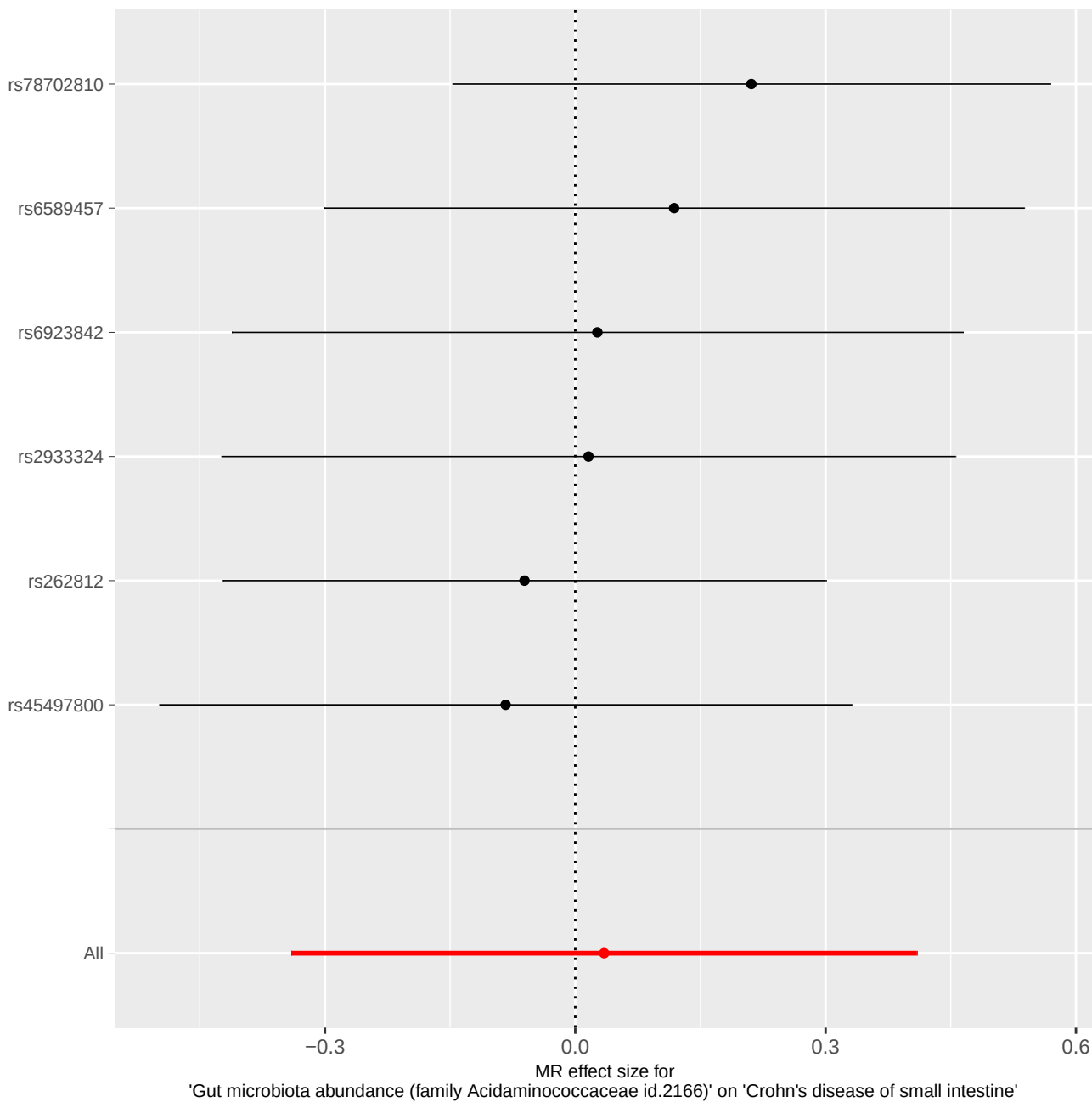


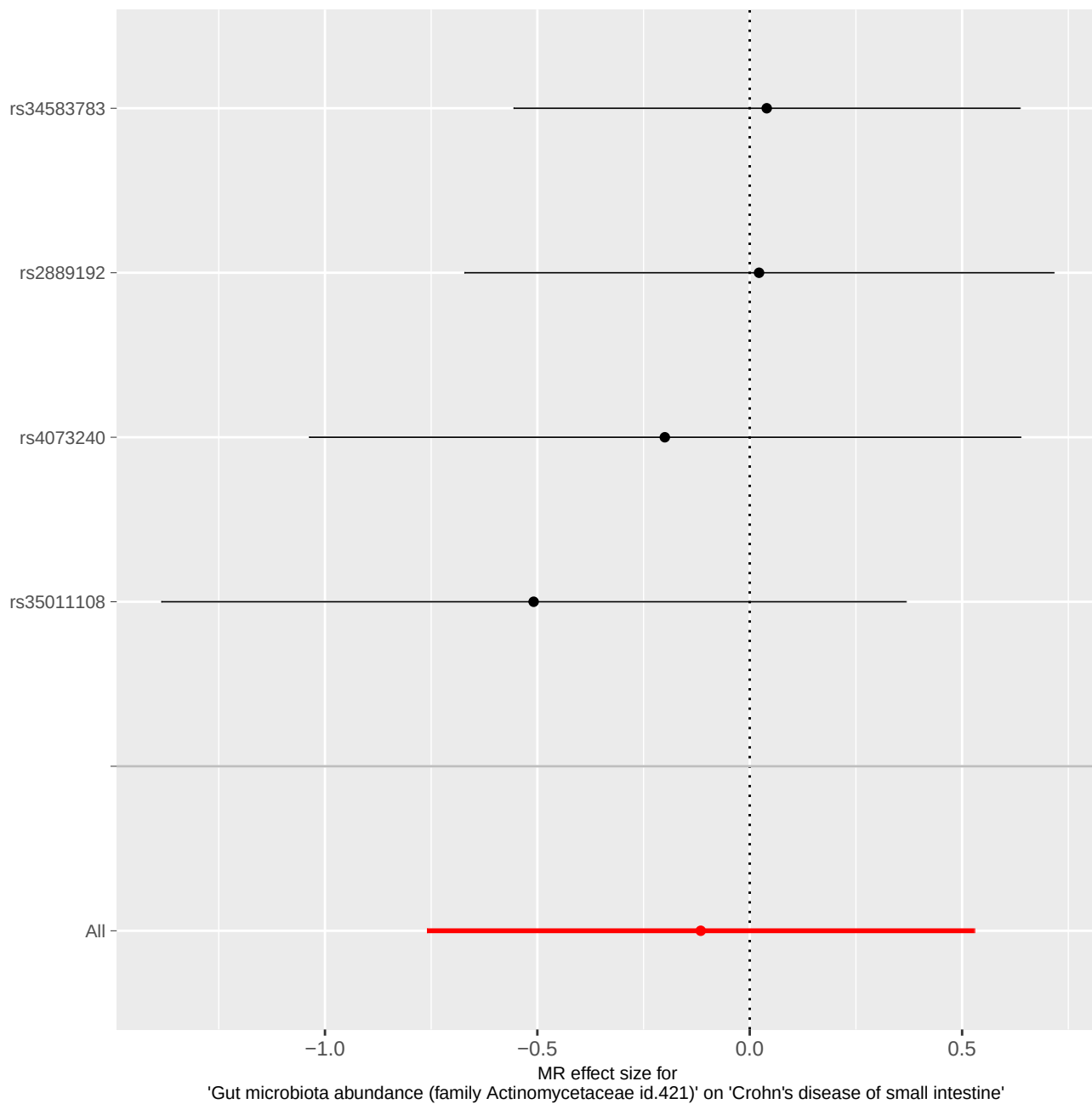
Batch 299 : Gut microbiota abundance (genus Tyzzerella3 id.11335) on Other Crohn's disease

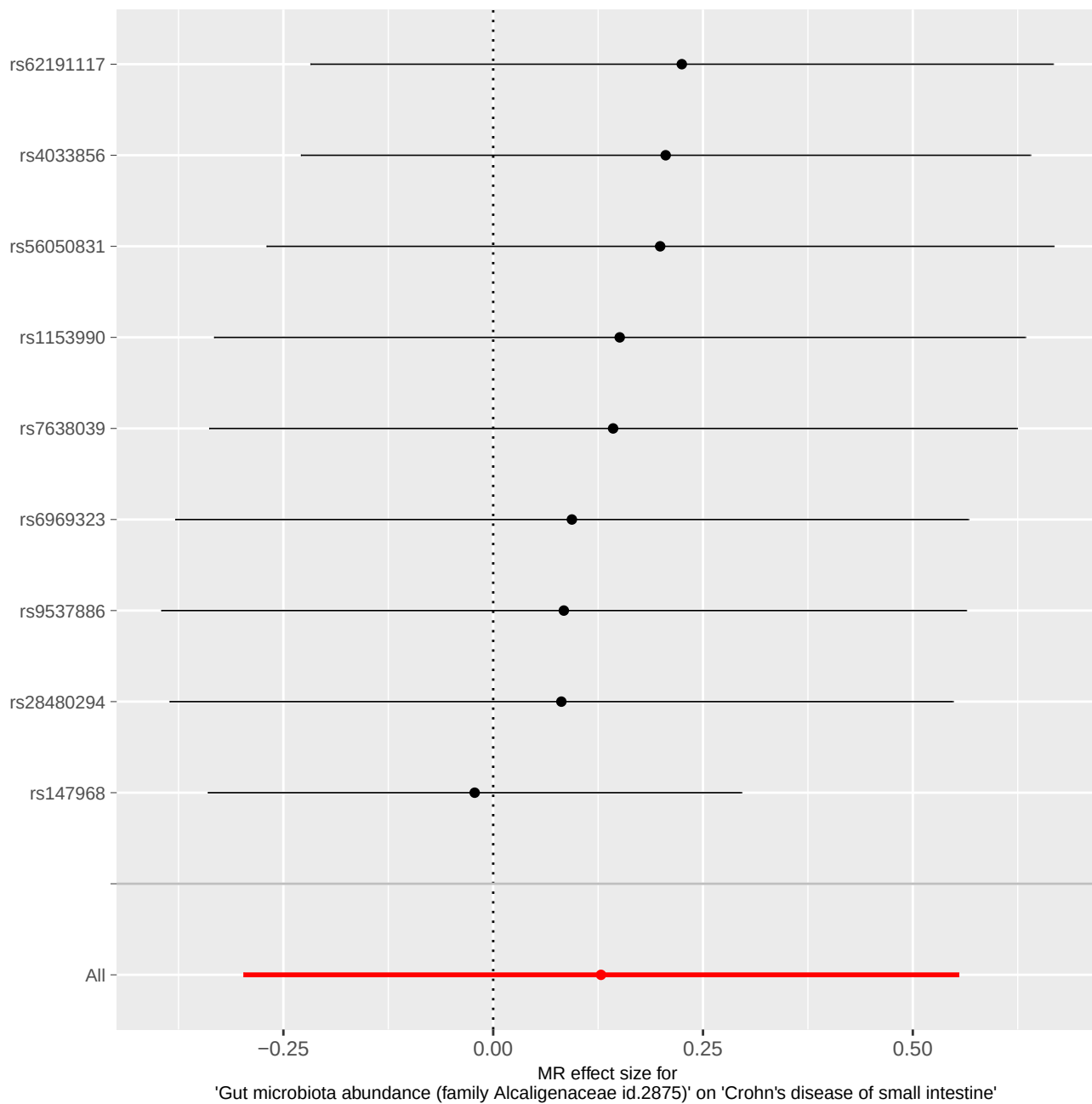


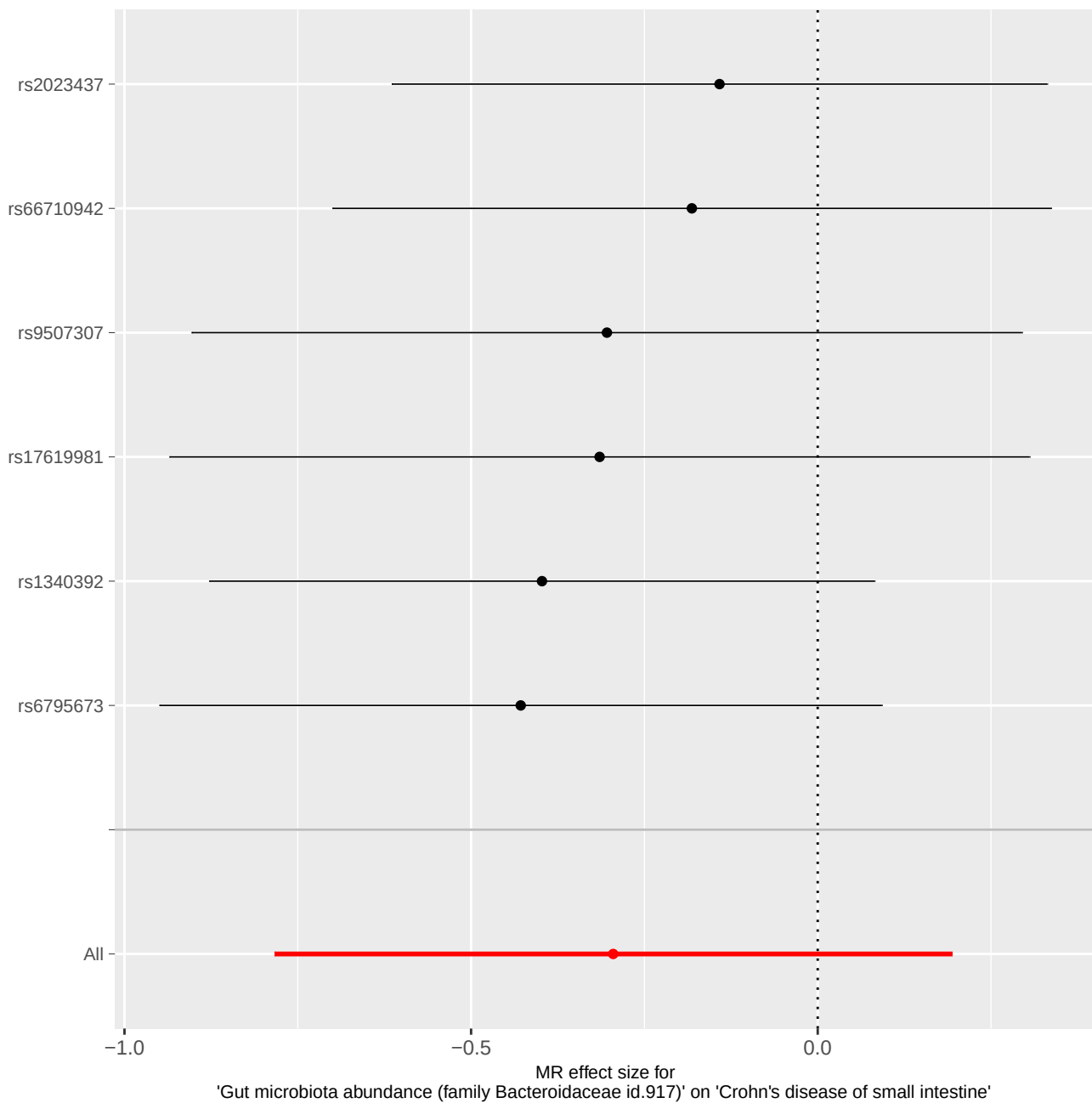


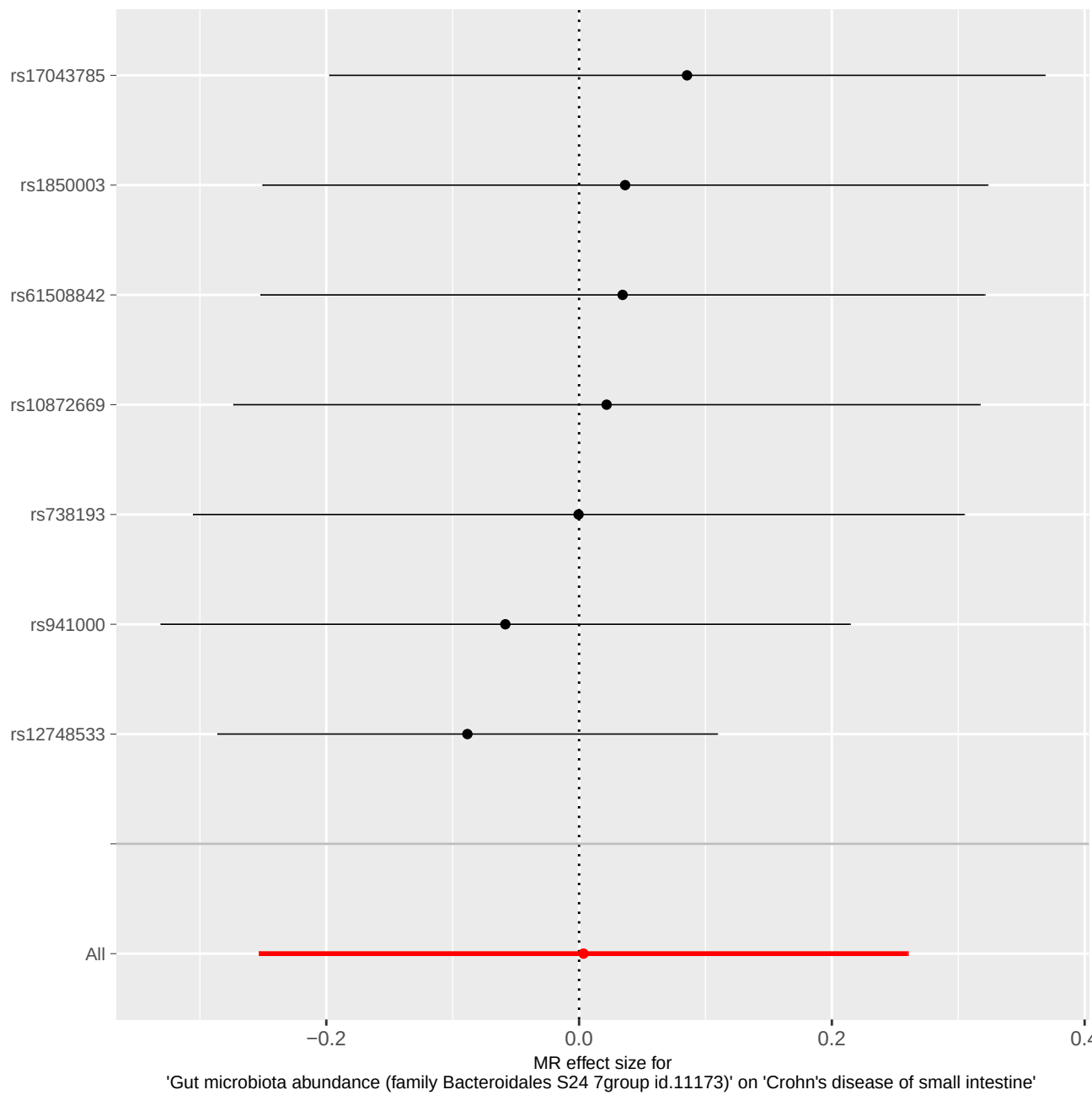
Batch 301 : Gut microbiota abundance (family Acidaminococcaceae id.2166) on Crohn's disease of small intestine

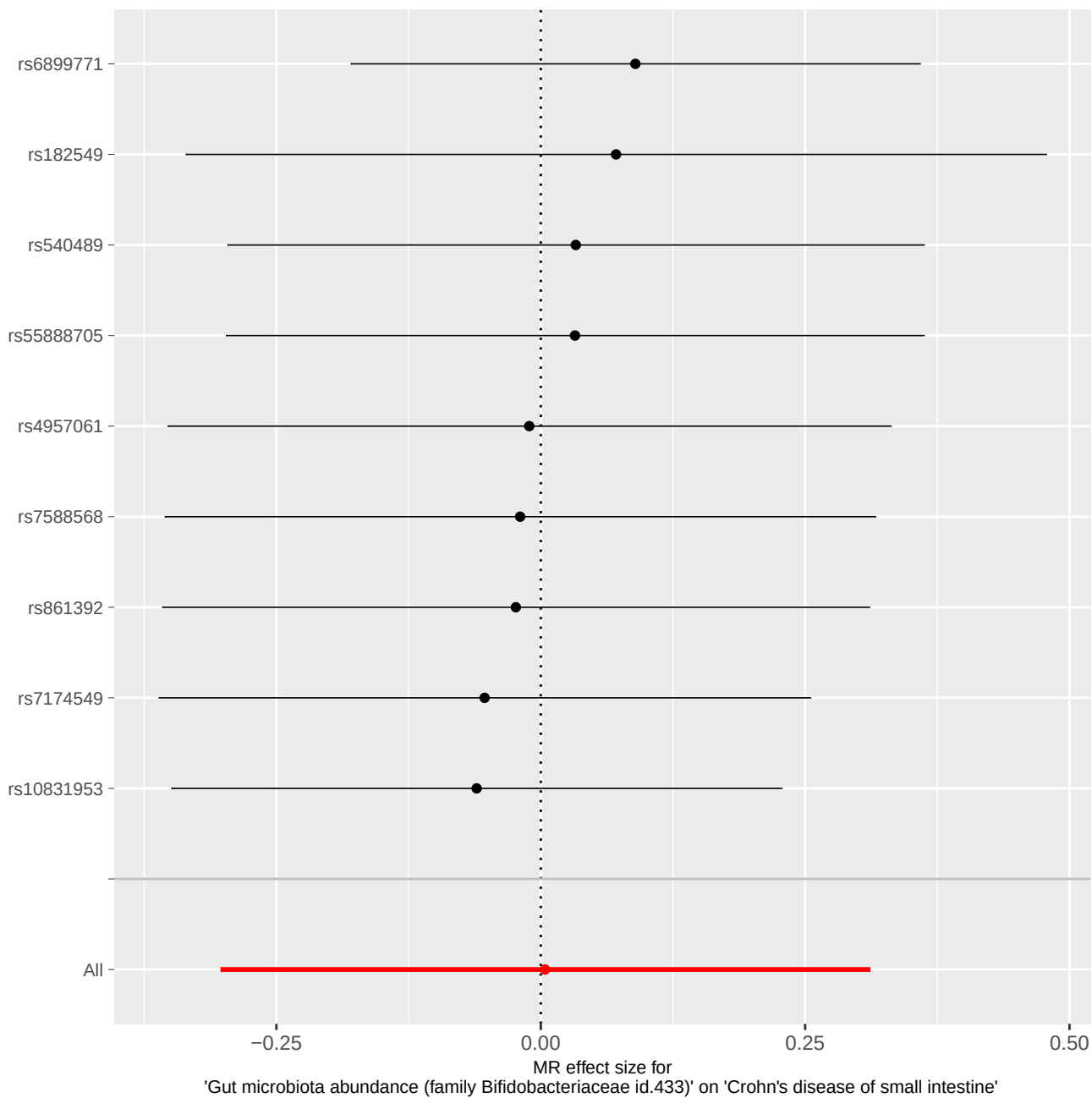




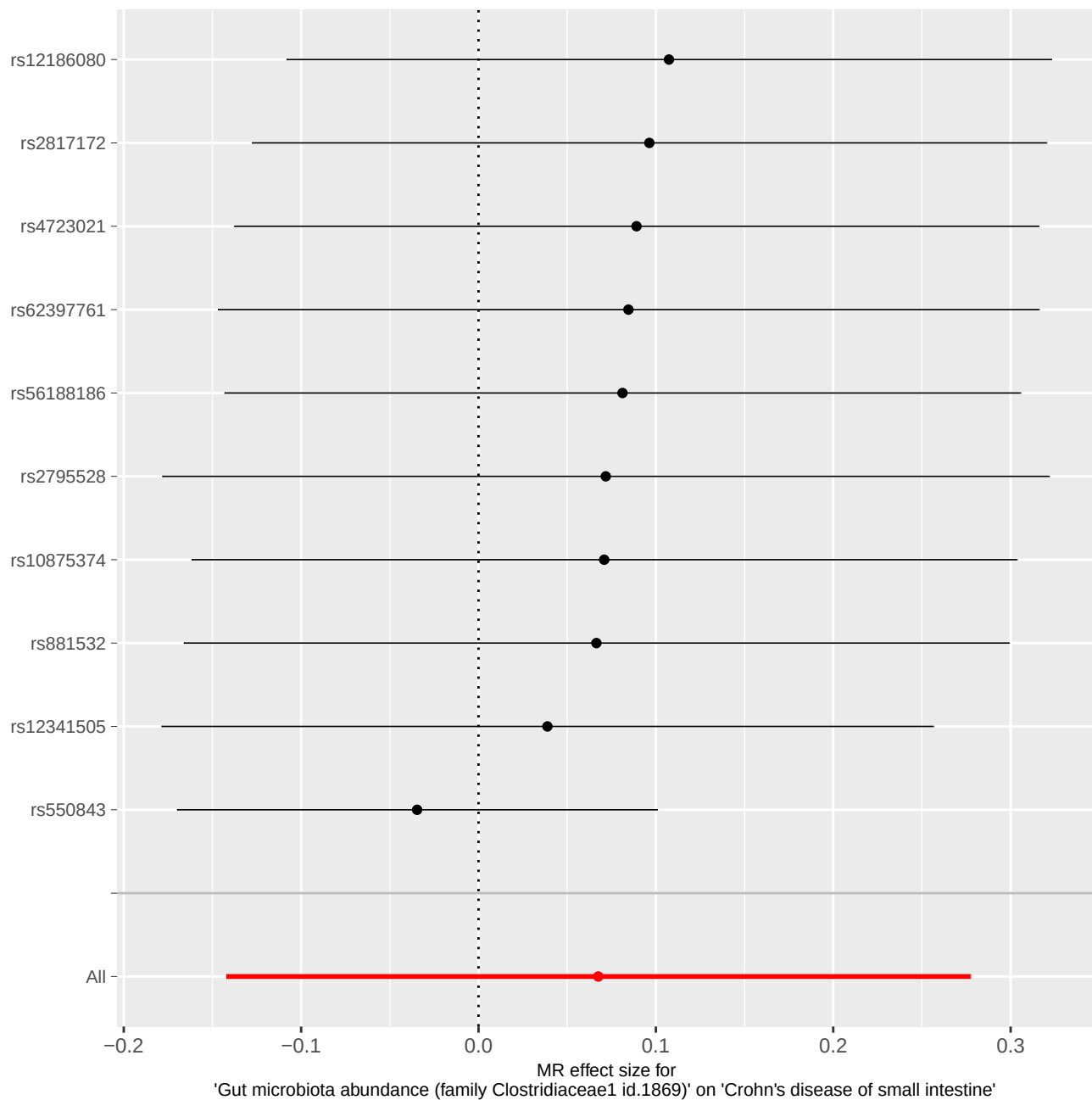


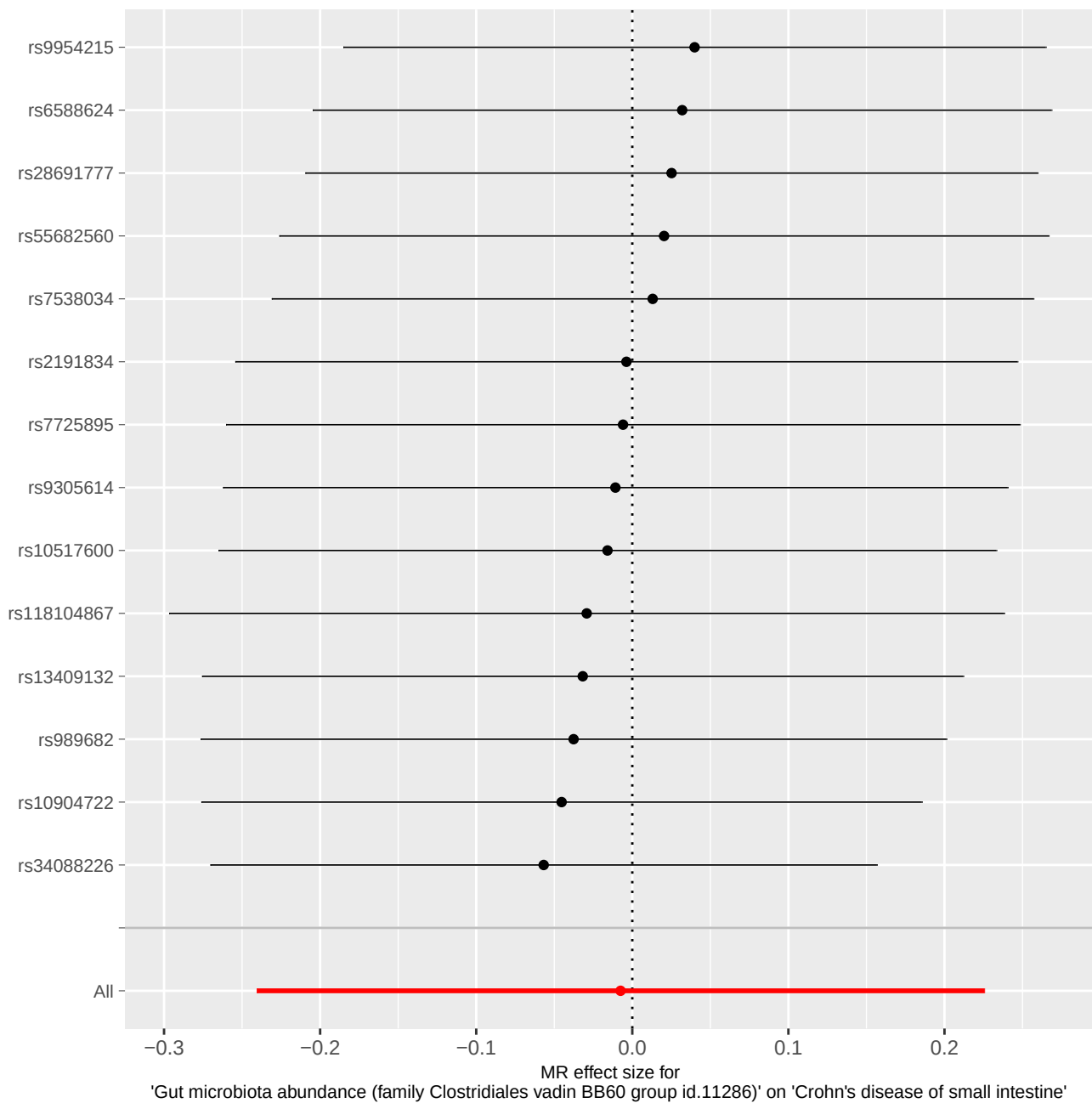


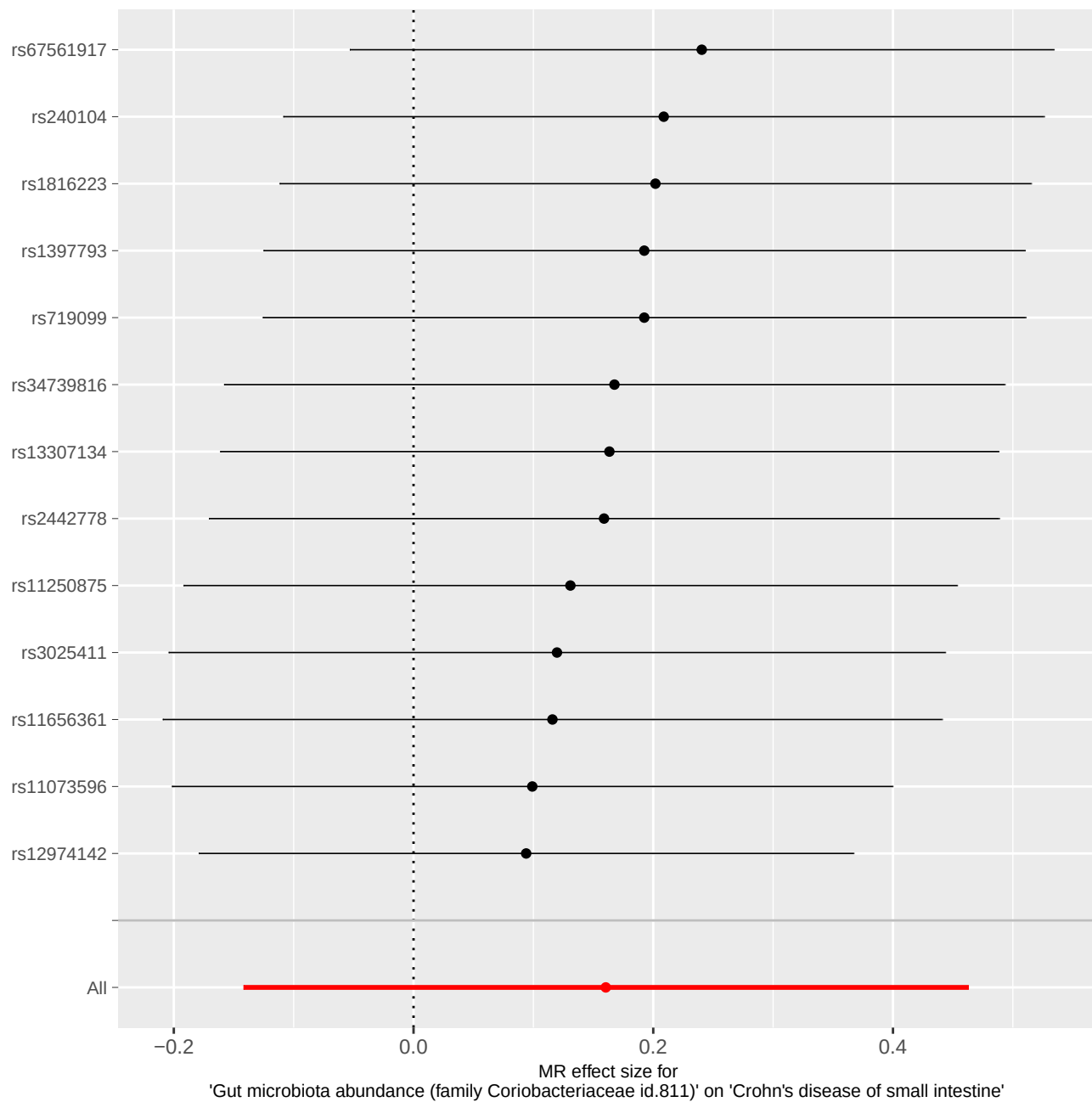


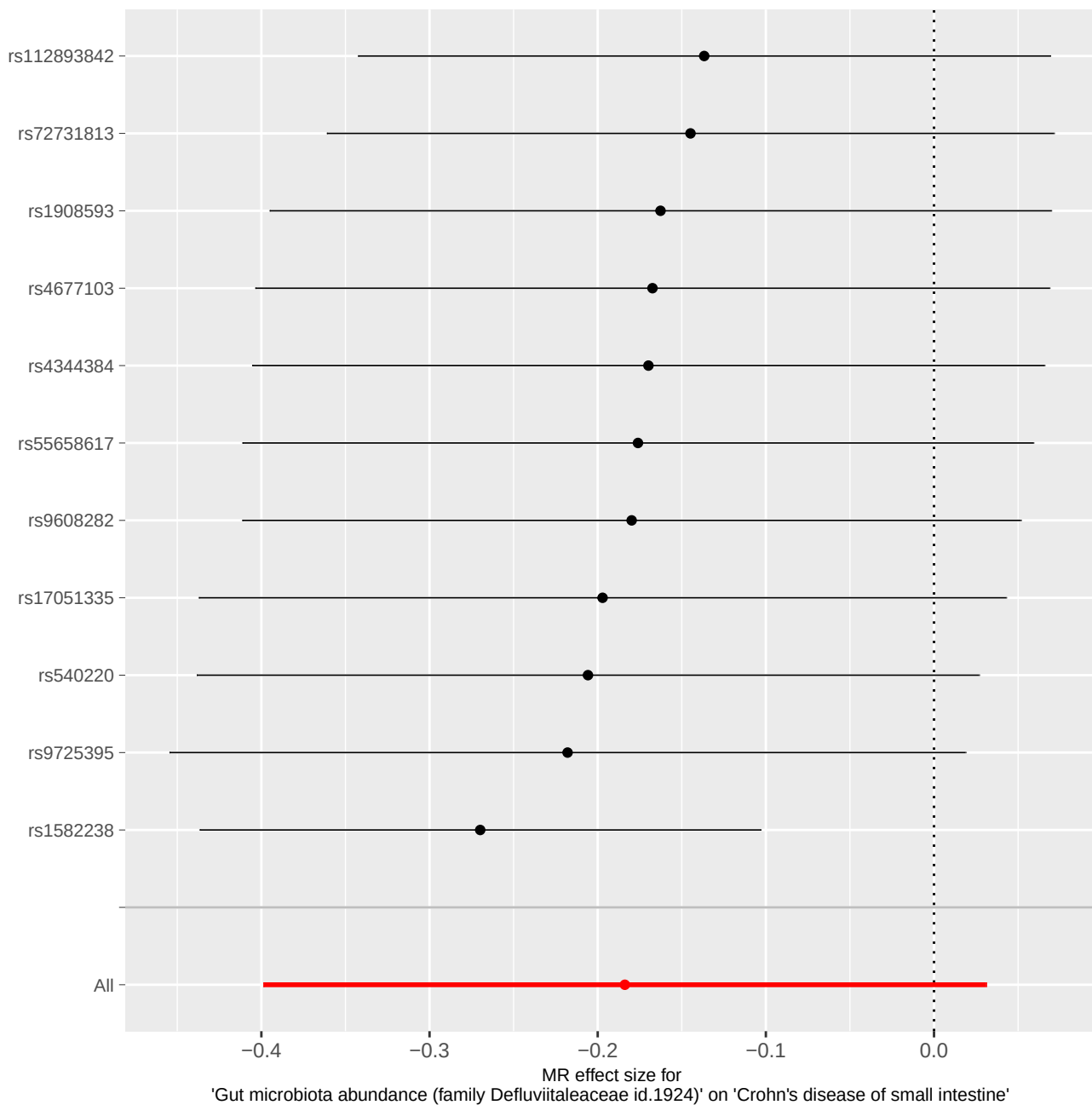


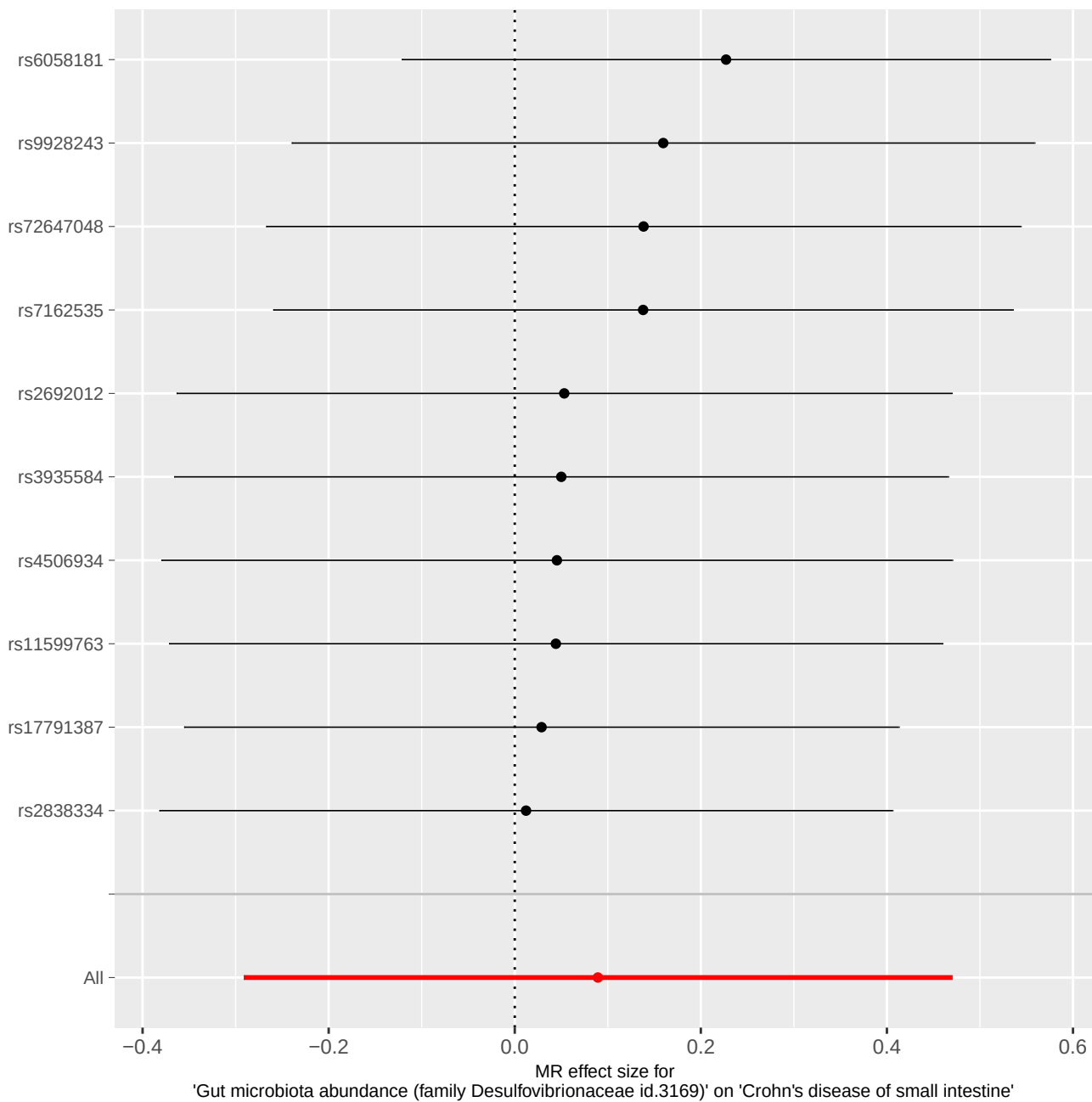
MR effect size for
'Gut microbiota abundance (family Bifidobacteriaceae id.433)' on 'Crohn's disease of small intestine'

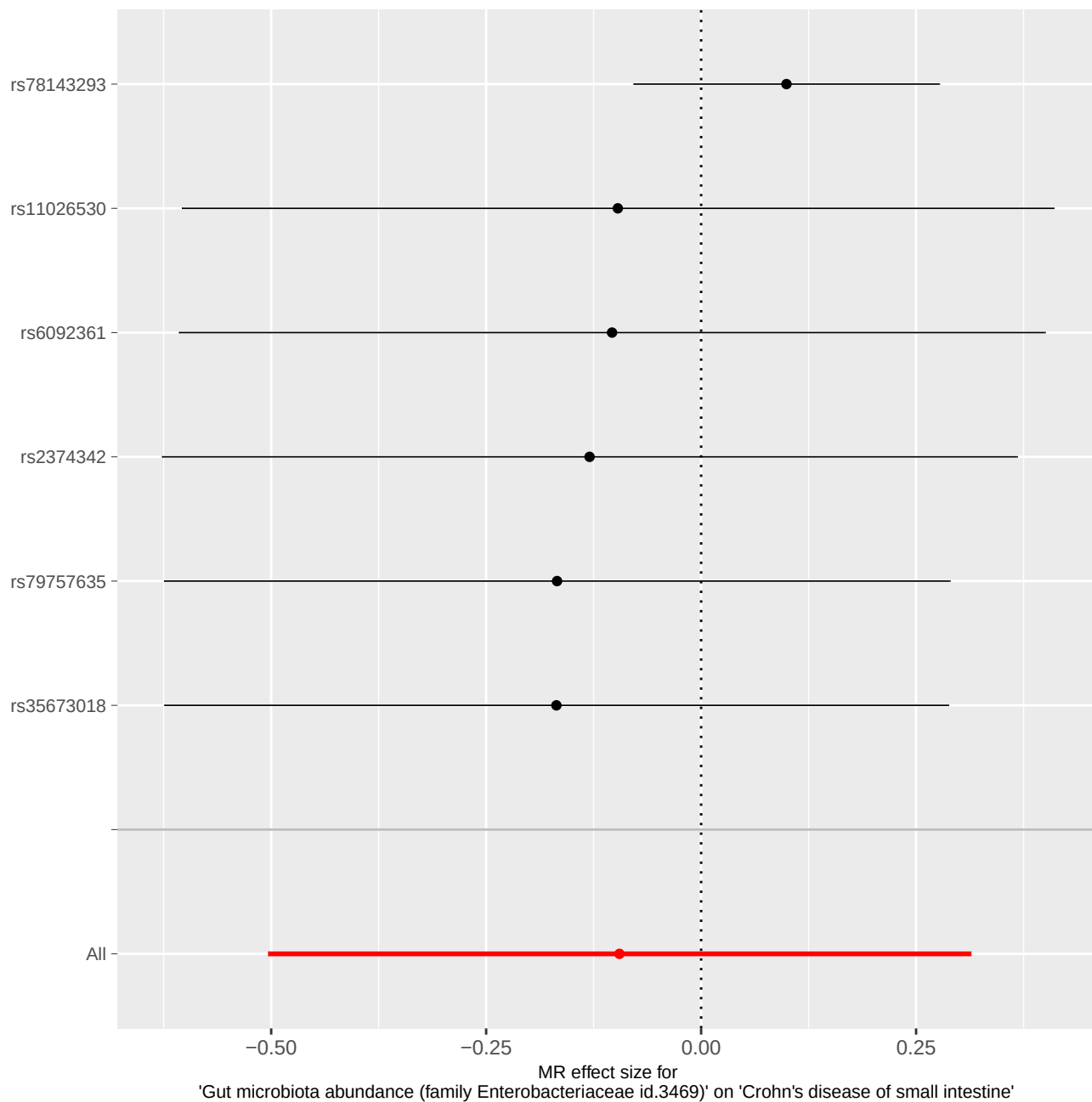


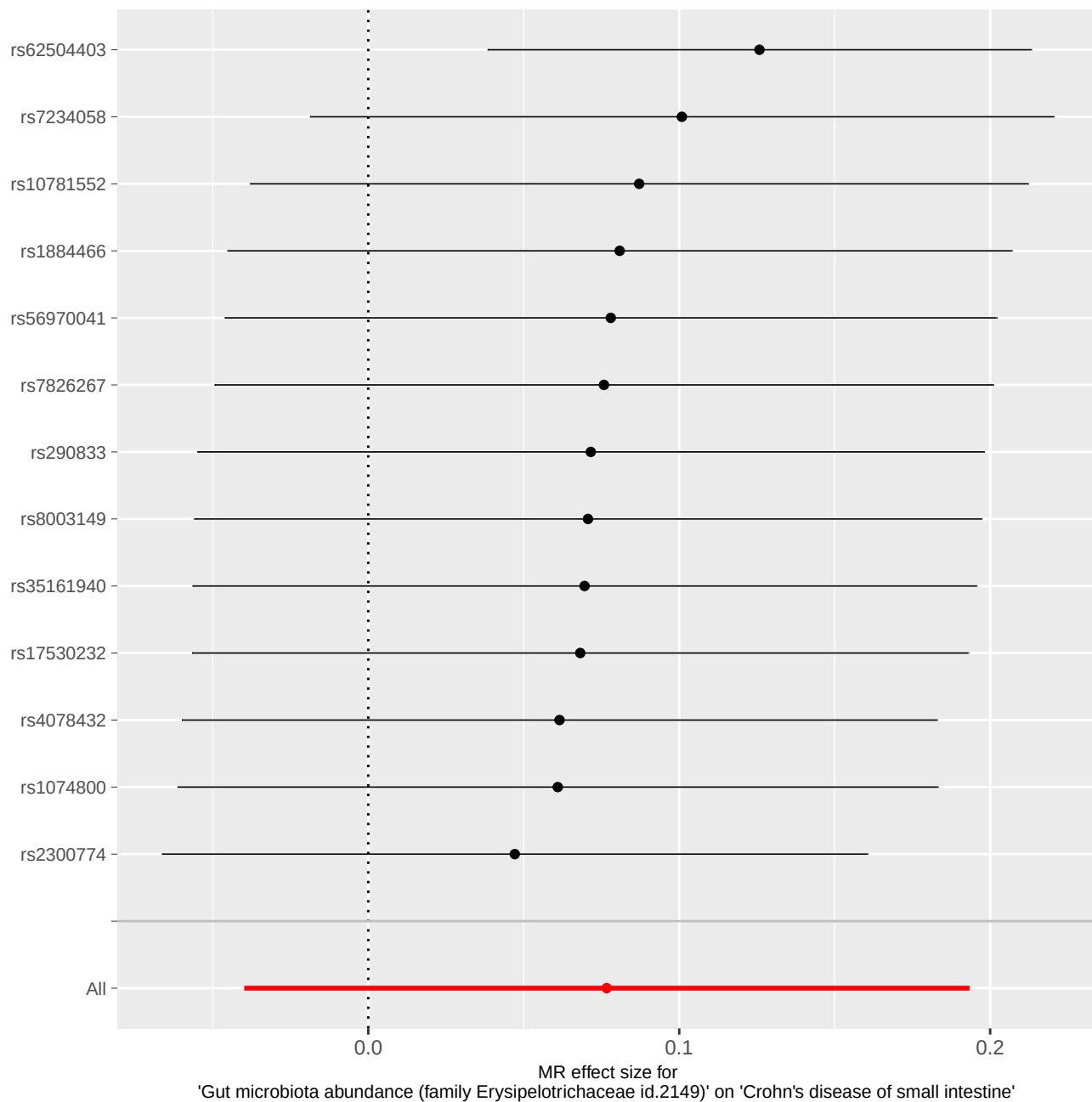


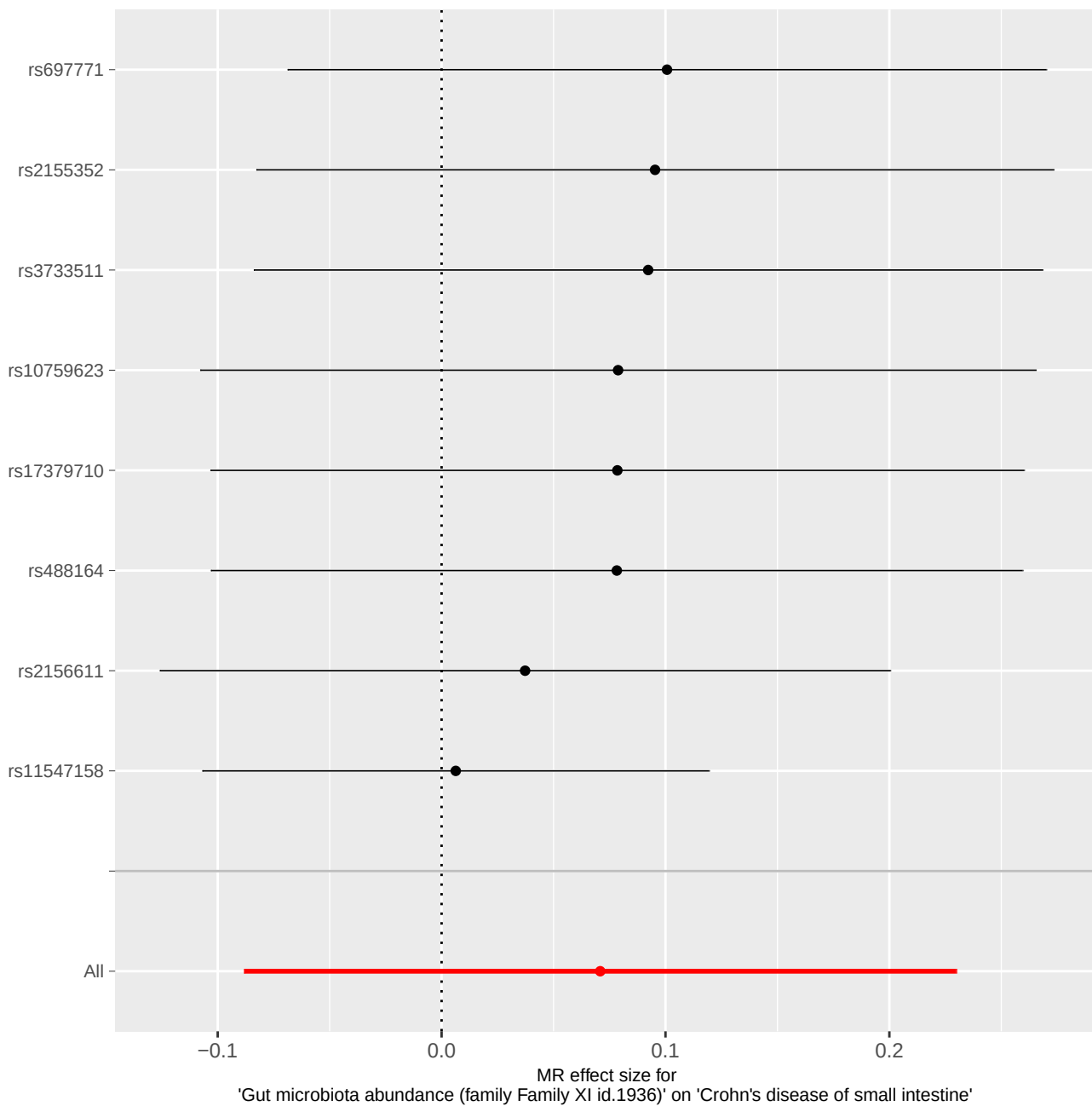


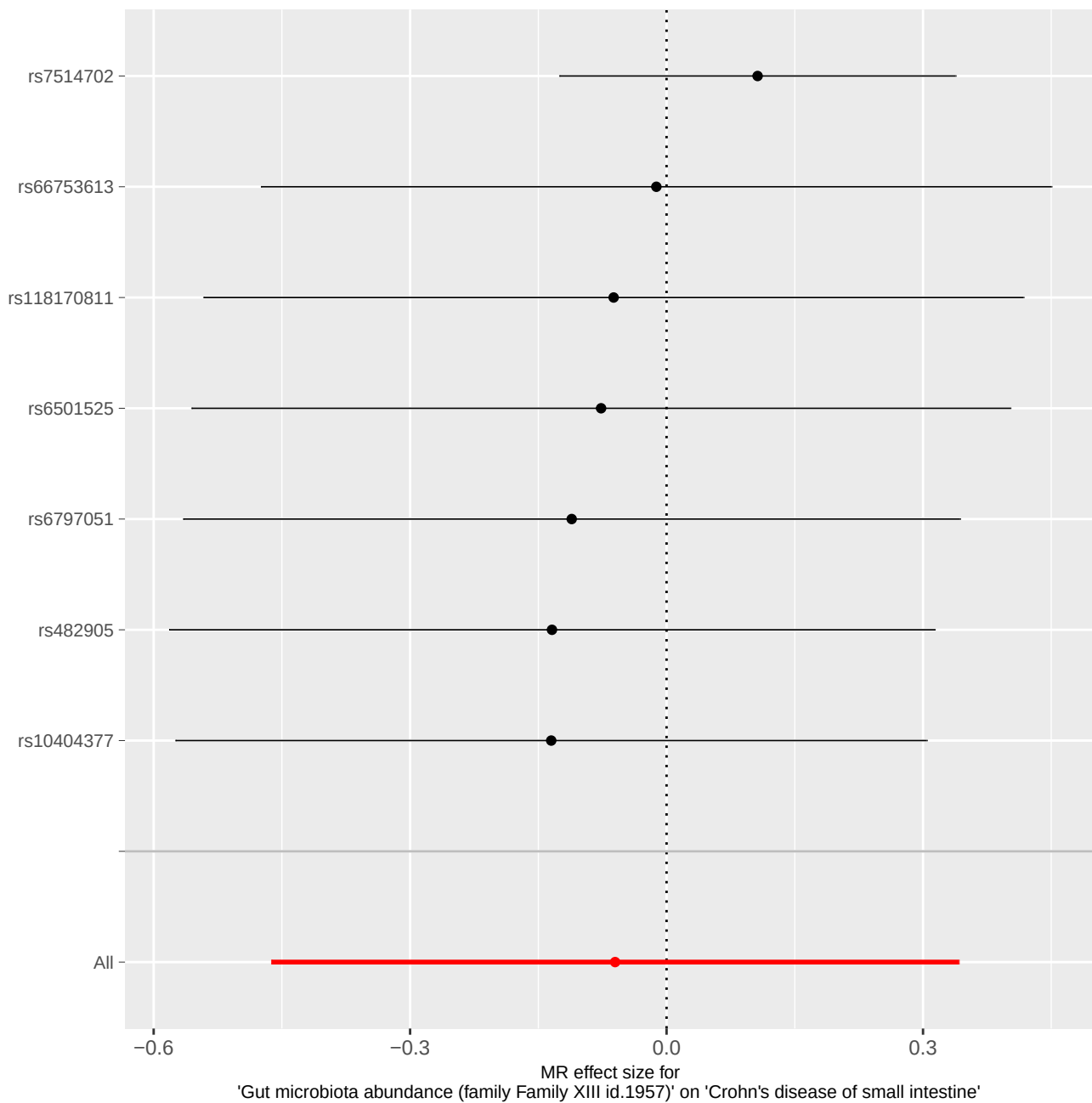


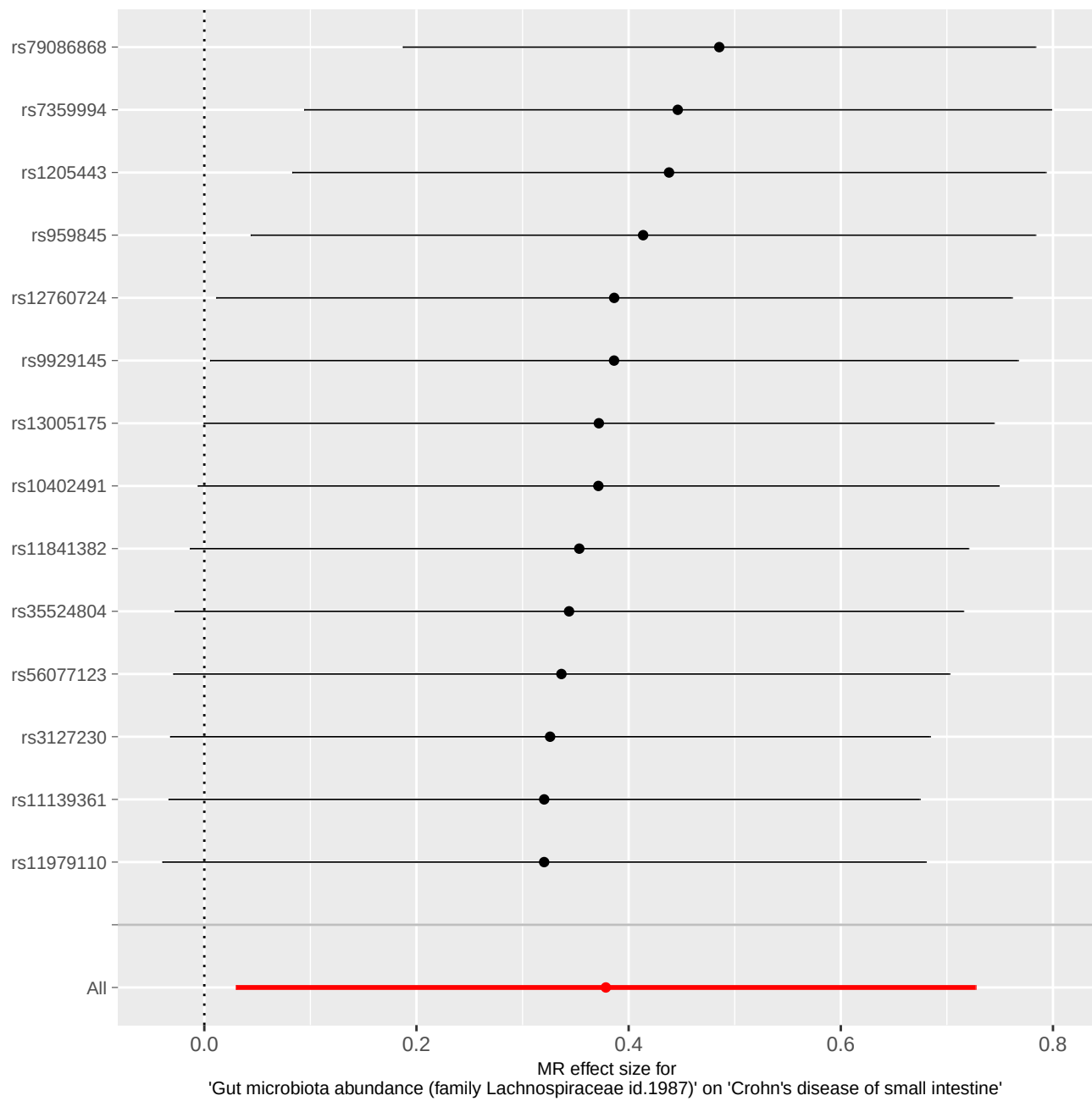


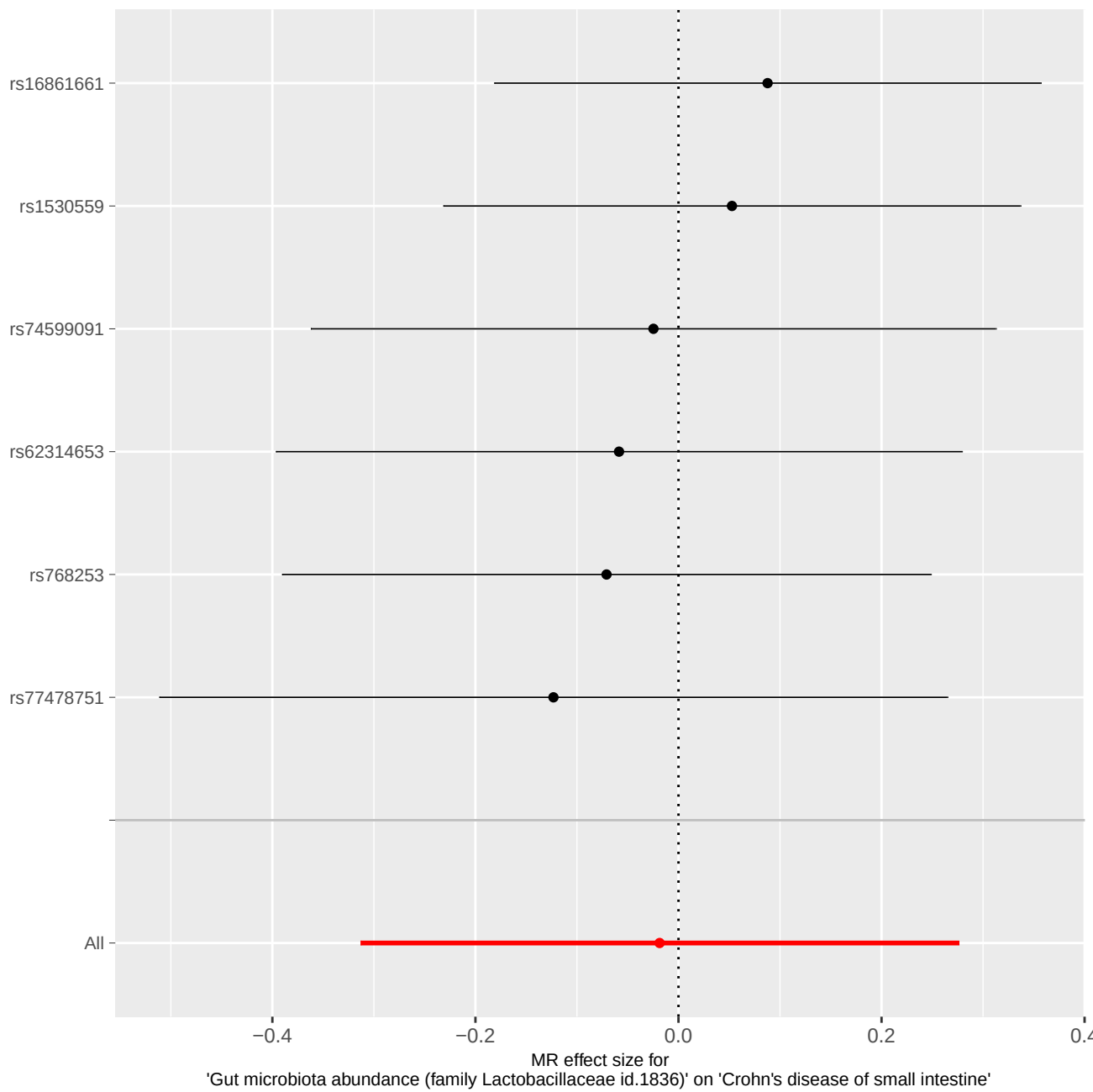


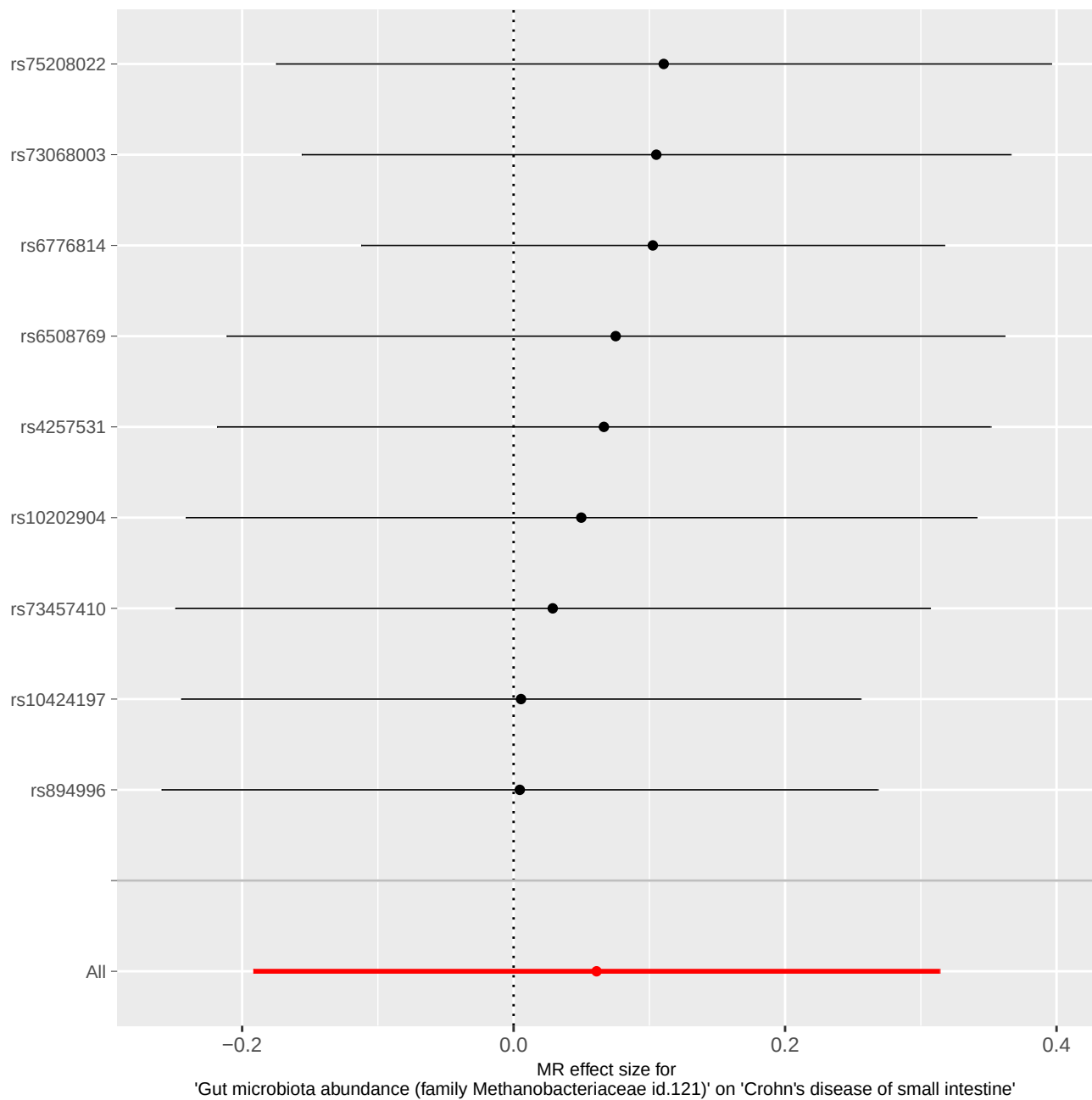


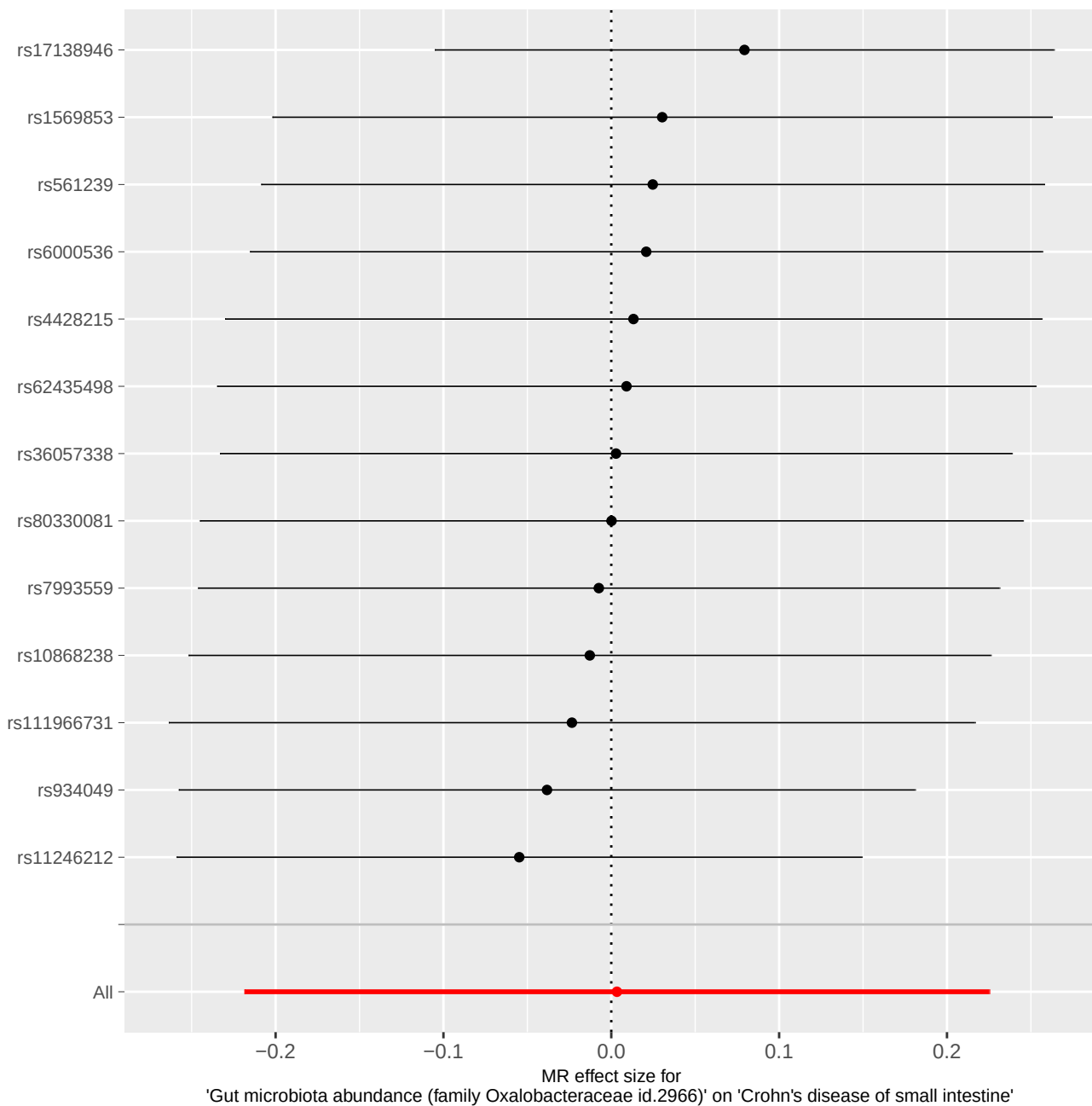




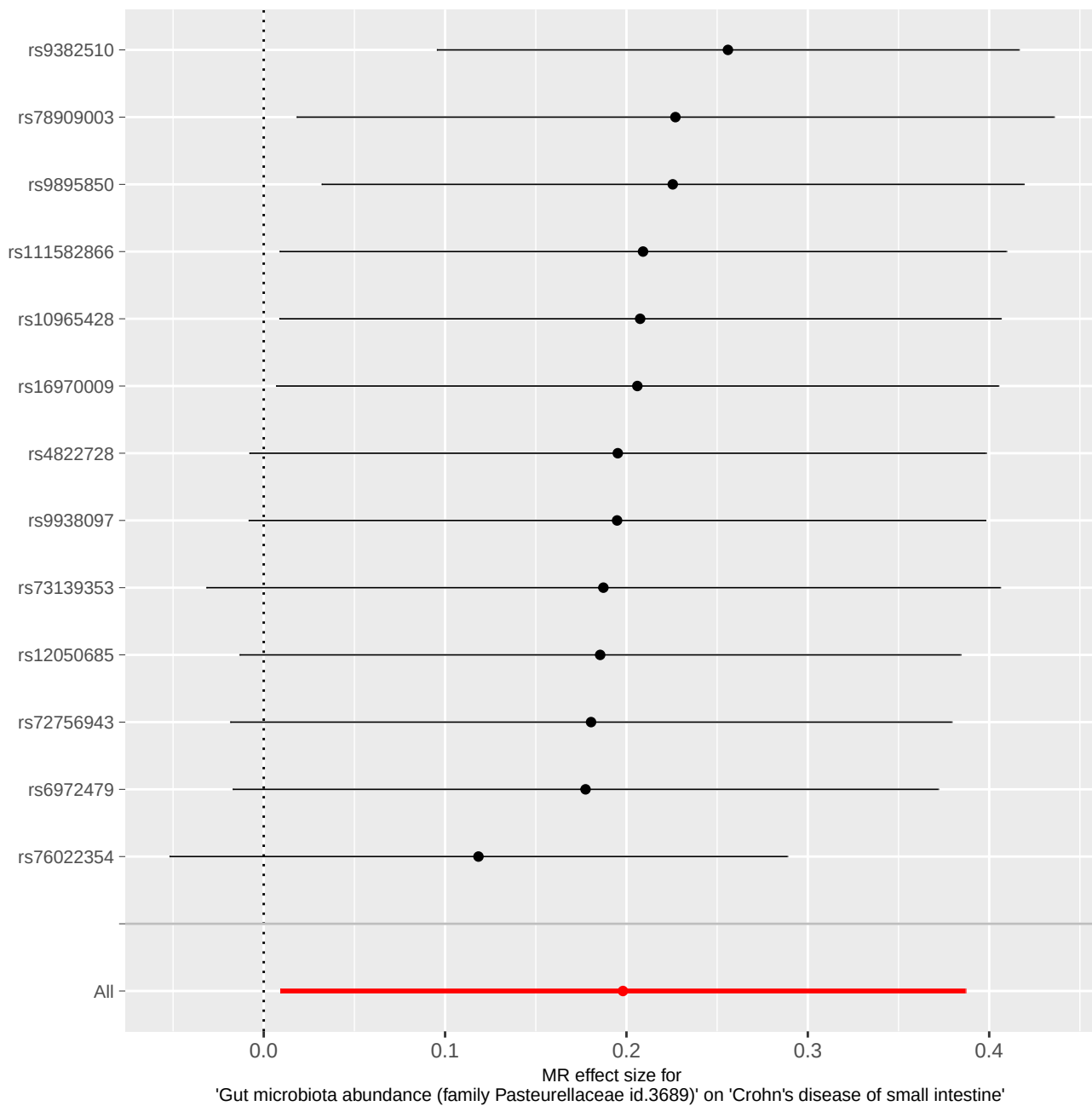


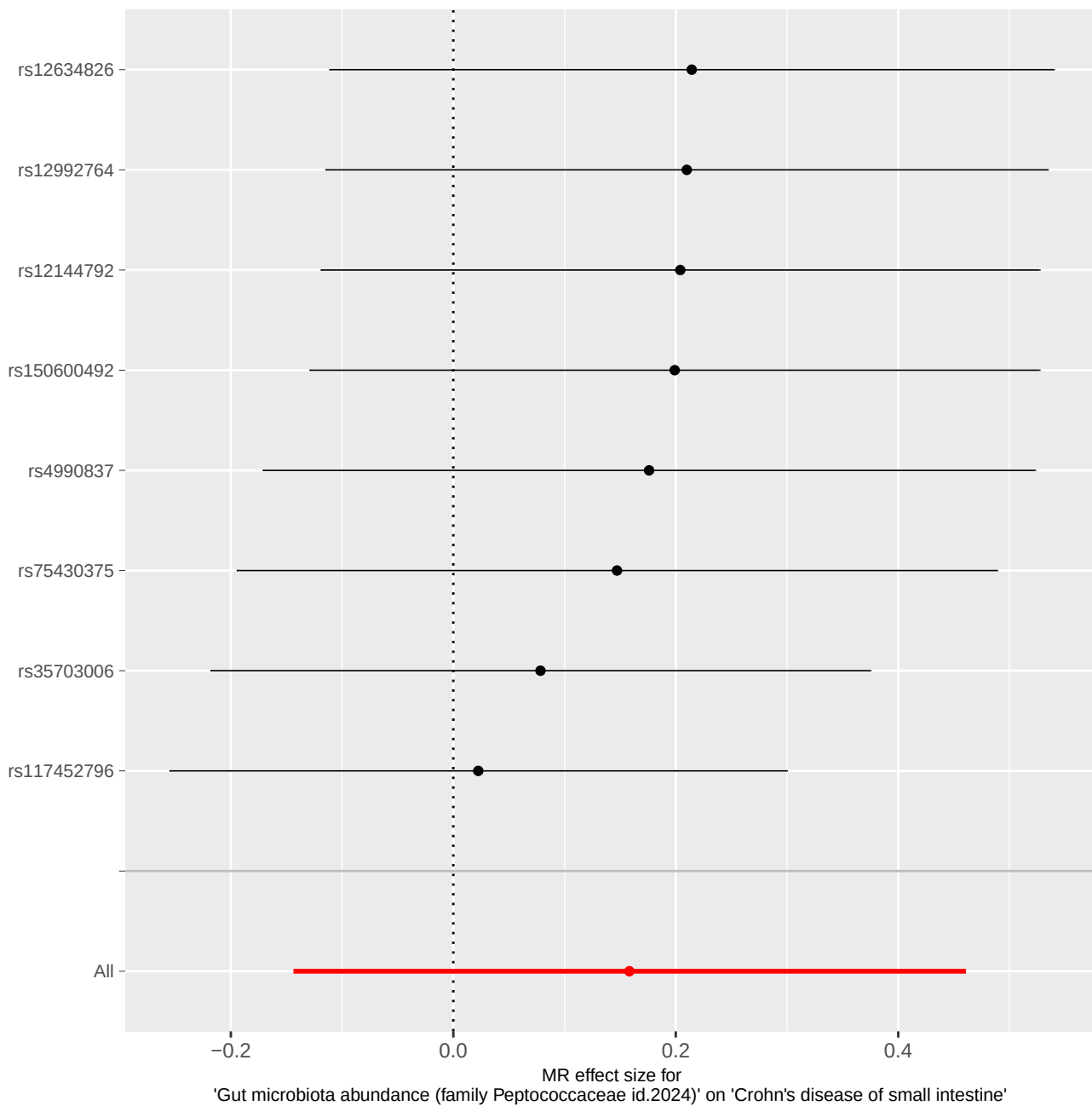


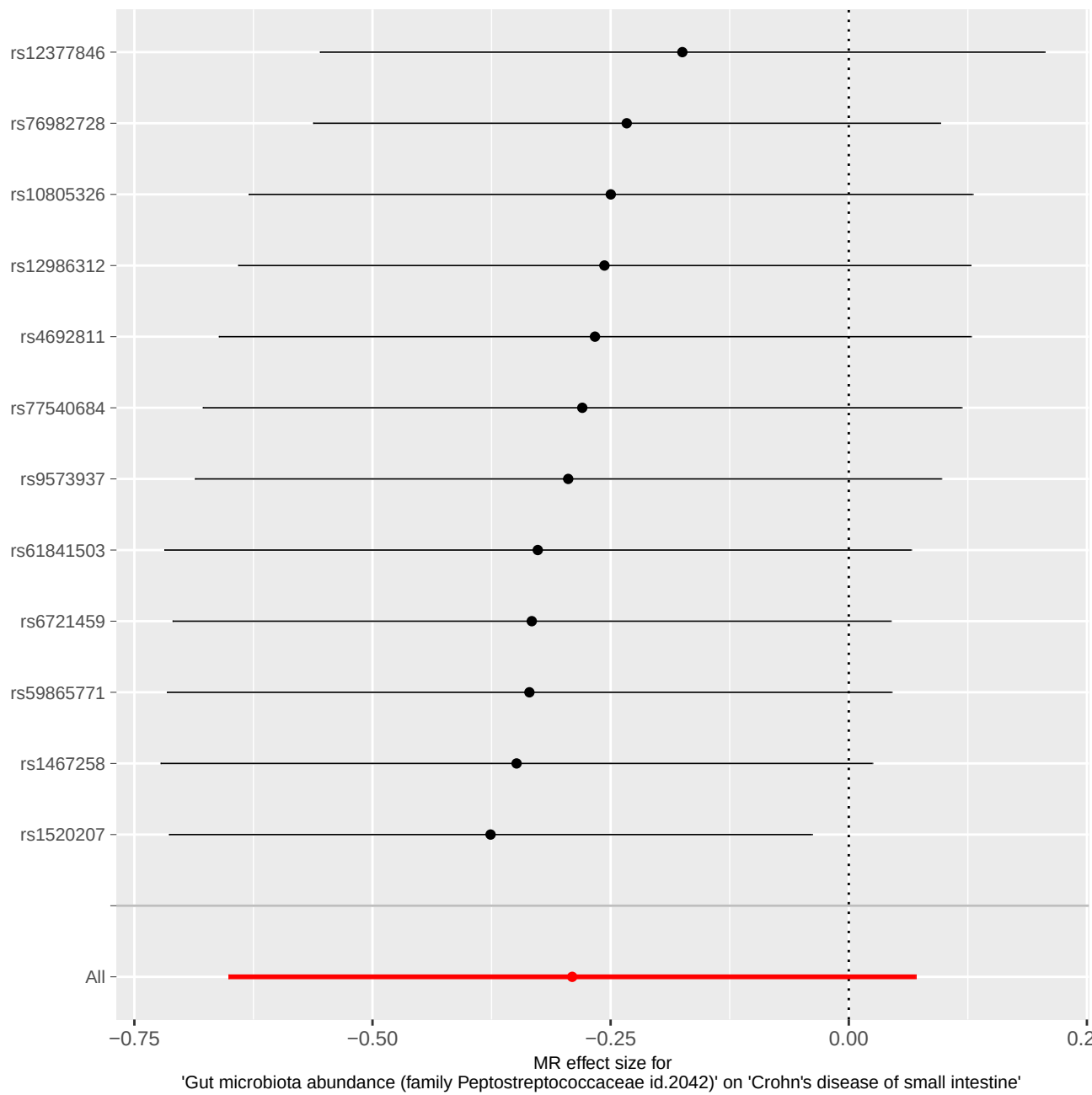


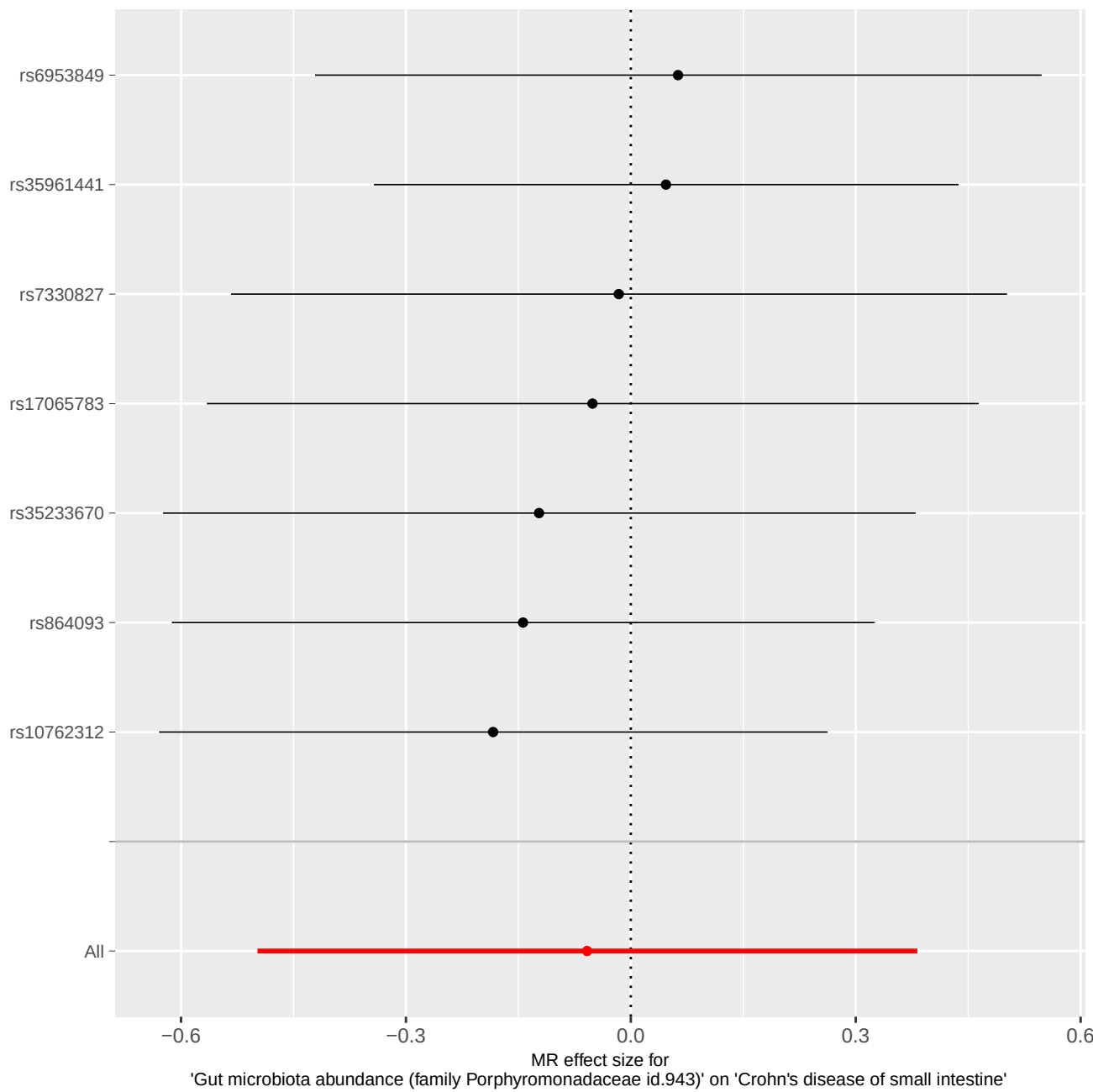


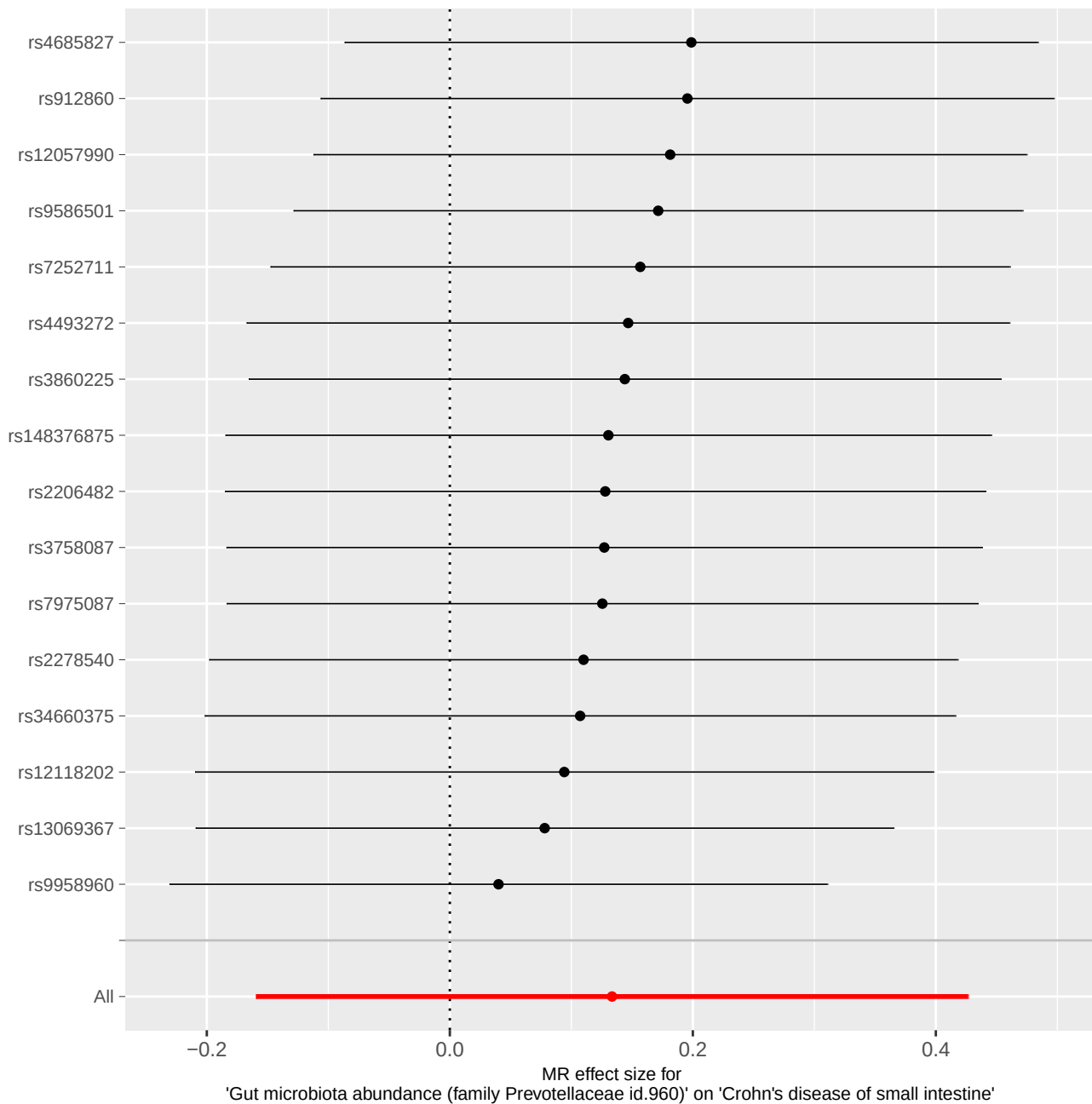
Batch 321 : Gut microbiota abundance (family Pasteurellaceae id.3689) on Crohn's disease of small intestine



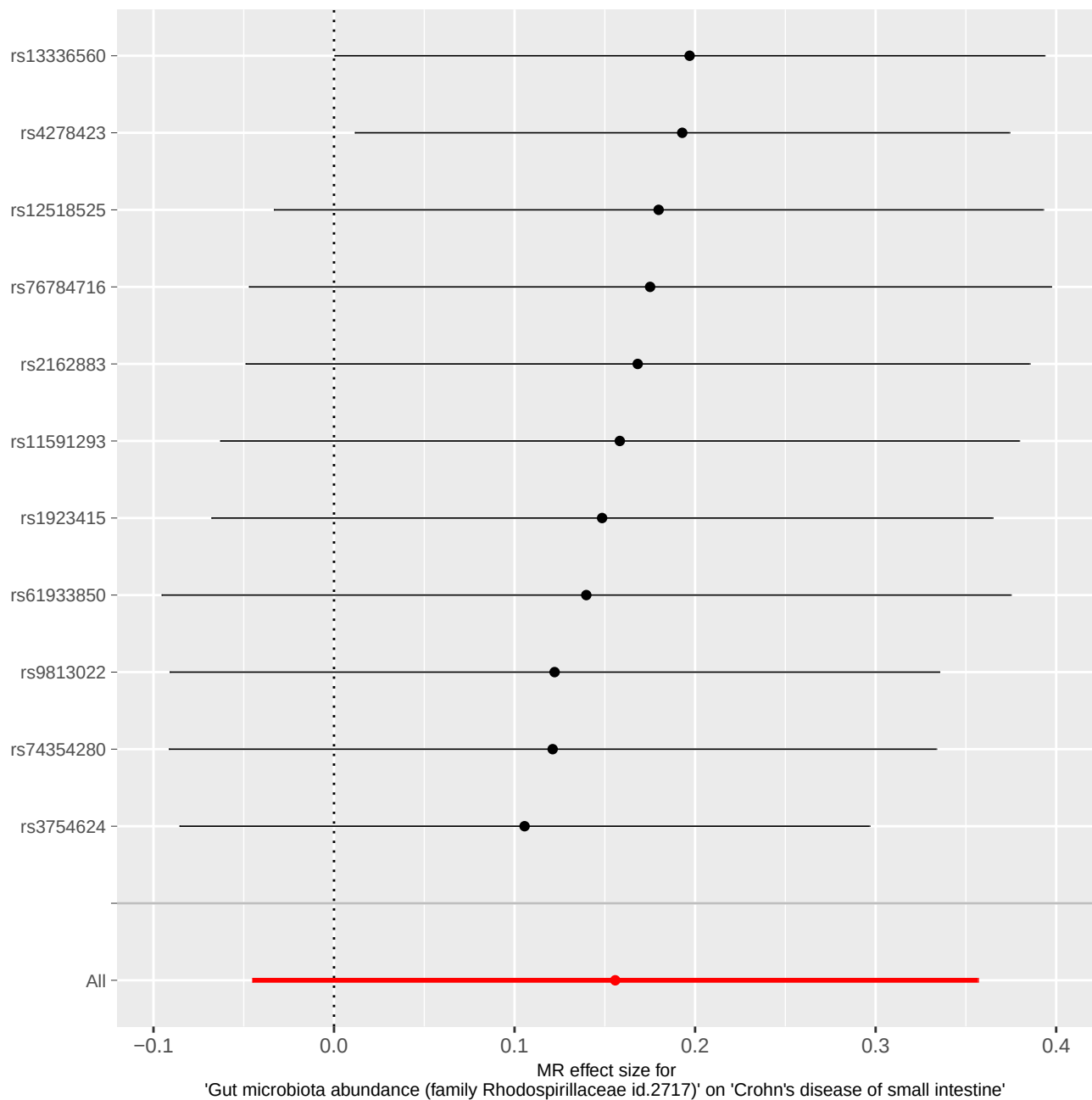




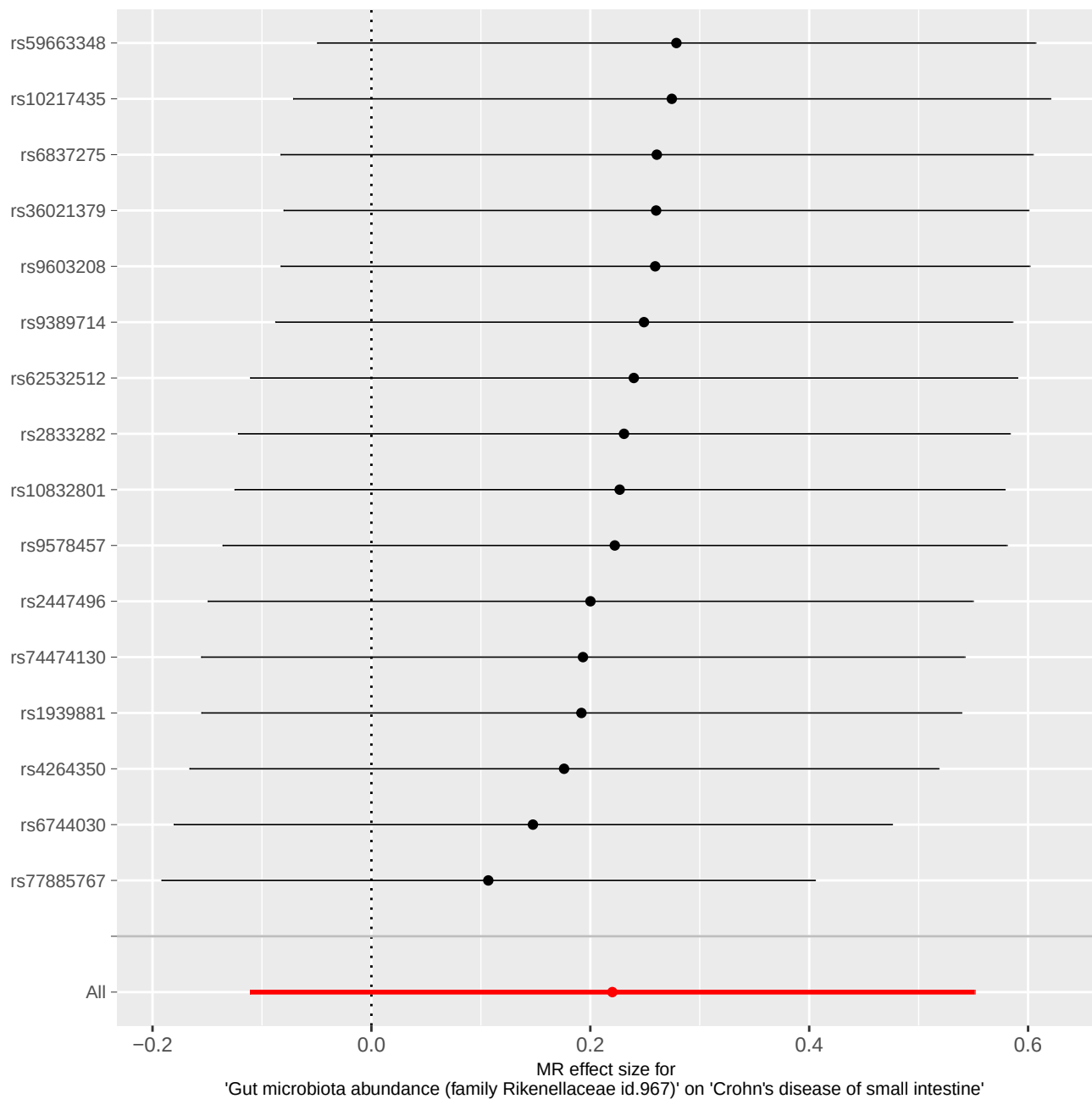


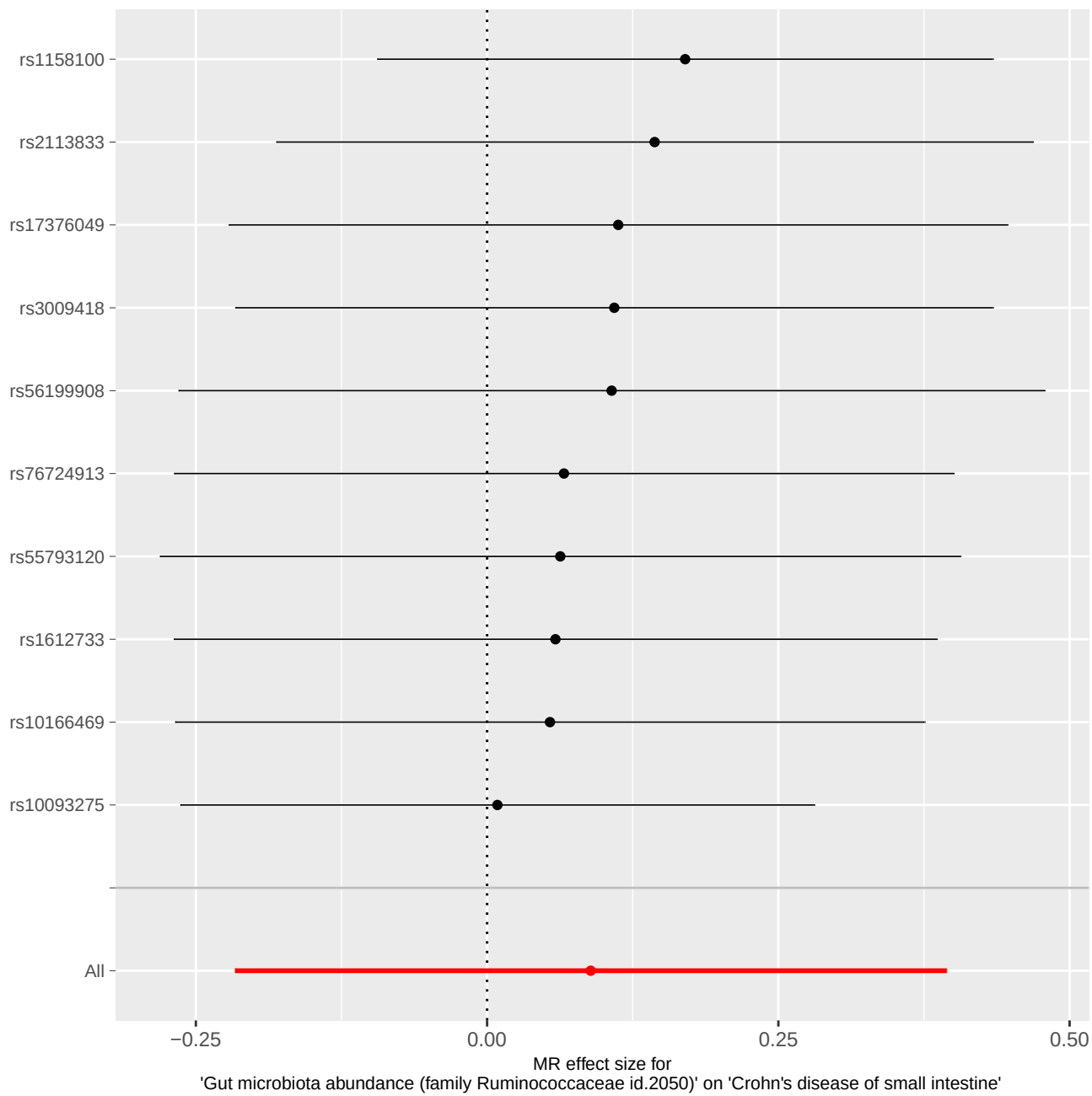


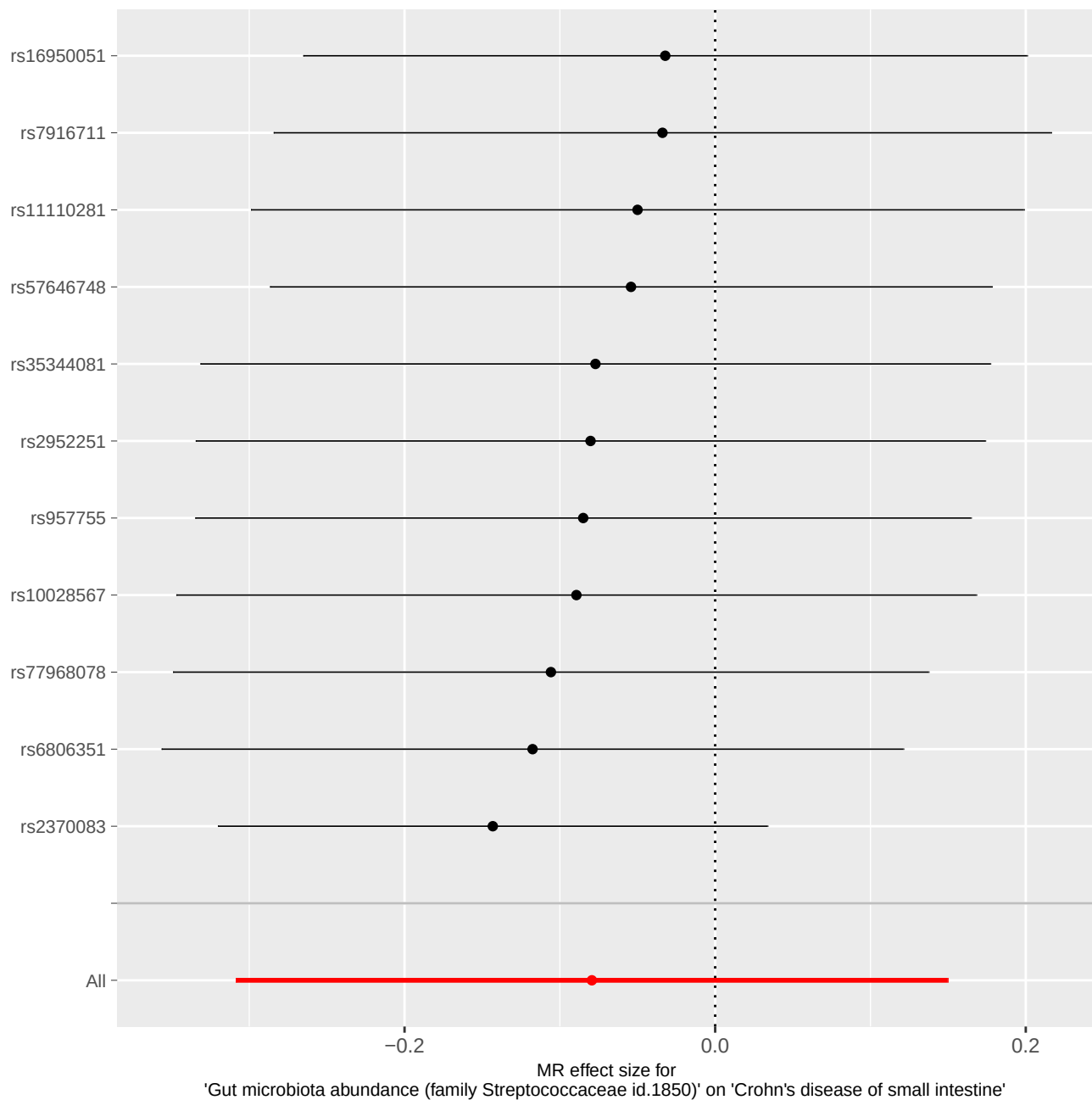
Batch 326 : Gut microbiota abundance (family Rhodospirillaceae id.2717) on Crohn's disease of small intestine

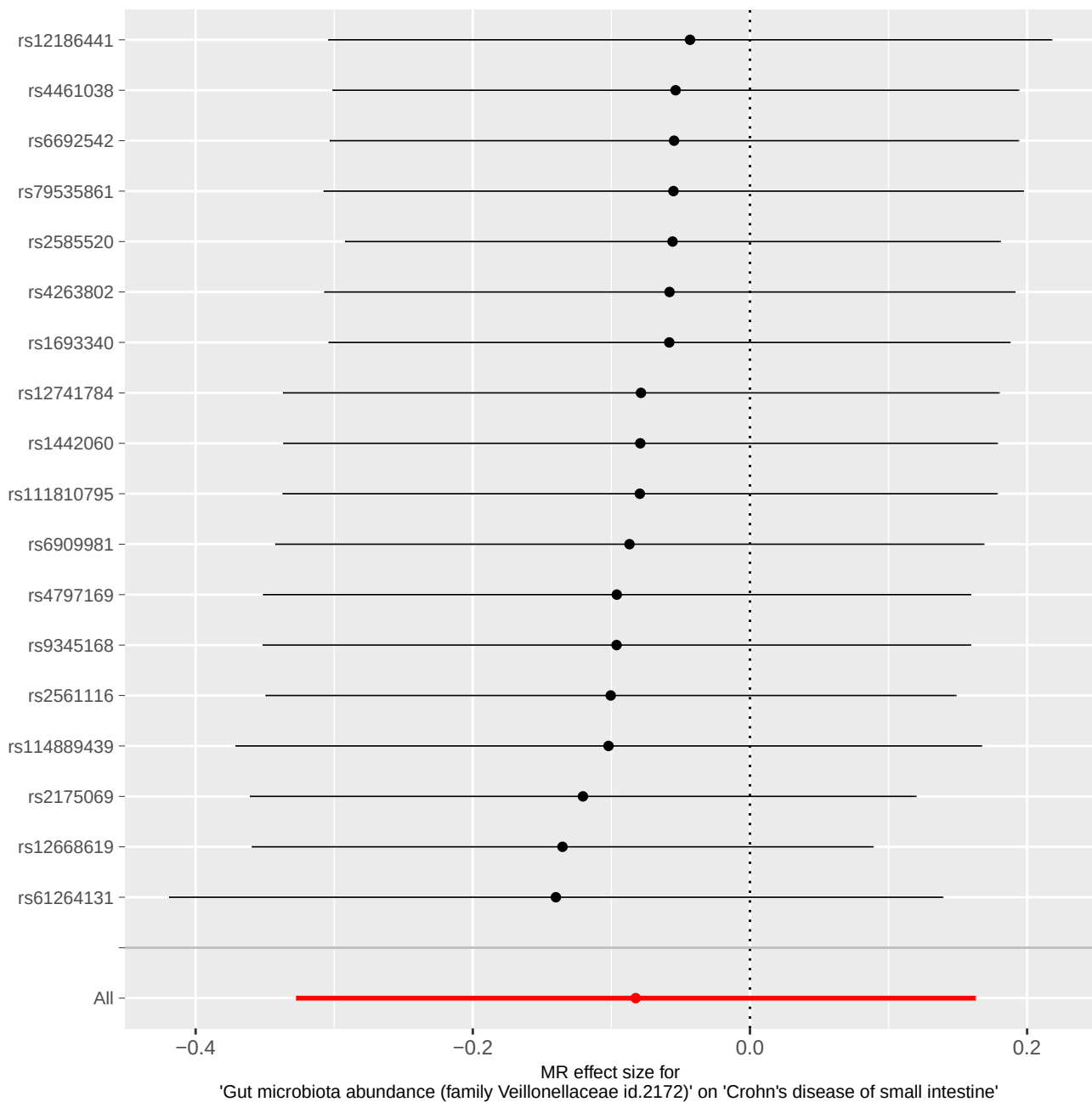


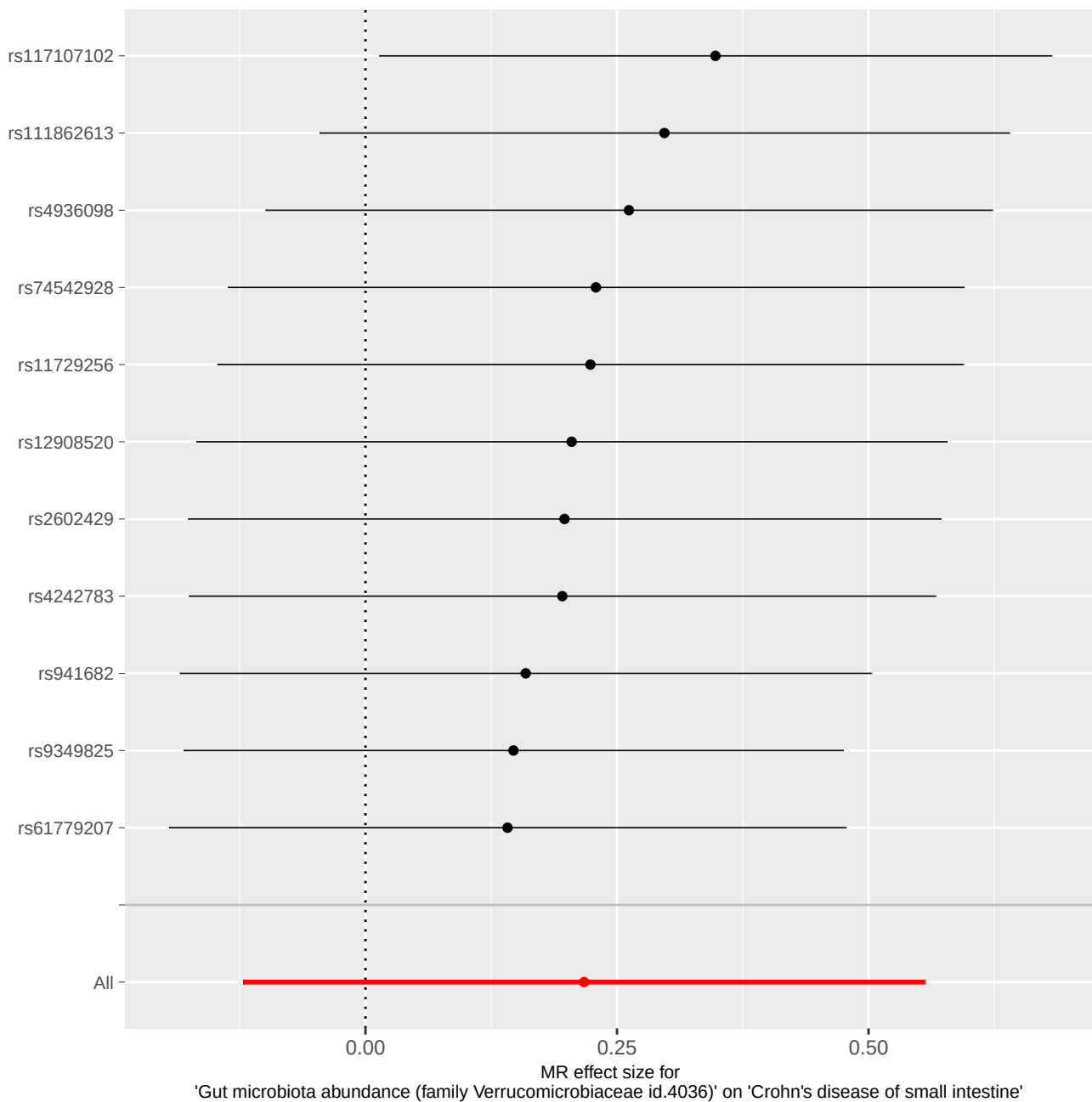
Batch 327 : Gut microbiota abundance (family Rikenellaceae id.967) on Crohn's disease of small intestine

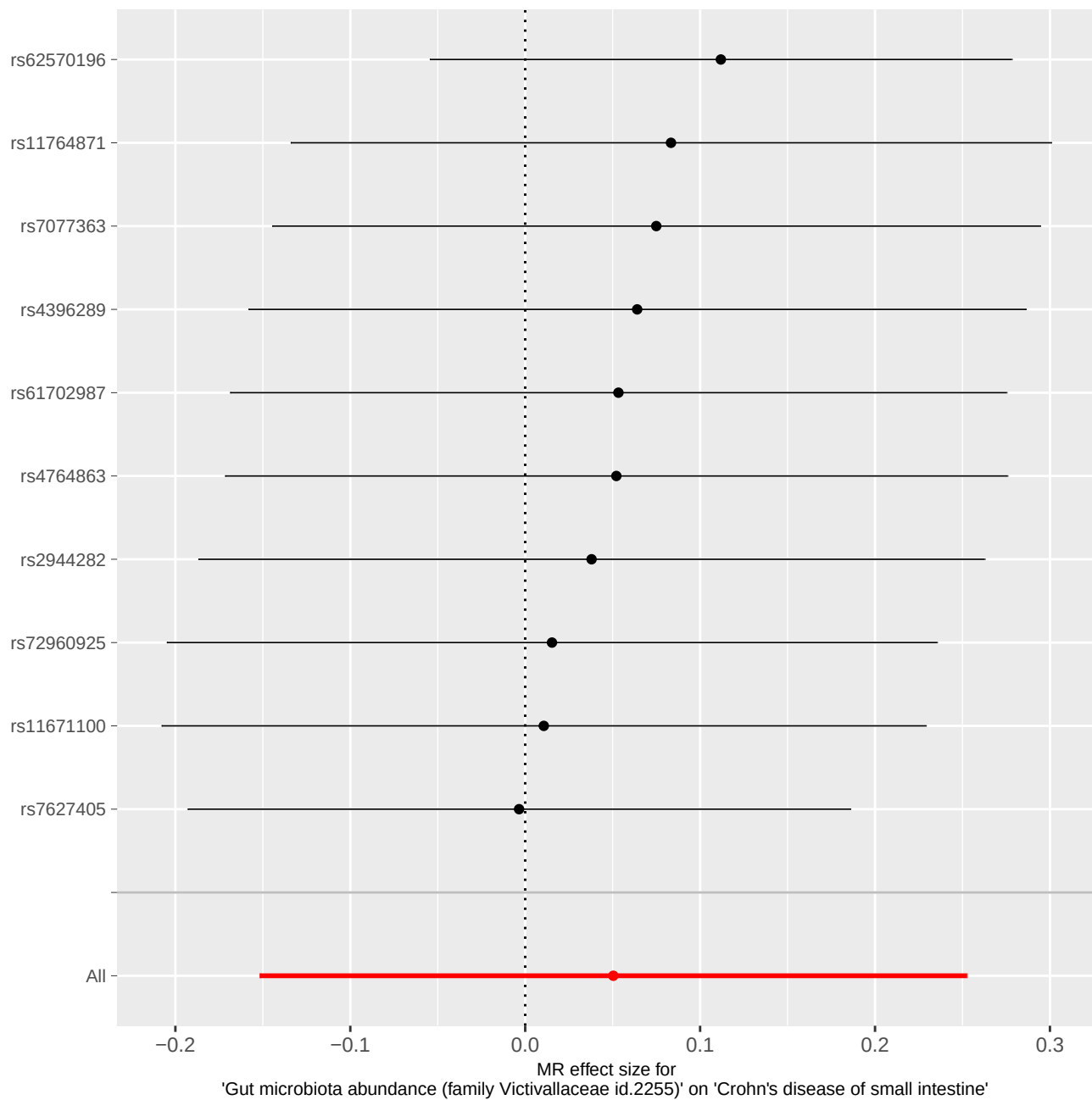




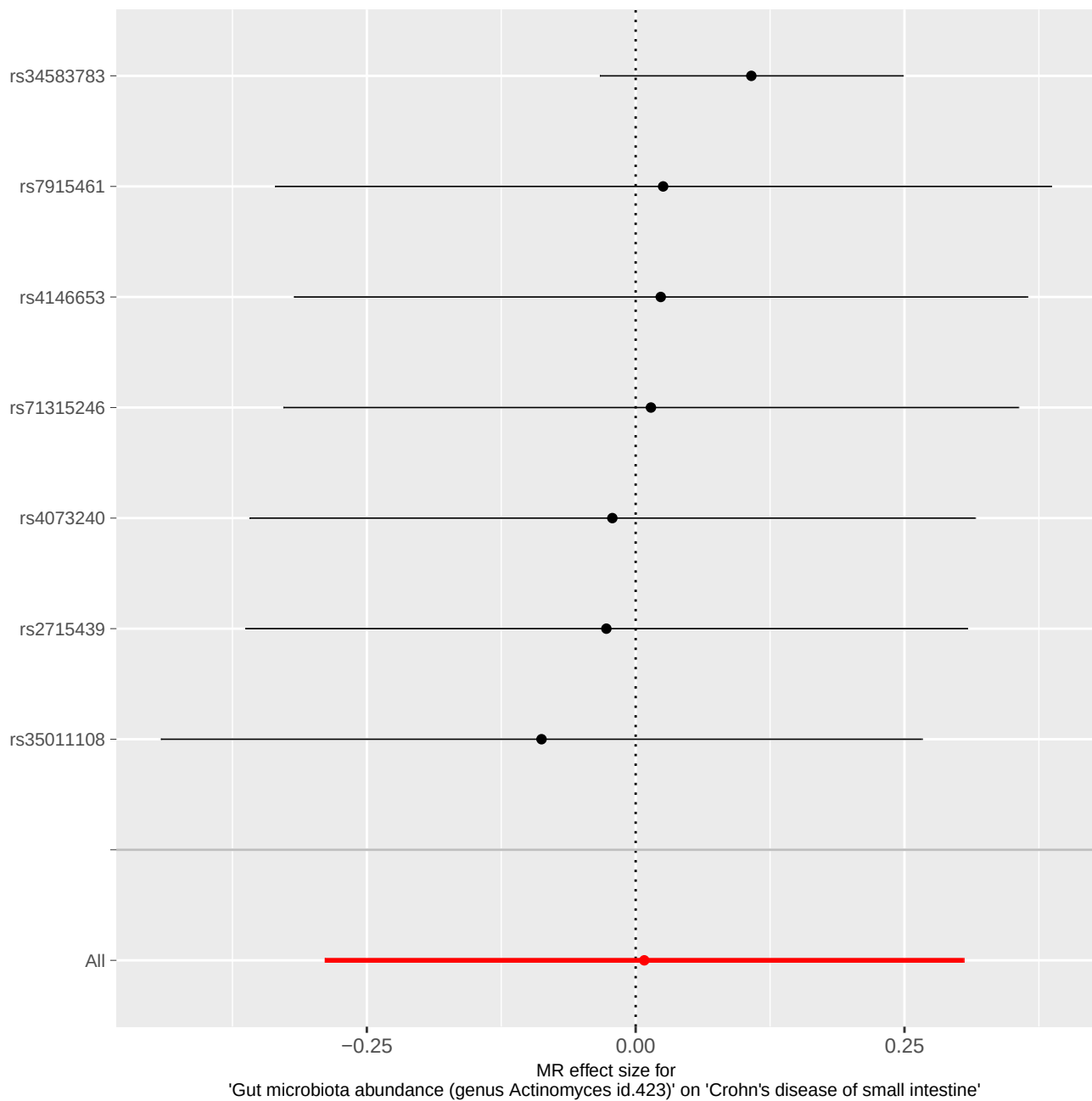


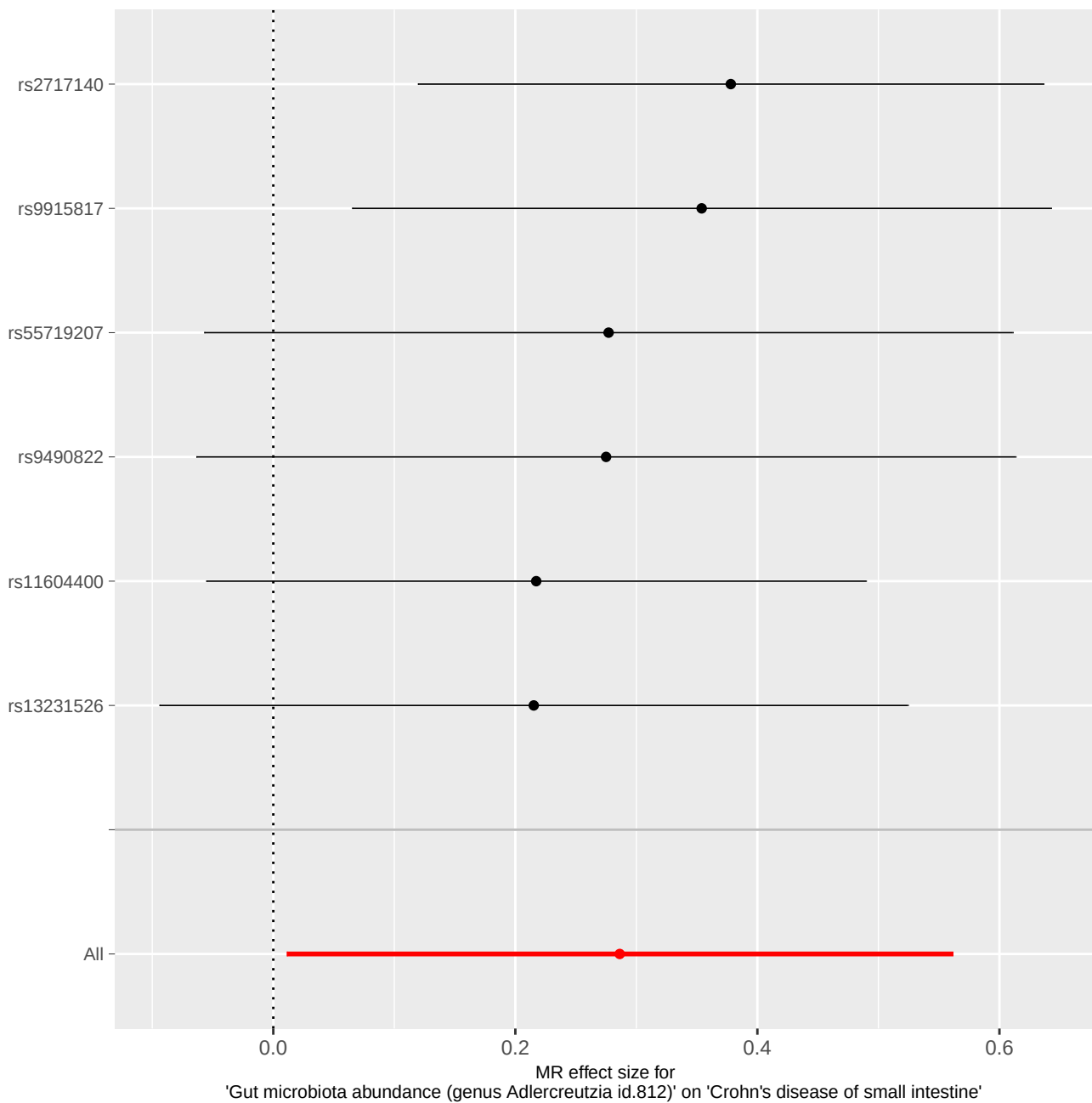


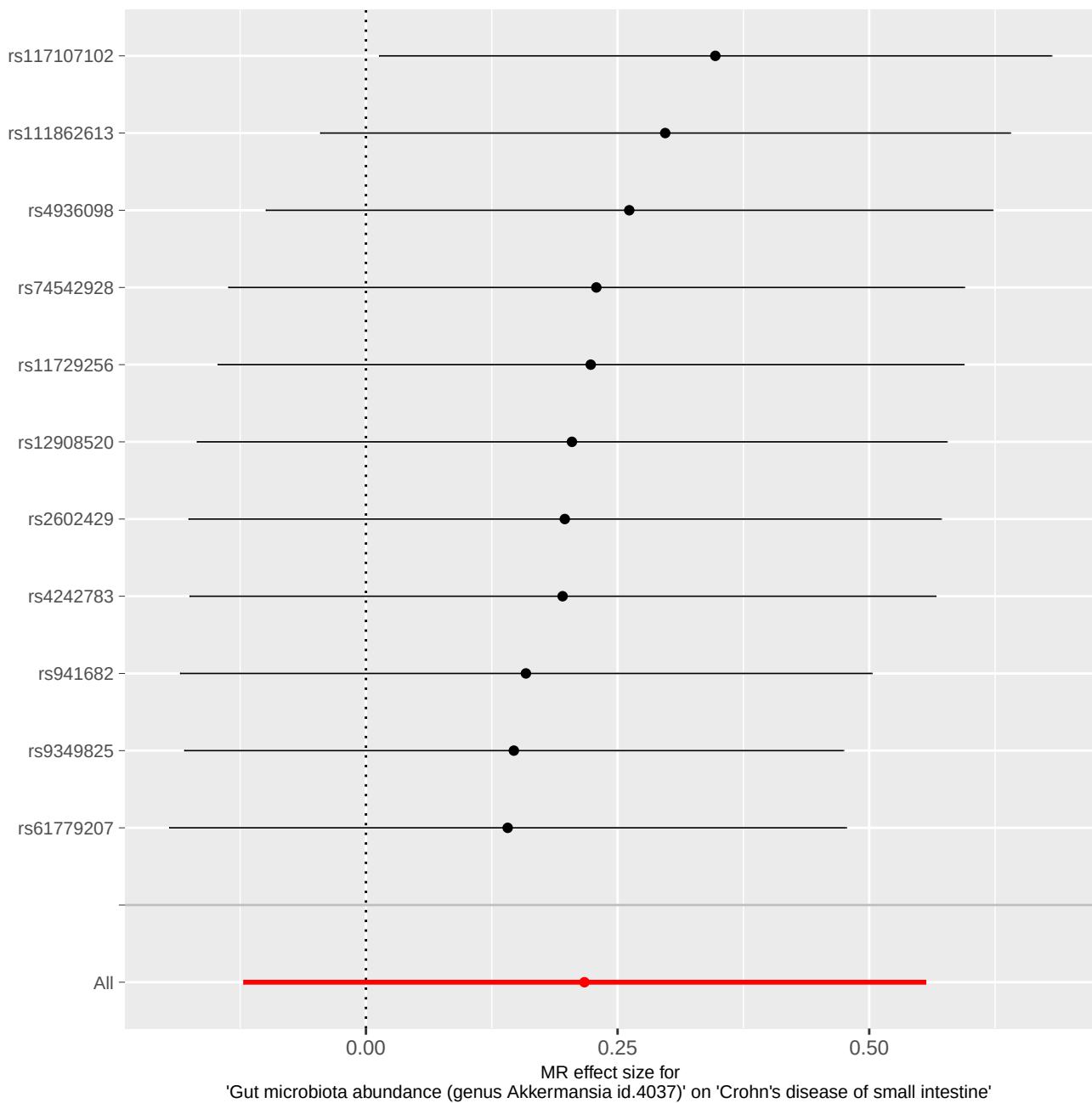




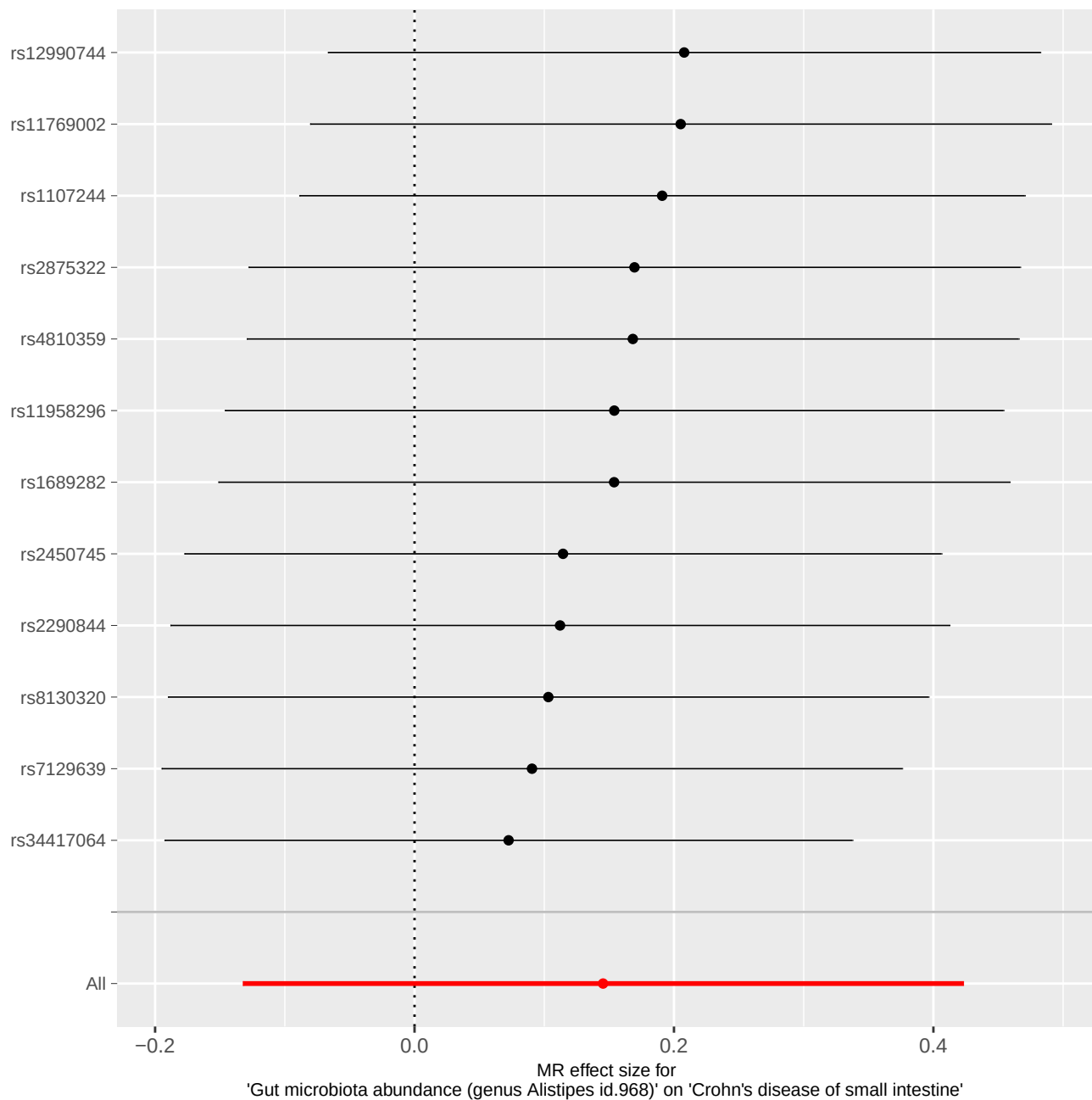
Batch 333 : Gut microbiota abundance (genus Actinomyces id.423) on Crohn's disease of small intestine

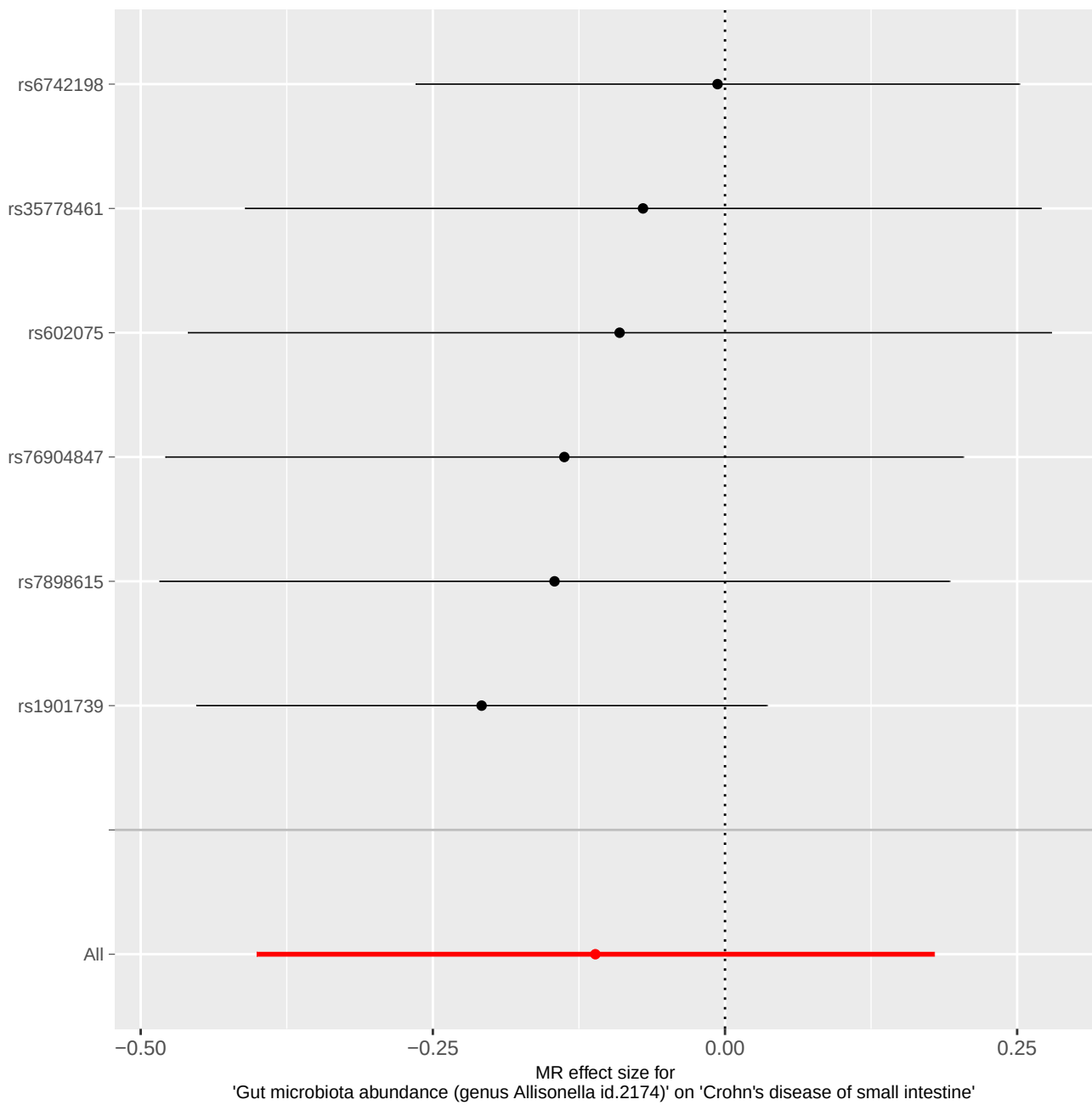




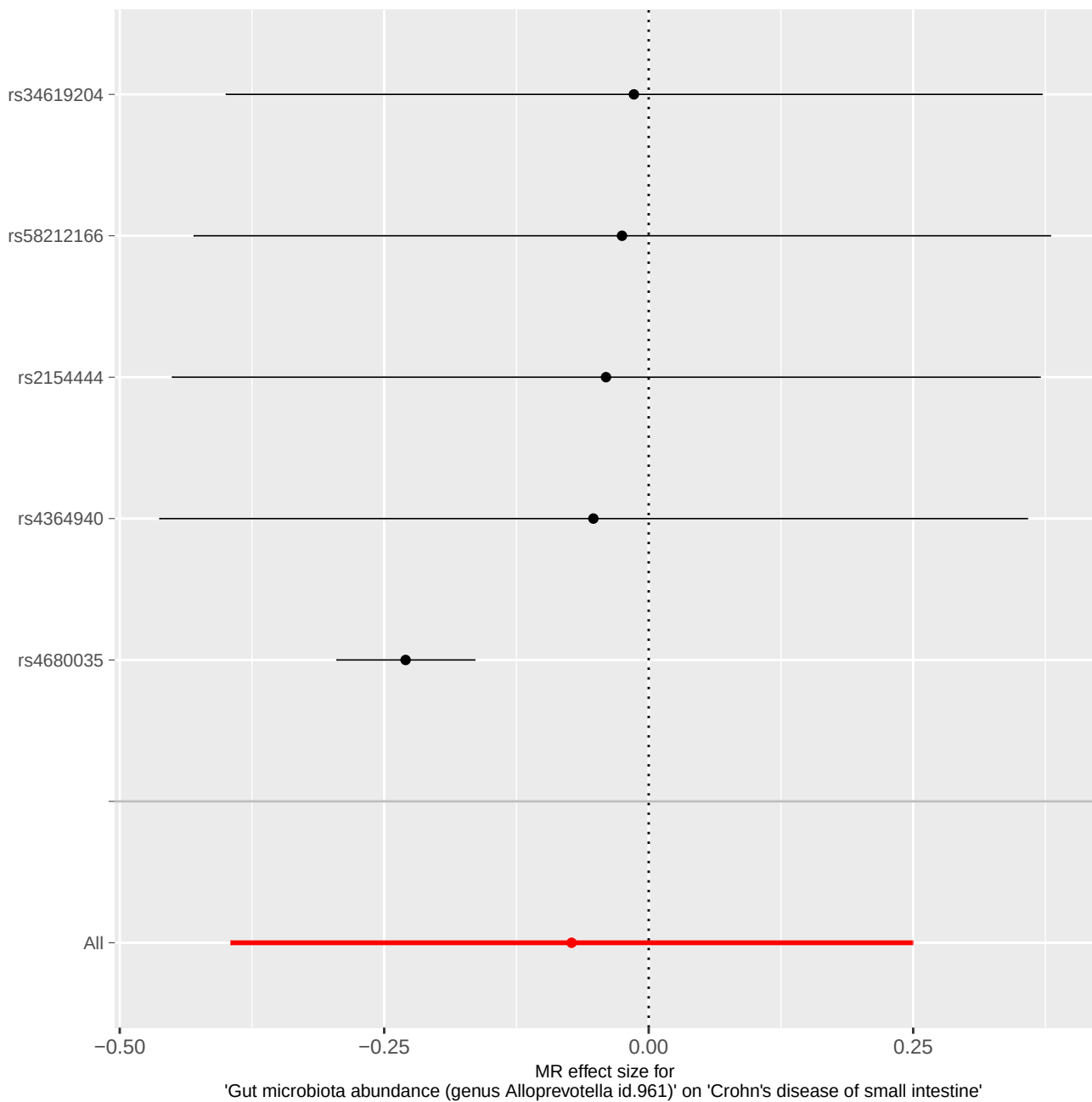


Batch 336 : Gut microbiota abundance (genus Alistipes id.968) on Crohn's disease of small intestine

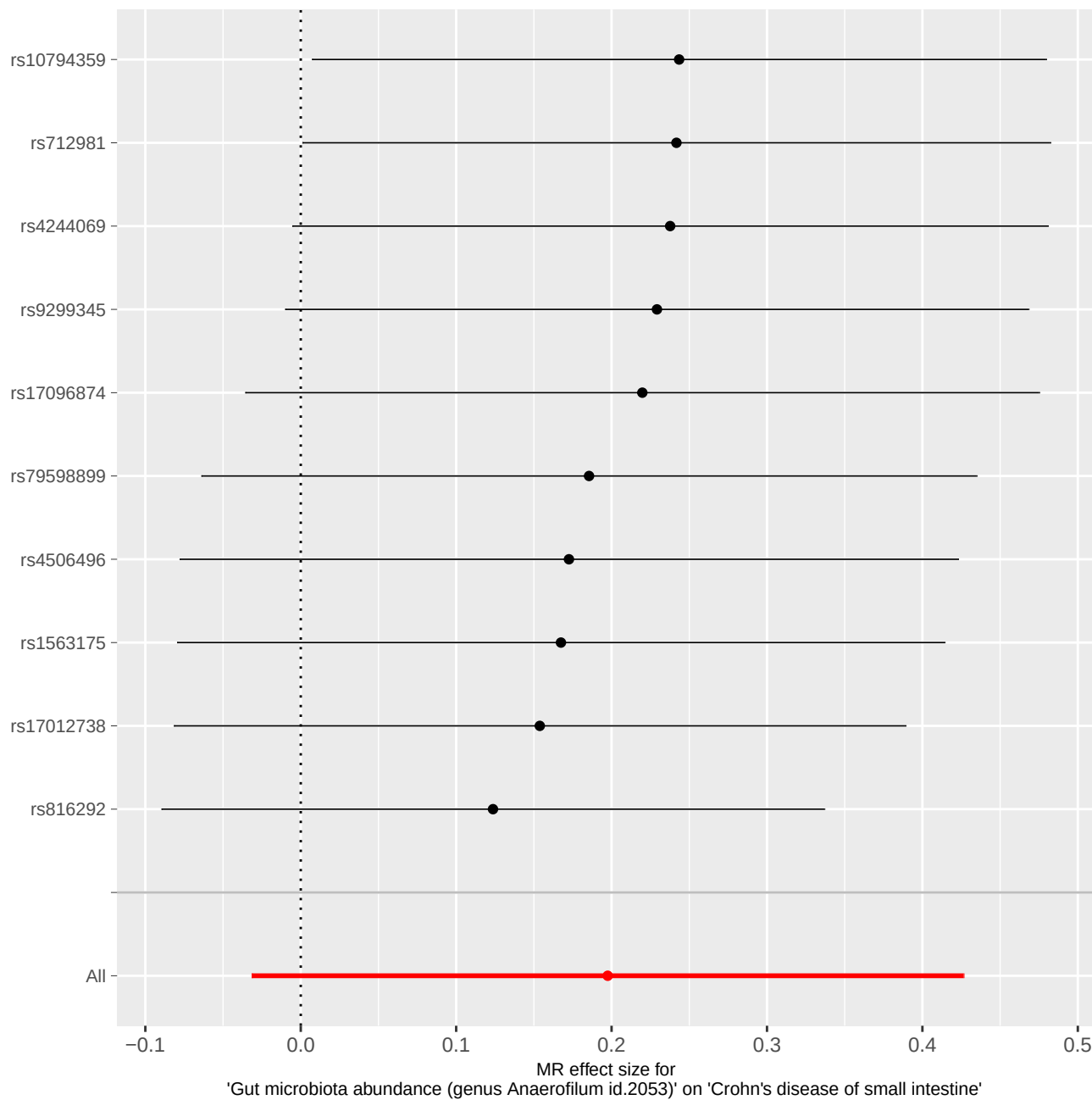


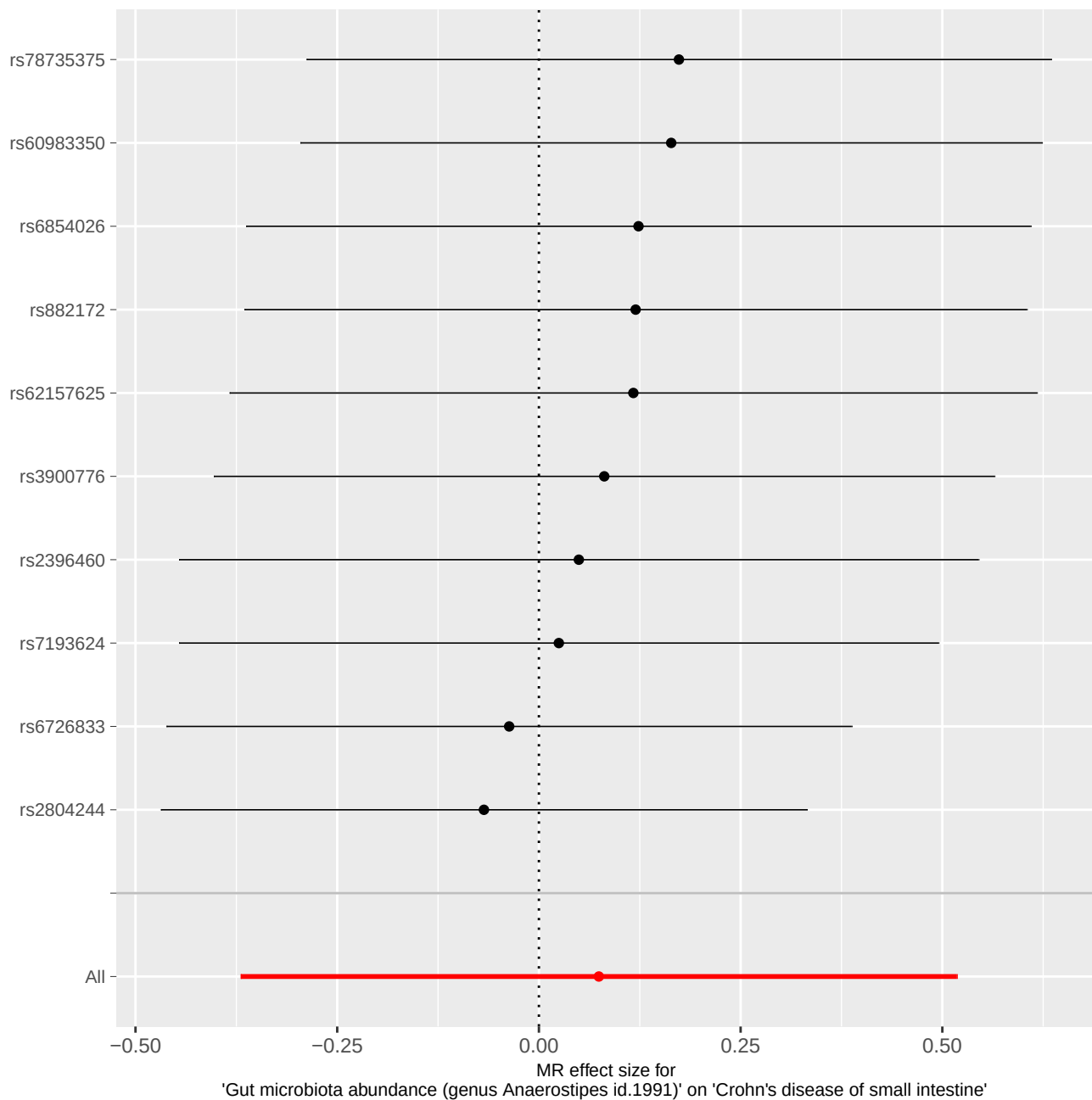


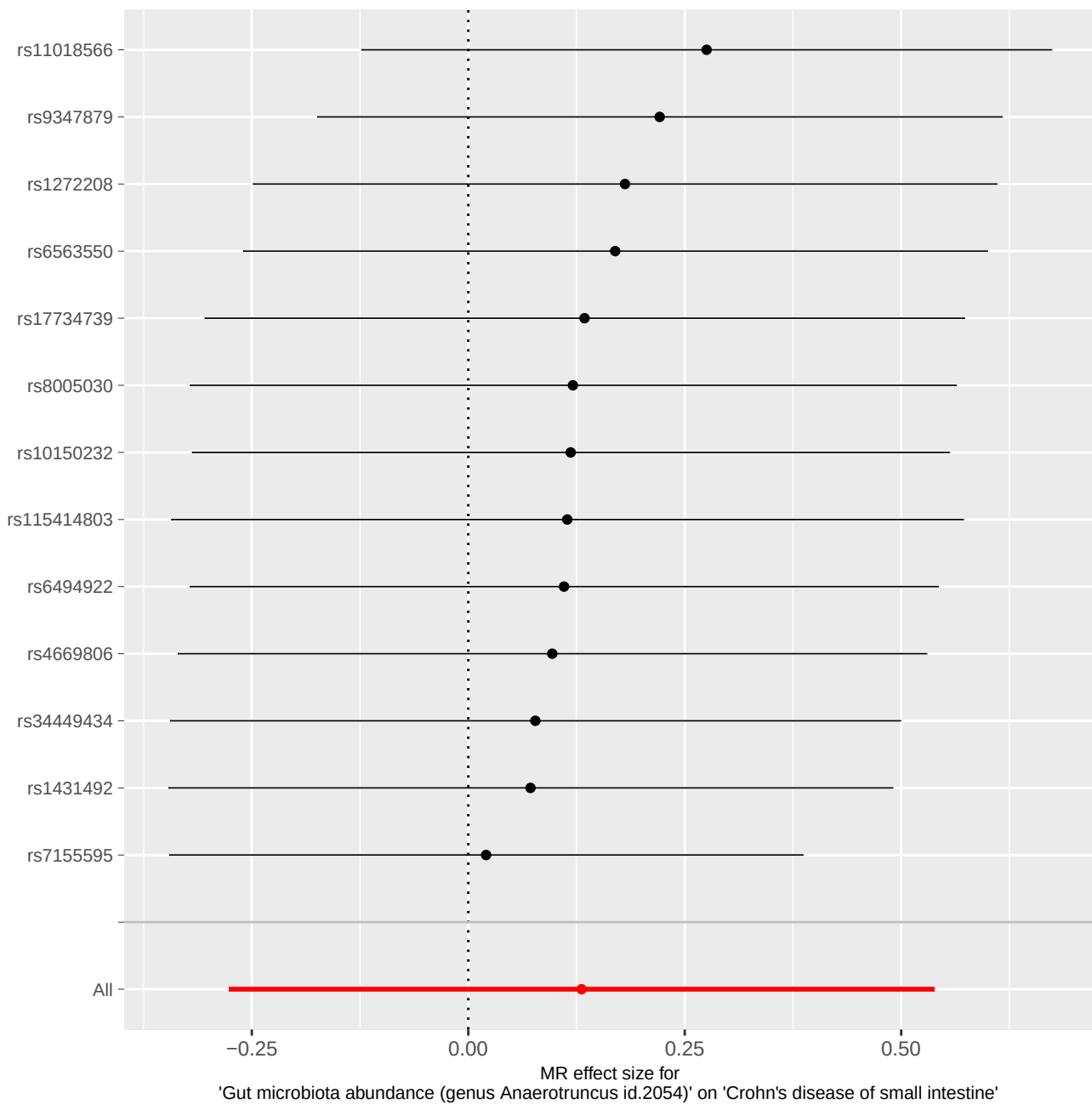
Batch 338 : Gut microbiota abundance (genus Alloprevotella id.961) on Crohn's disease of small intestine

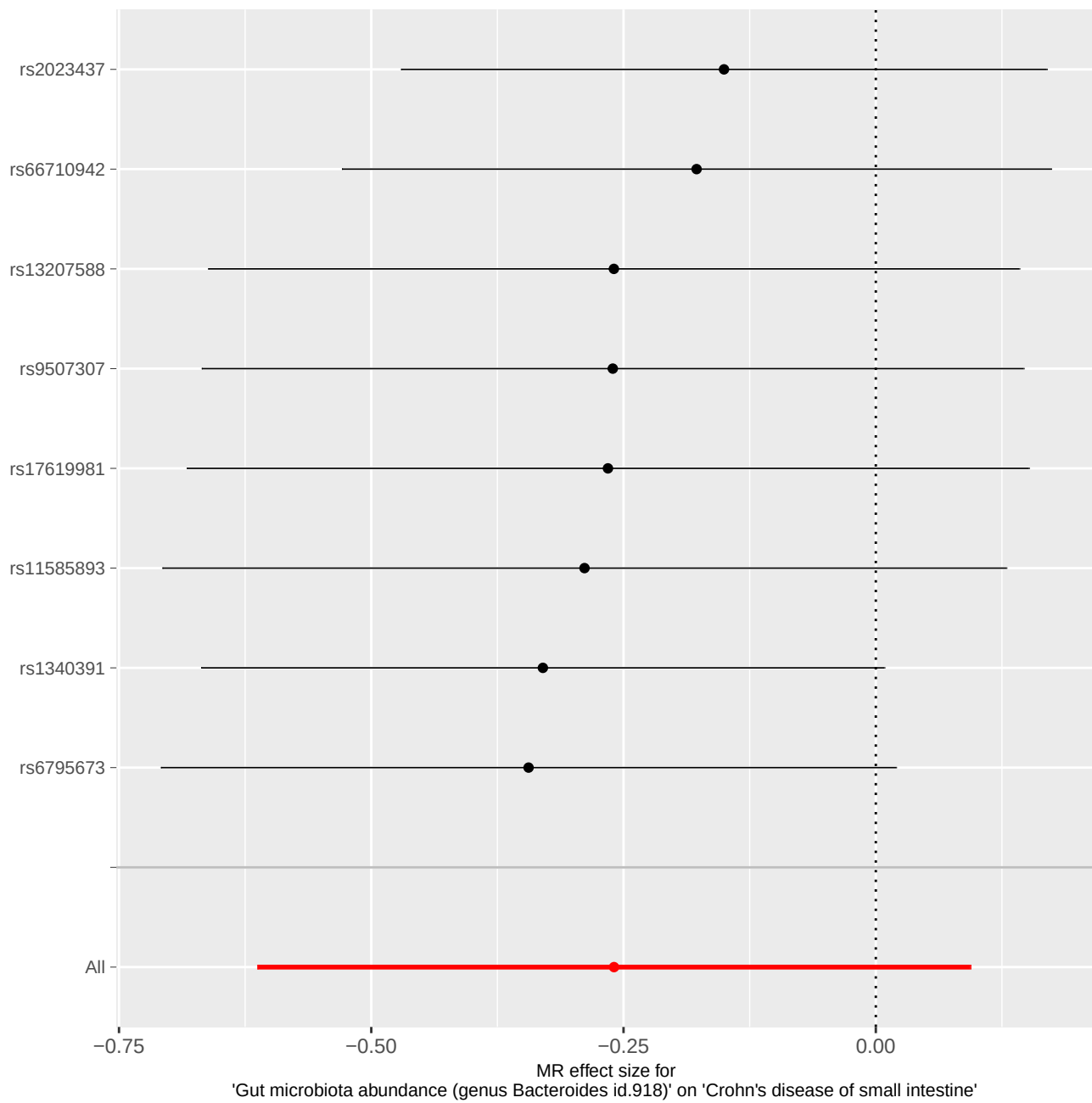


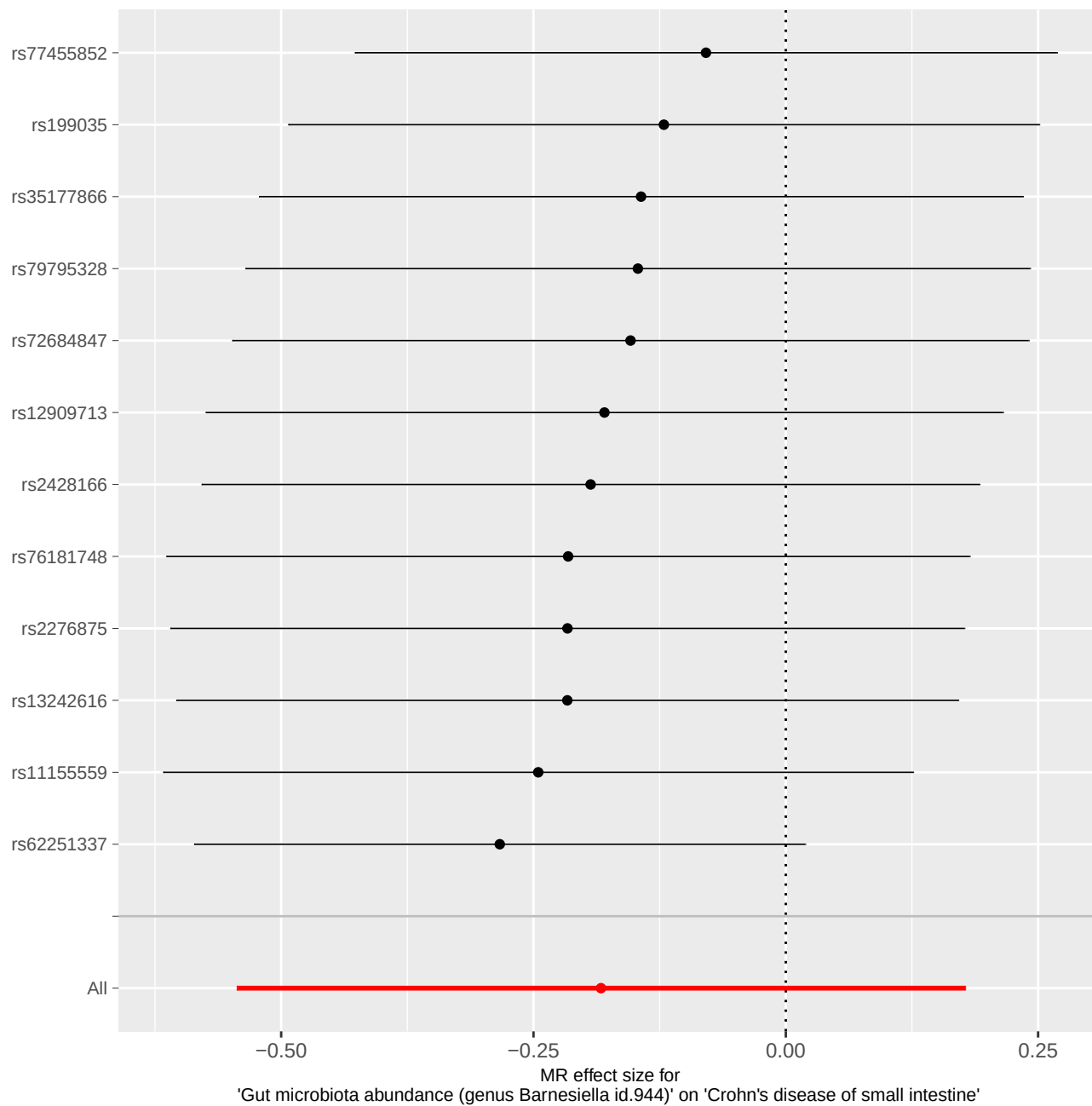
Batch 339 : Gut microbiota abundance (genus Anaerofilum id.2053) on Crohn's disease of small intestine

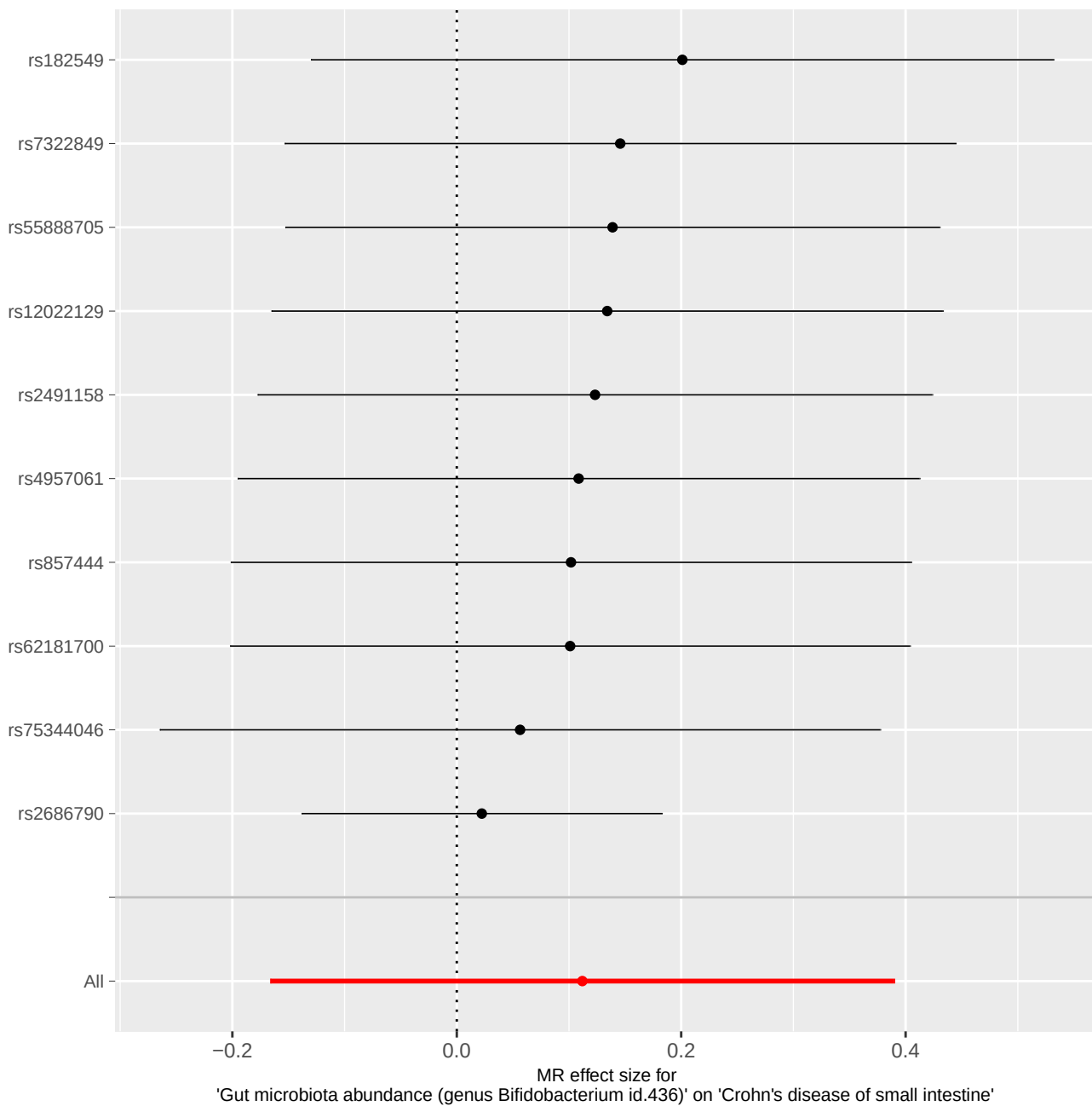




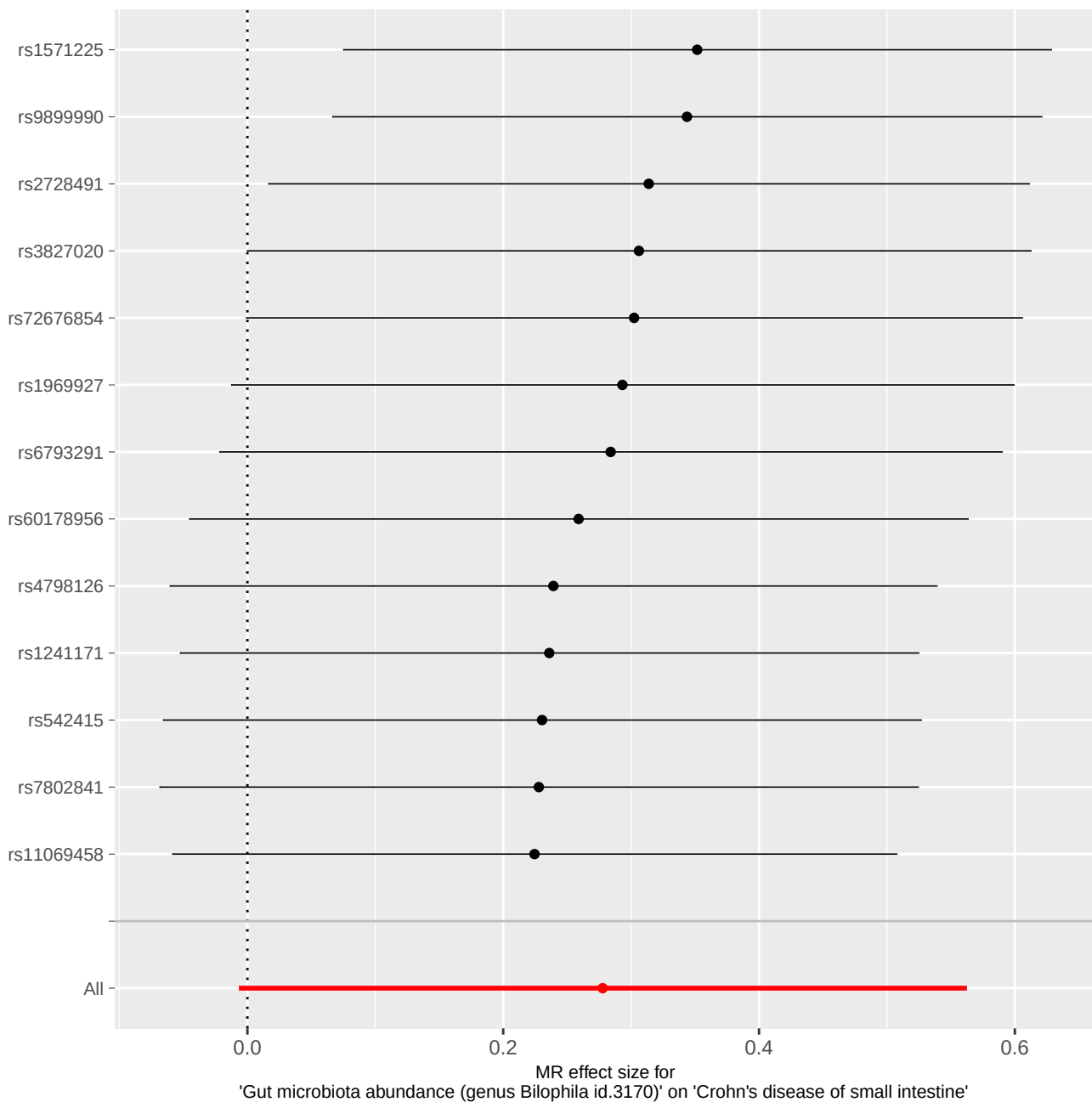


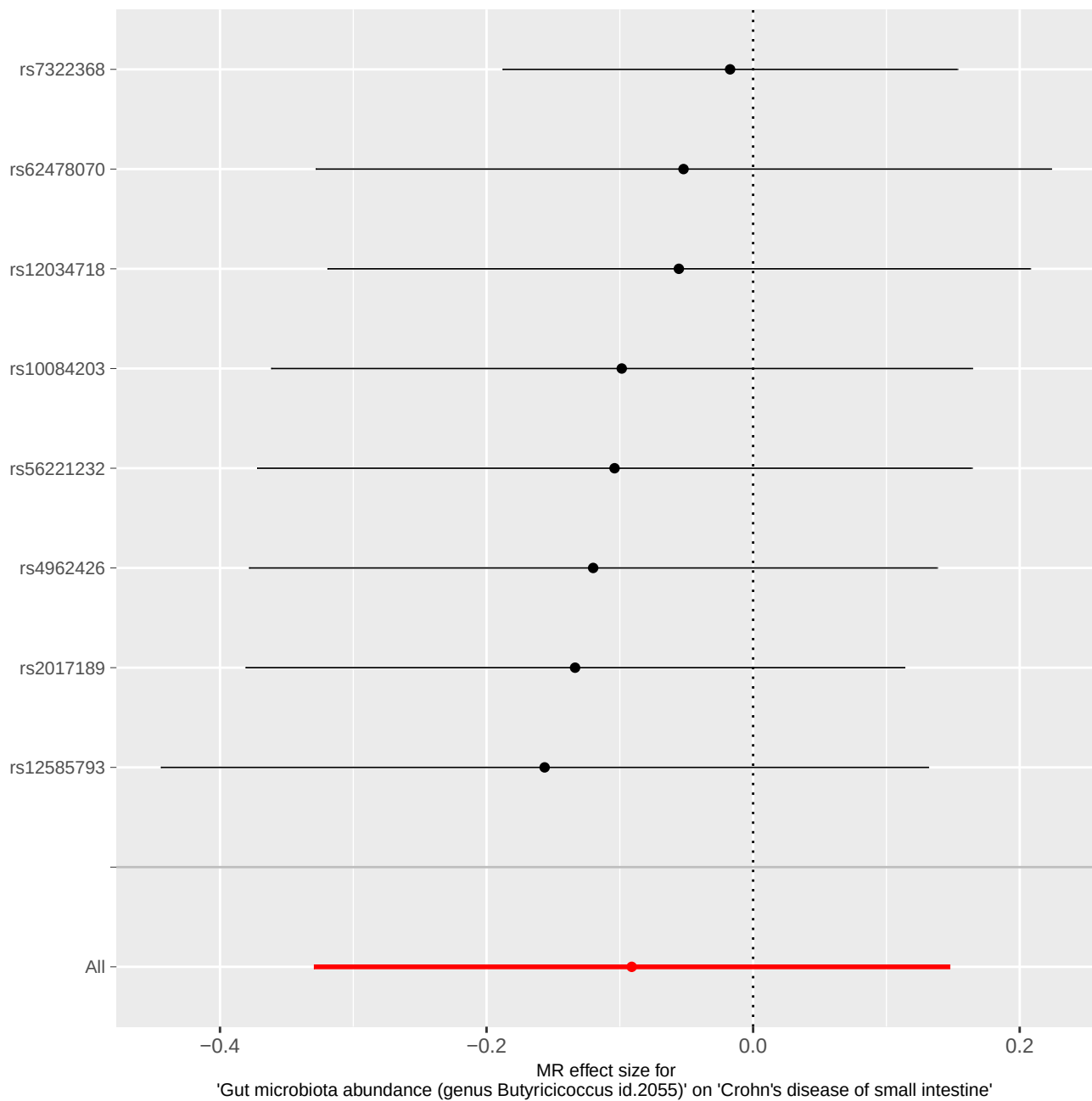




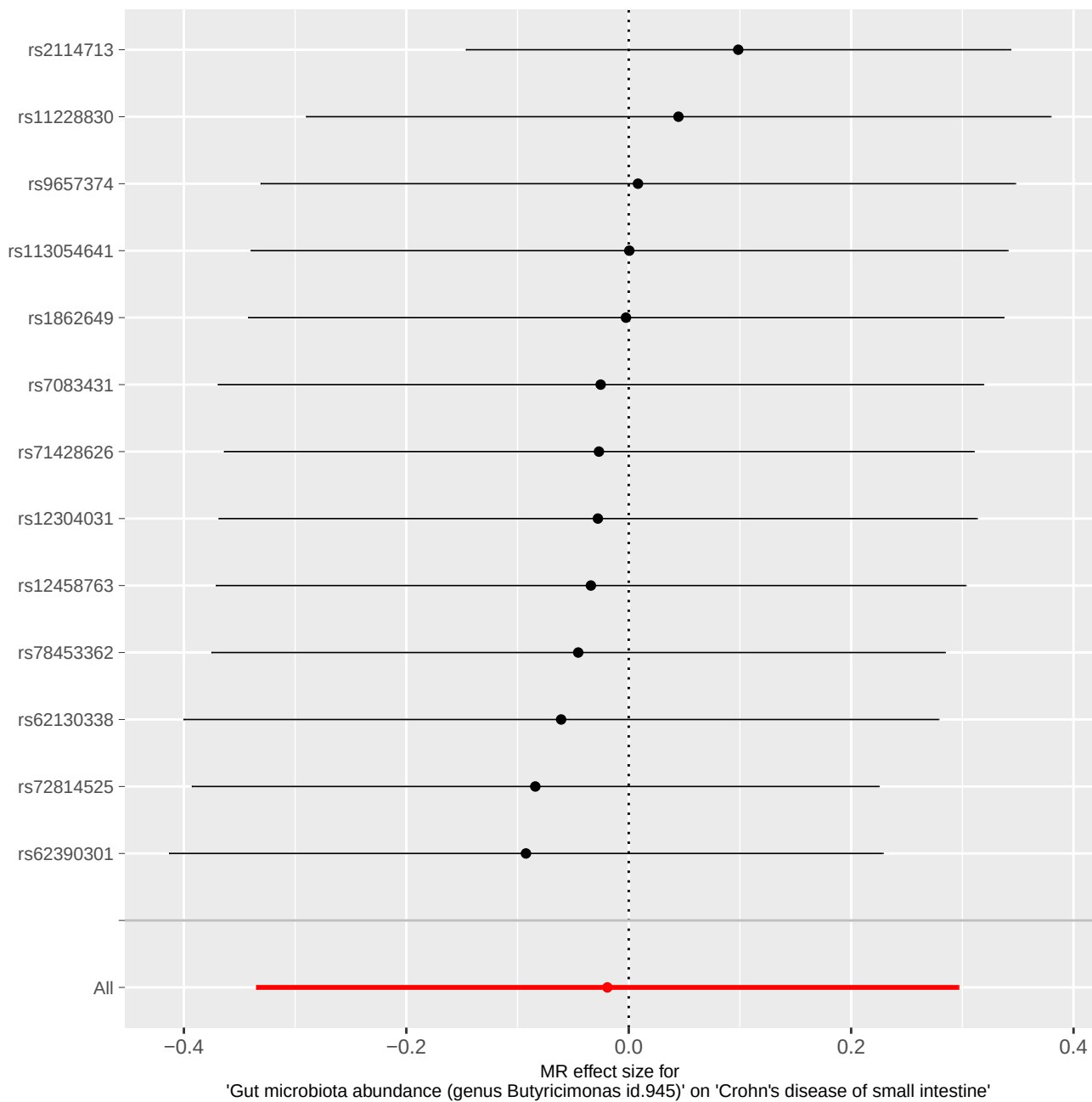


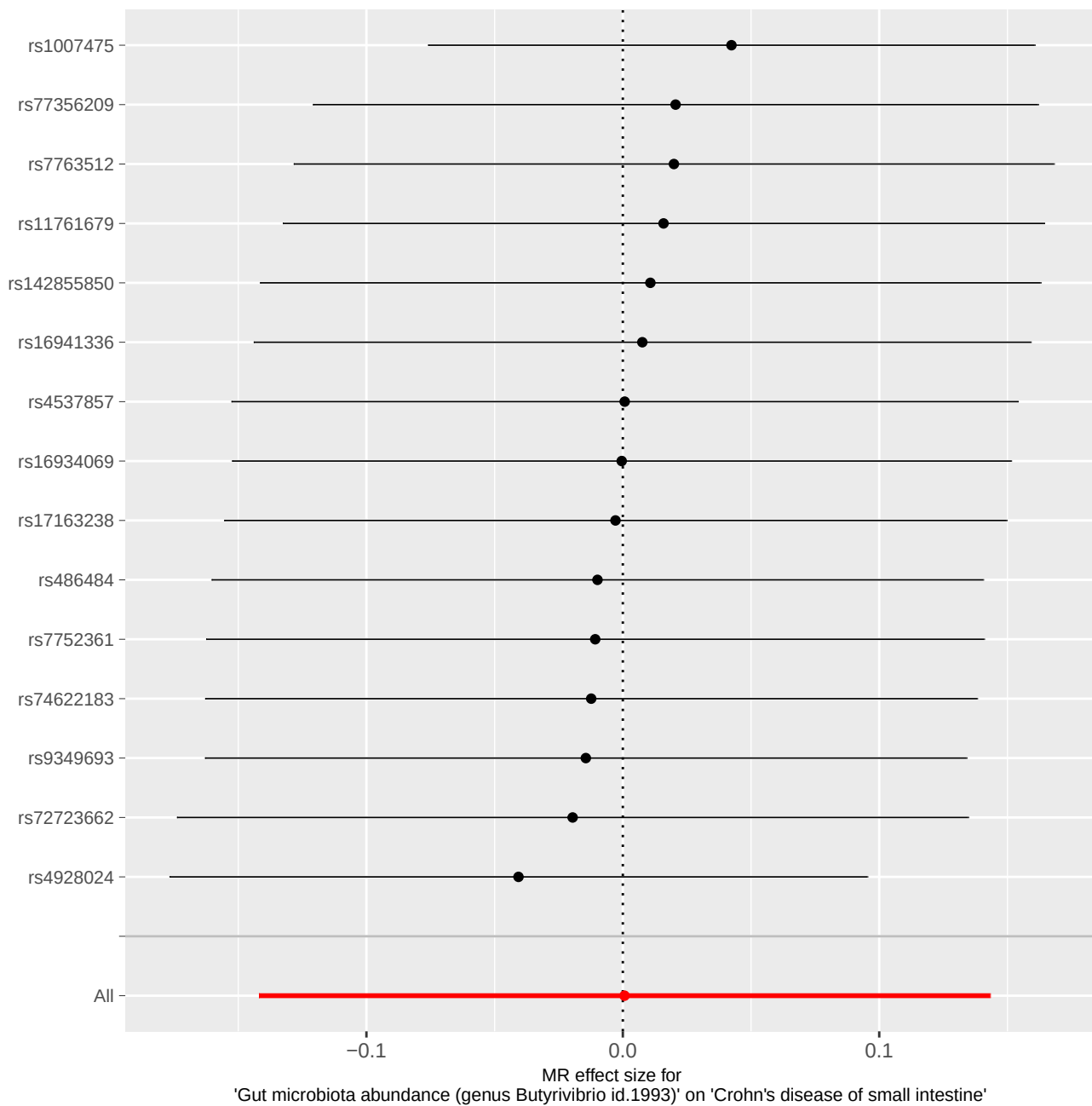
Batch 345 : Gut microbiota abundance (genus Bilophila id.3170) on Crohn's disease of small intestine

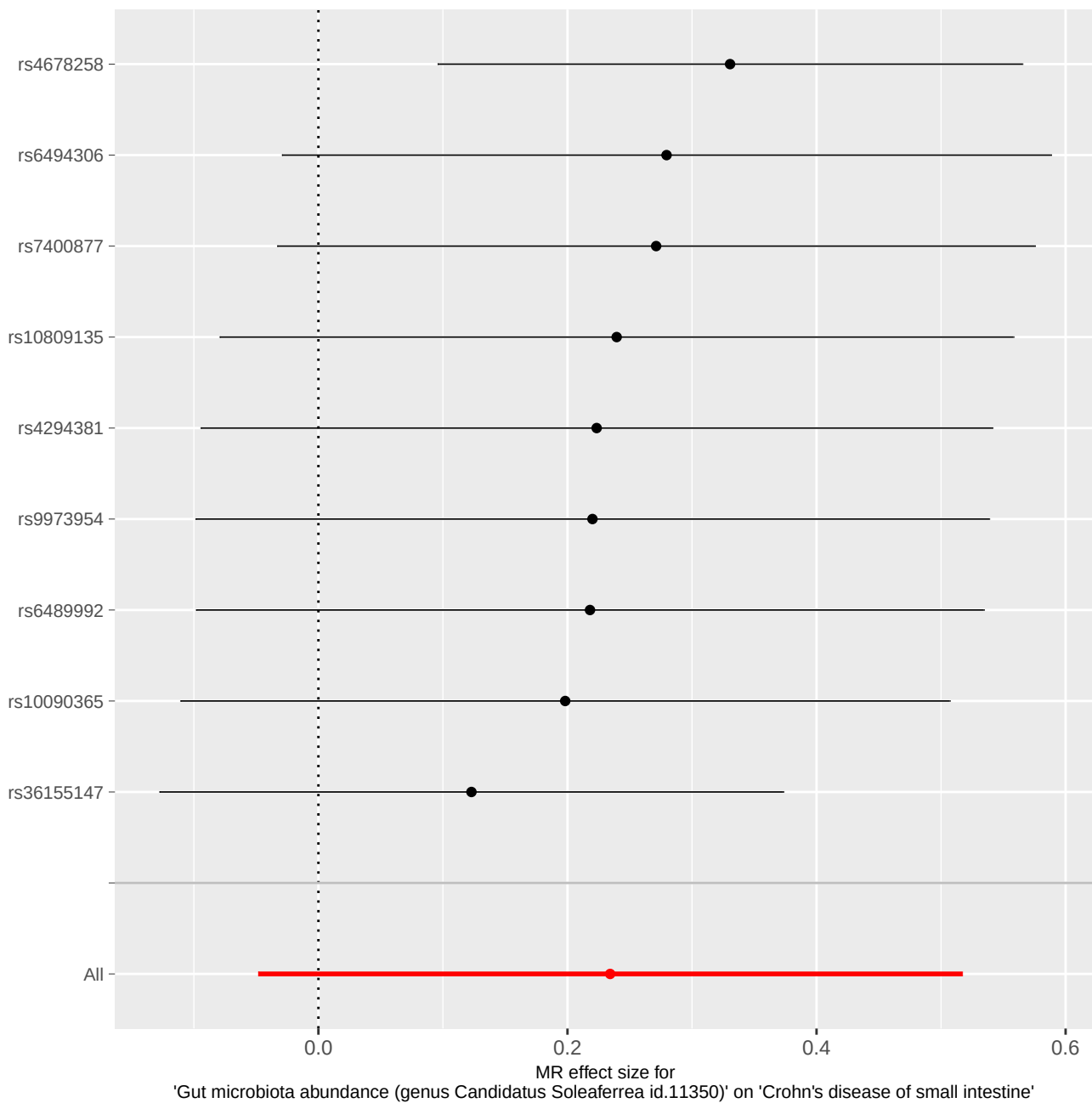


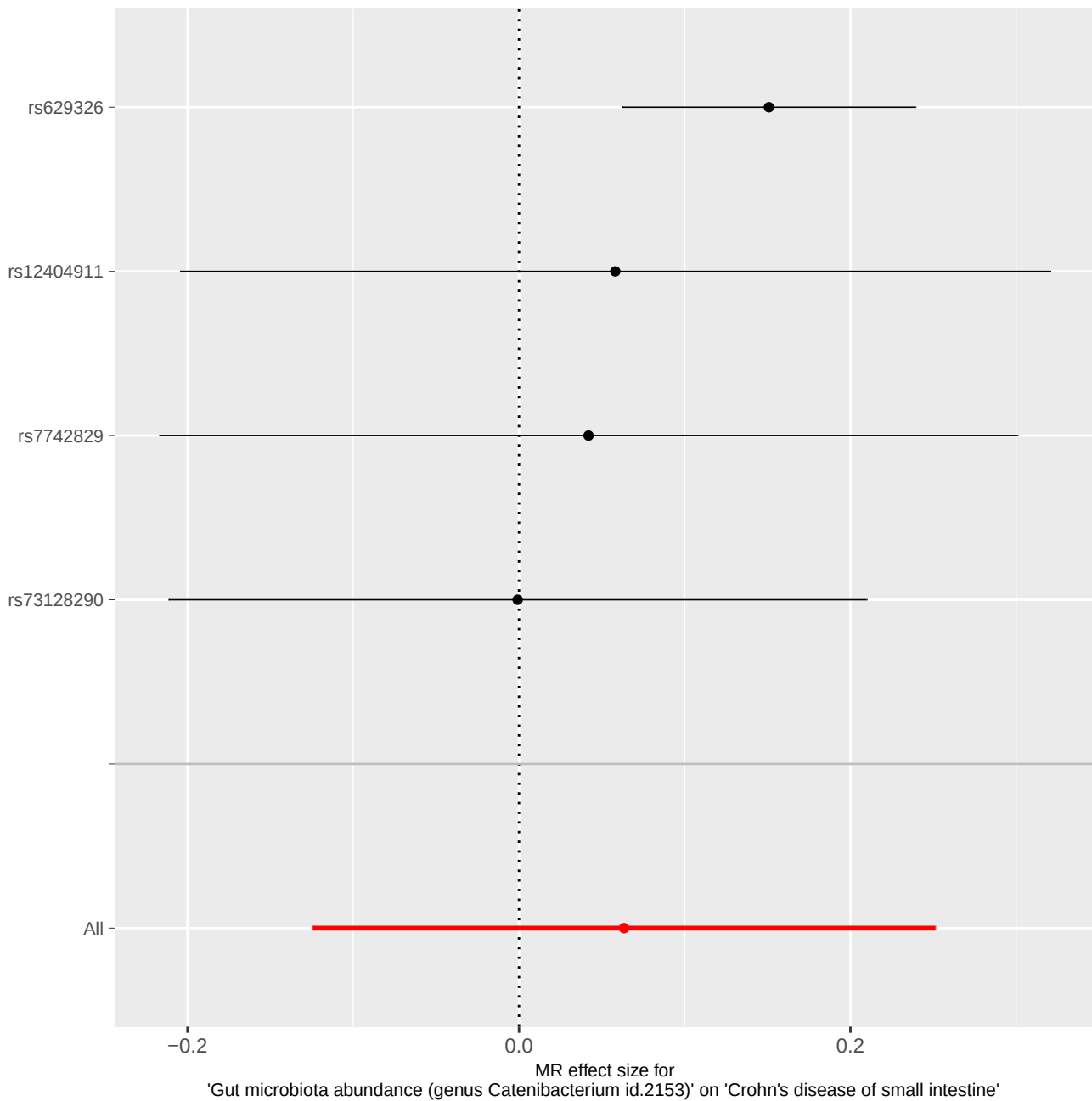


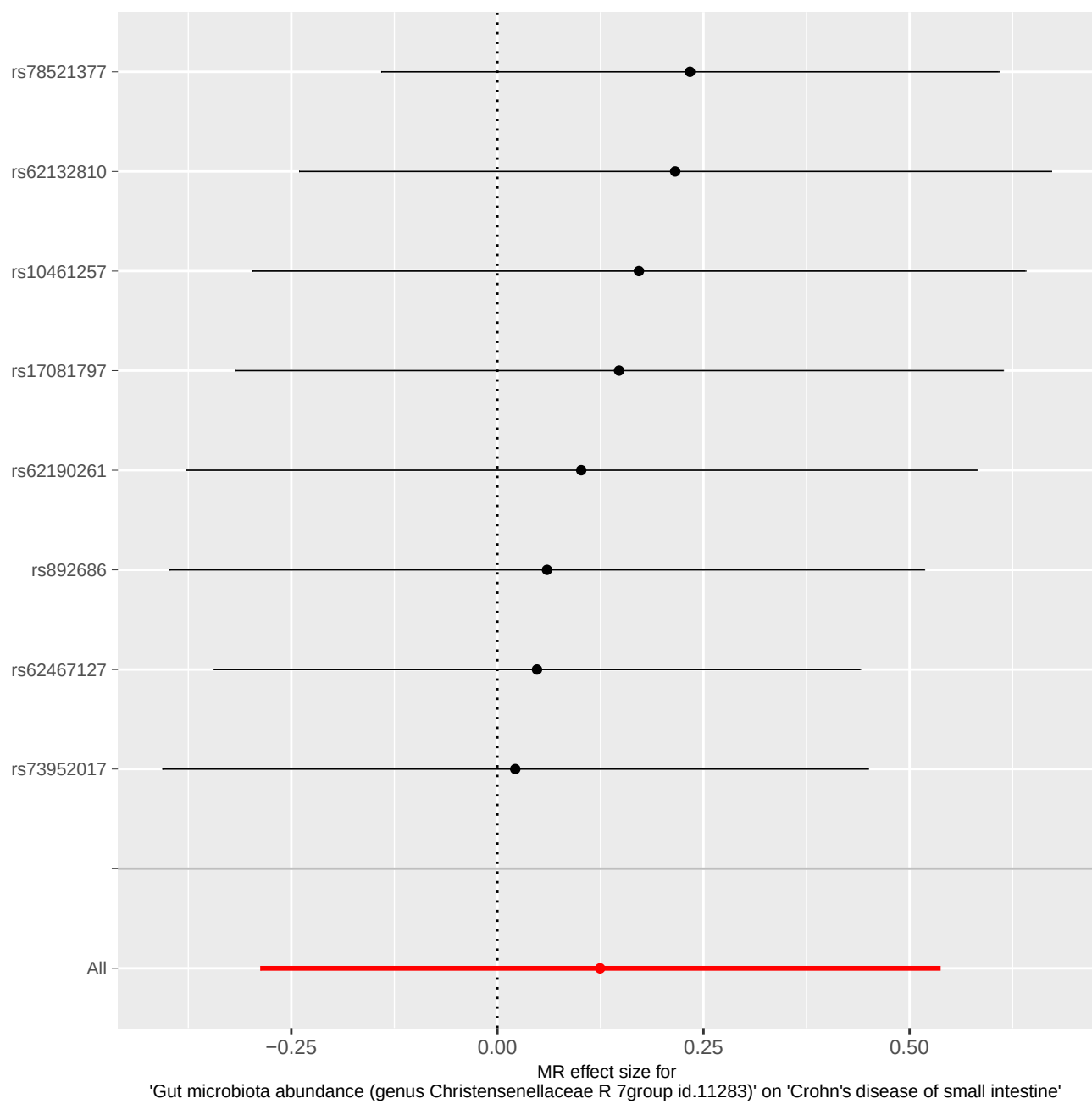
Batch 348 : Gut microbiota abundance (genus Butyricimonas id.945) on Crohn's disease of small intestine

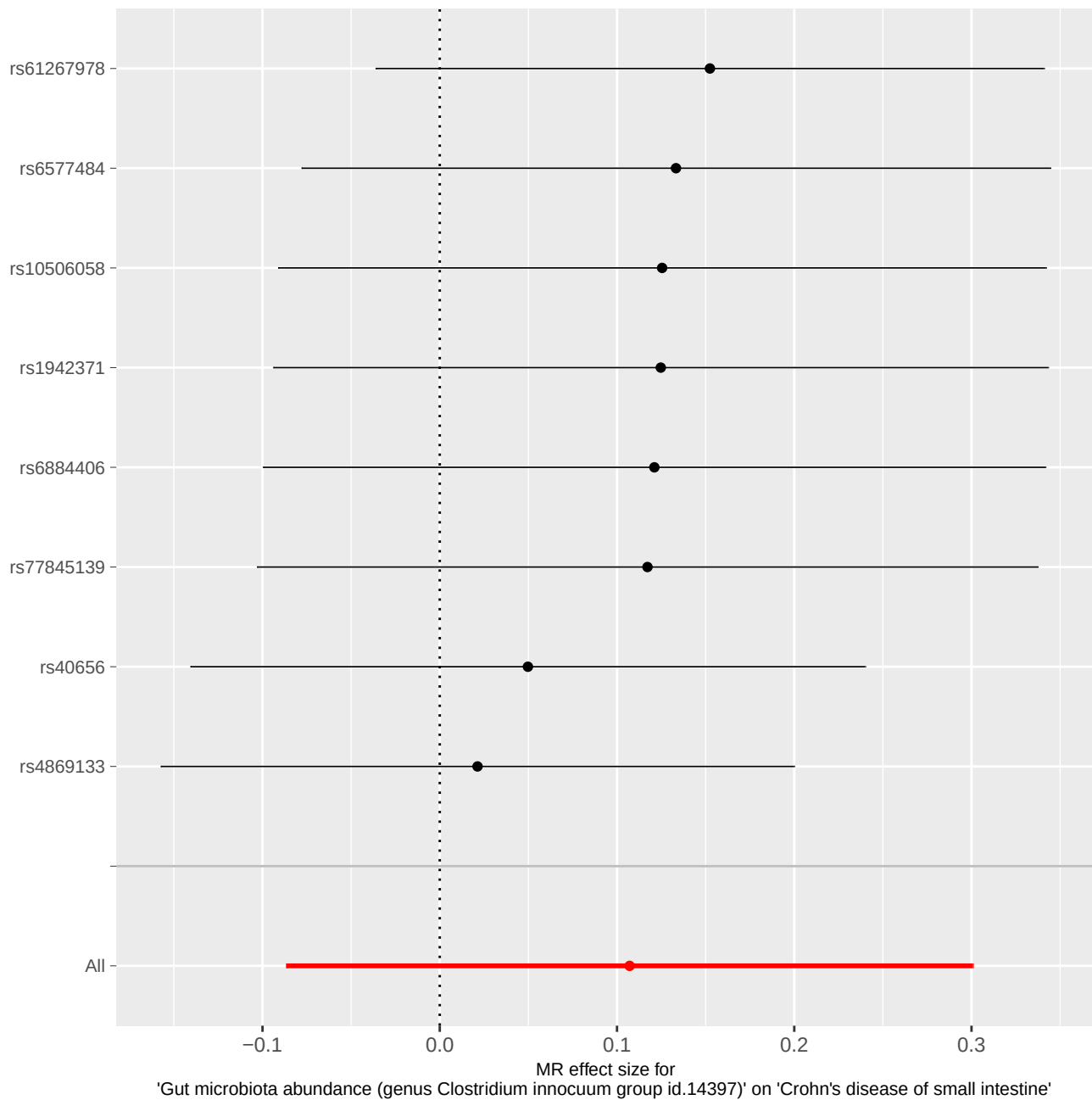


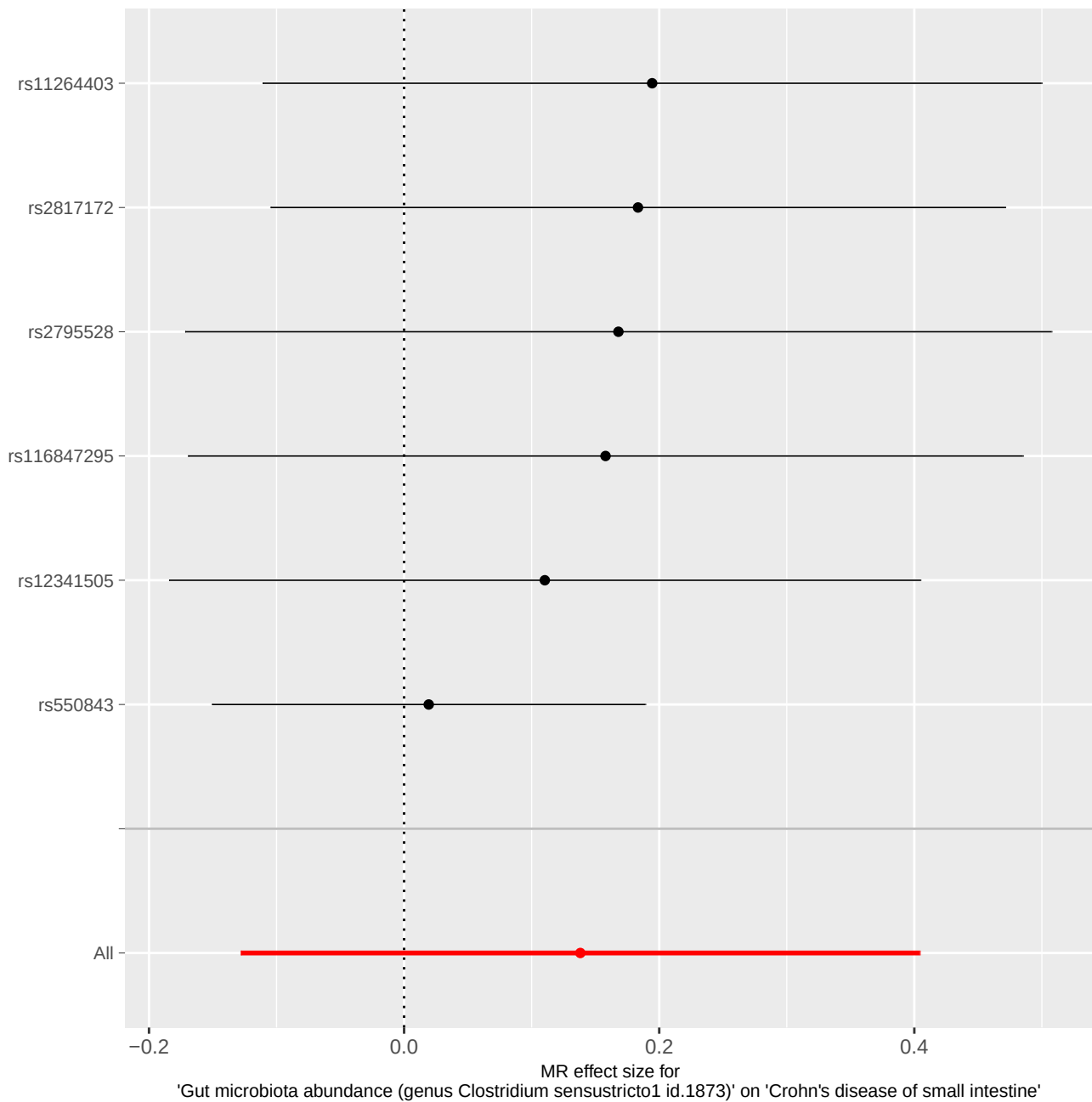


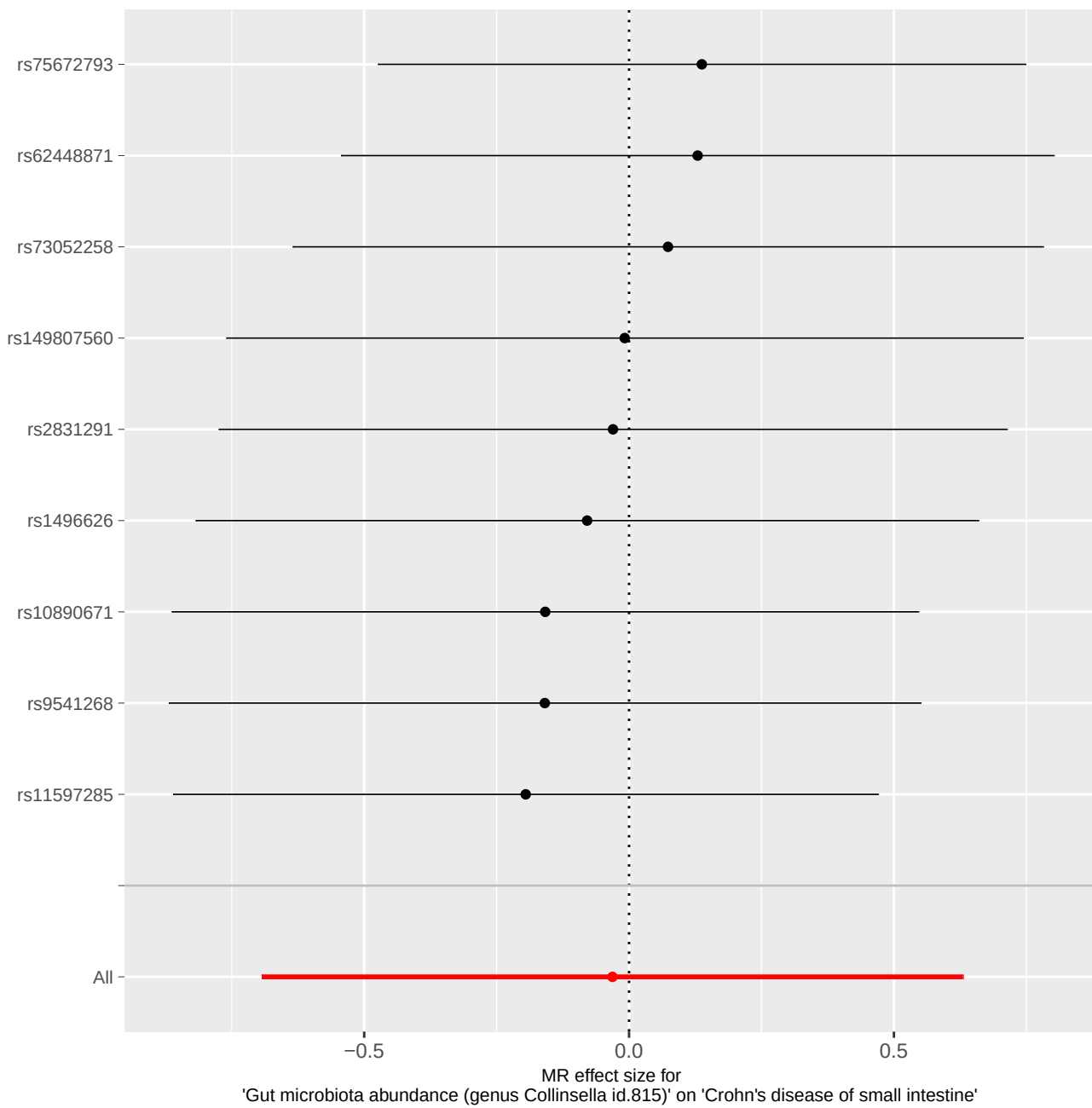


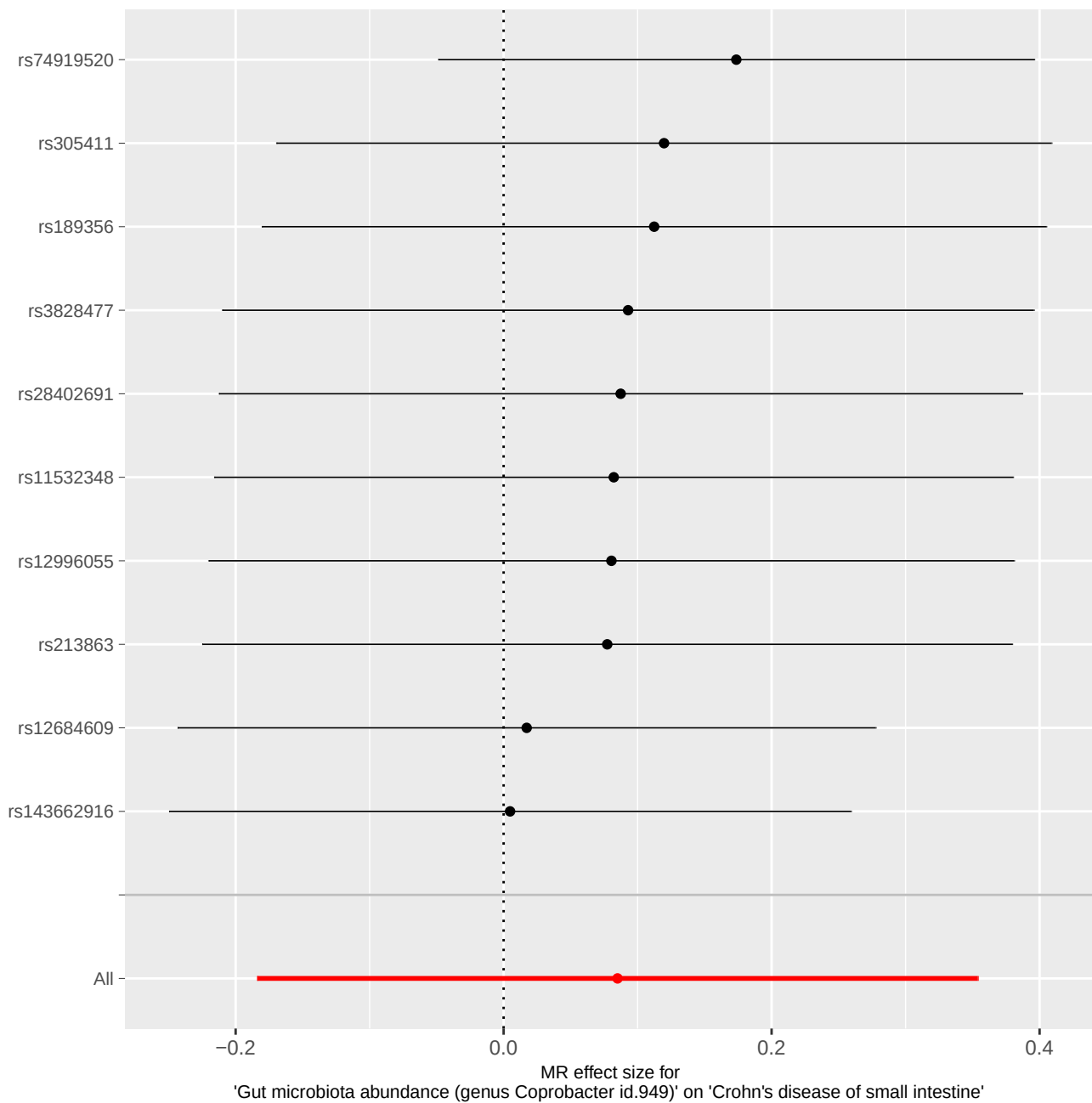


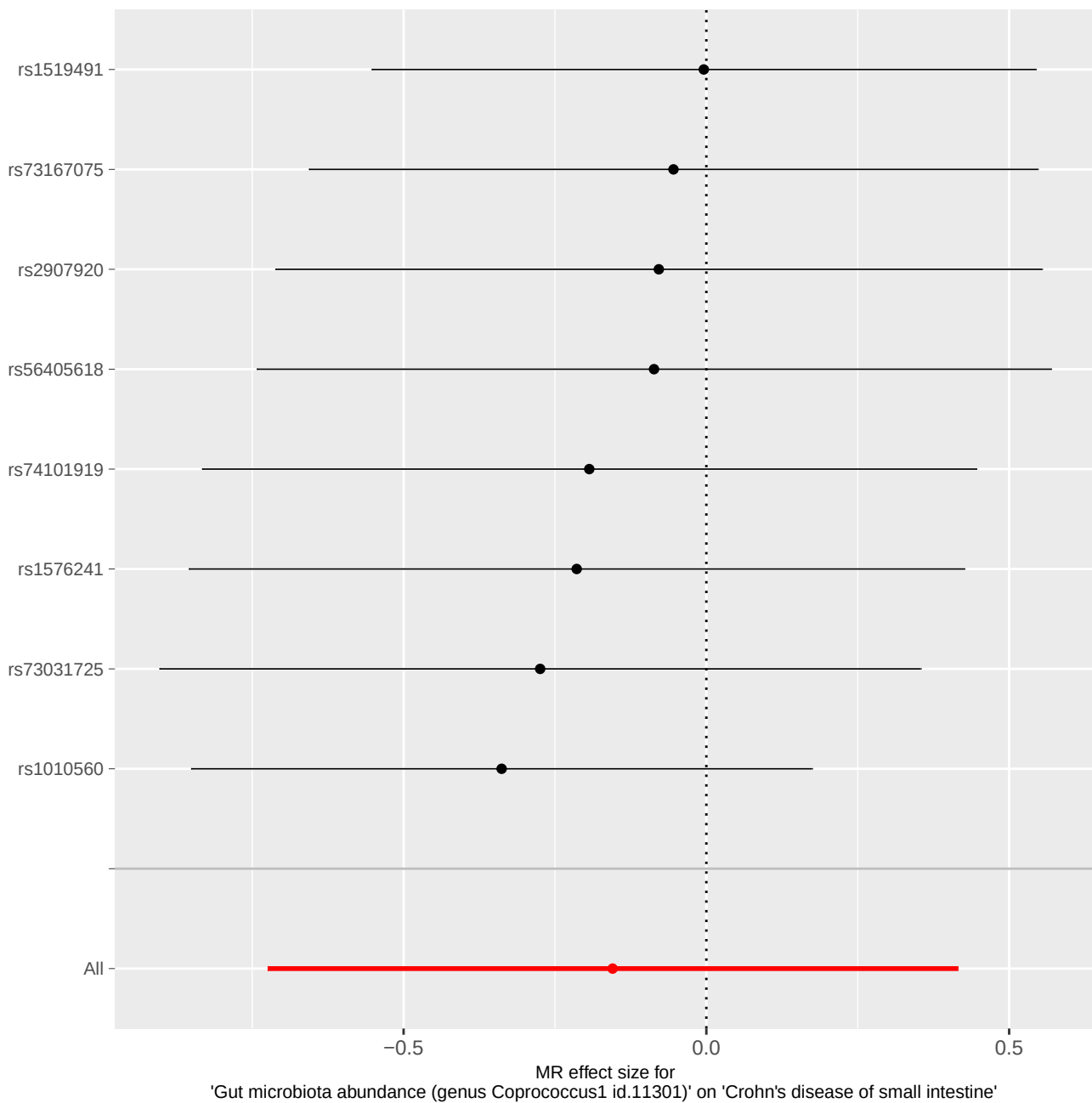




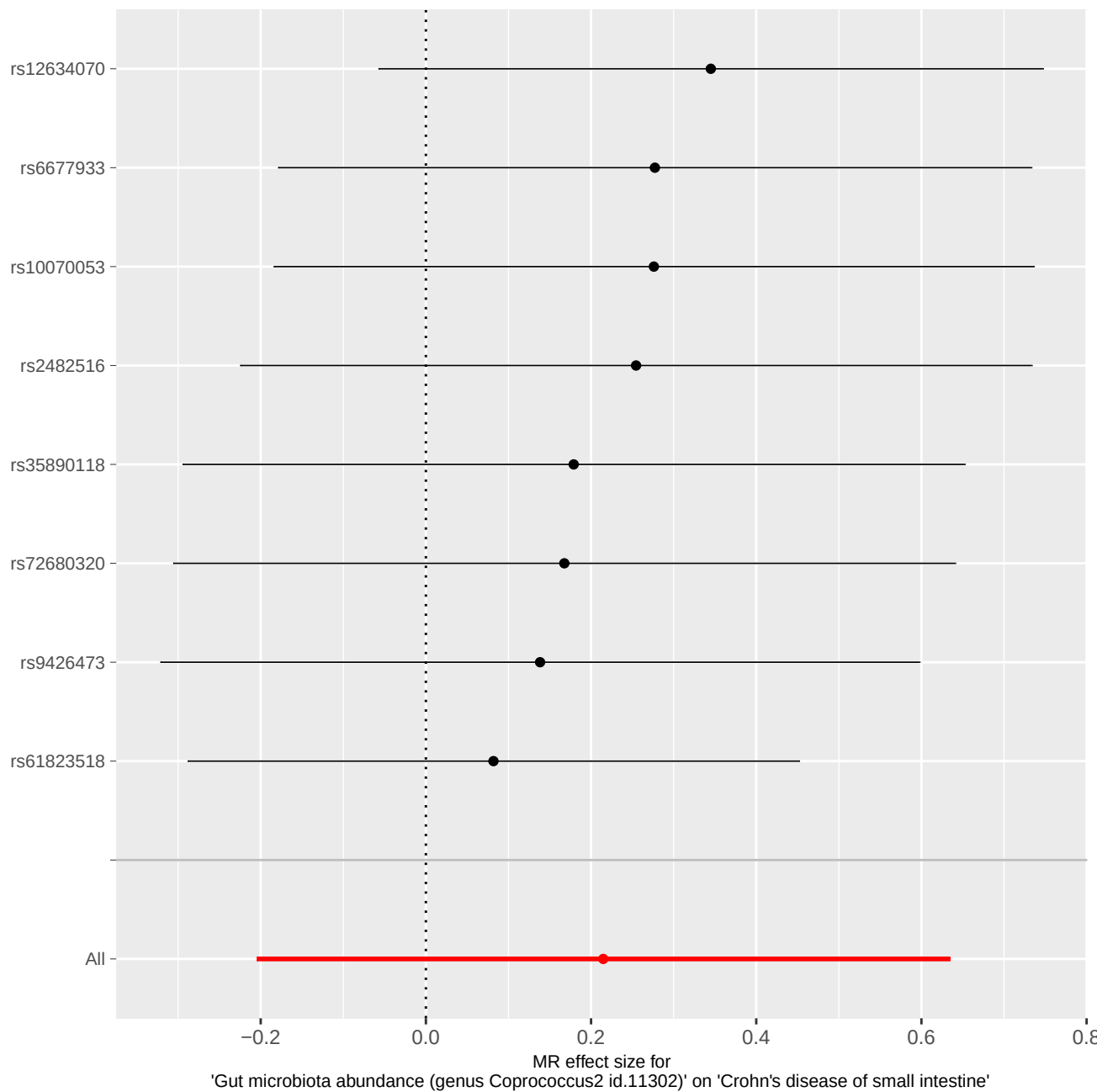




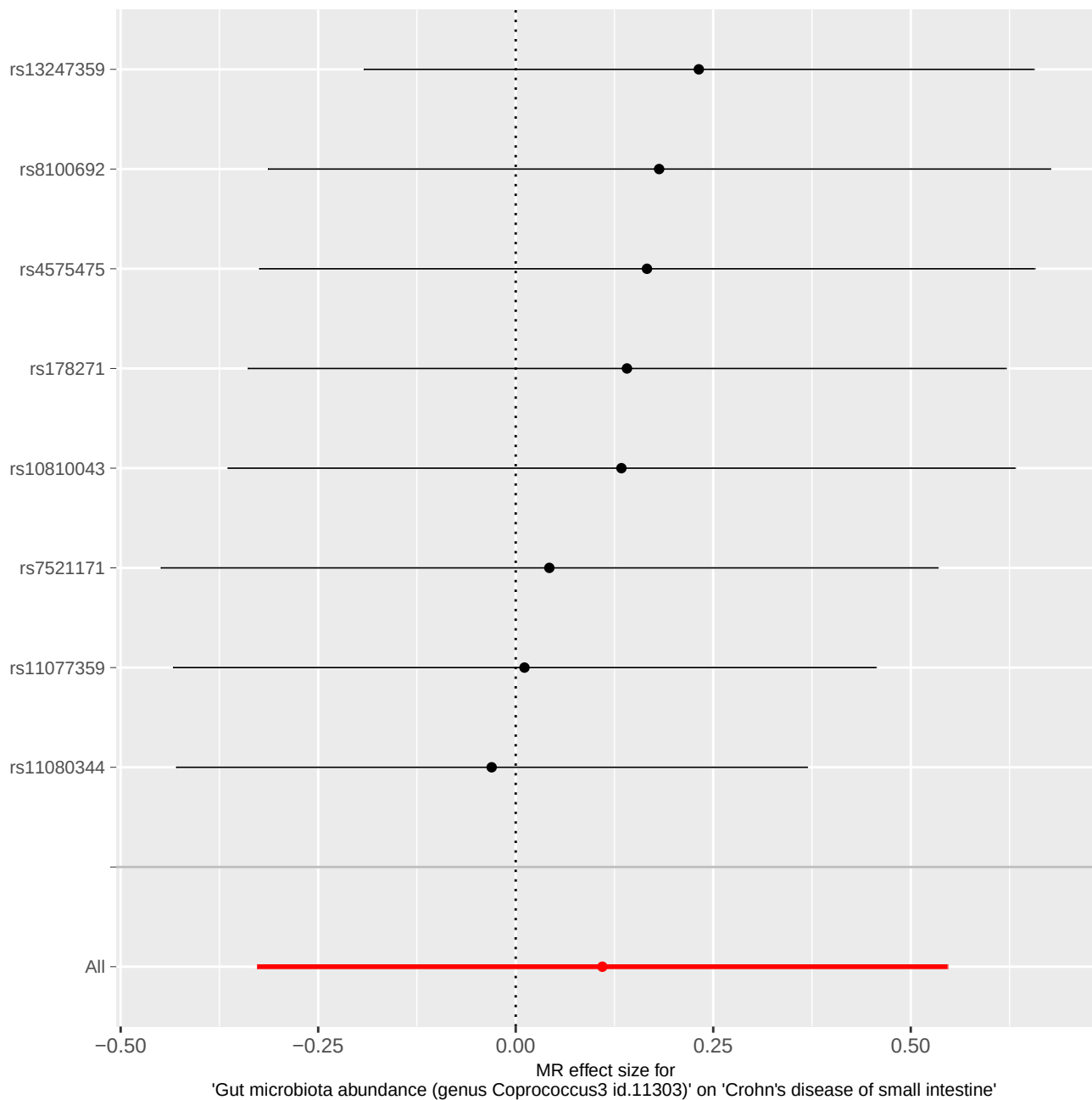


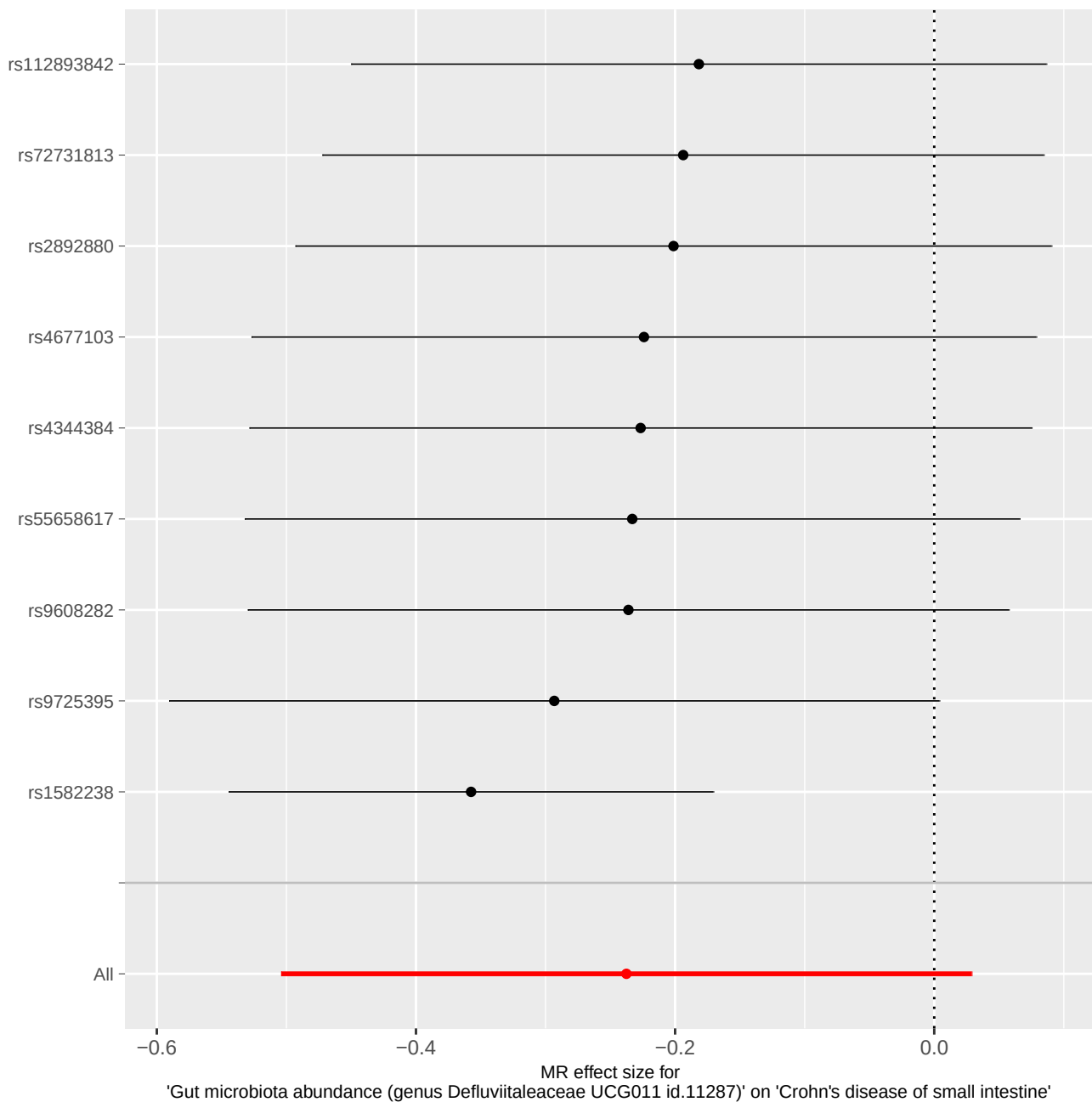


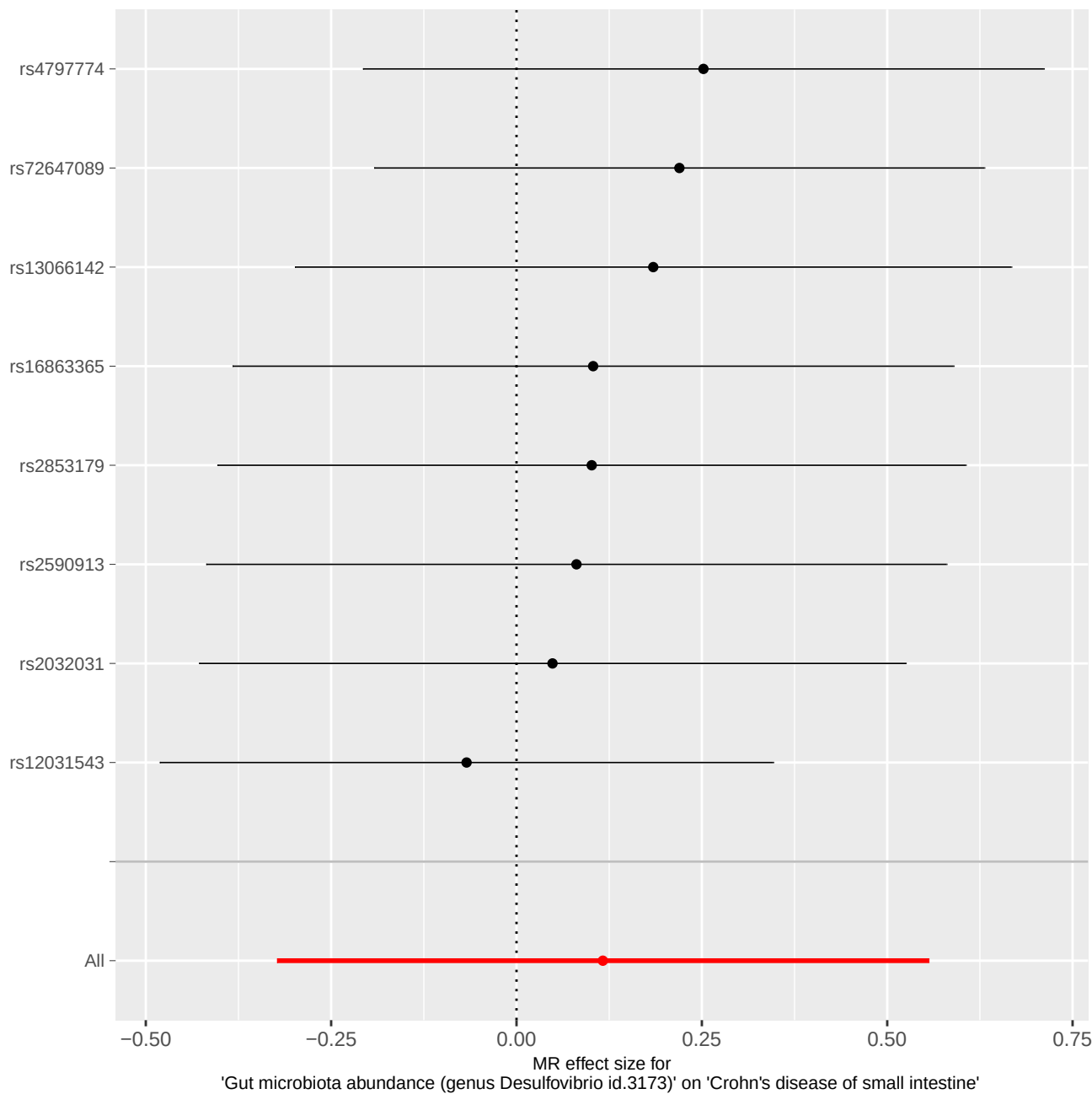
Batch 358 : Gut microbiota abundance (genus Coprococcus2 id.11302) on Crohn's disease of small intestine

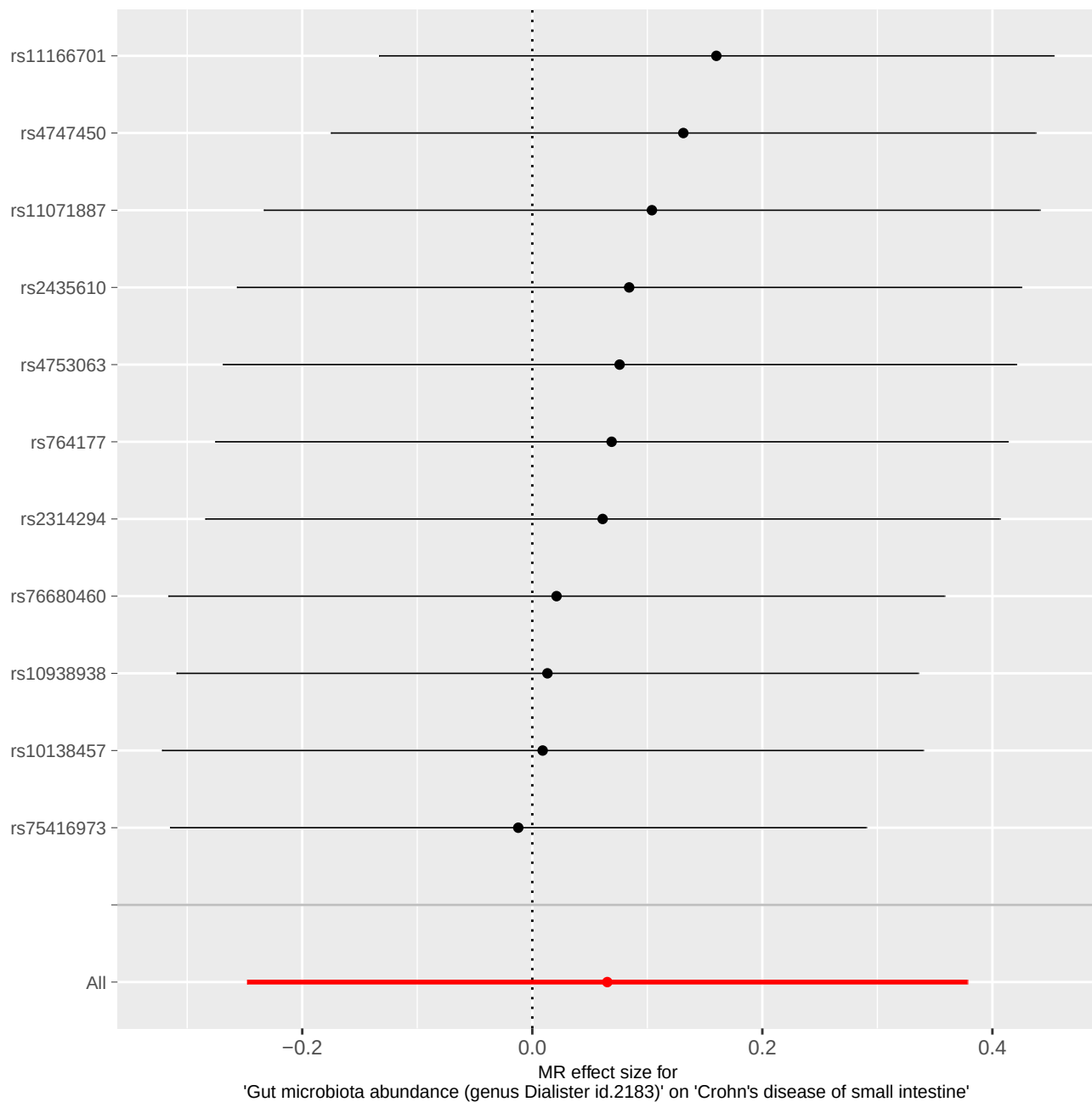


Batch 359 : Gut microbiota abundance (genus Coprococcus3 id.11303) on Crohn's disease of small intestine

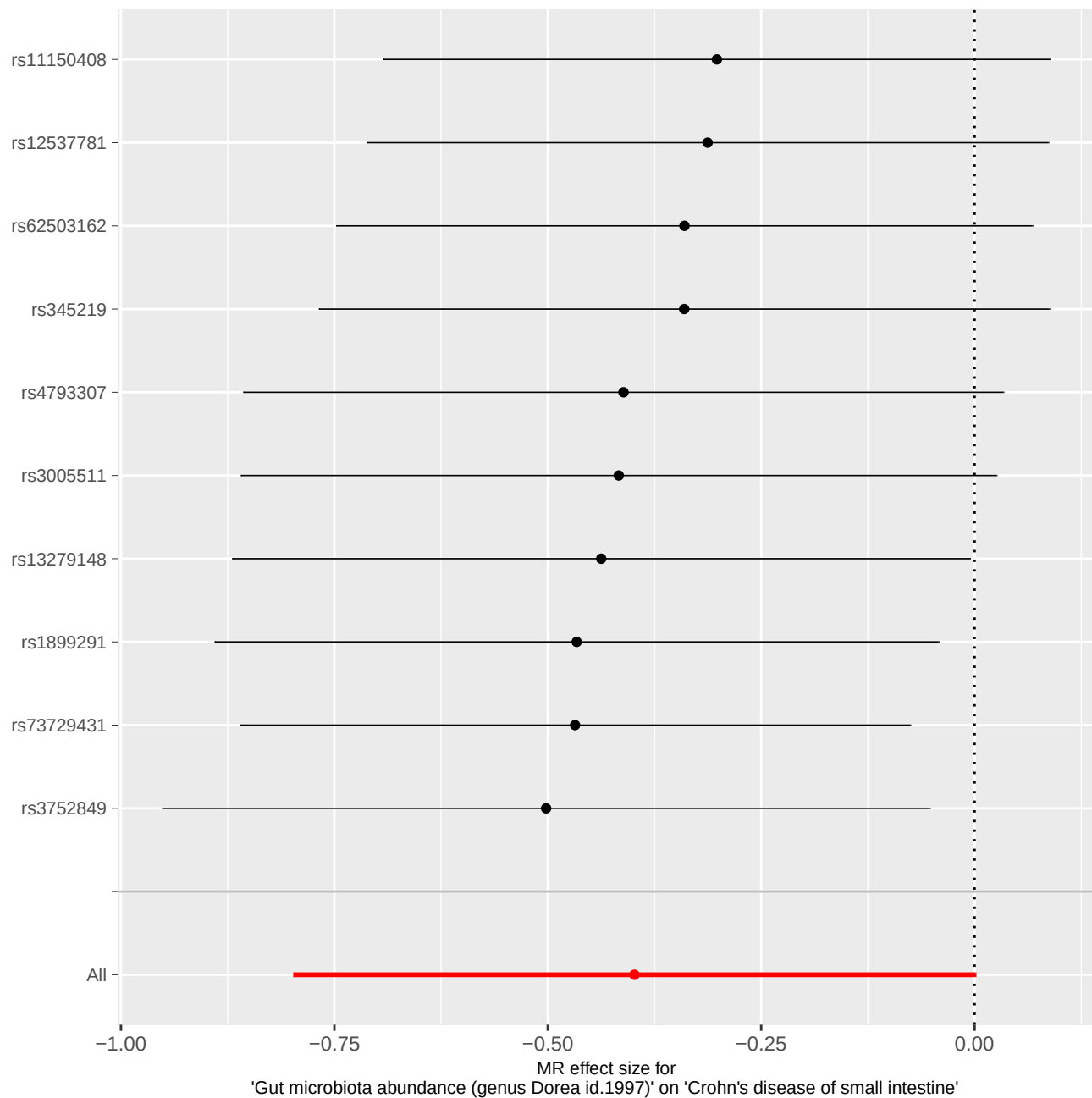


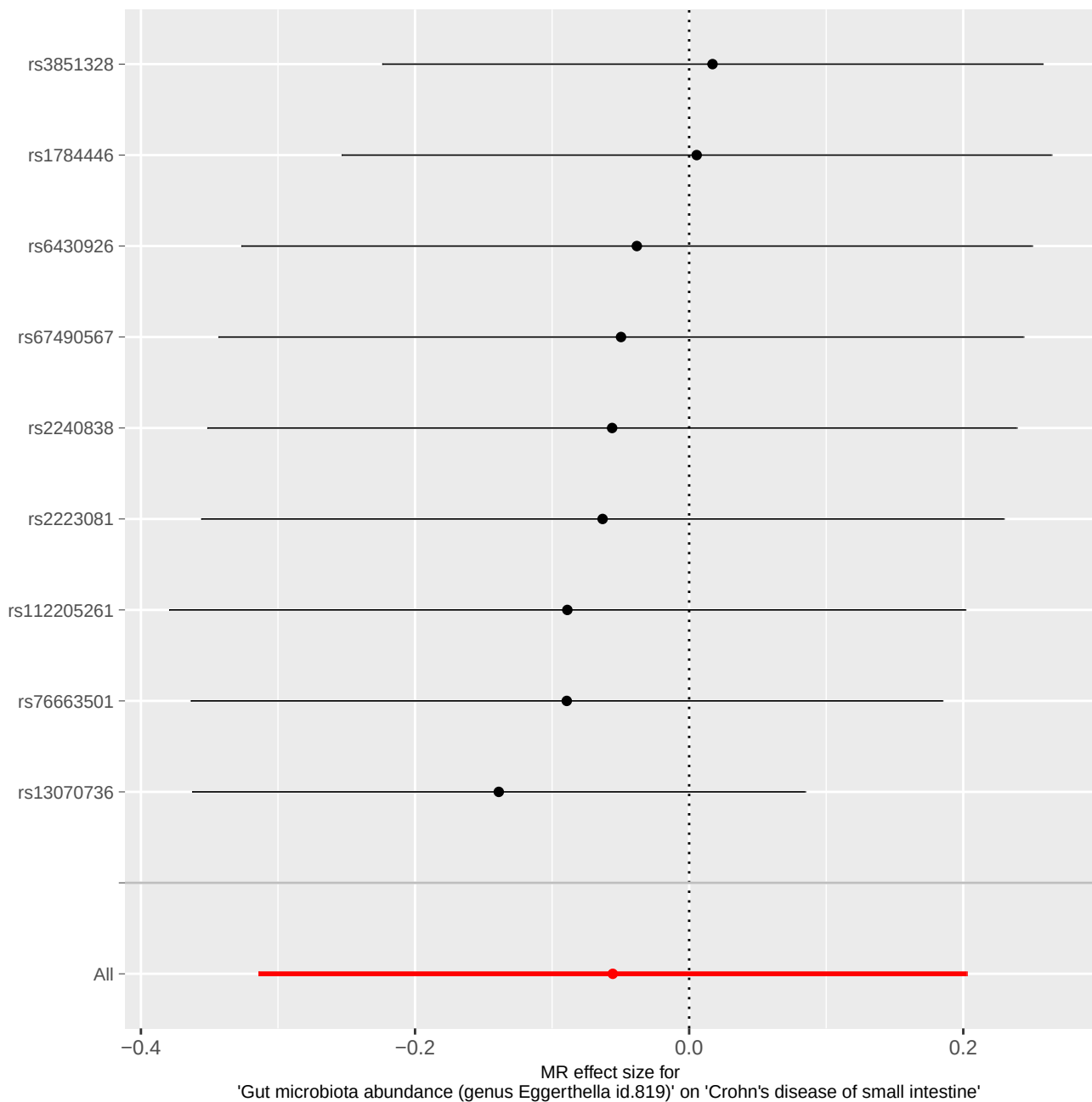


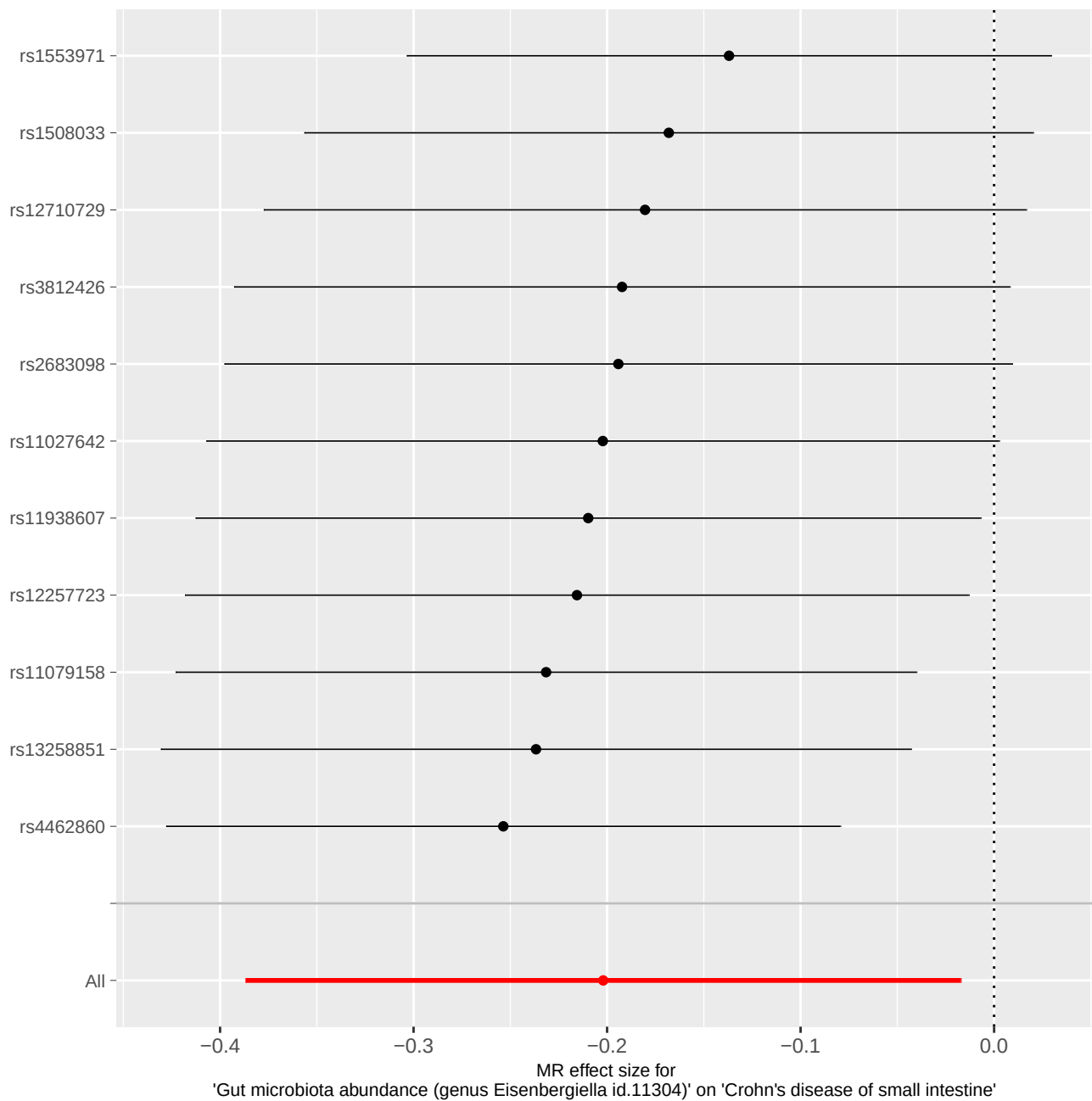


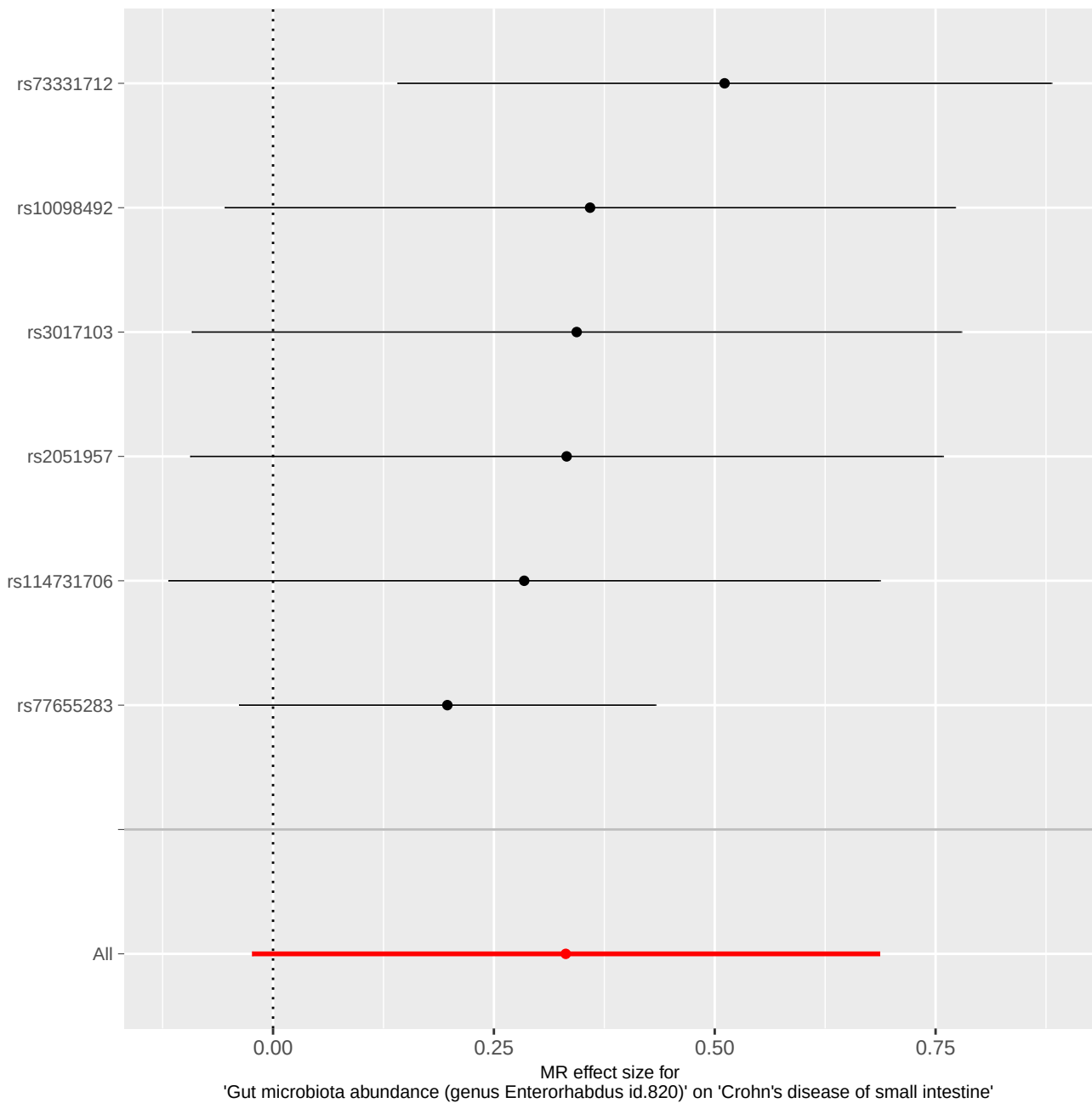


Batch 363 : Gut microbiota abundance (genus Dorea id.1997) on Crohn's disease of small intestine

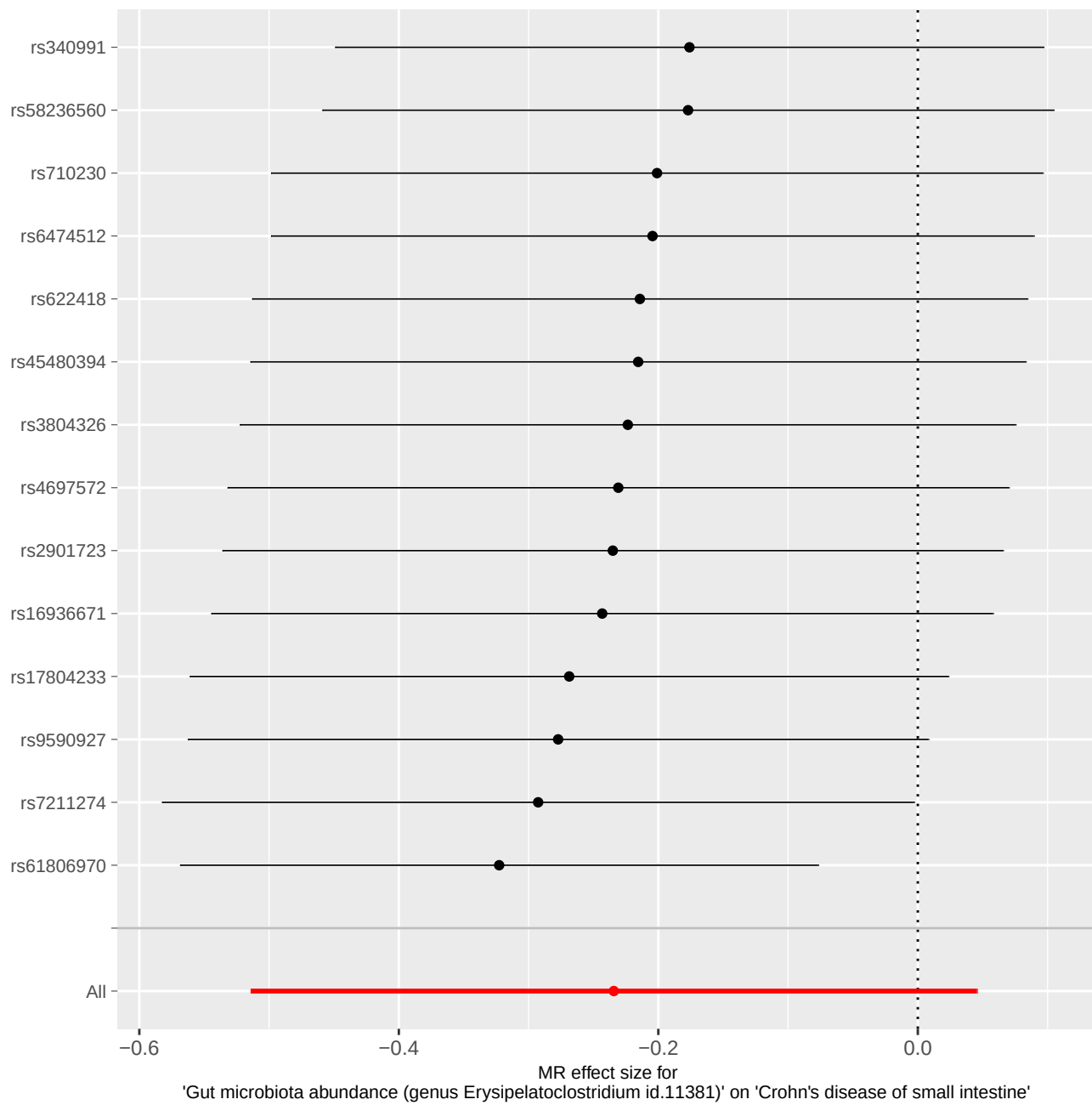


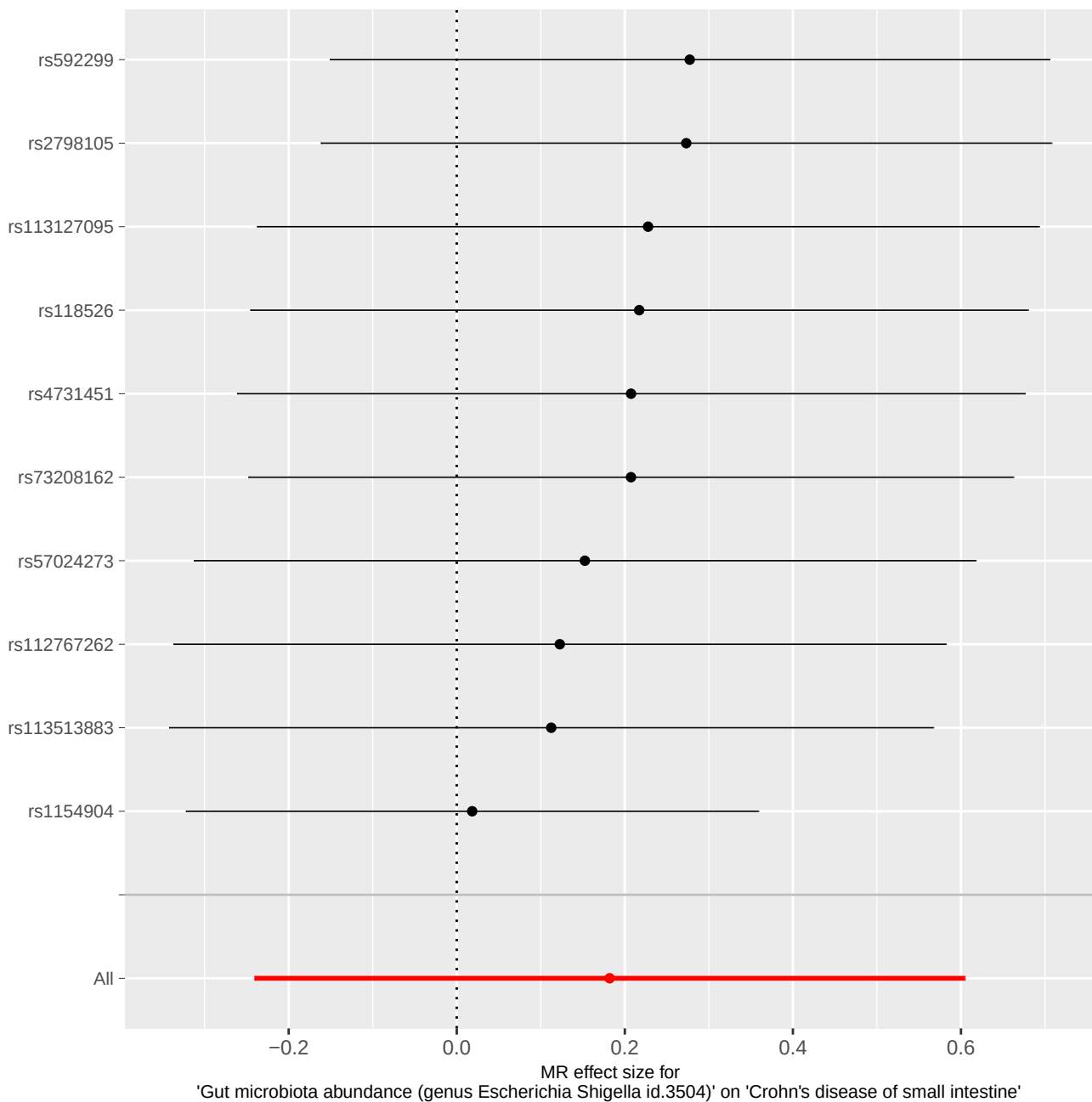


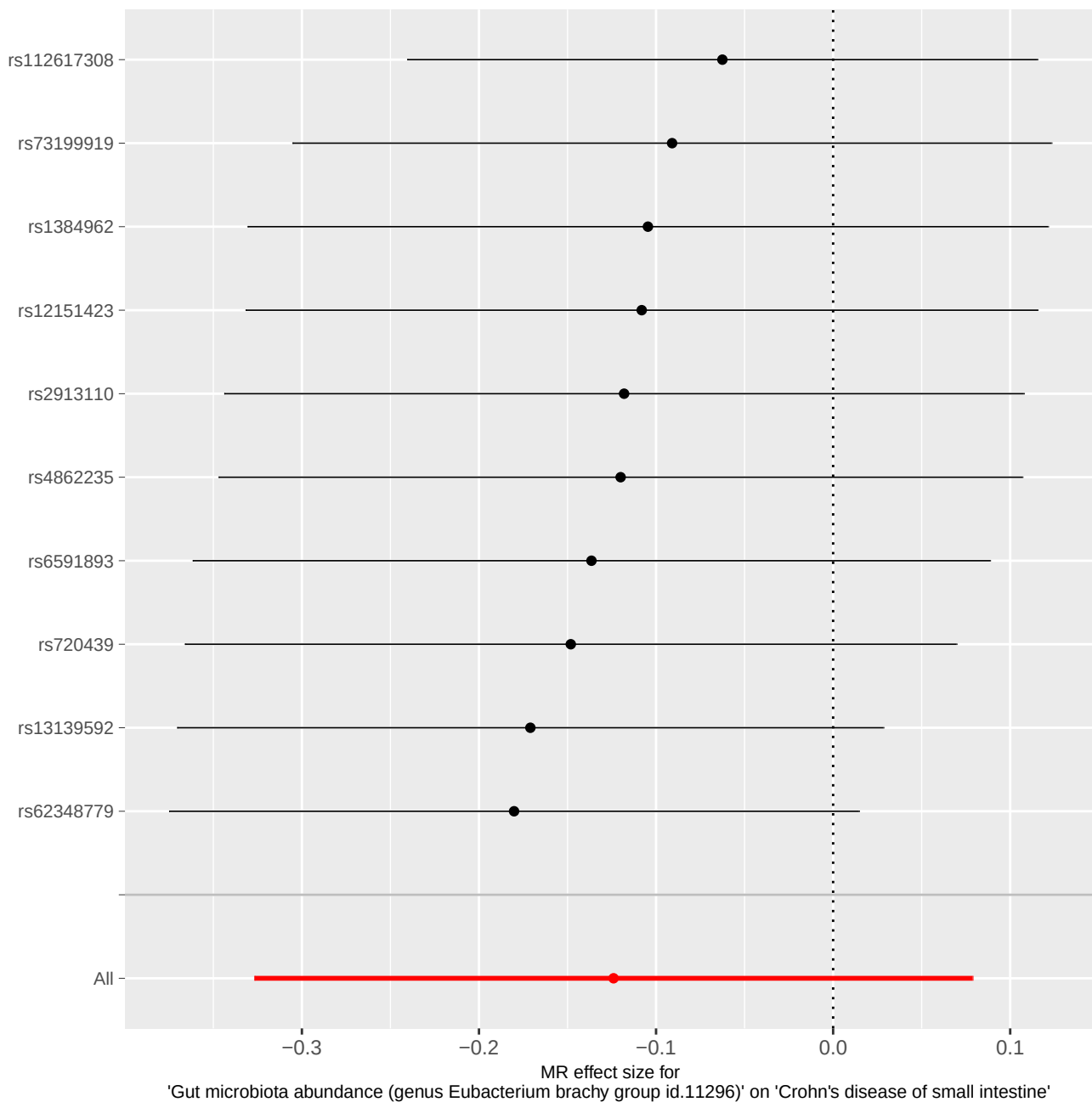


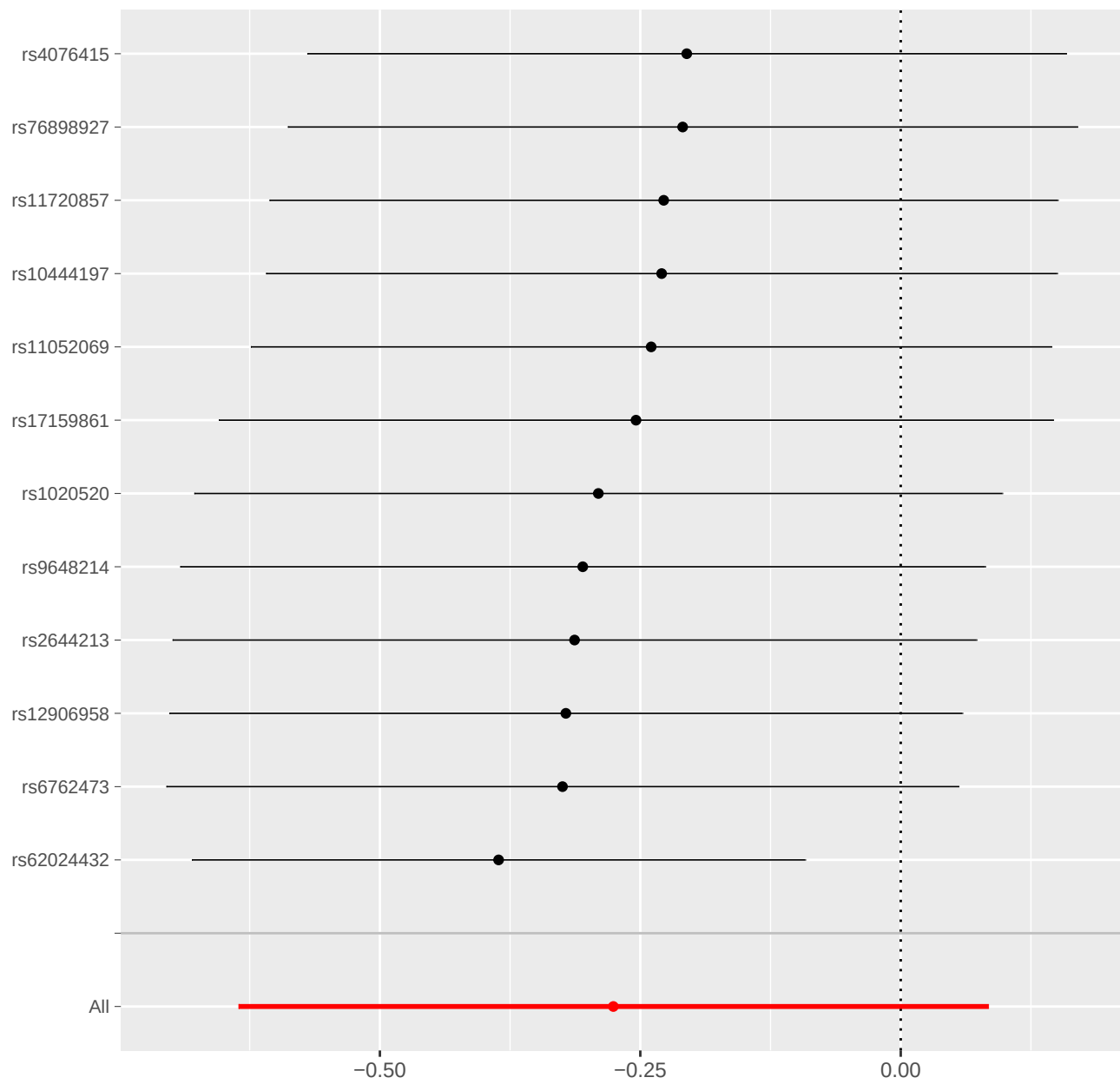


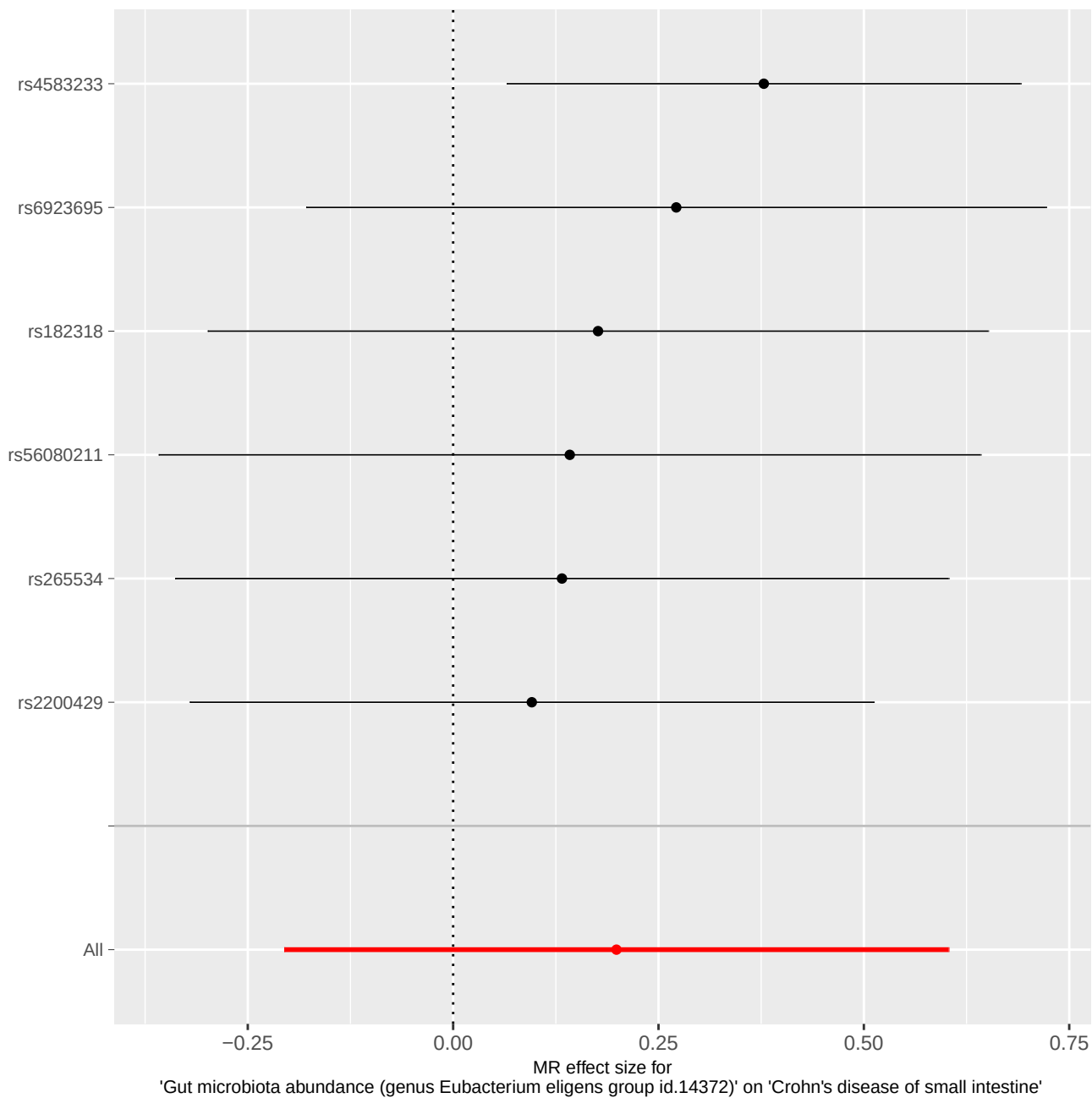
Batch 367 : Gut microbiota abundance (genus Erysipelatoclostridium id.11381) on Crohn's disease of small intestine

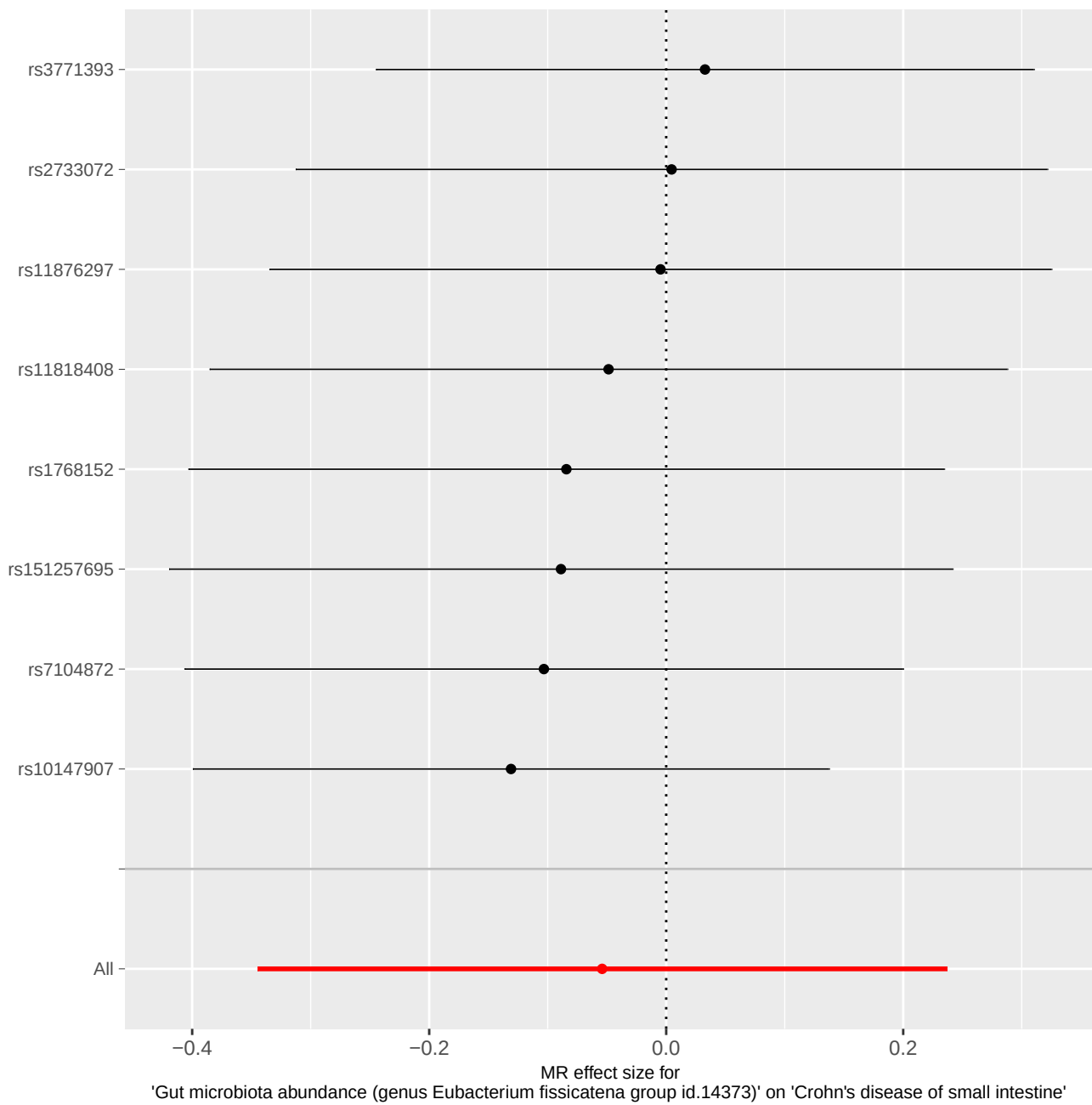


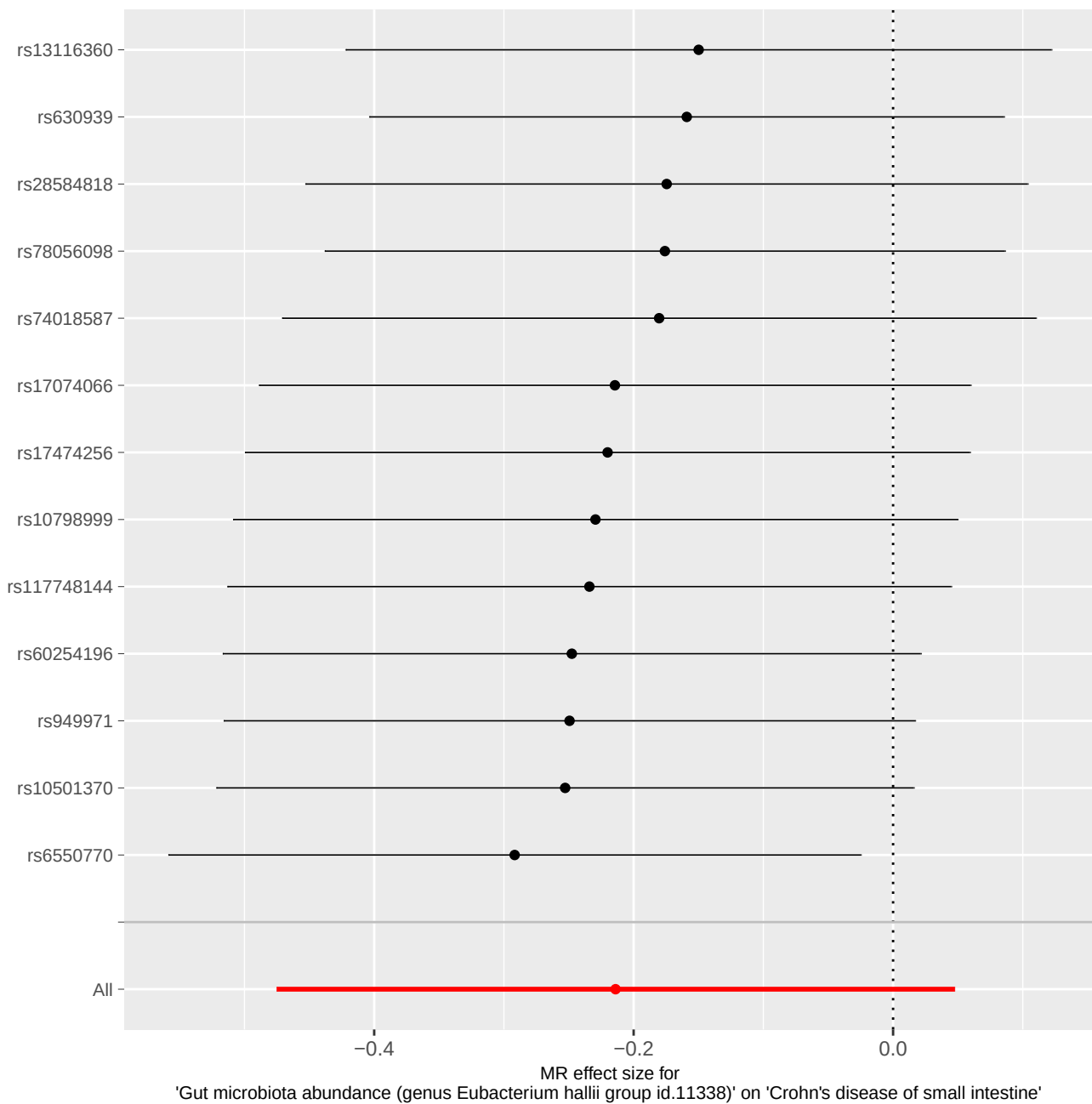


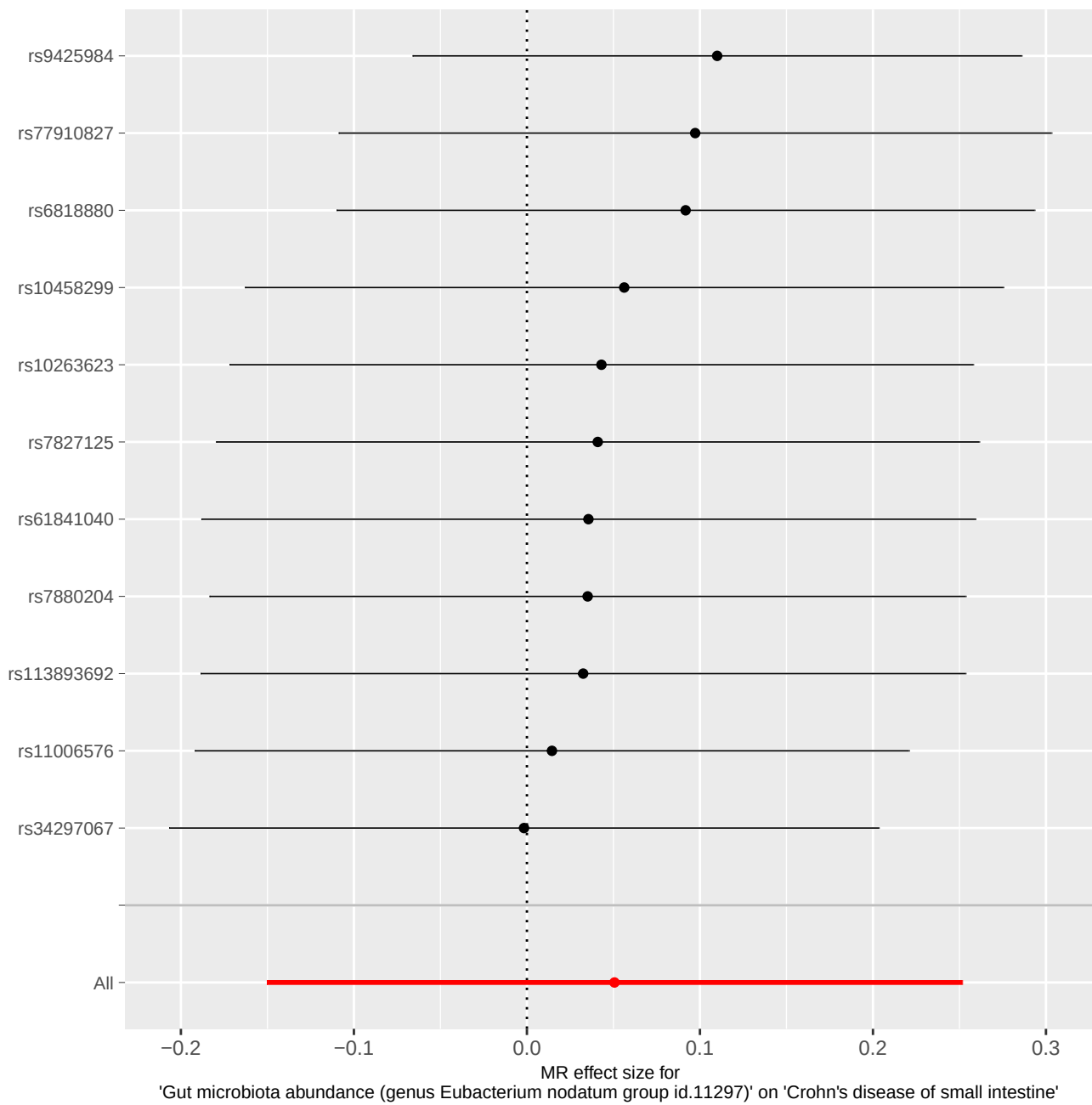


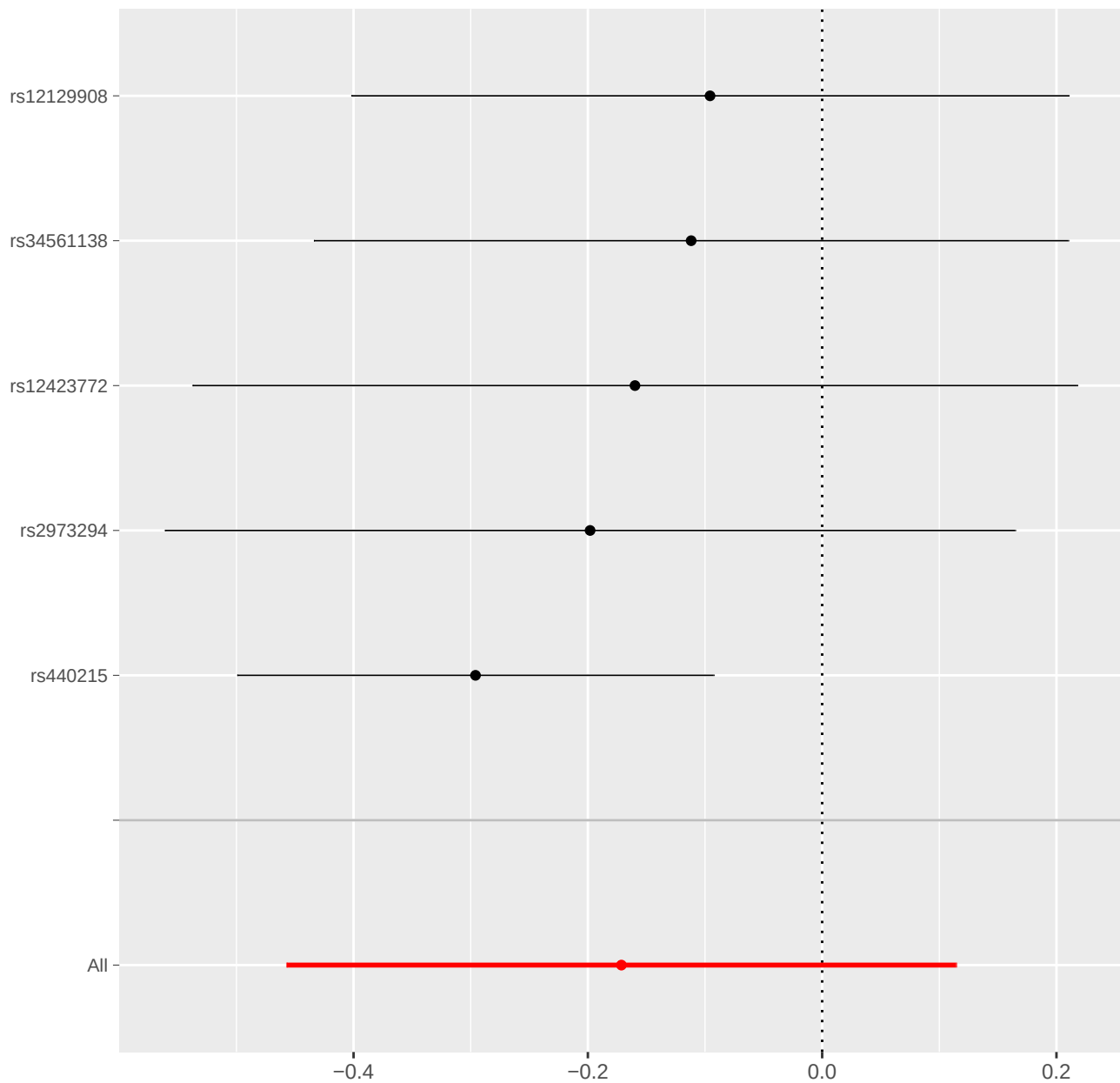


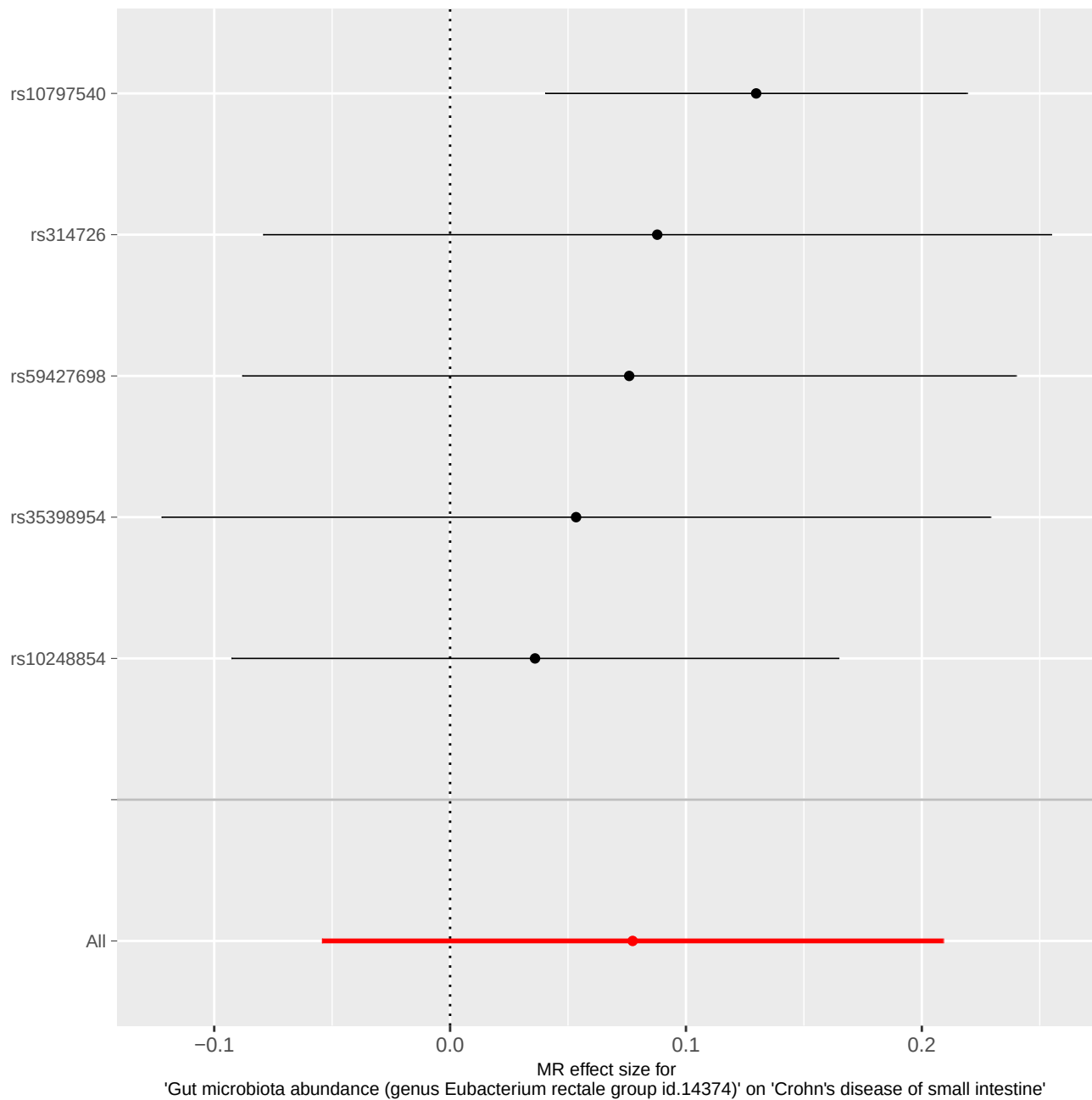


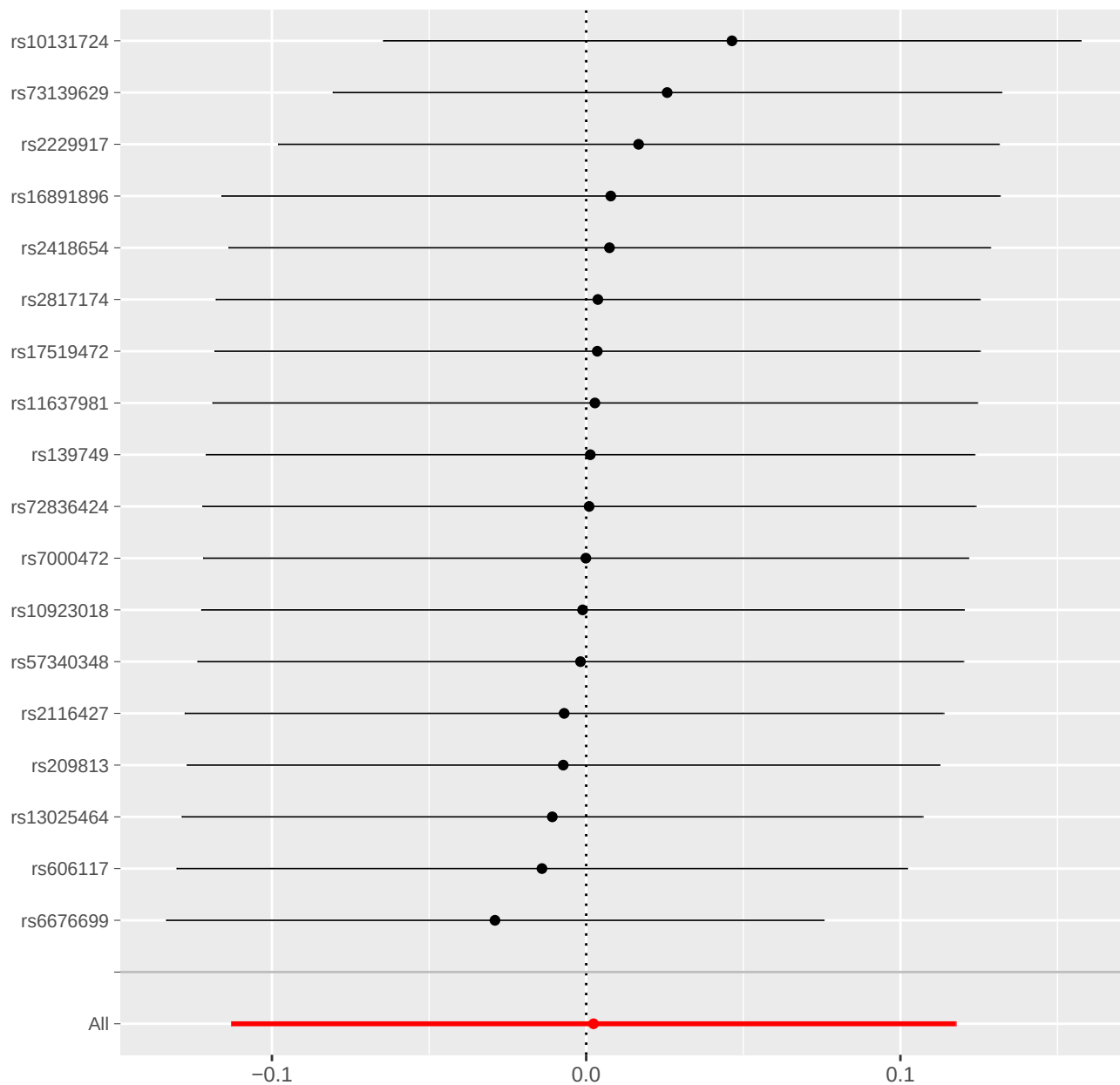




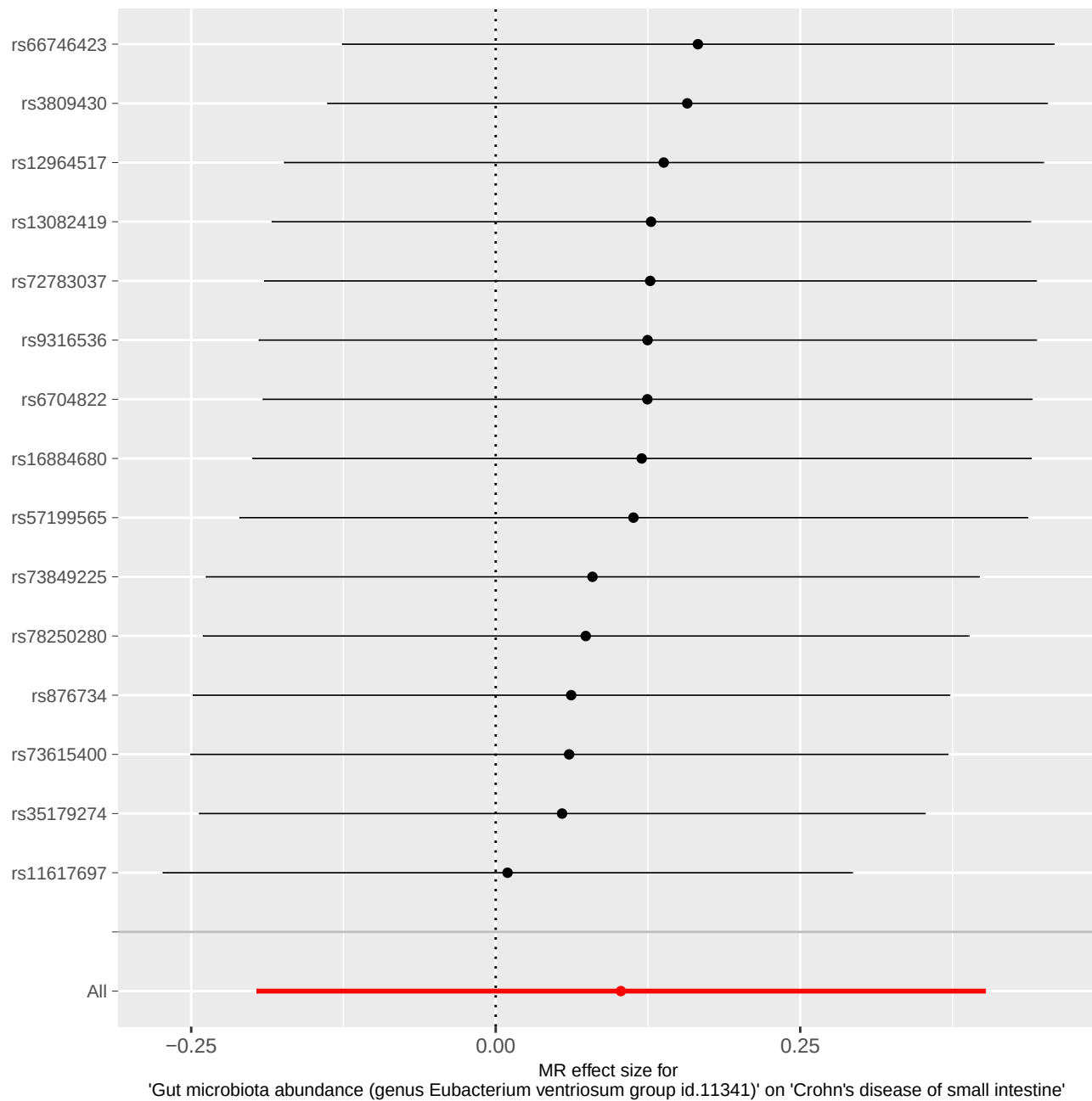




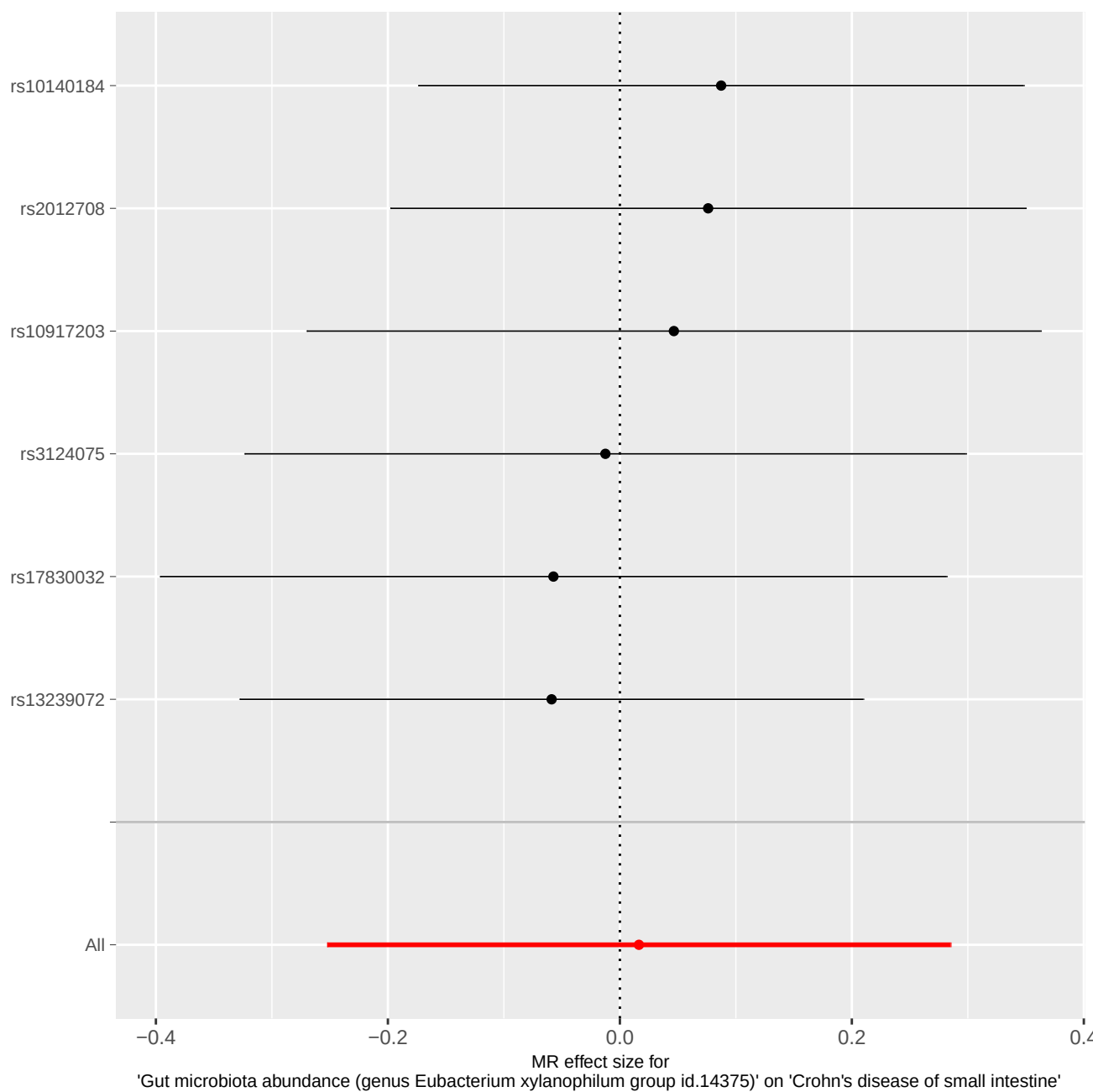


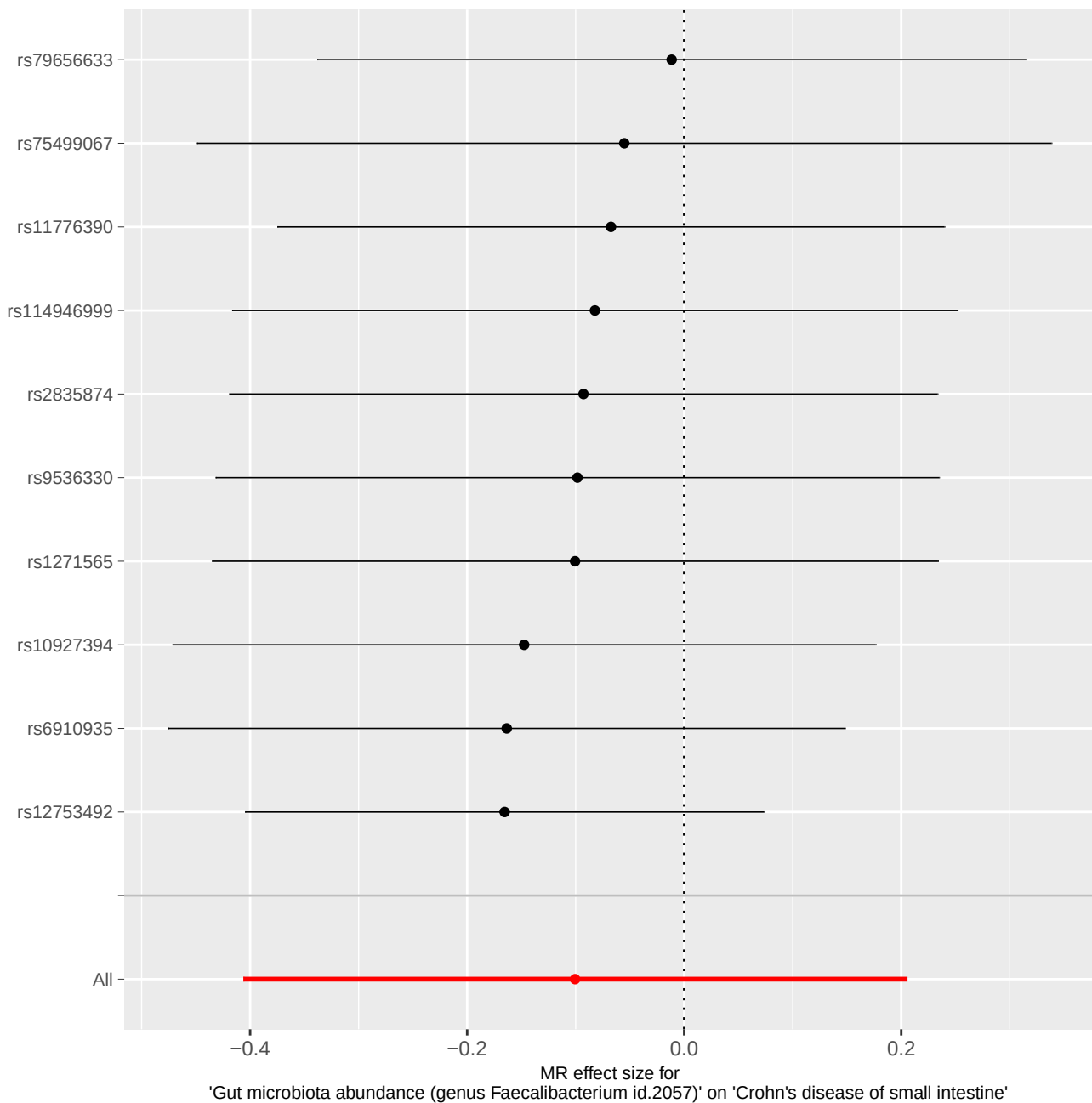


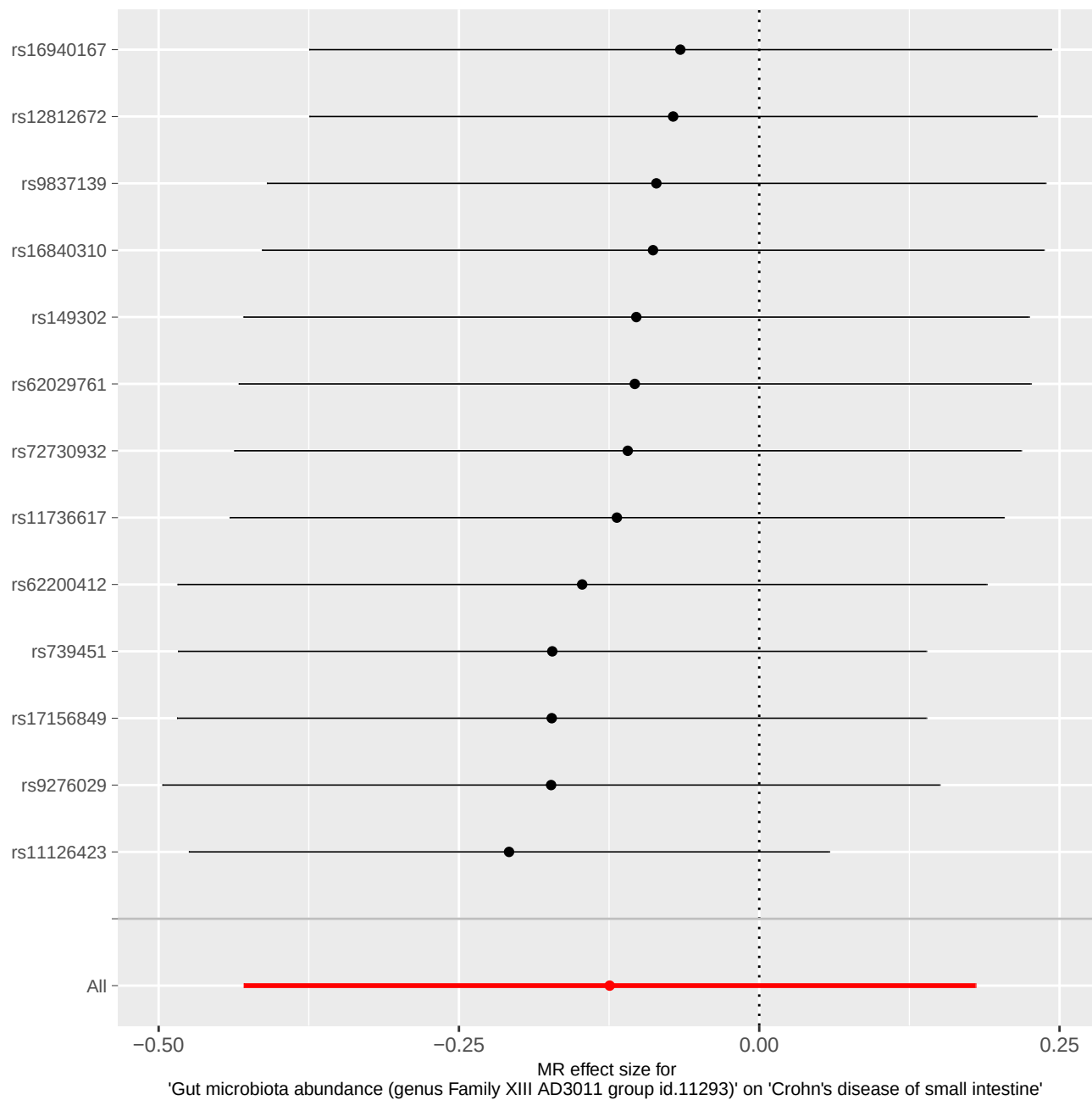
MR effect size for
'Gut microbiota abundance (genus Eubacterium ruminantium group id.11340)' on 'Crohn's disease of small intestine'

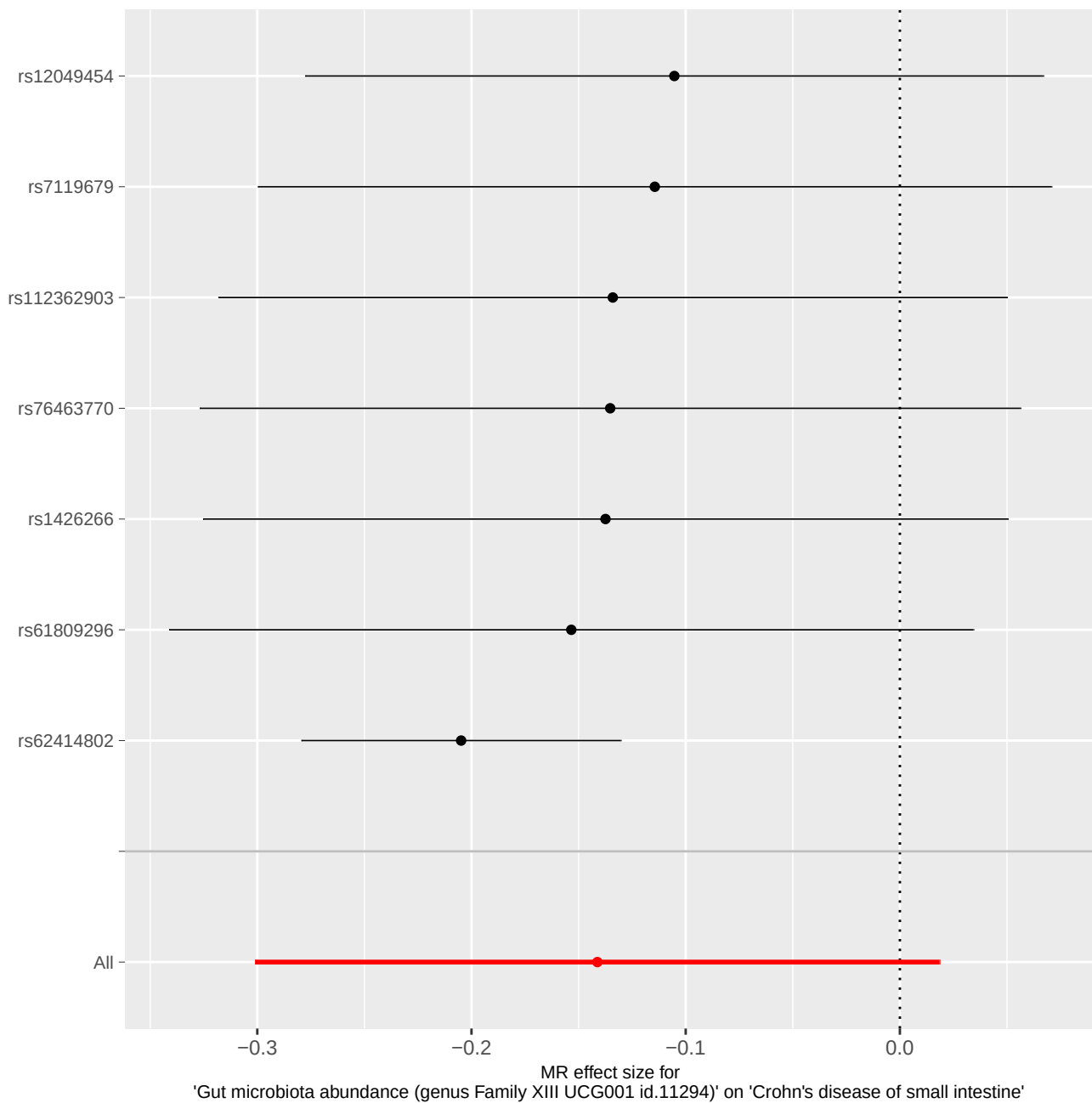


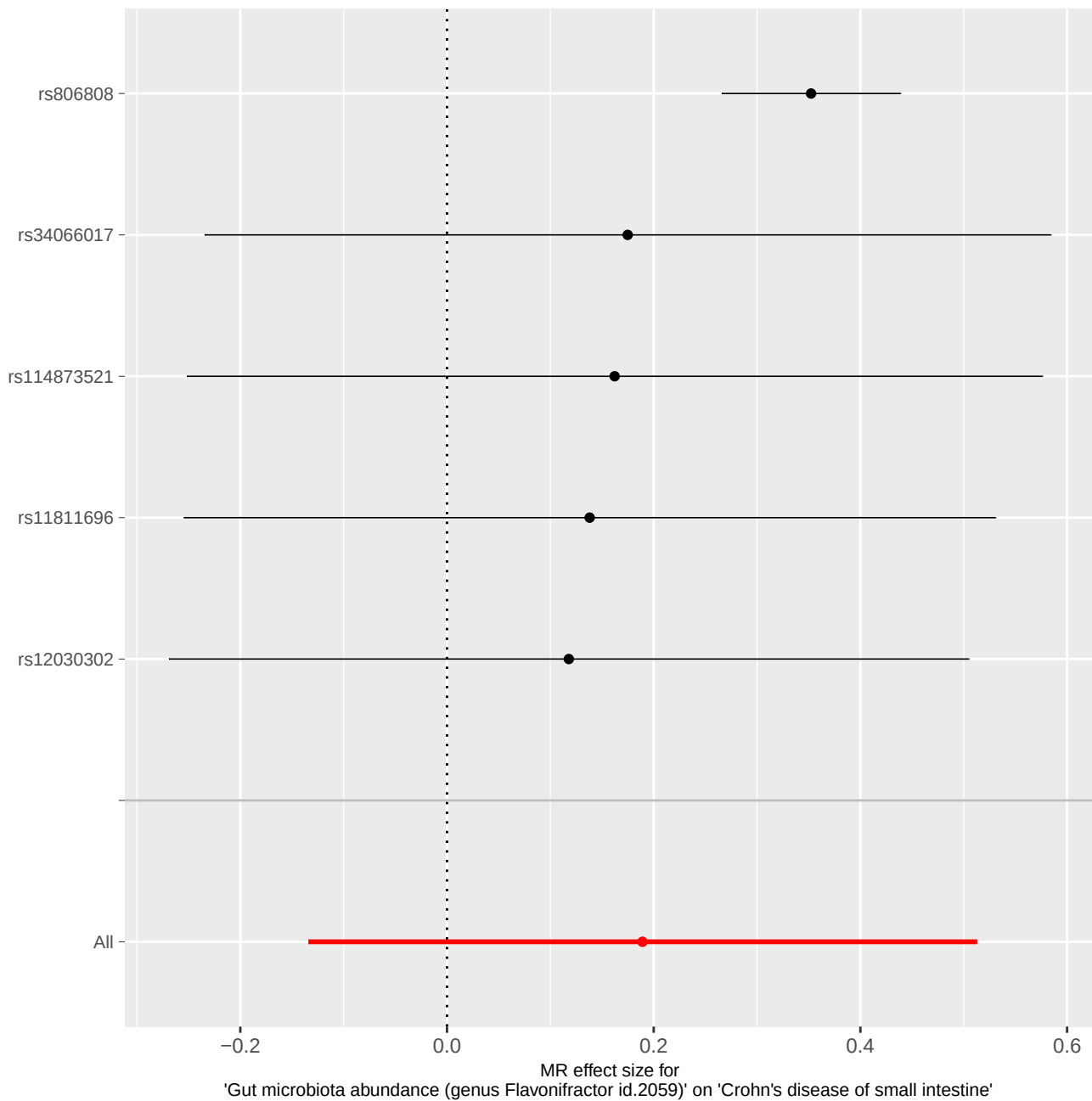
MR effect size for
'Gut microbiota abundance (genus Eubacterium ventriosum group id.11341)' on 'Crohn's disease of small intestine'

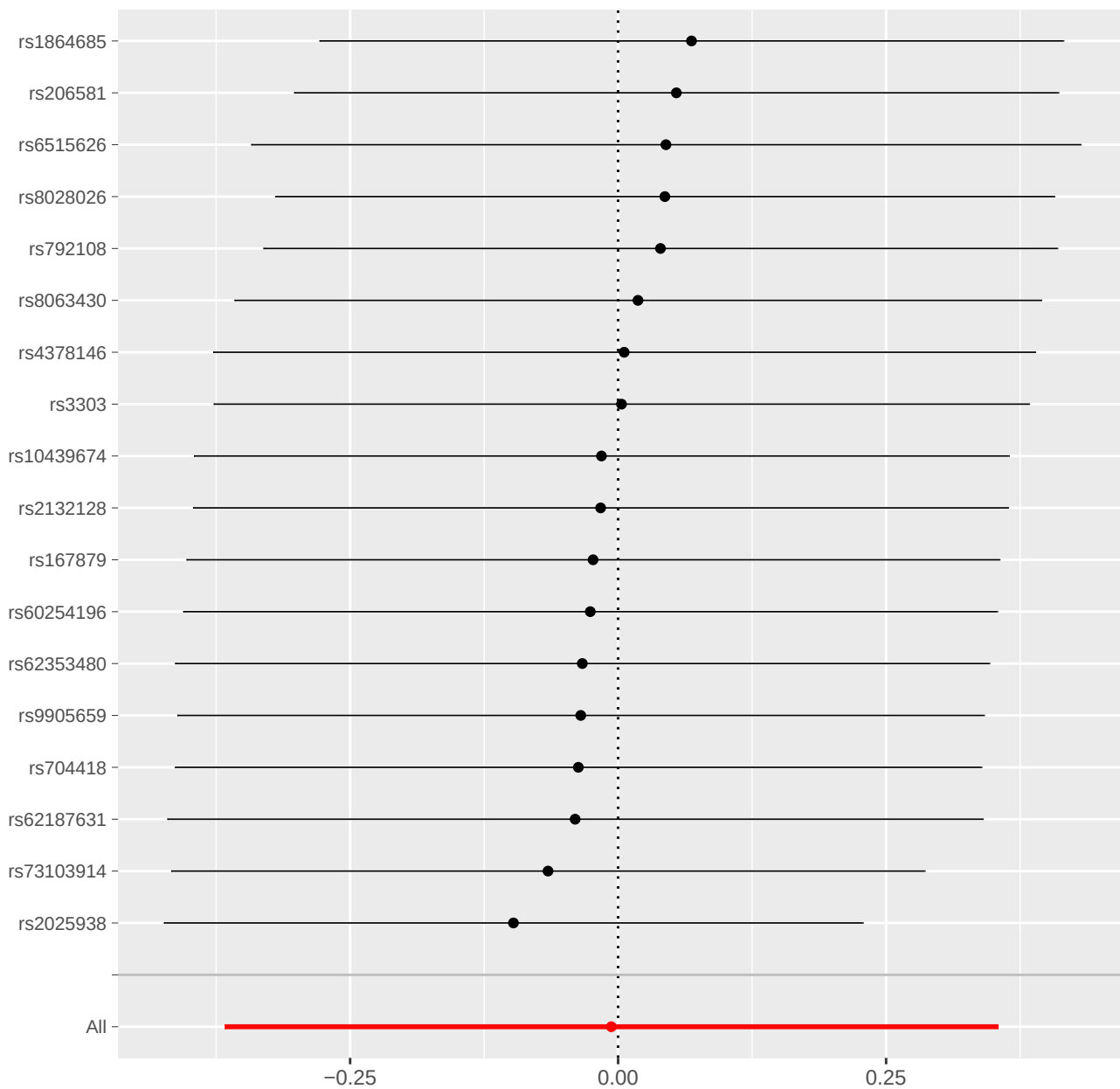


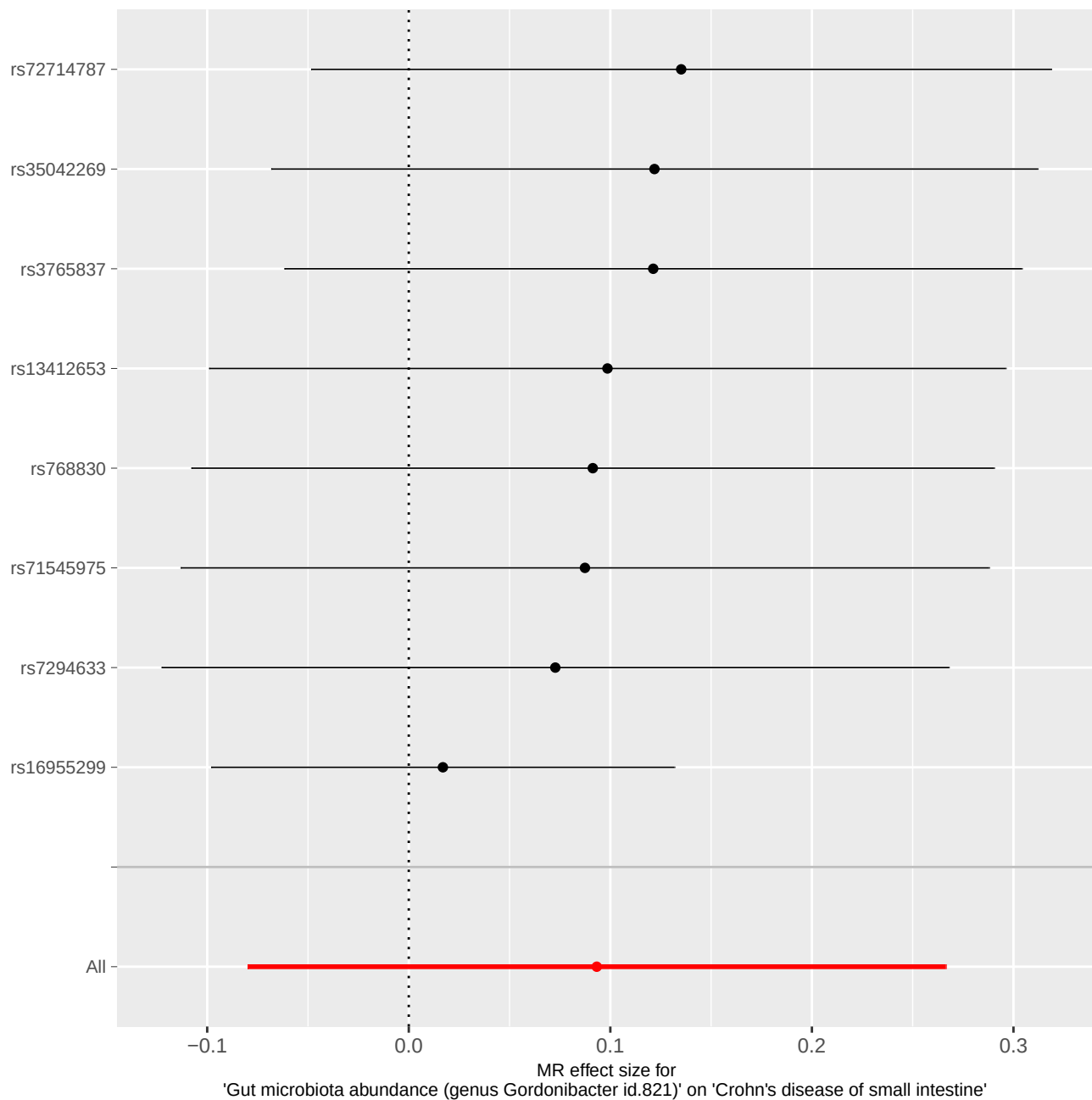


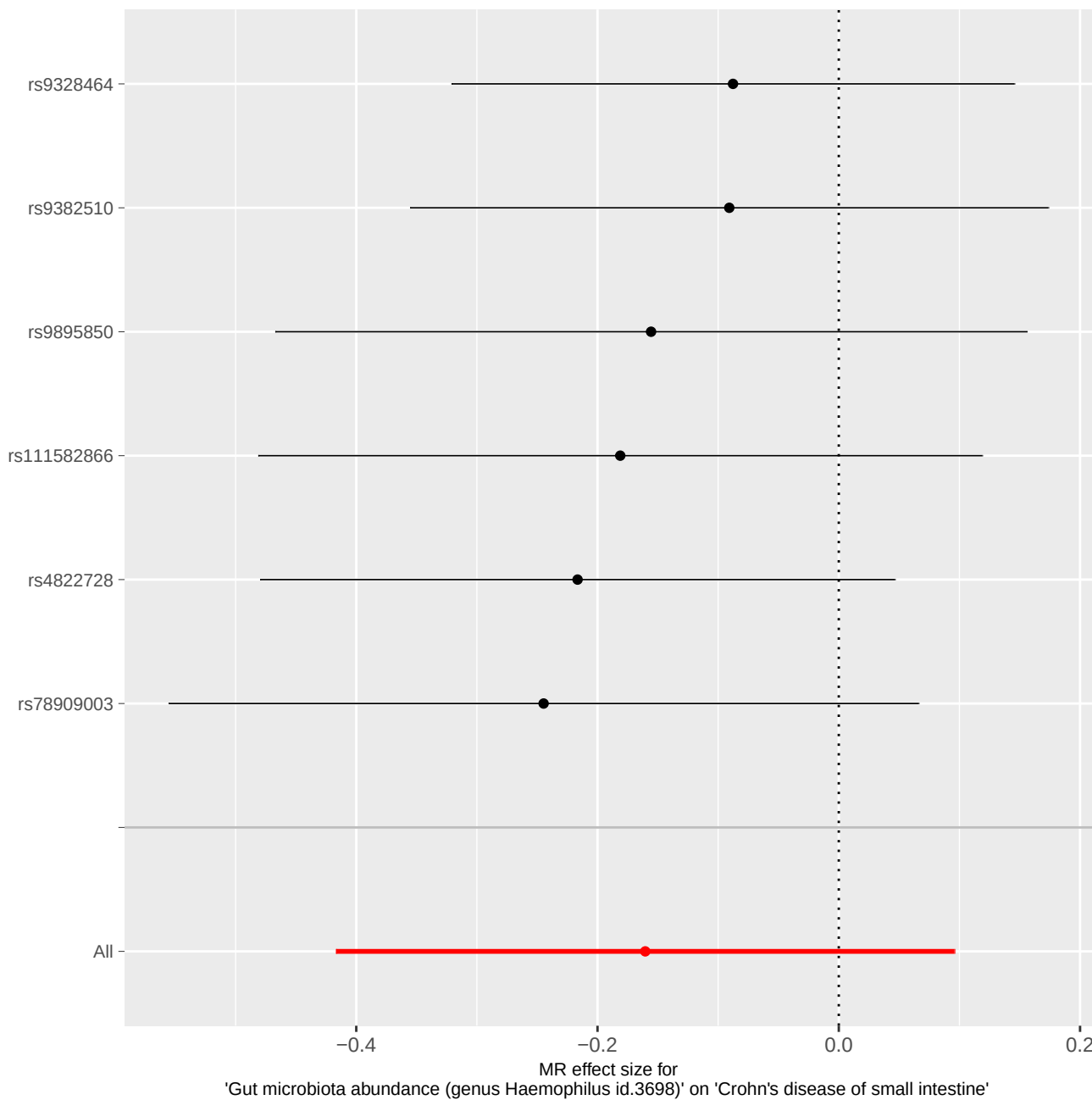


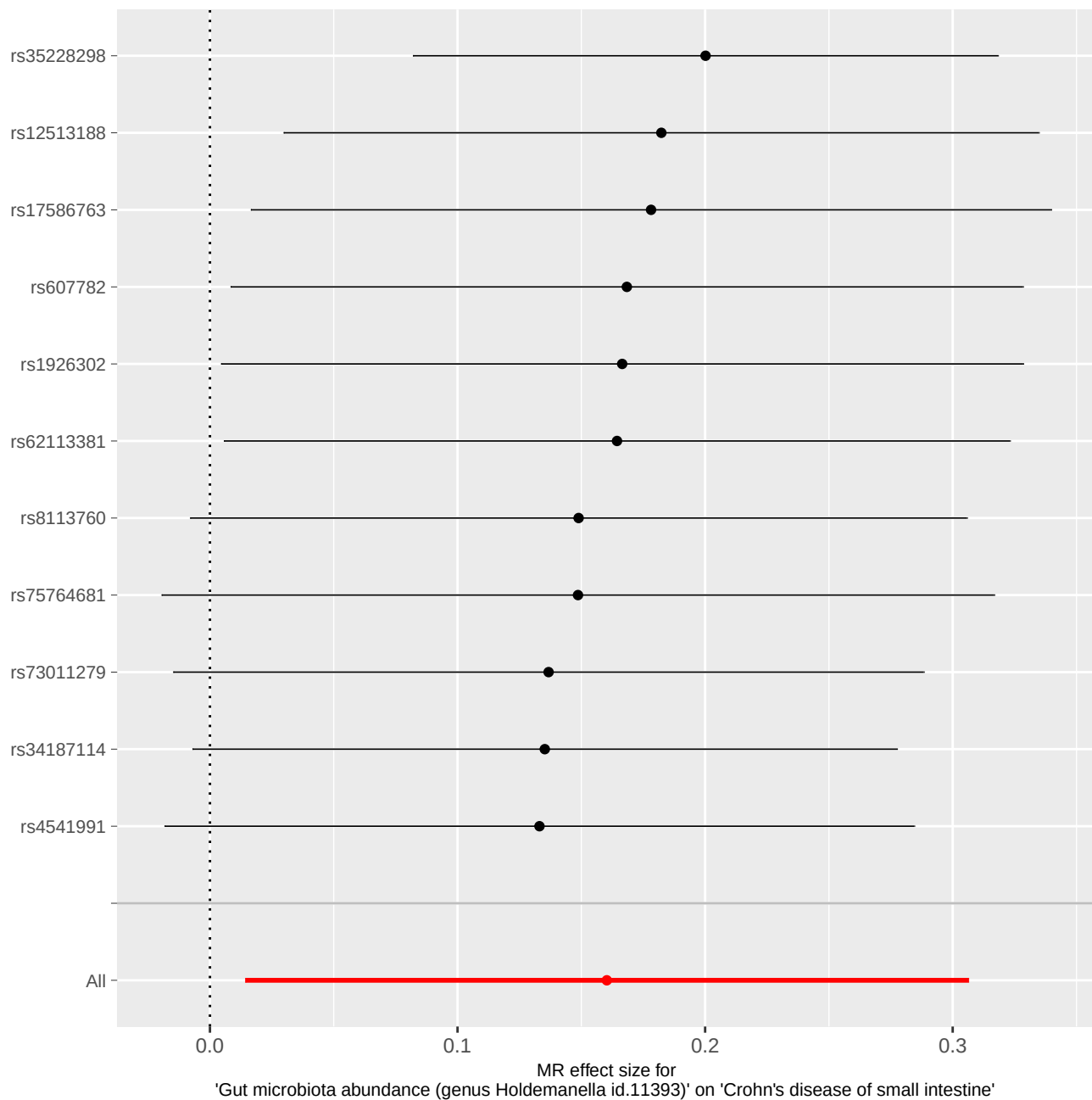


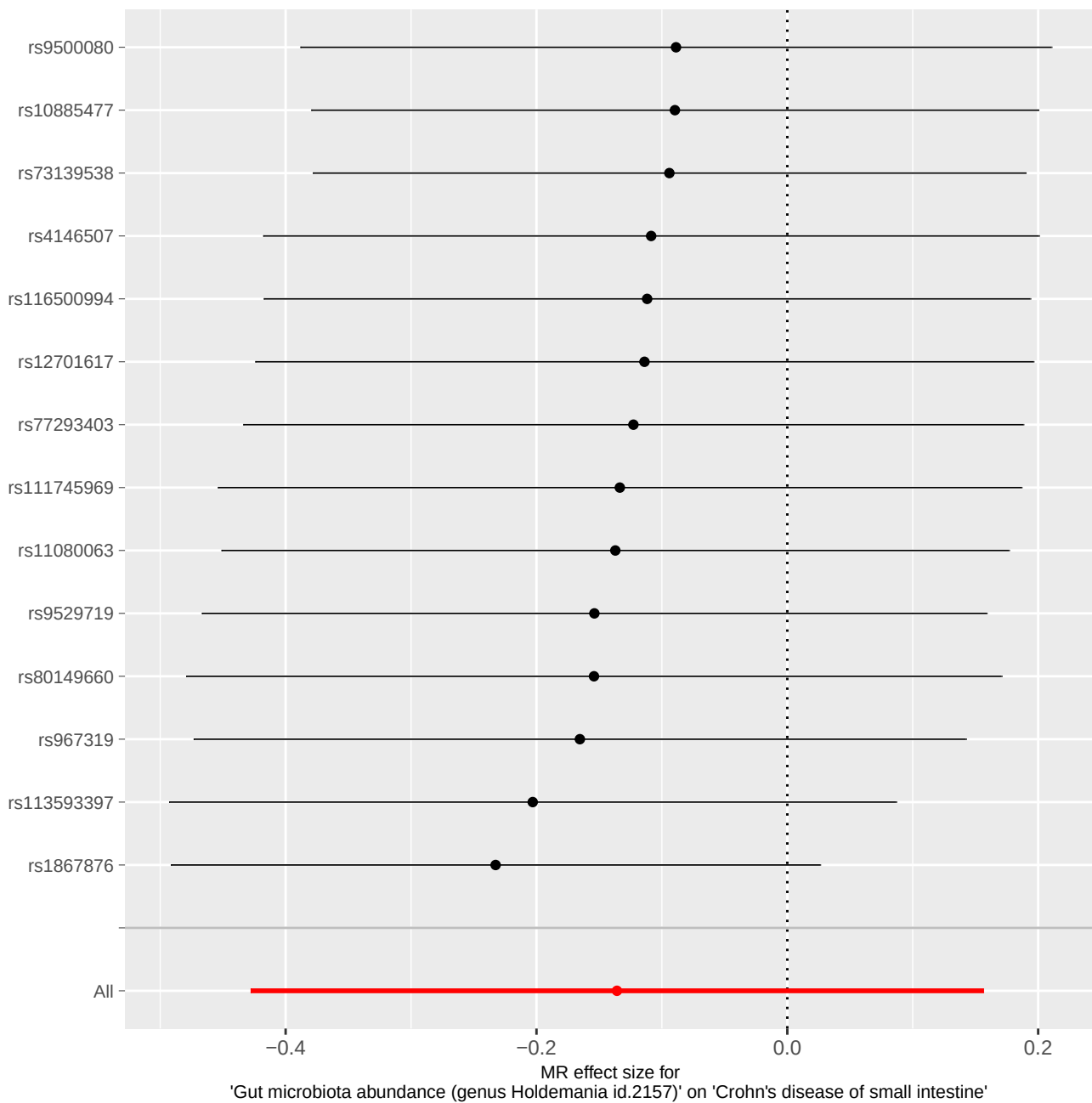


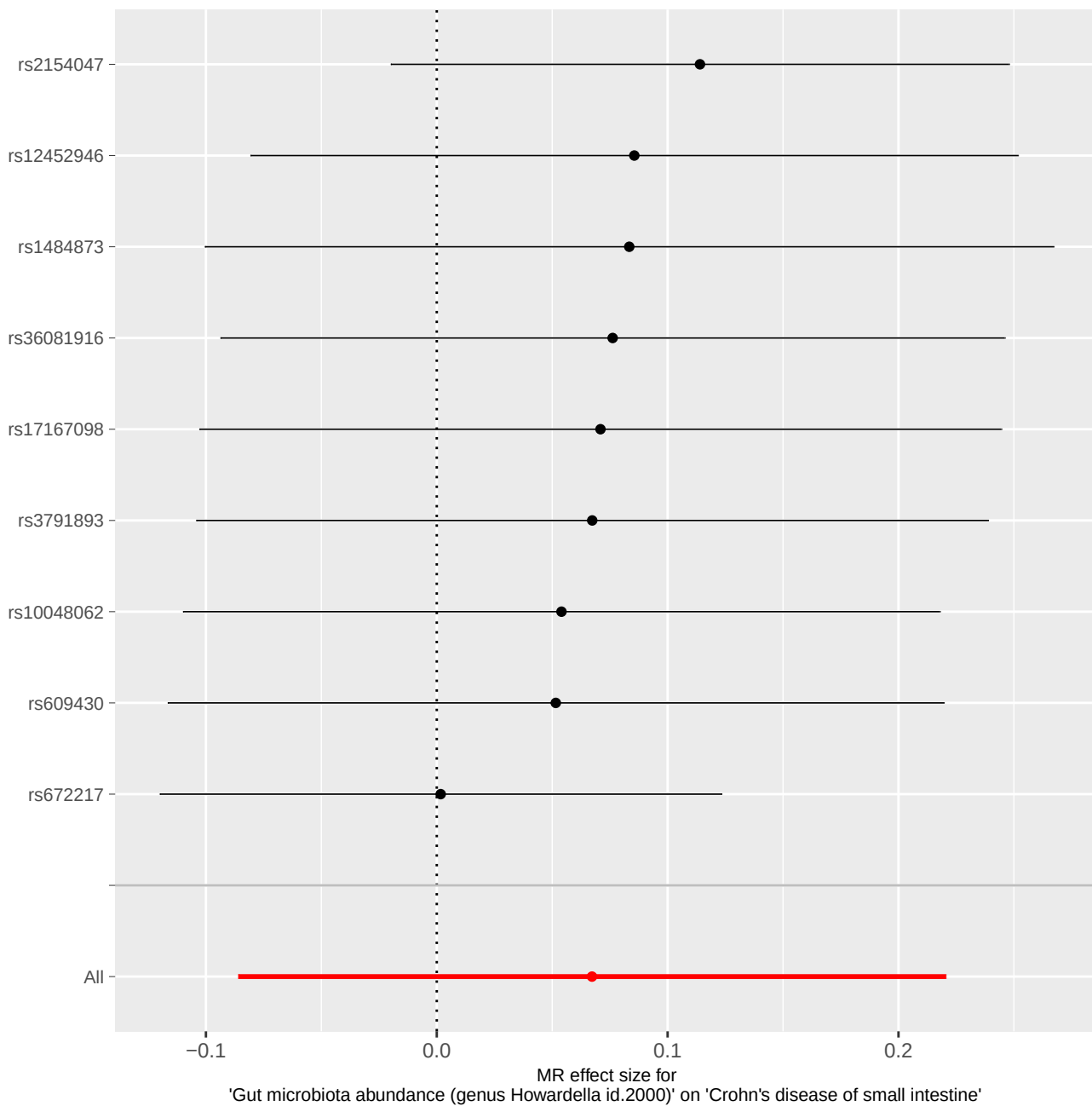


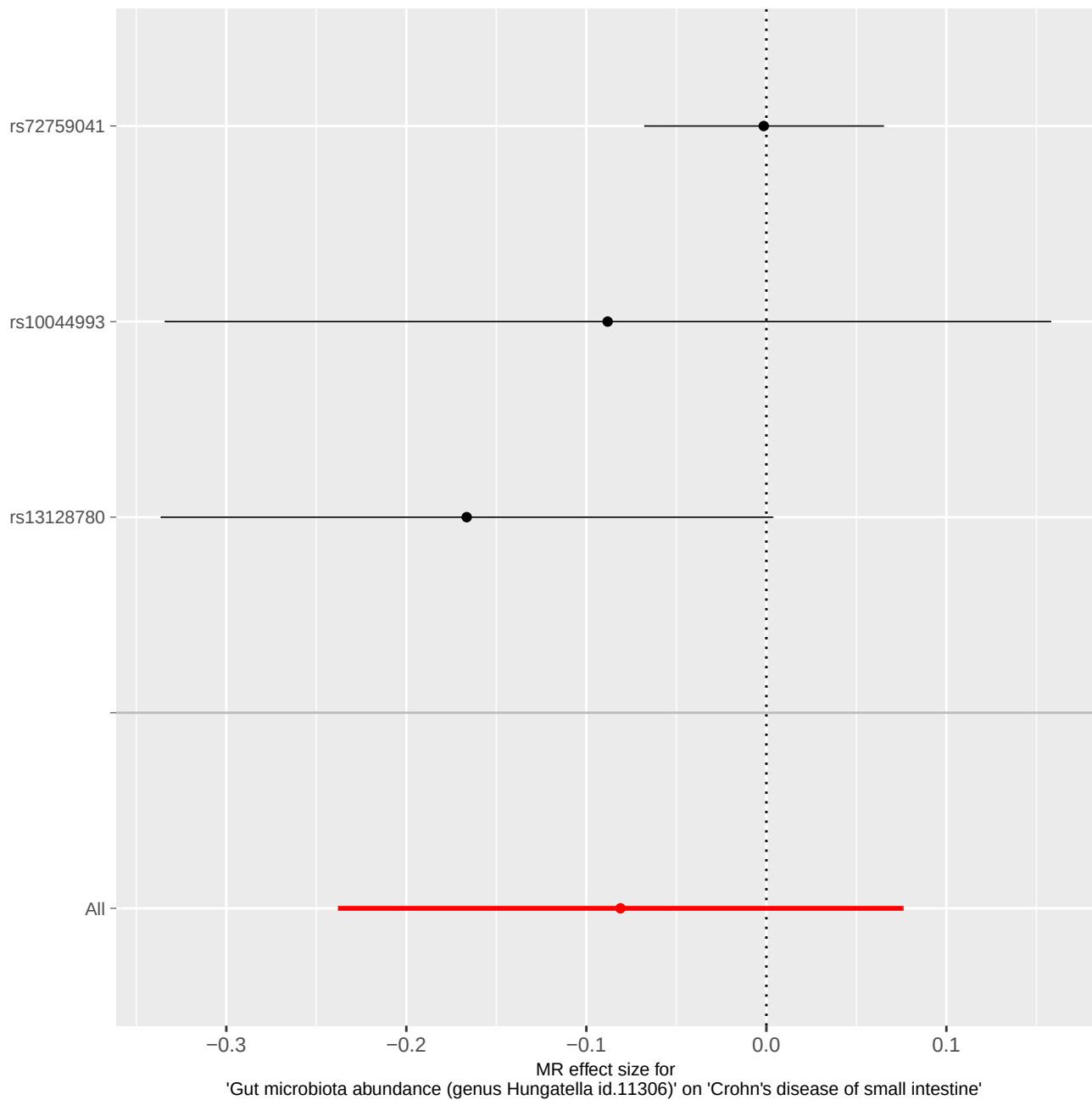


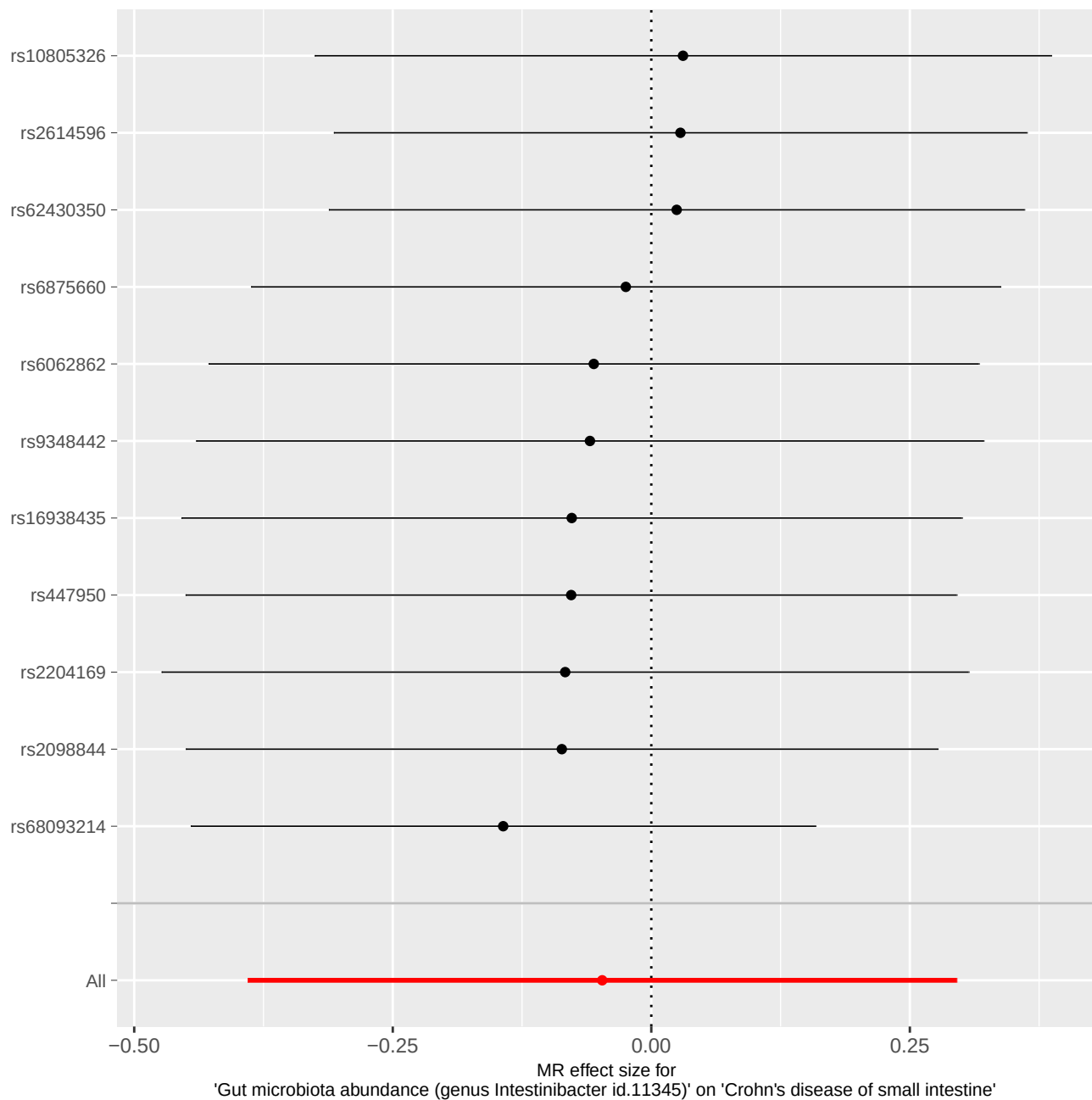




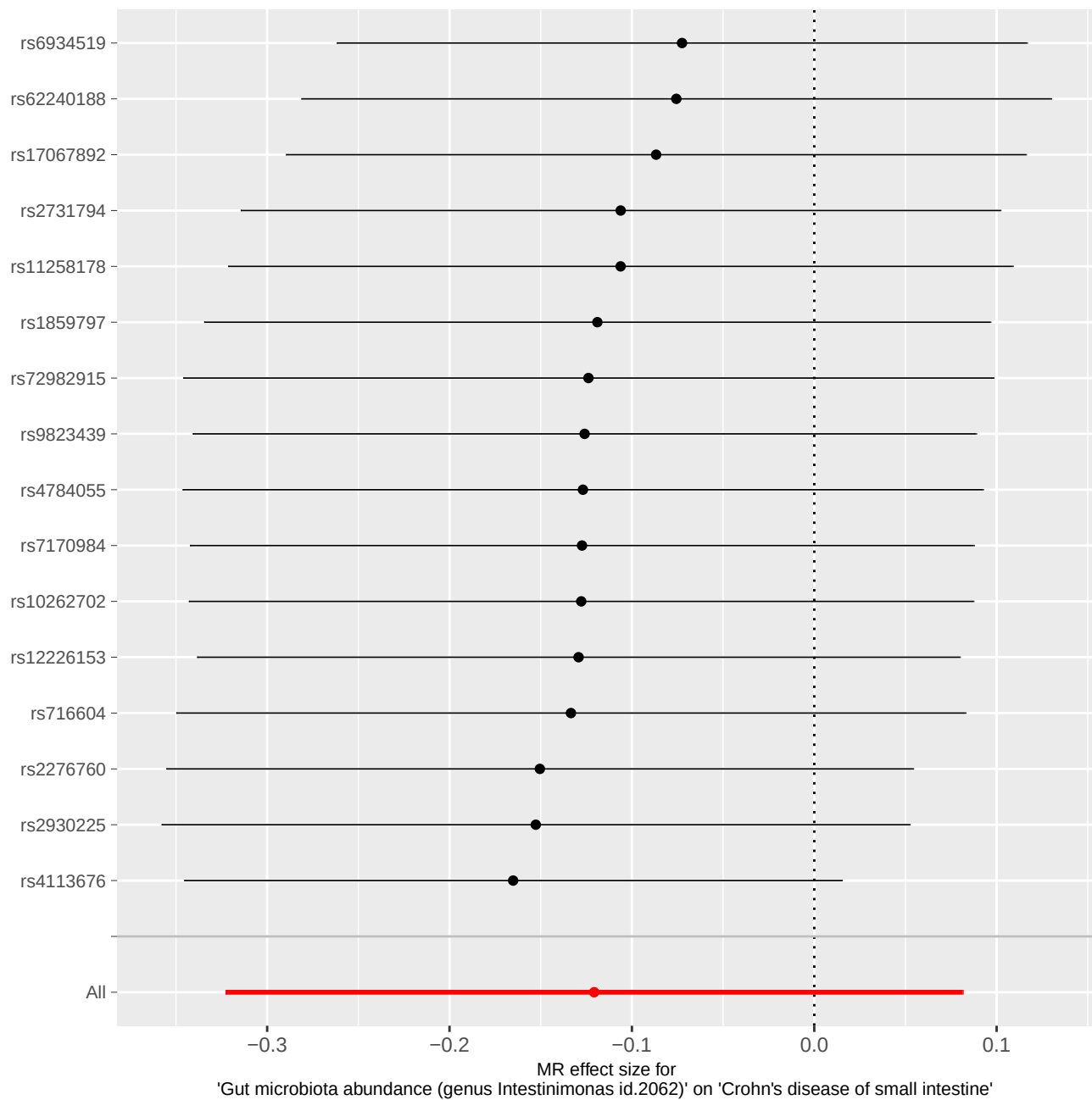


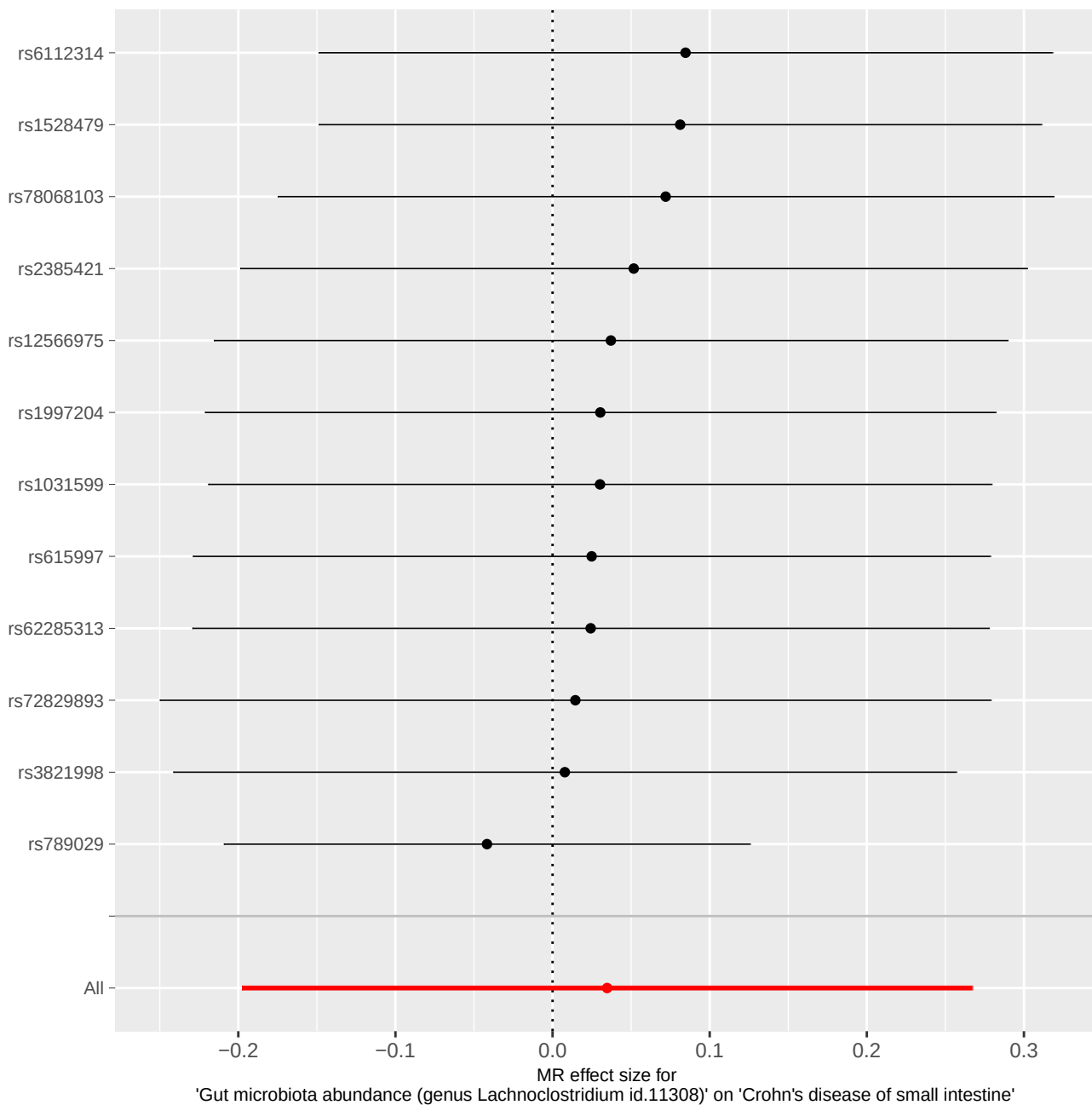


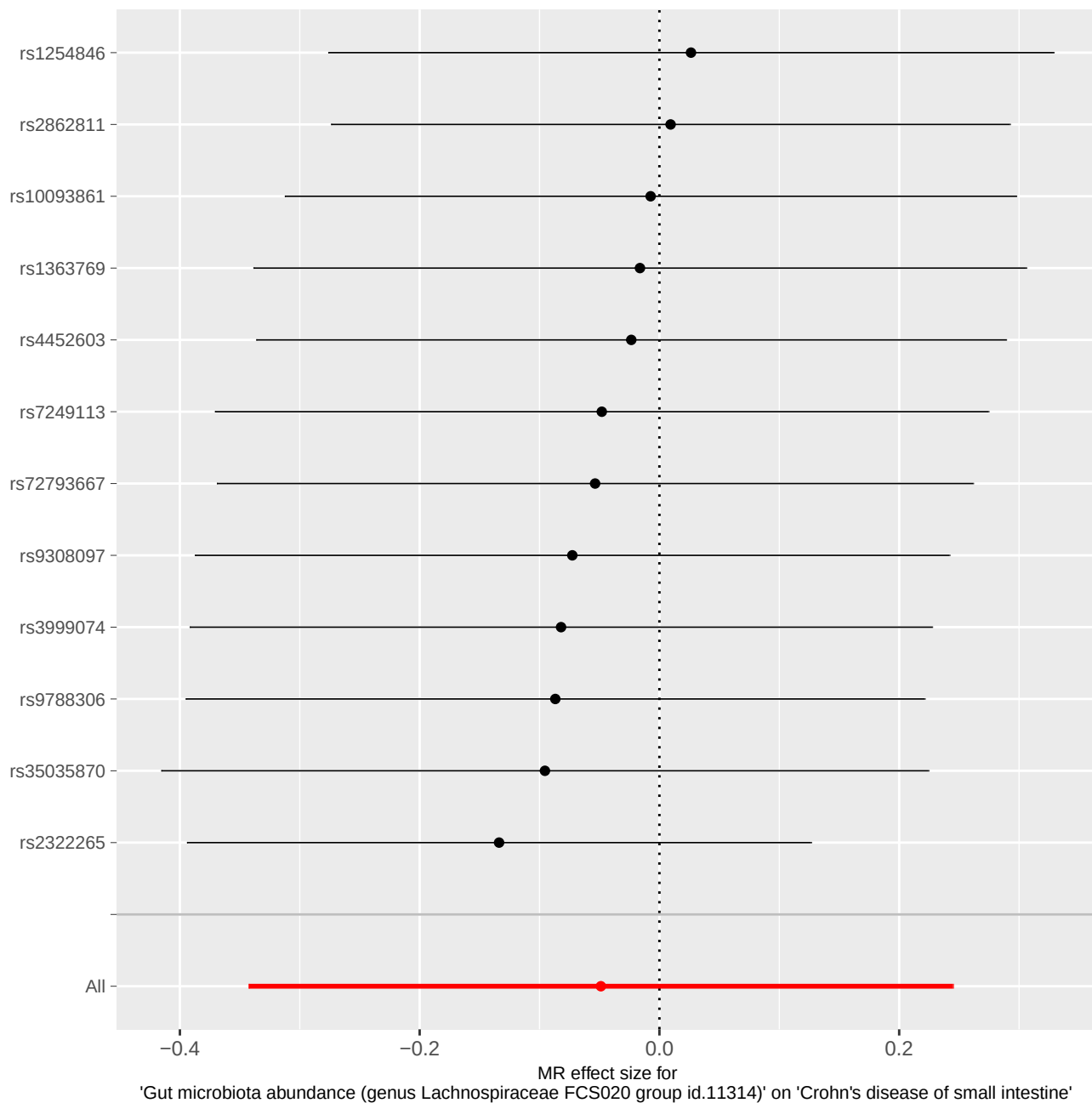


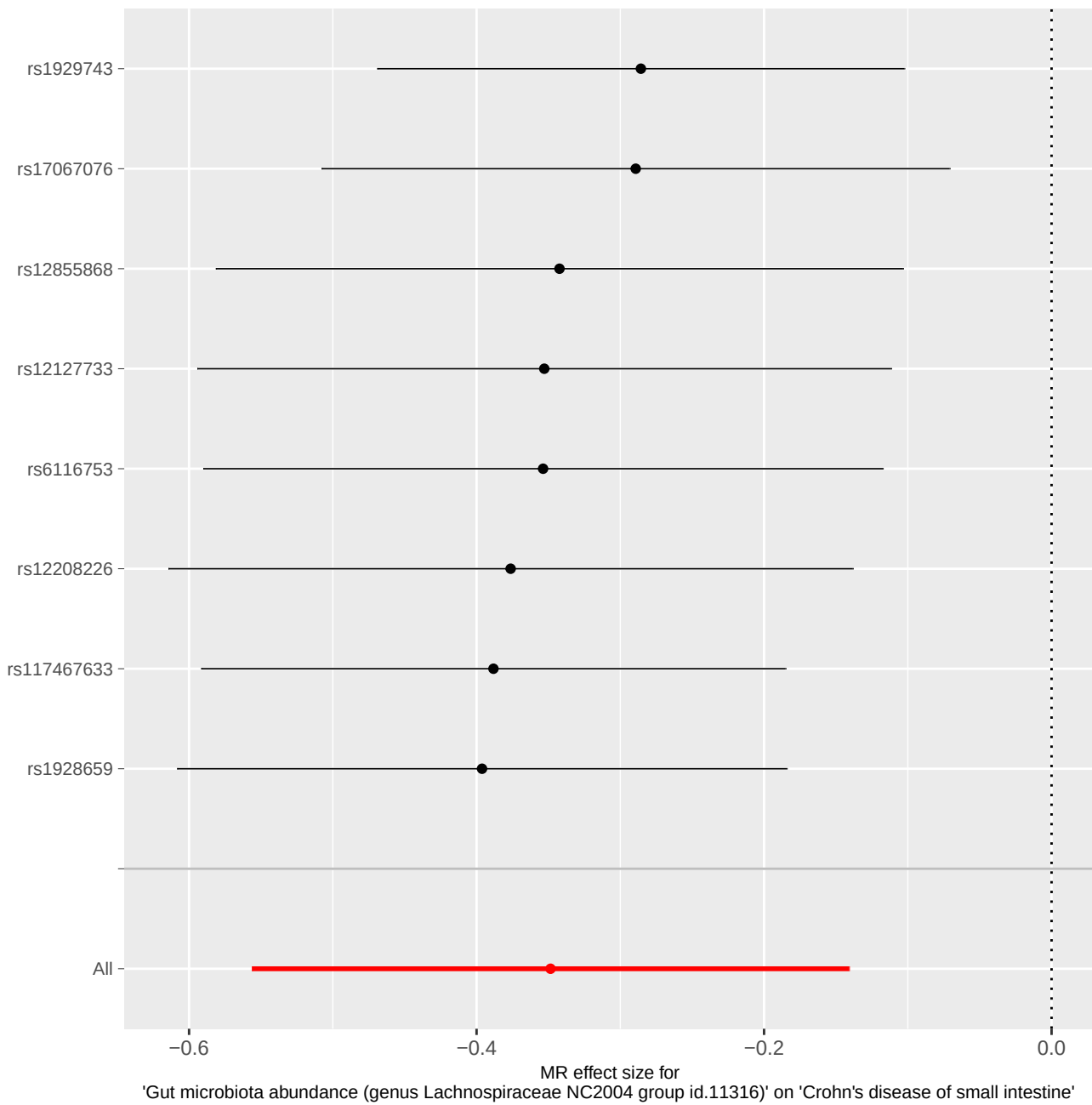


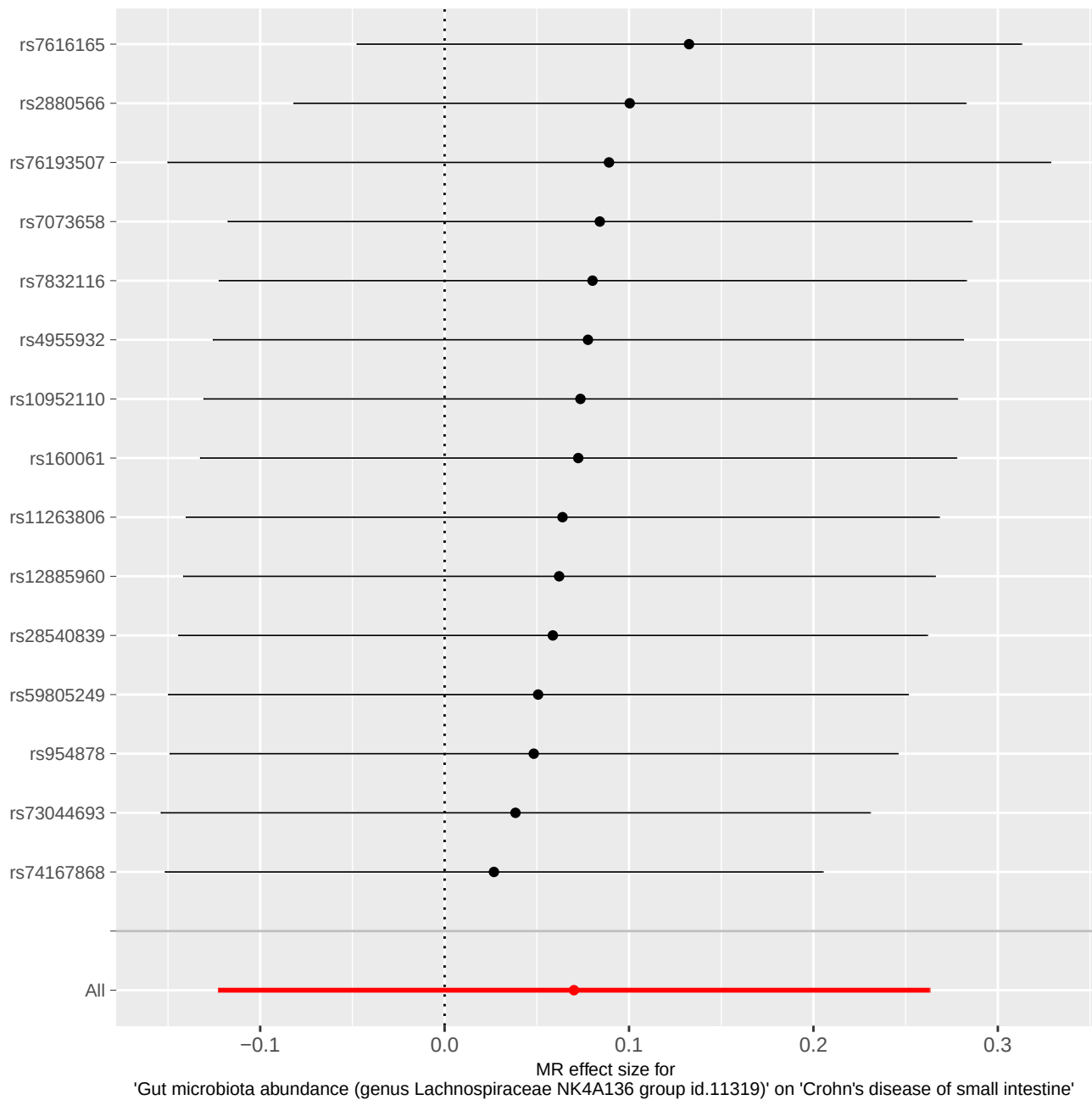
Batch 393 : Gut microbiota abundance (genus Intestinimonas id.2062) on Crohn's disease of small intestine

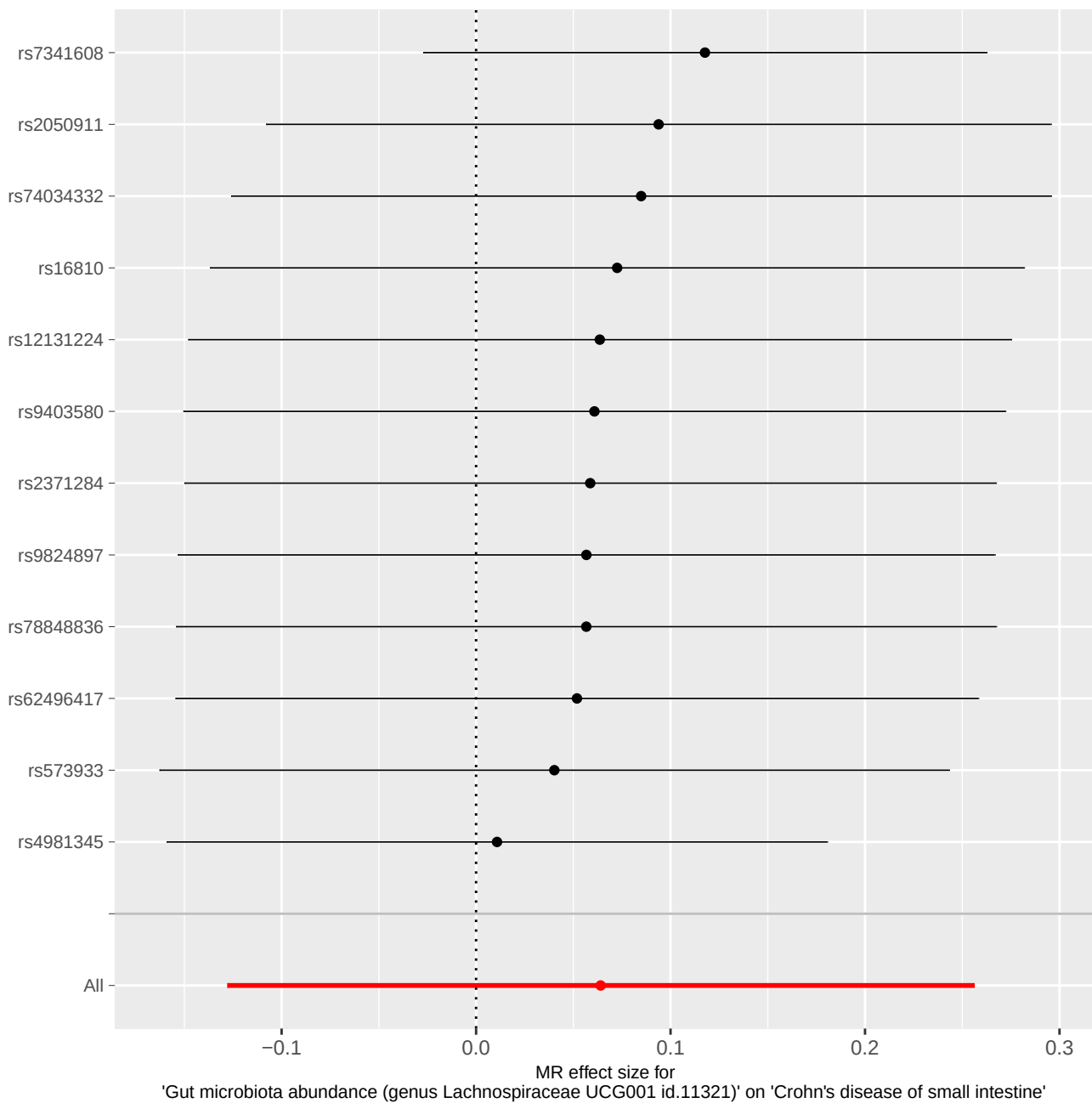


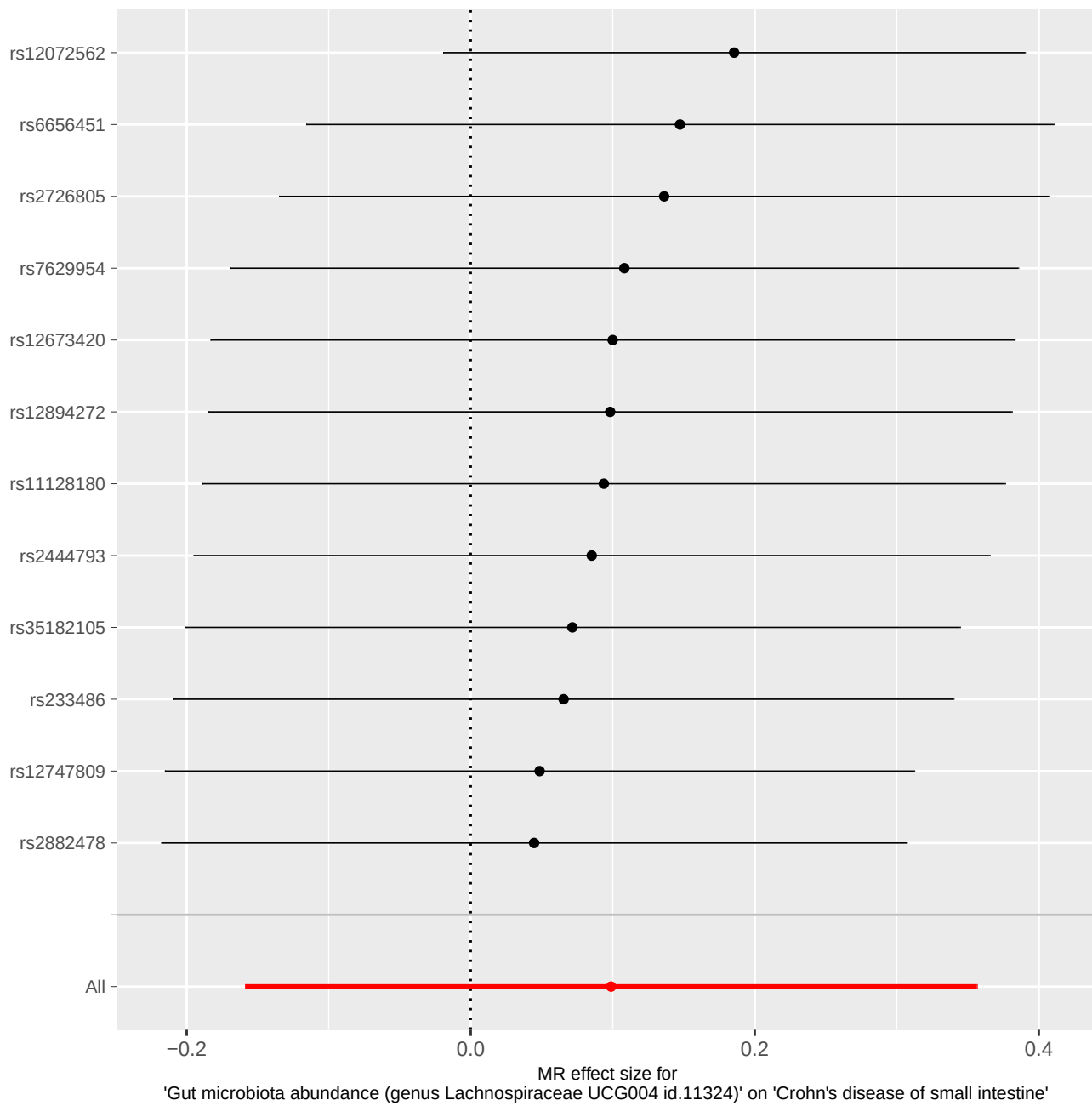


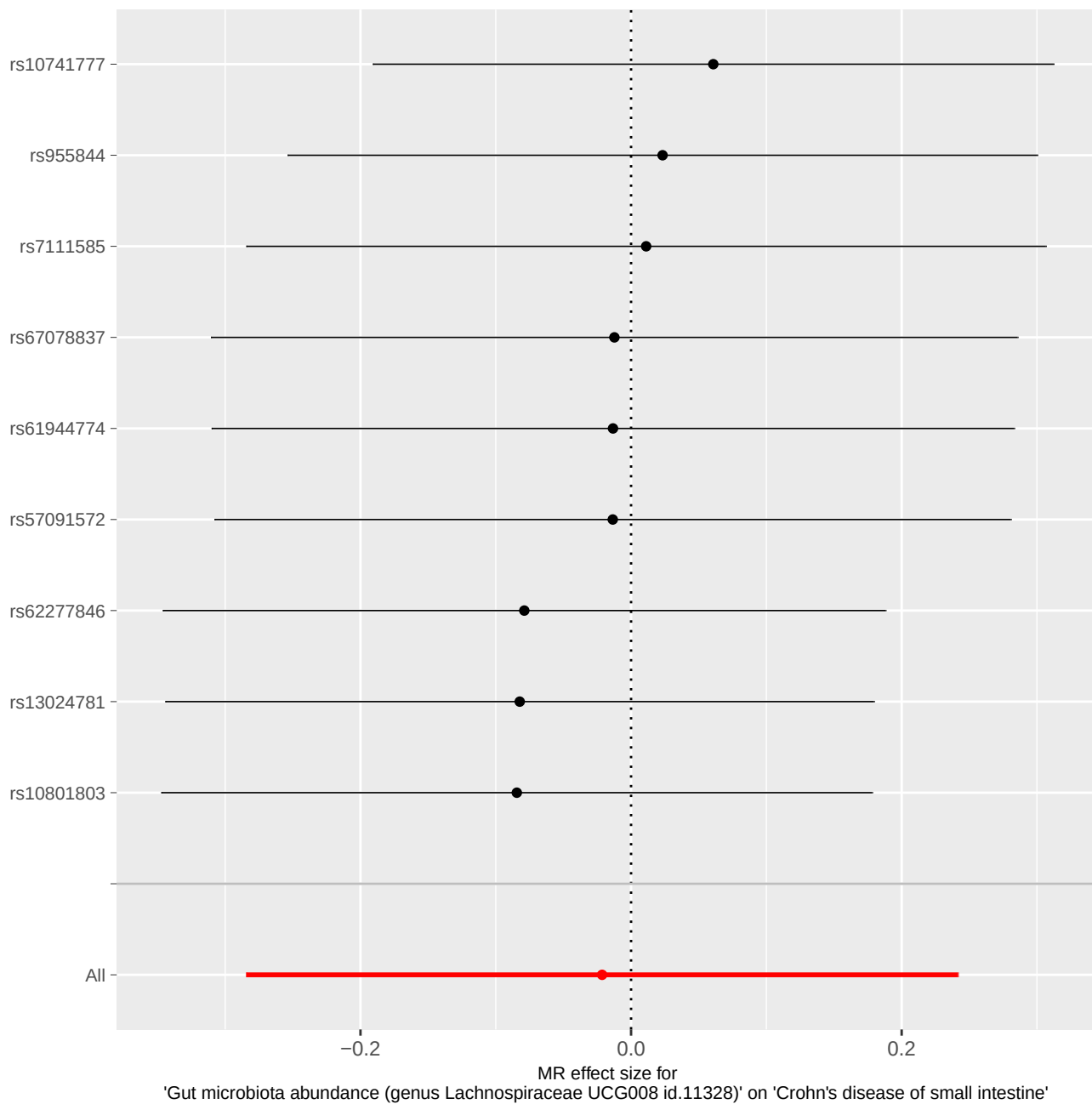


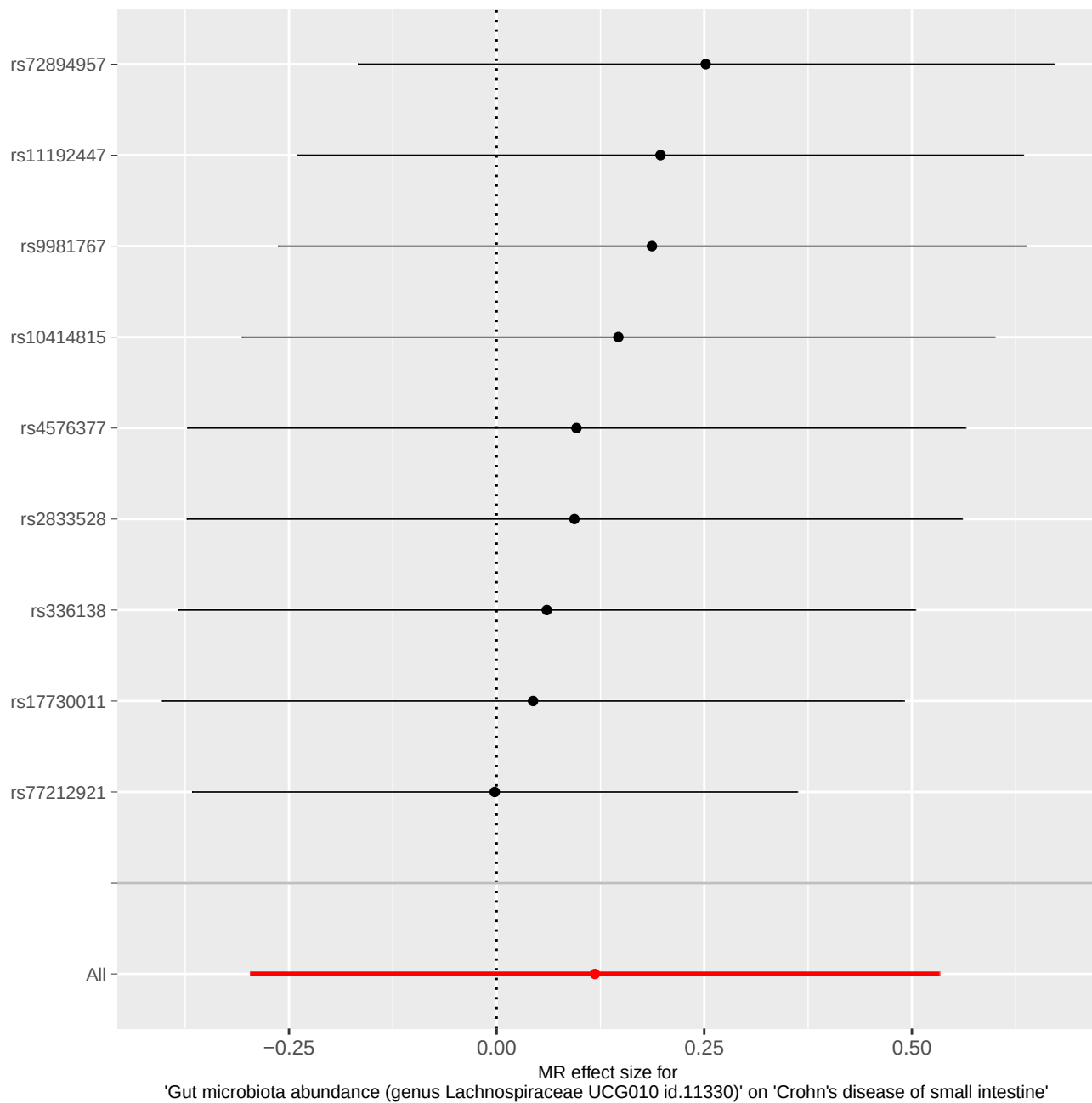


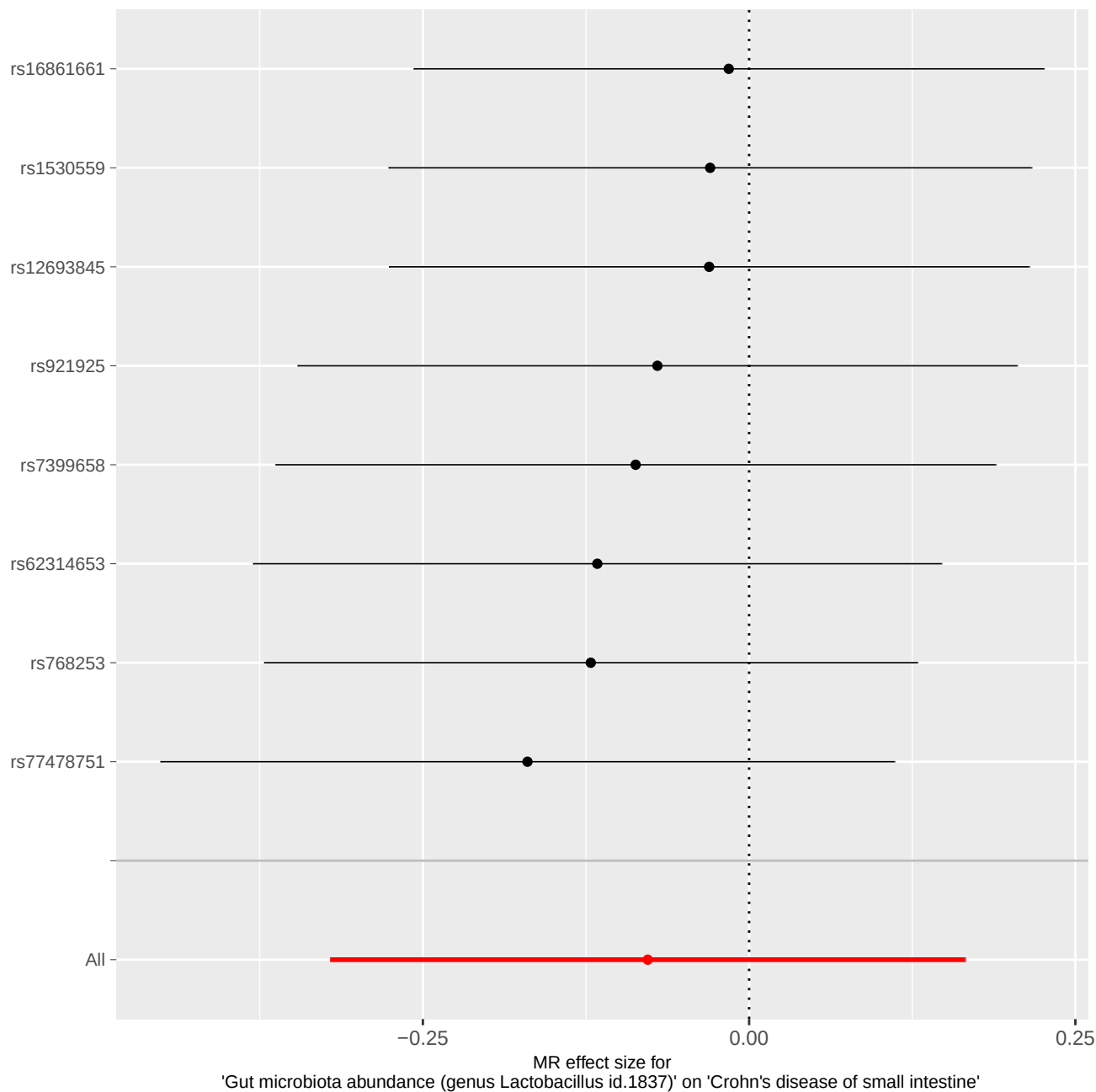


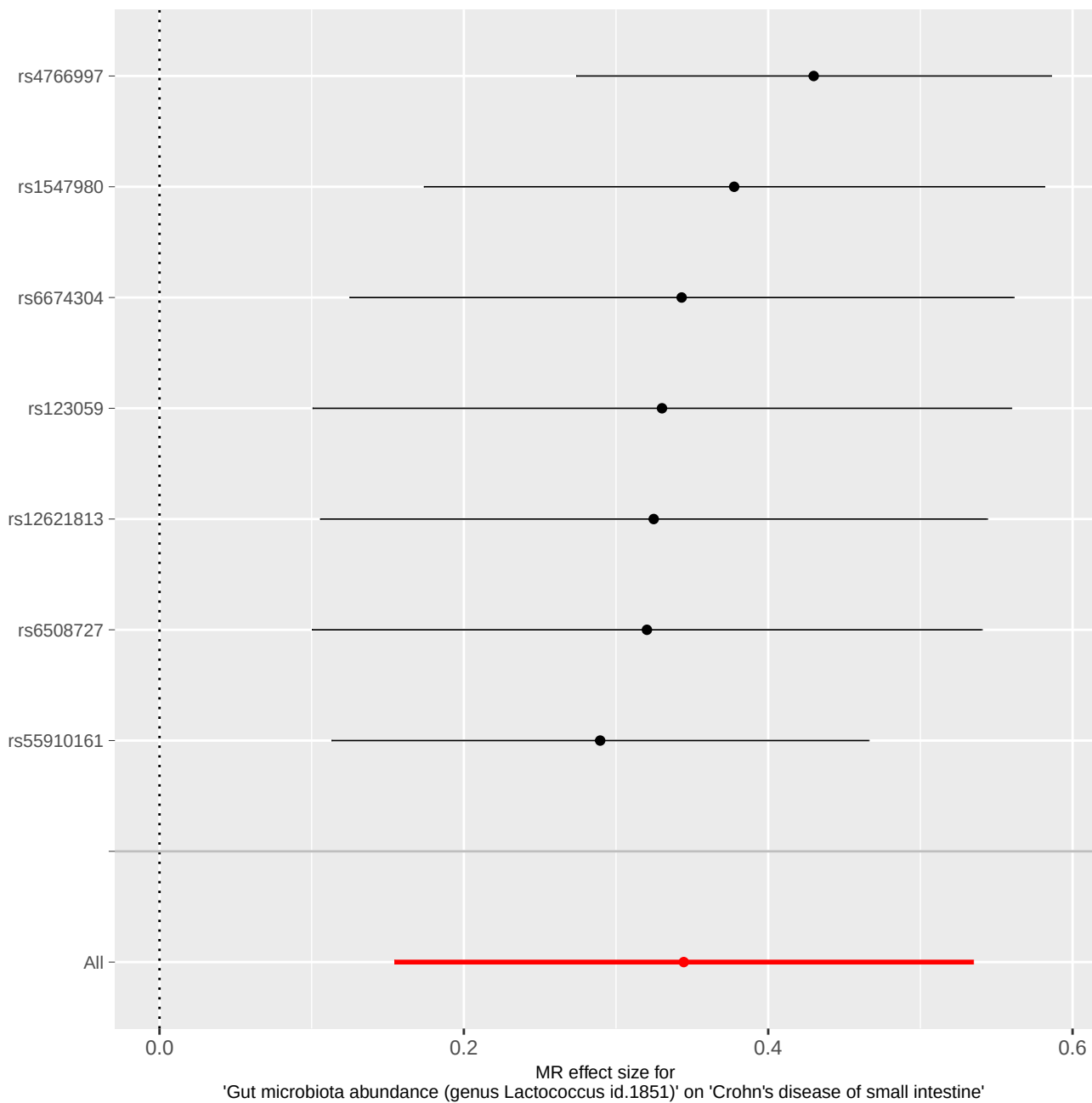


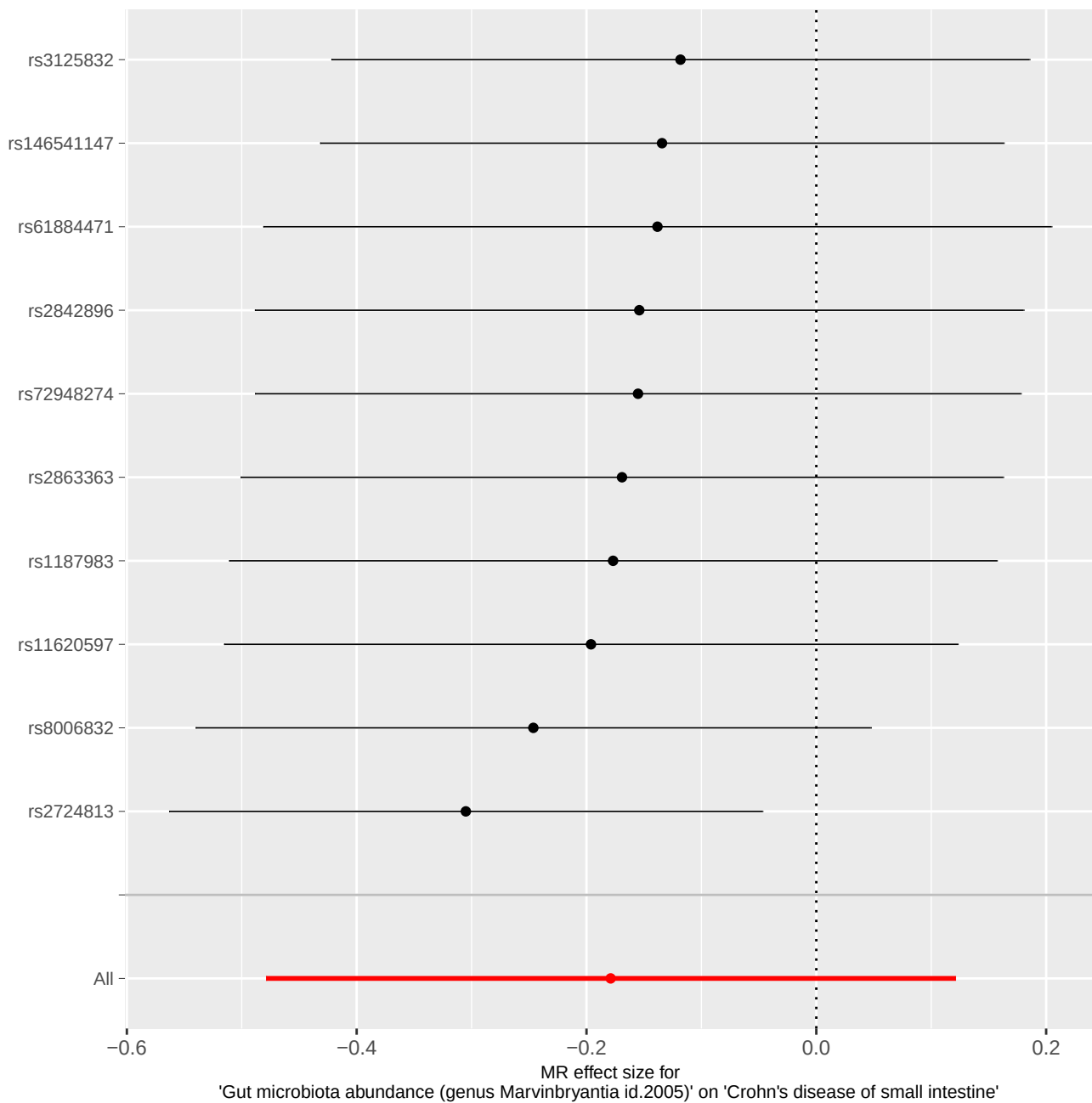


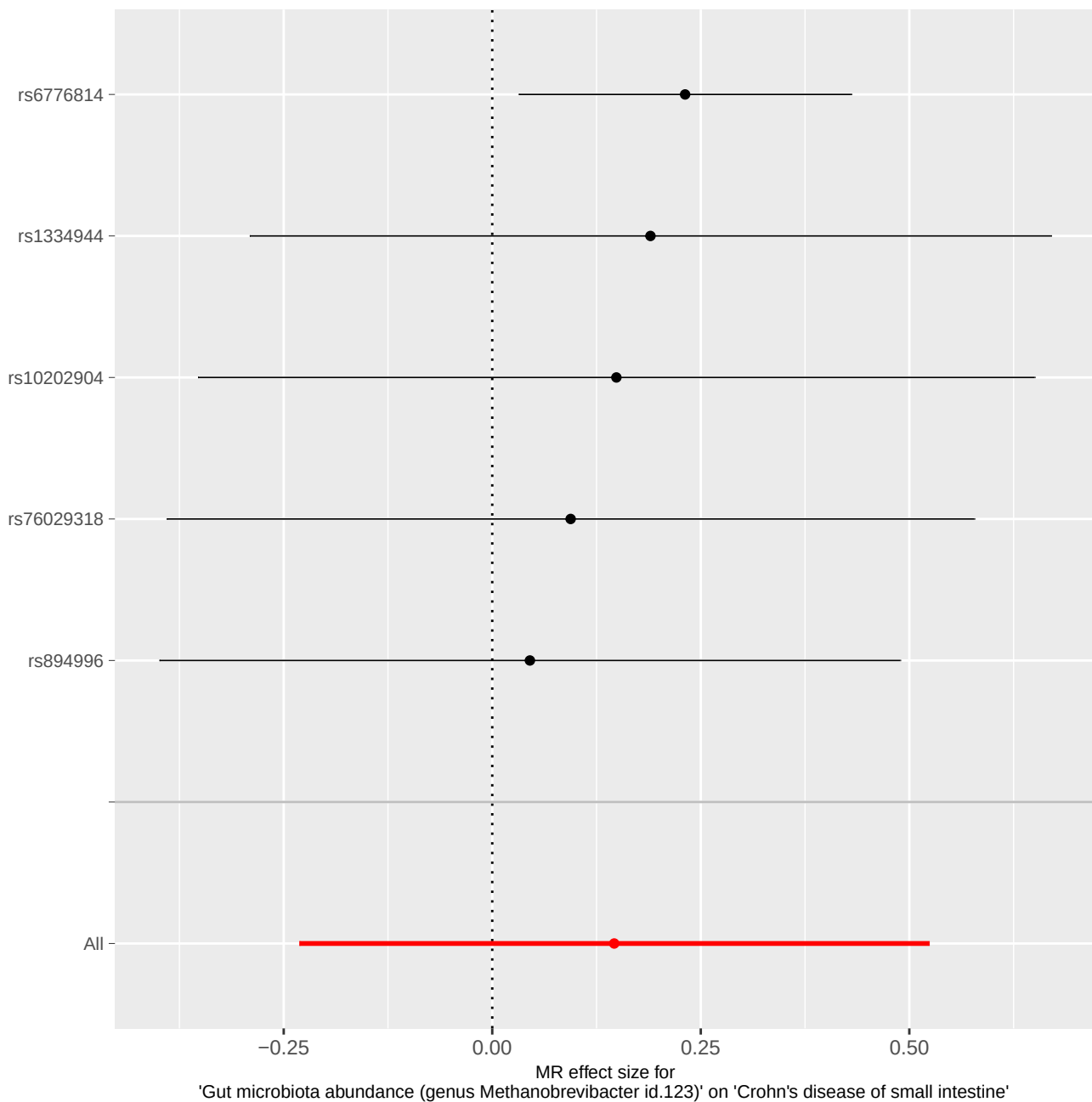


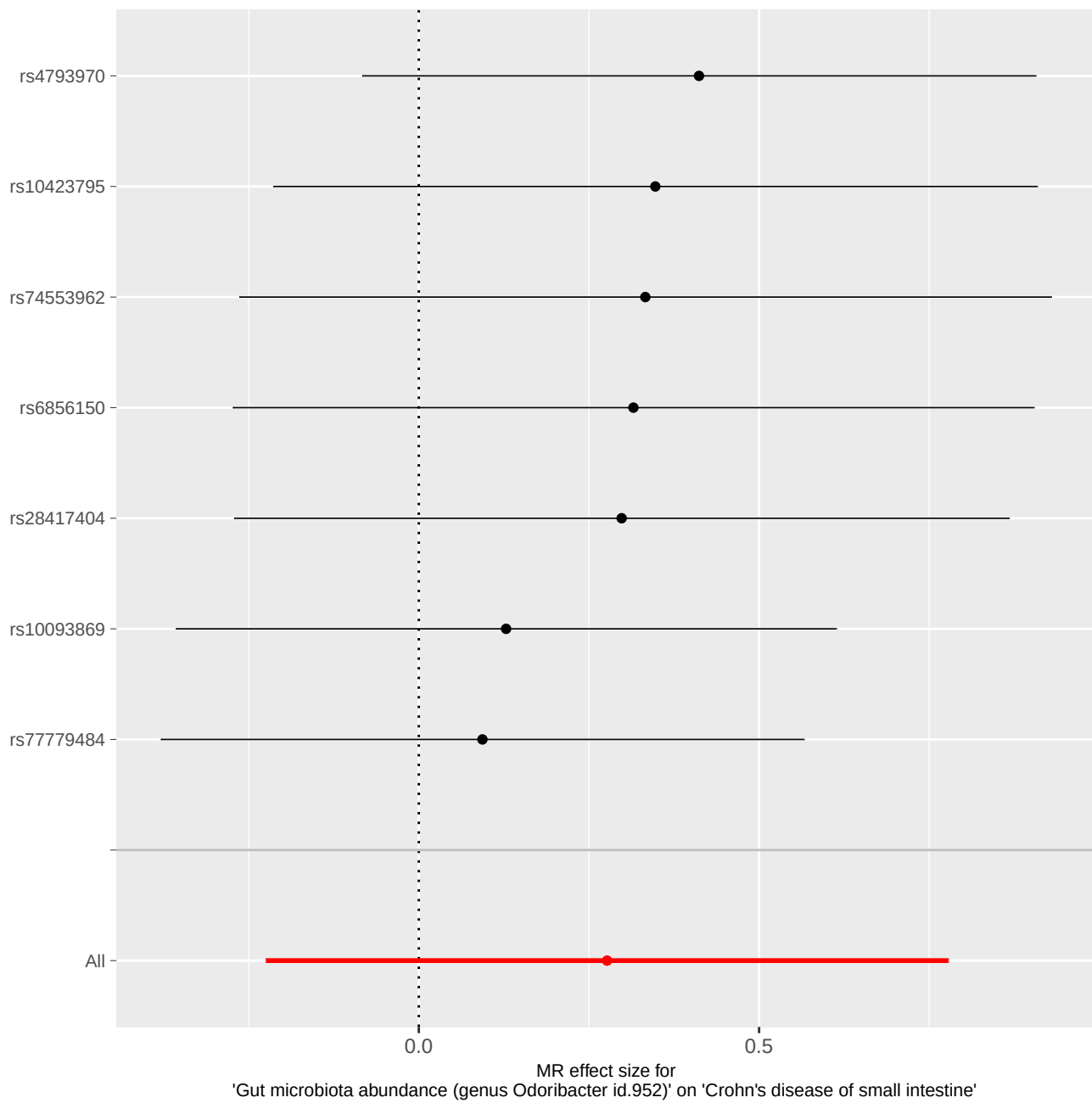


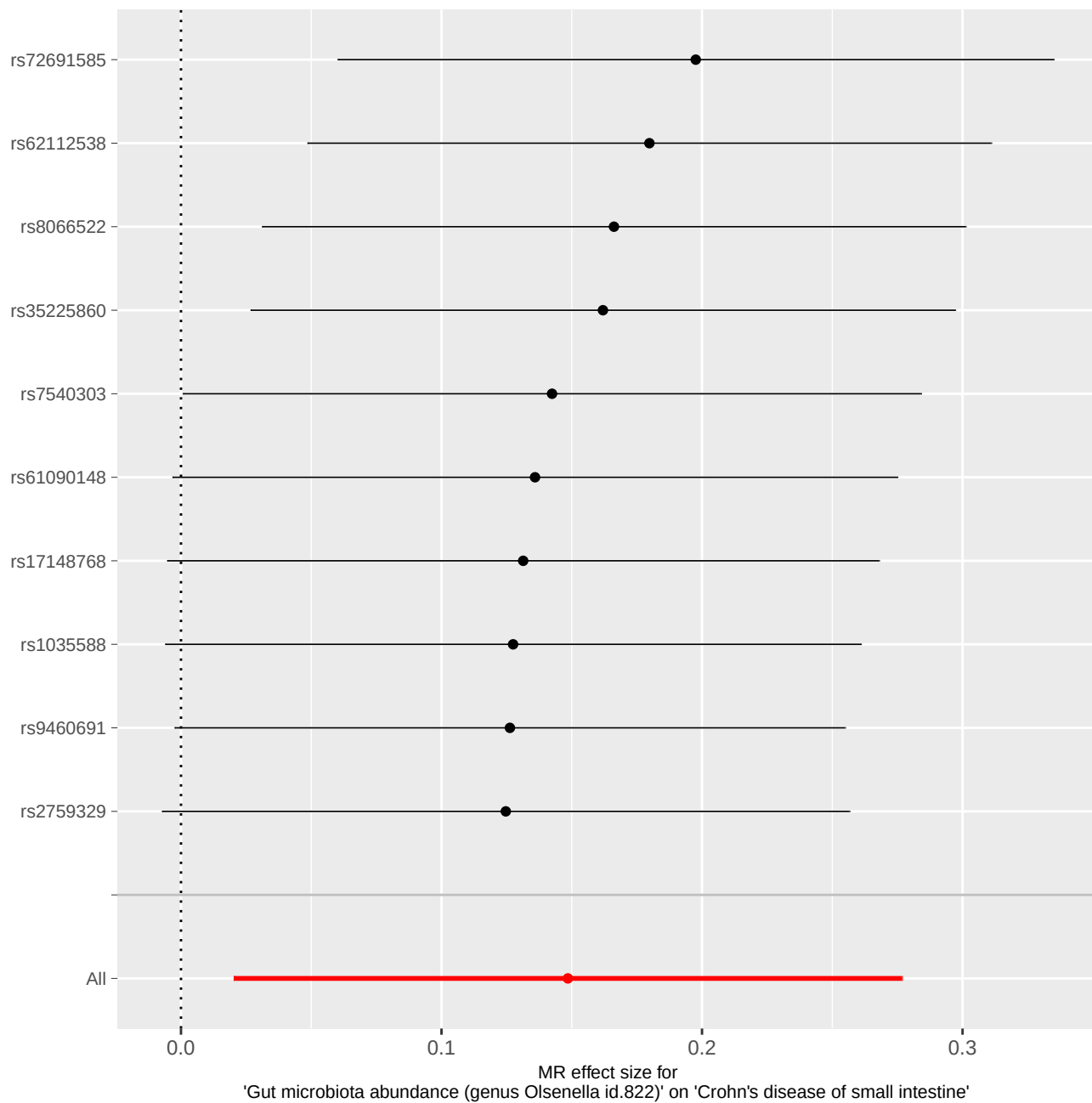


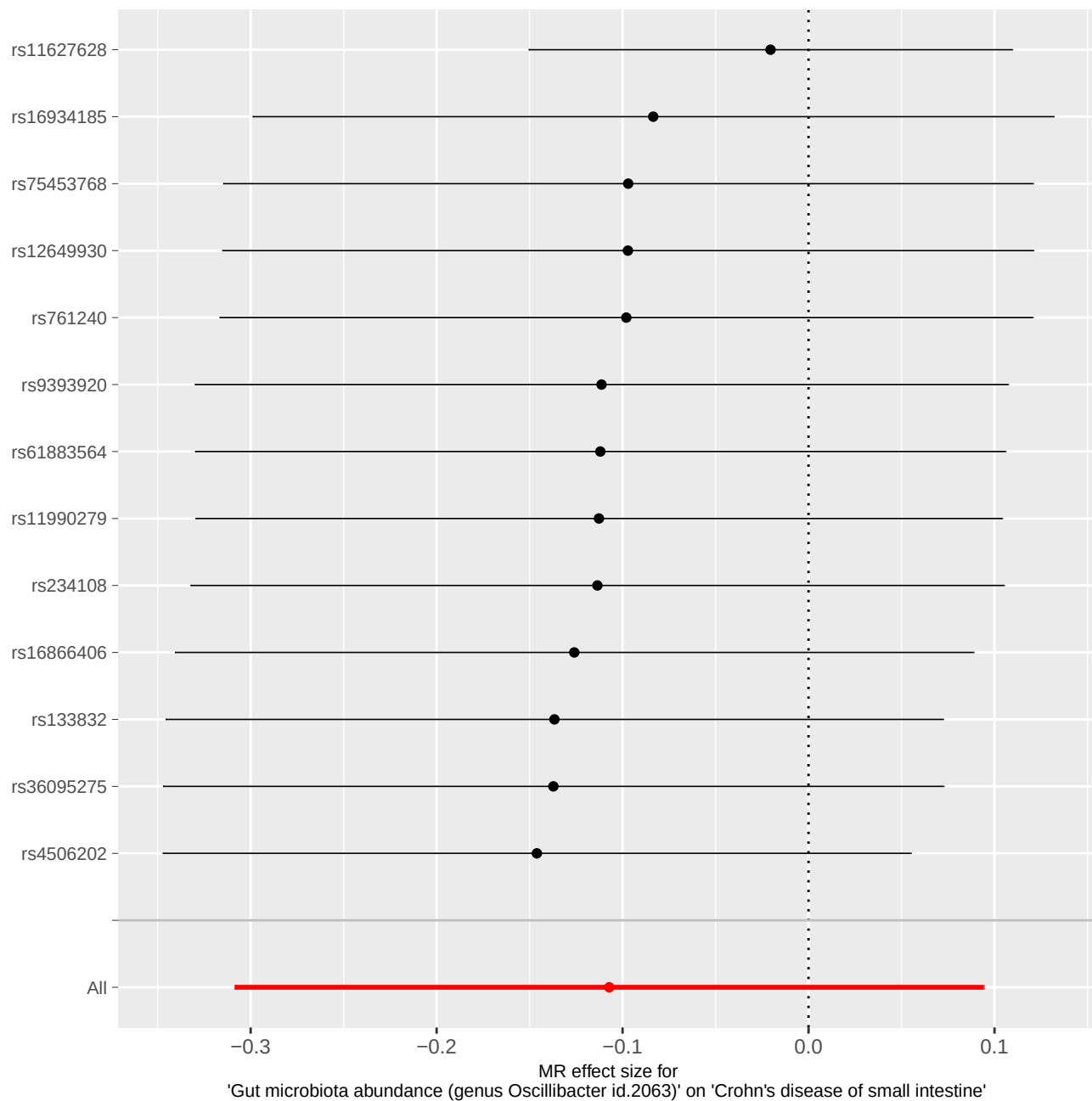




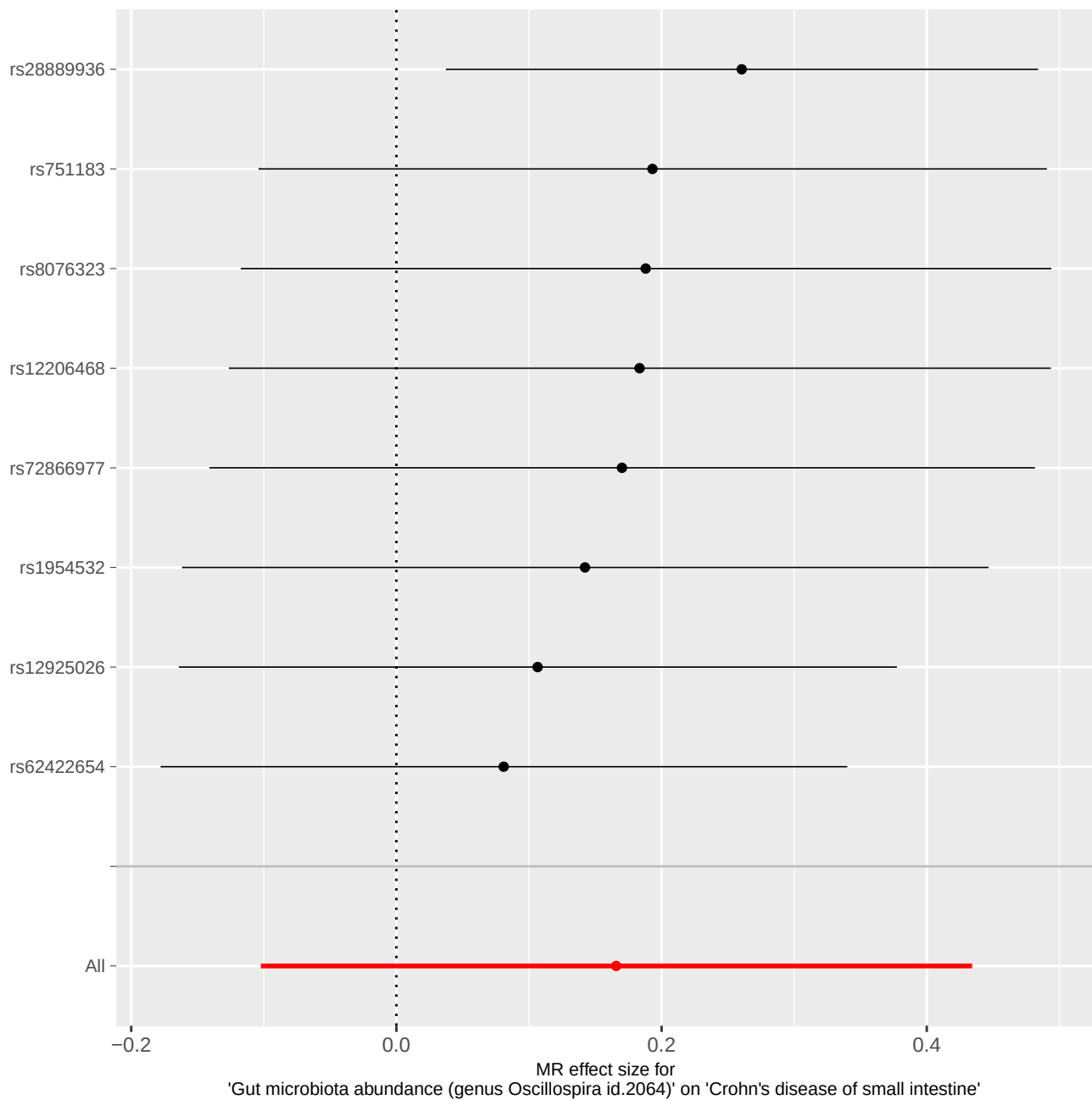




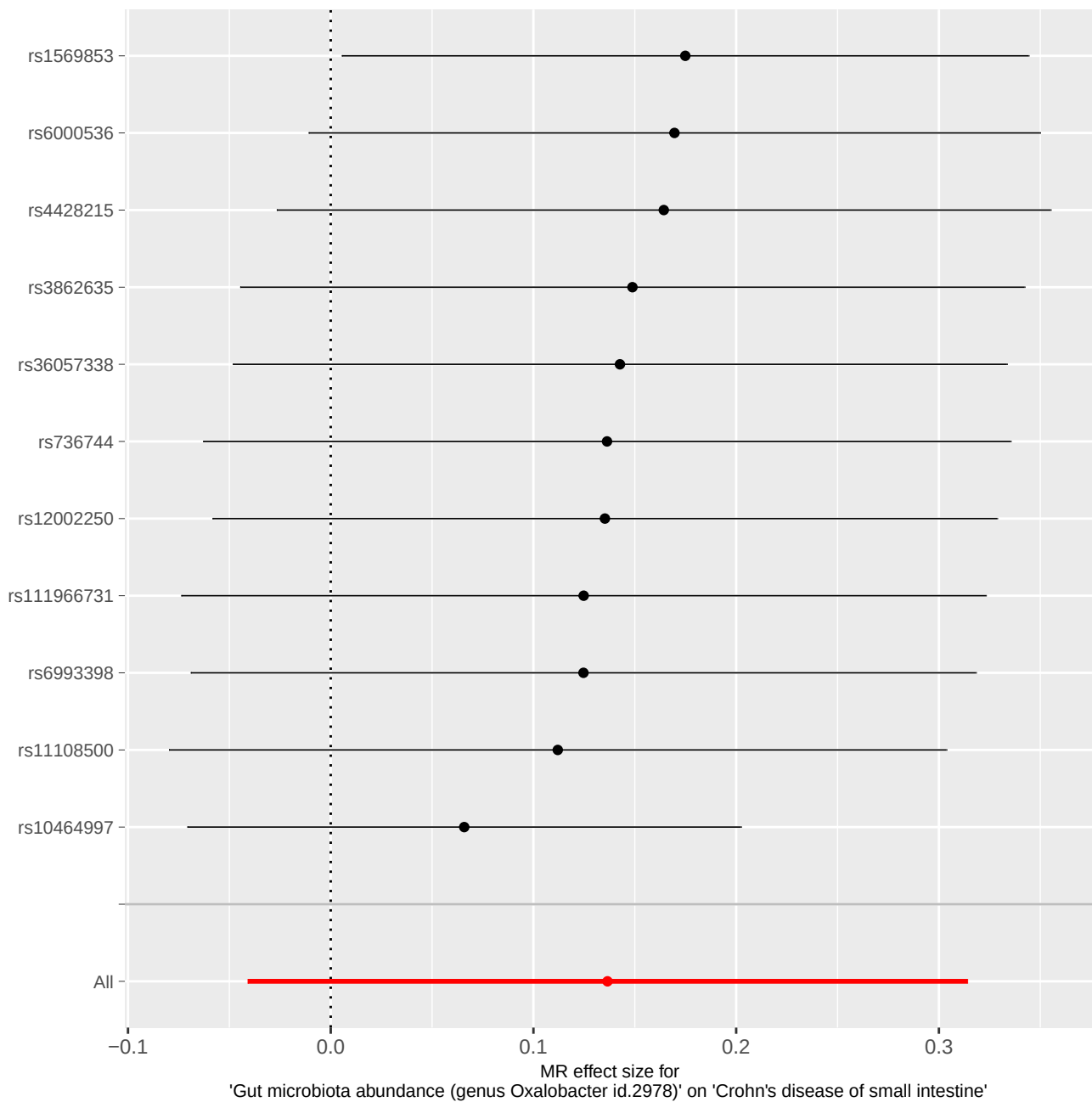


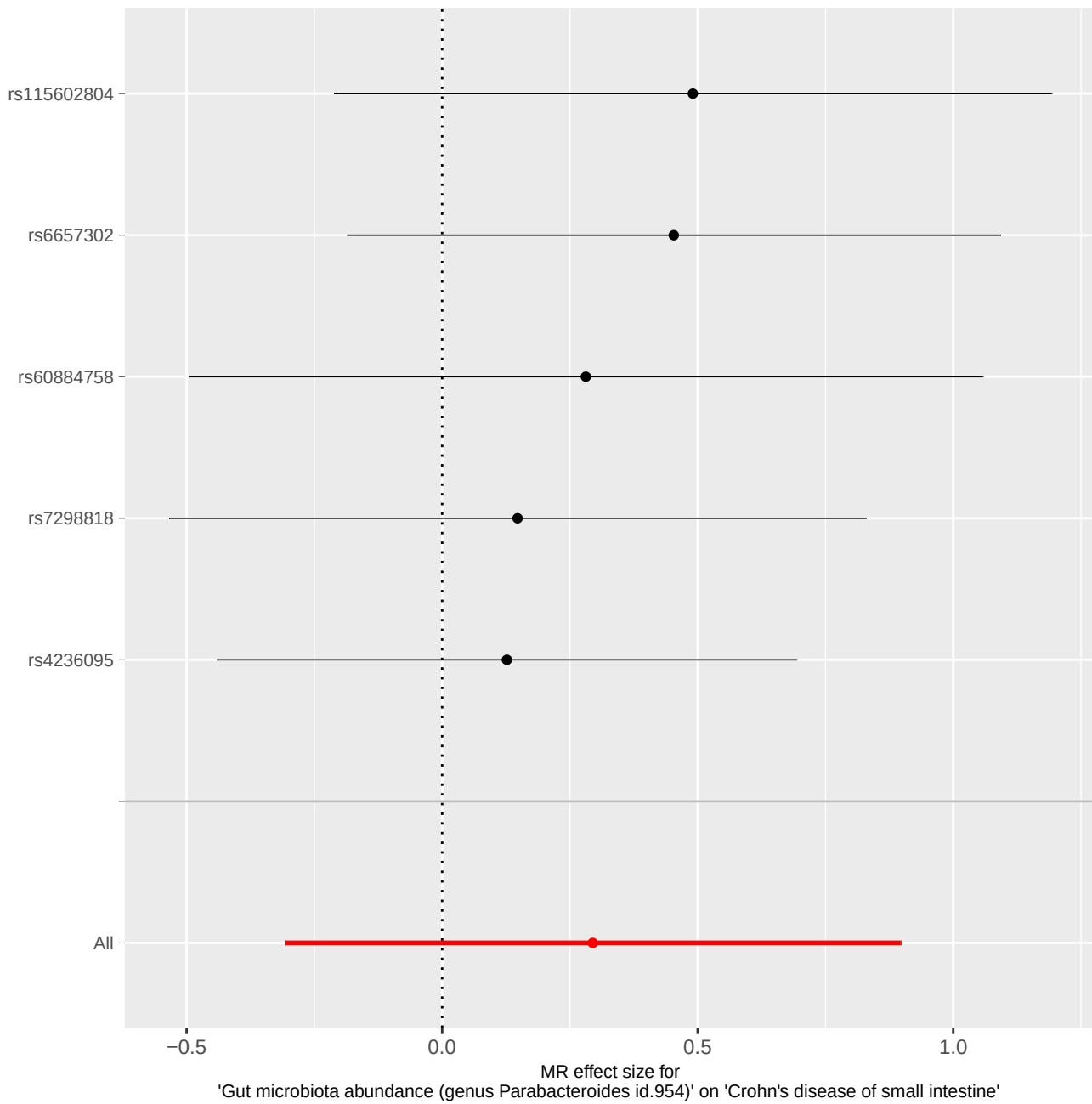


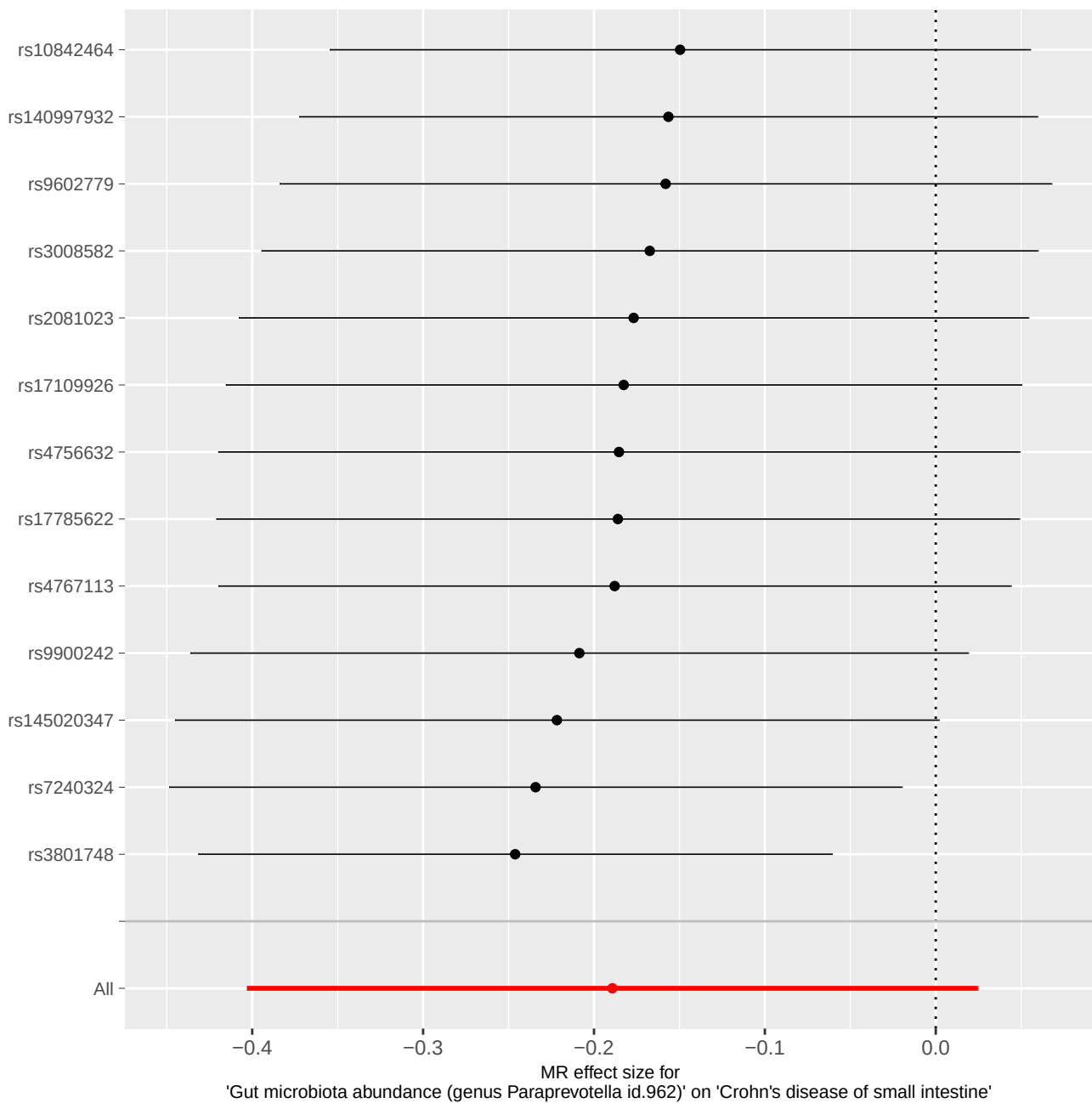
Batch 411 : Gut microbiota abundance (genus Oscillospira id.2064) on Crohn's disease of small intestine

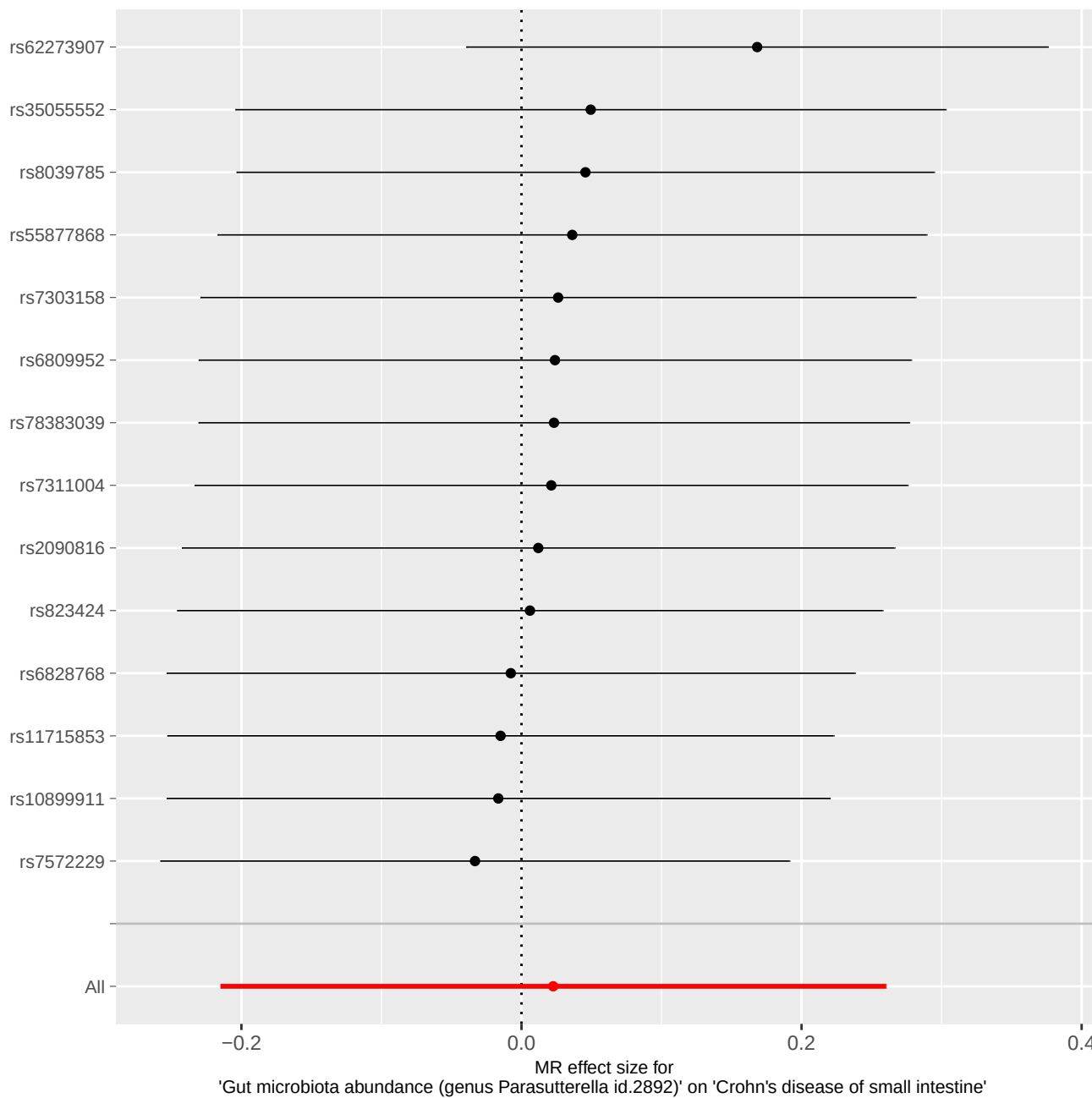


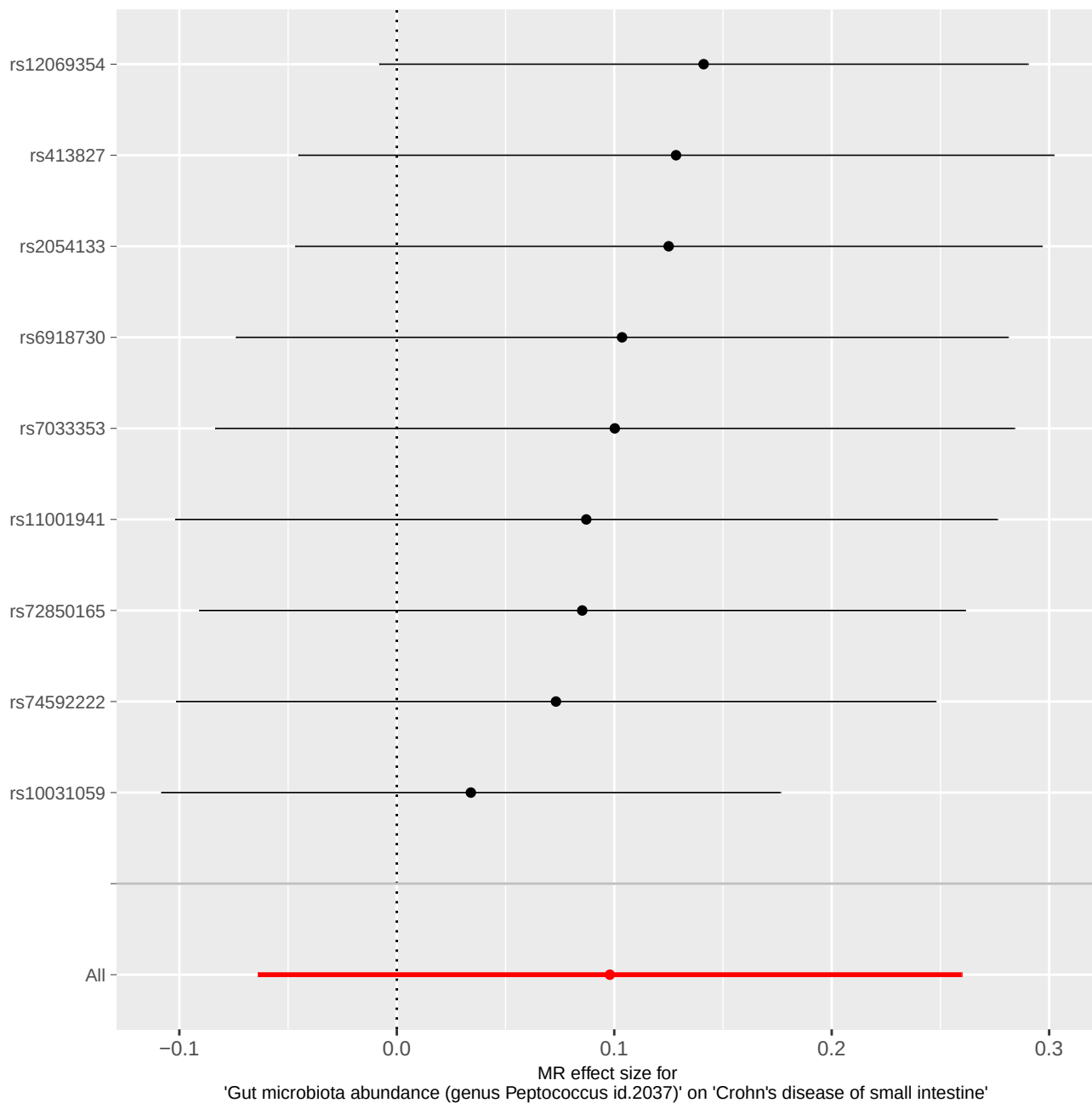
Batch 412 : Gut microbiota abundance (genus Oxalobacter id.2978) on Crohn's disease of small intestine

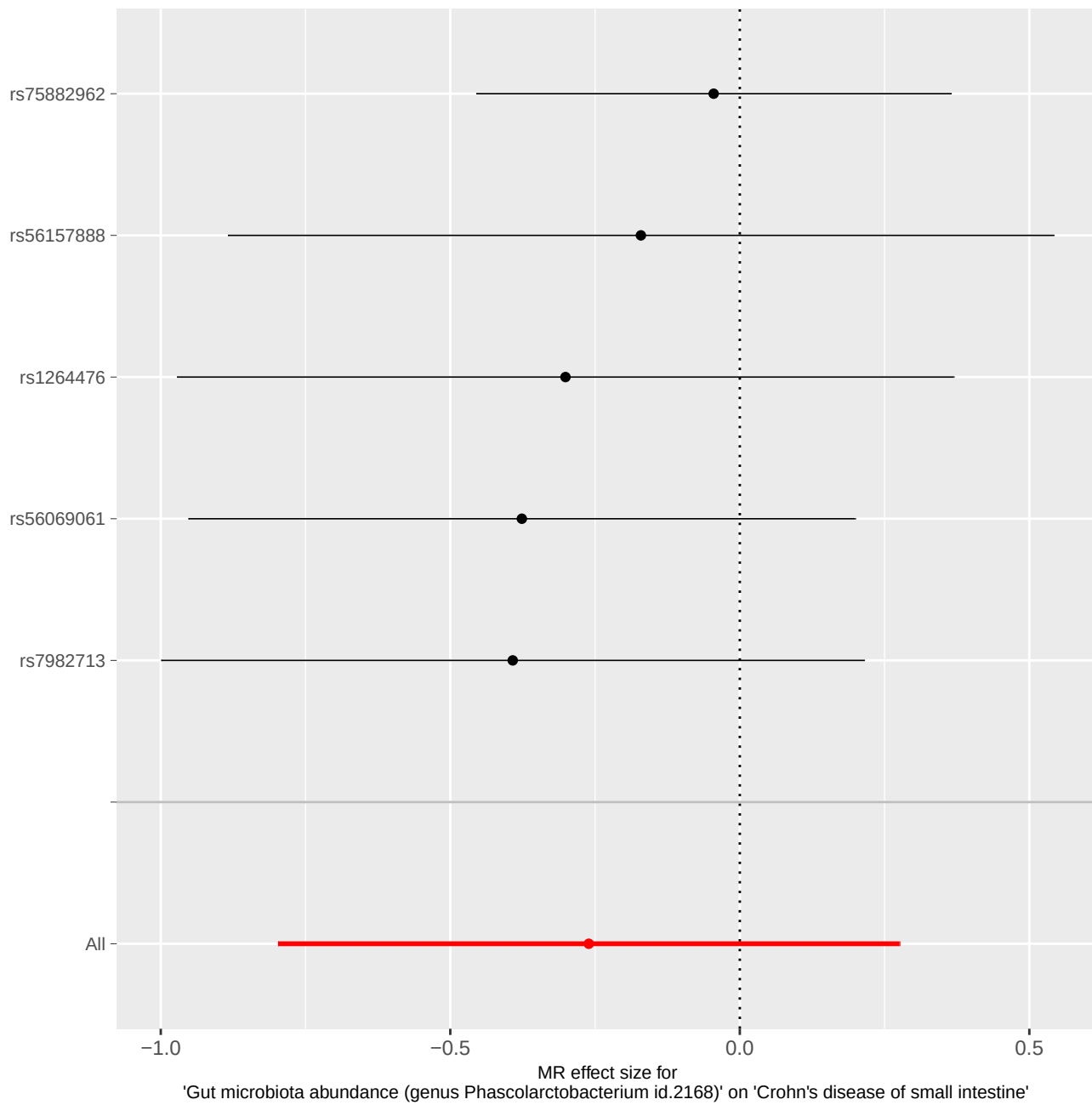


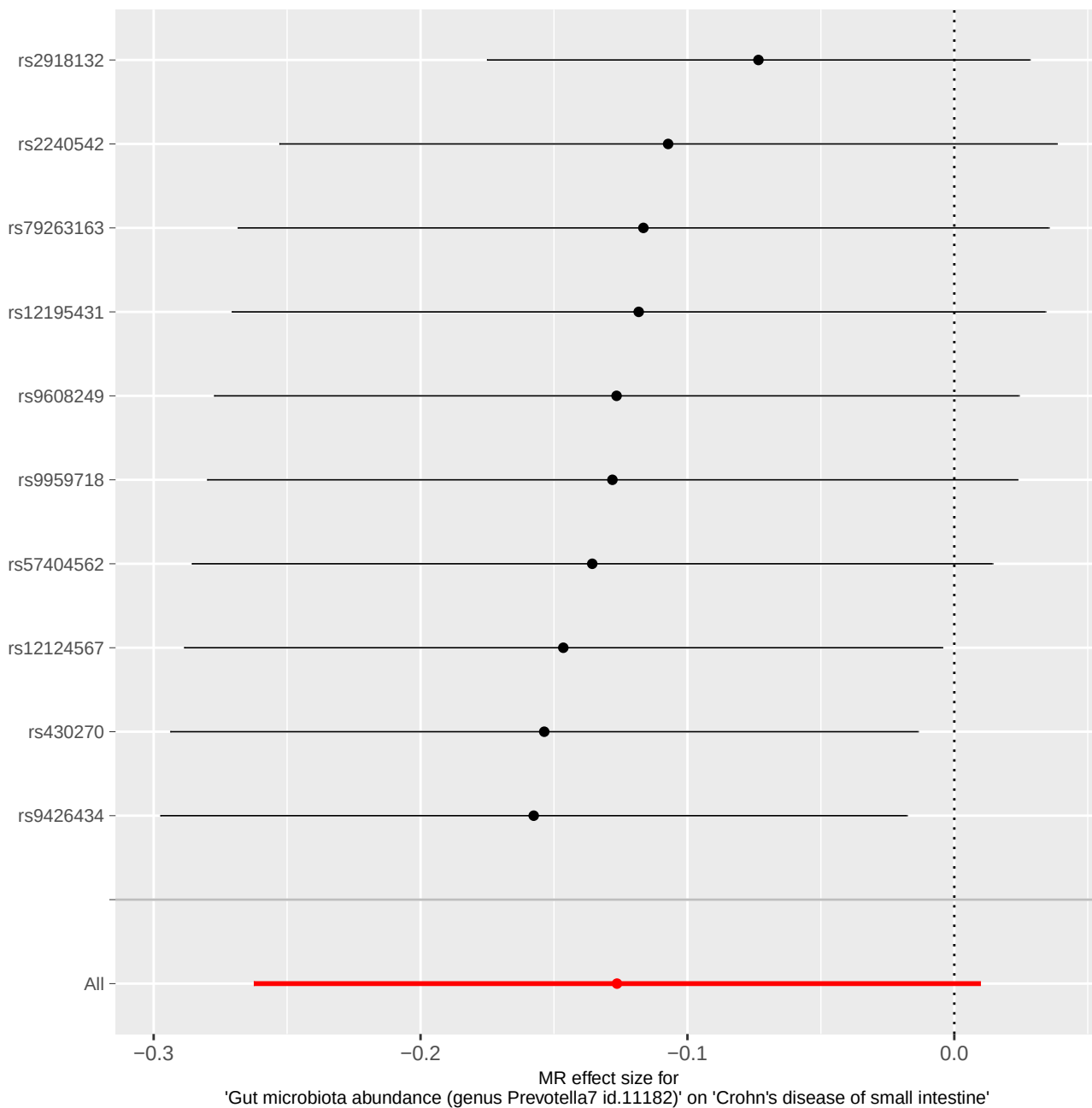


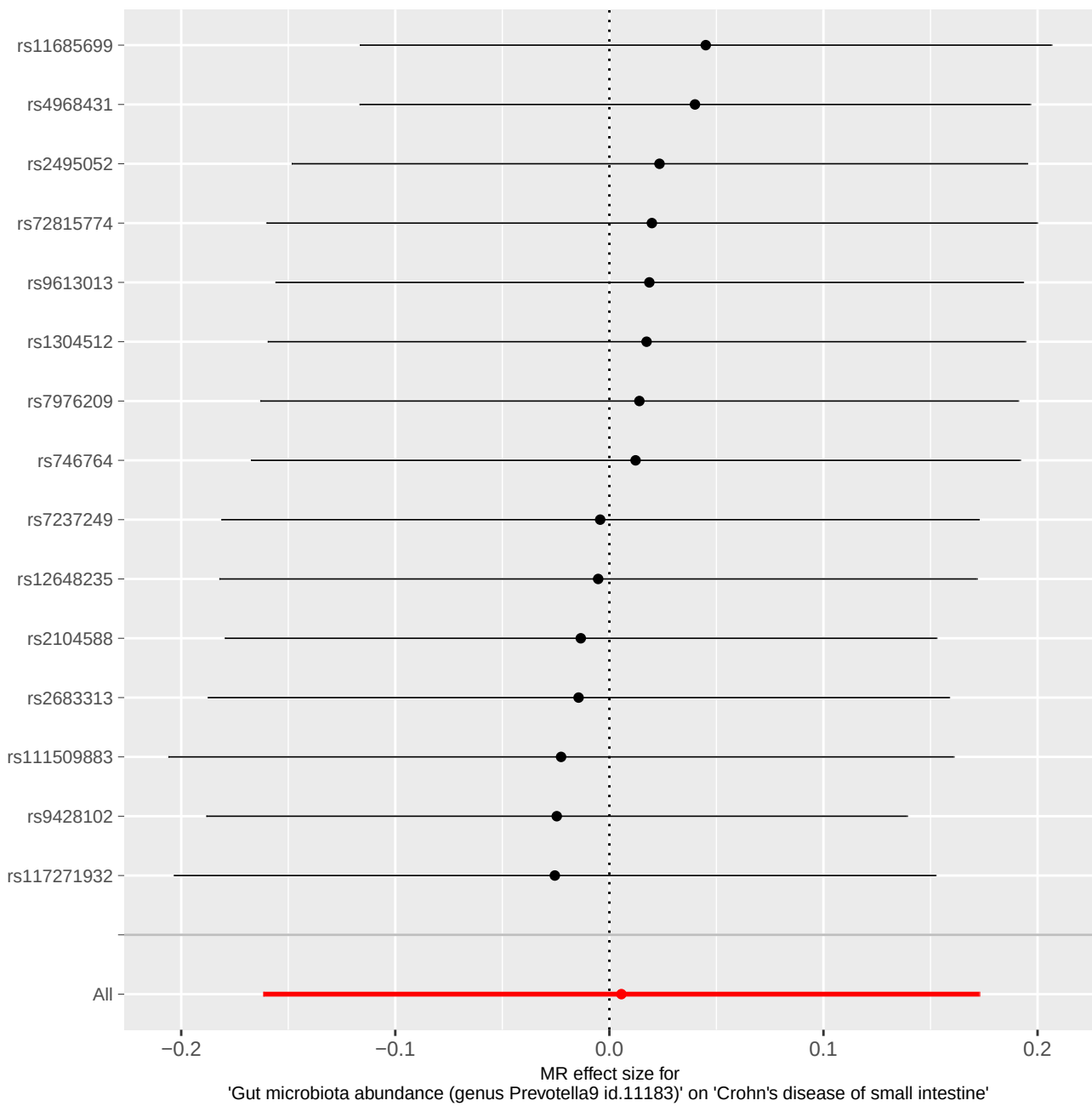


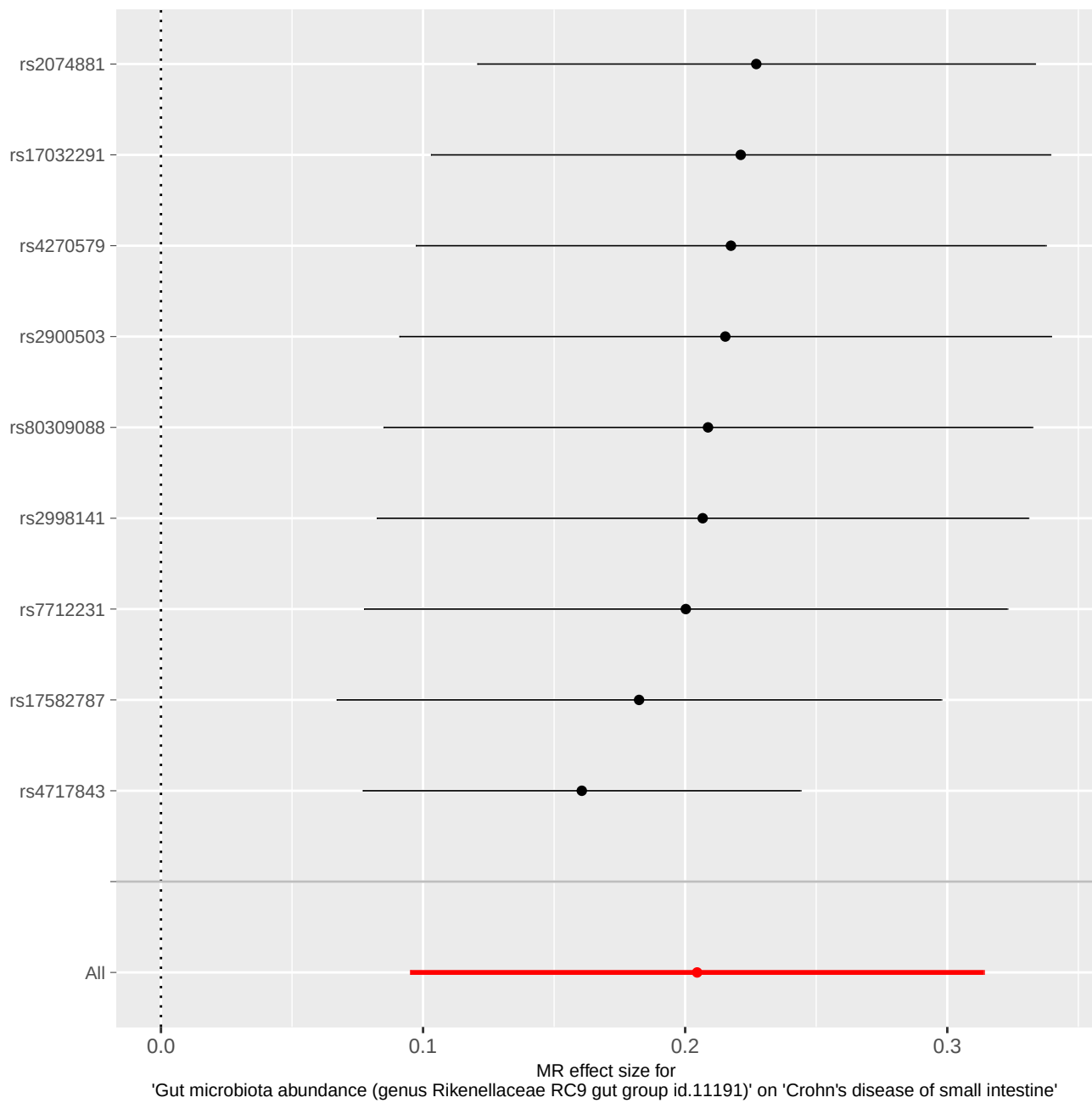


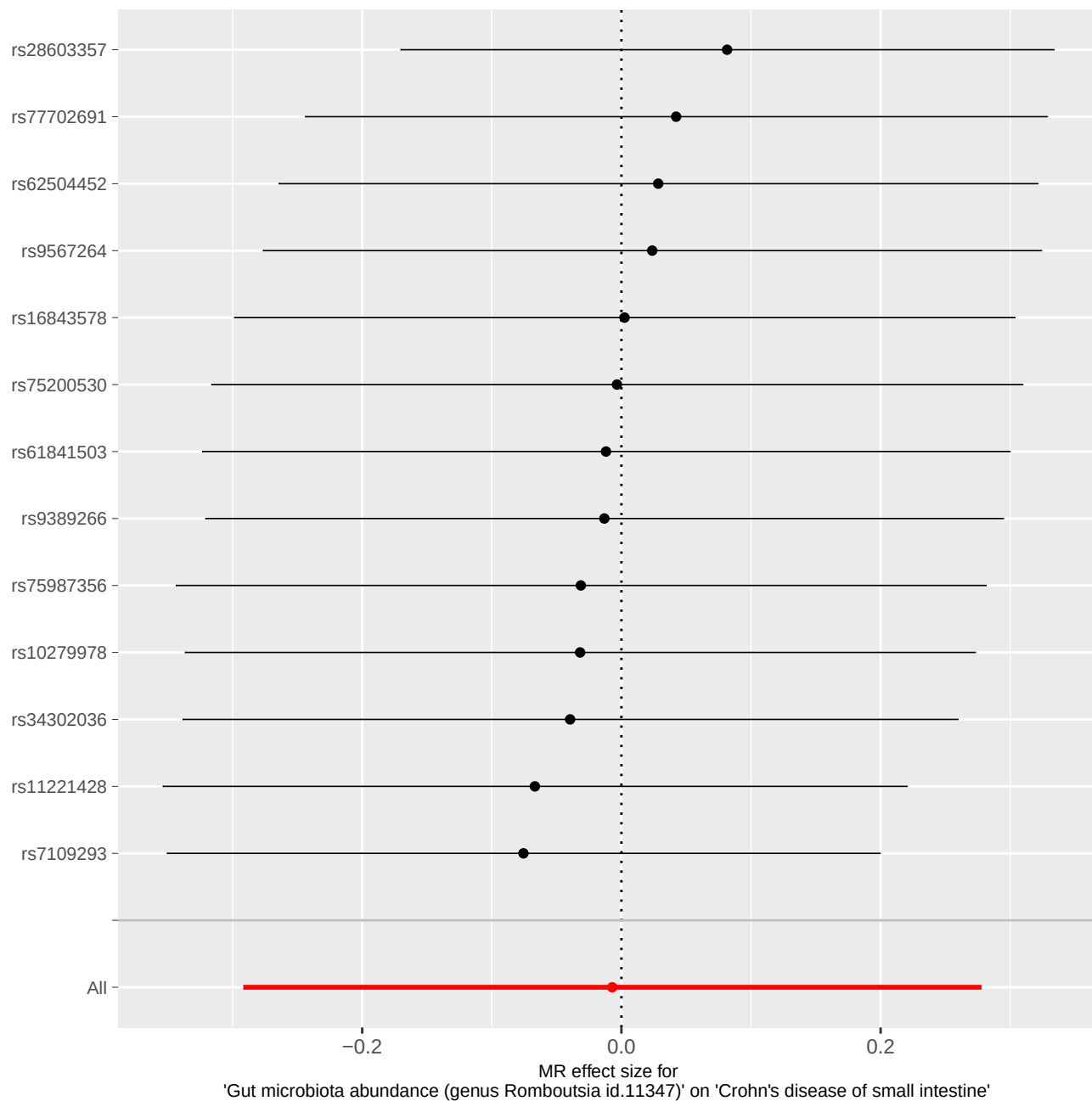


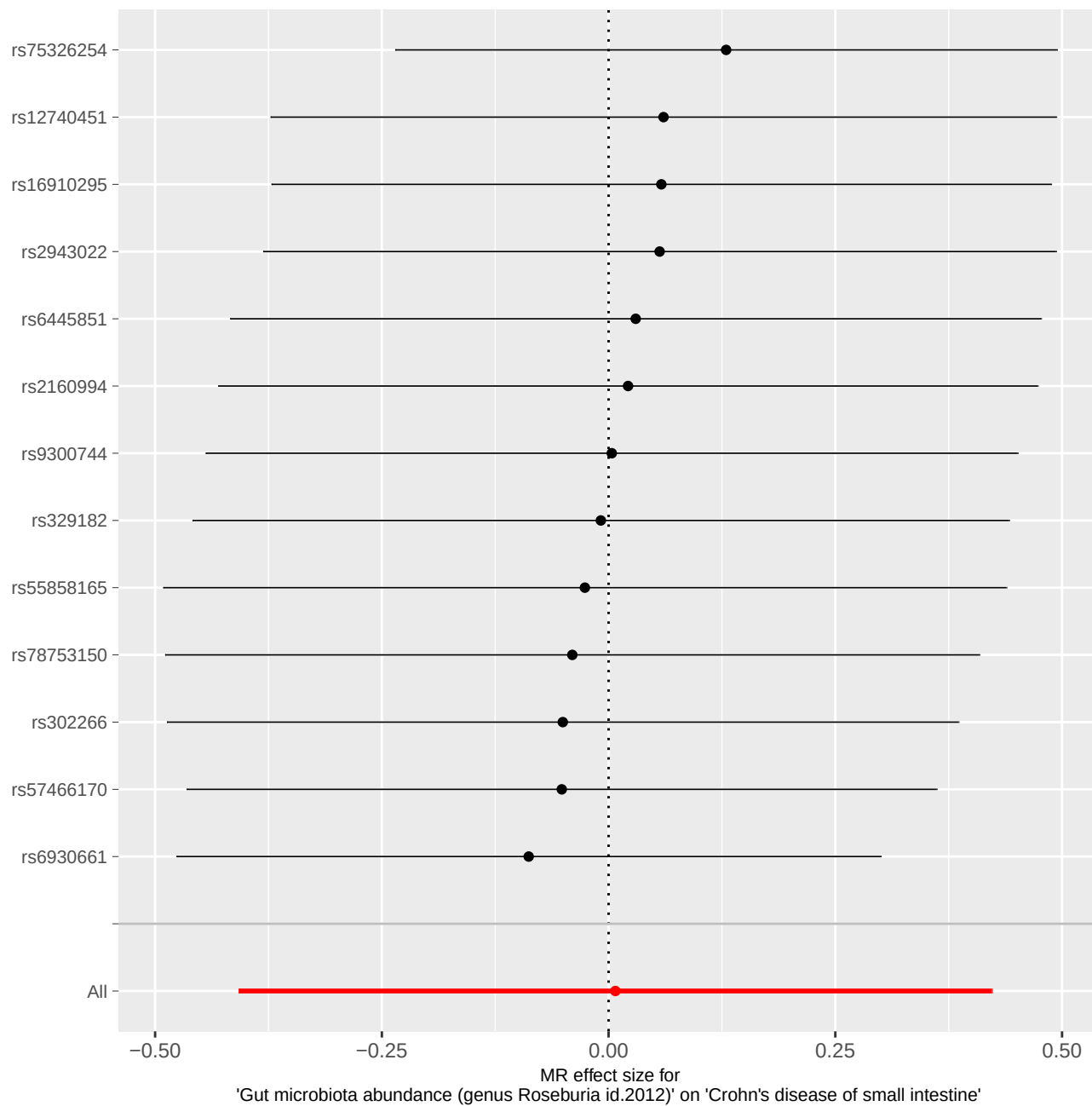


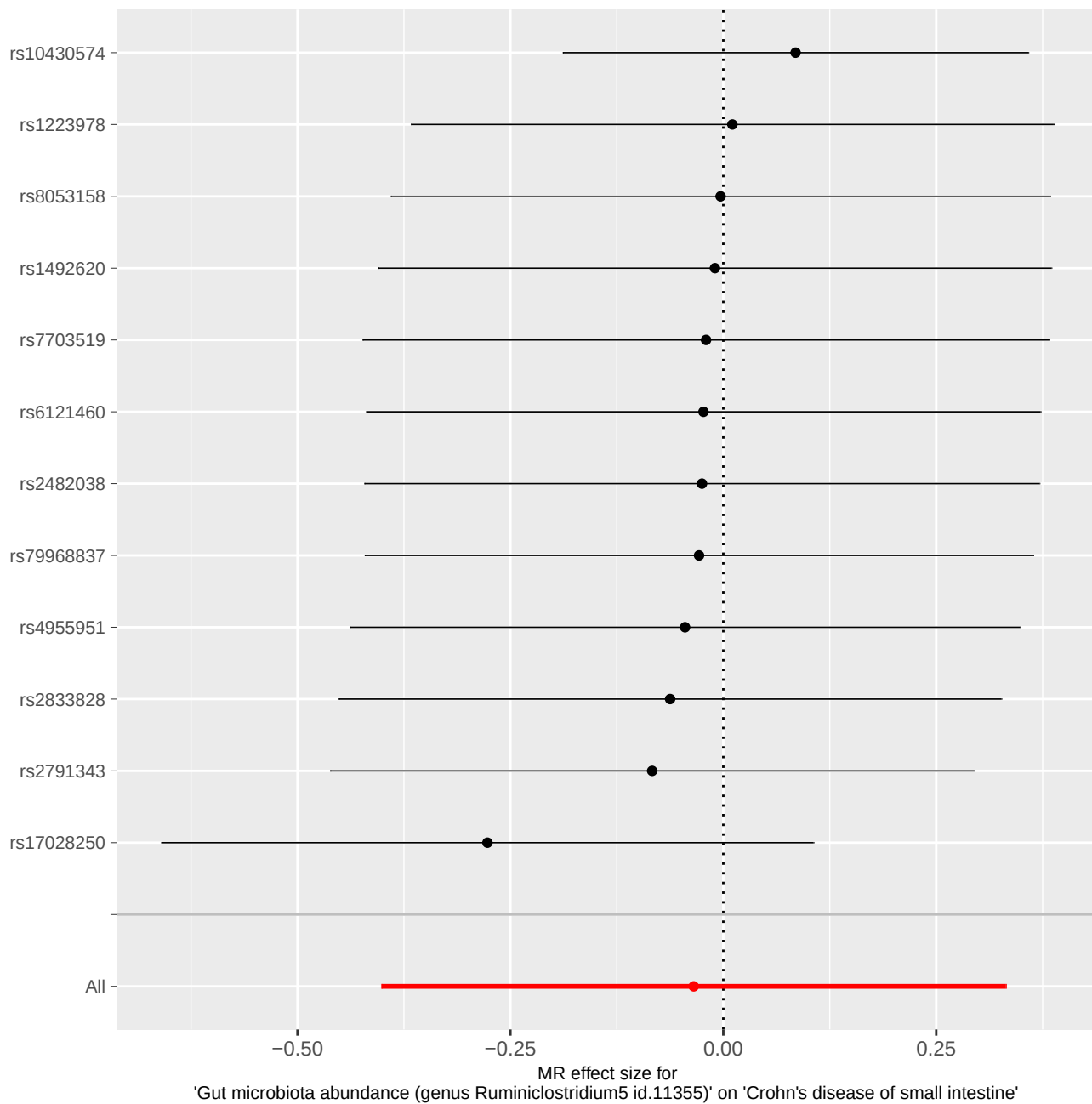


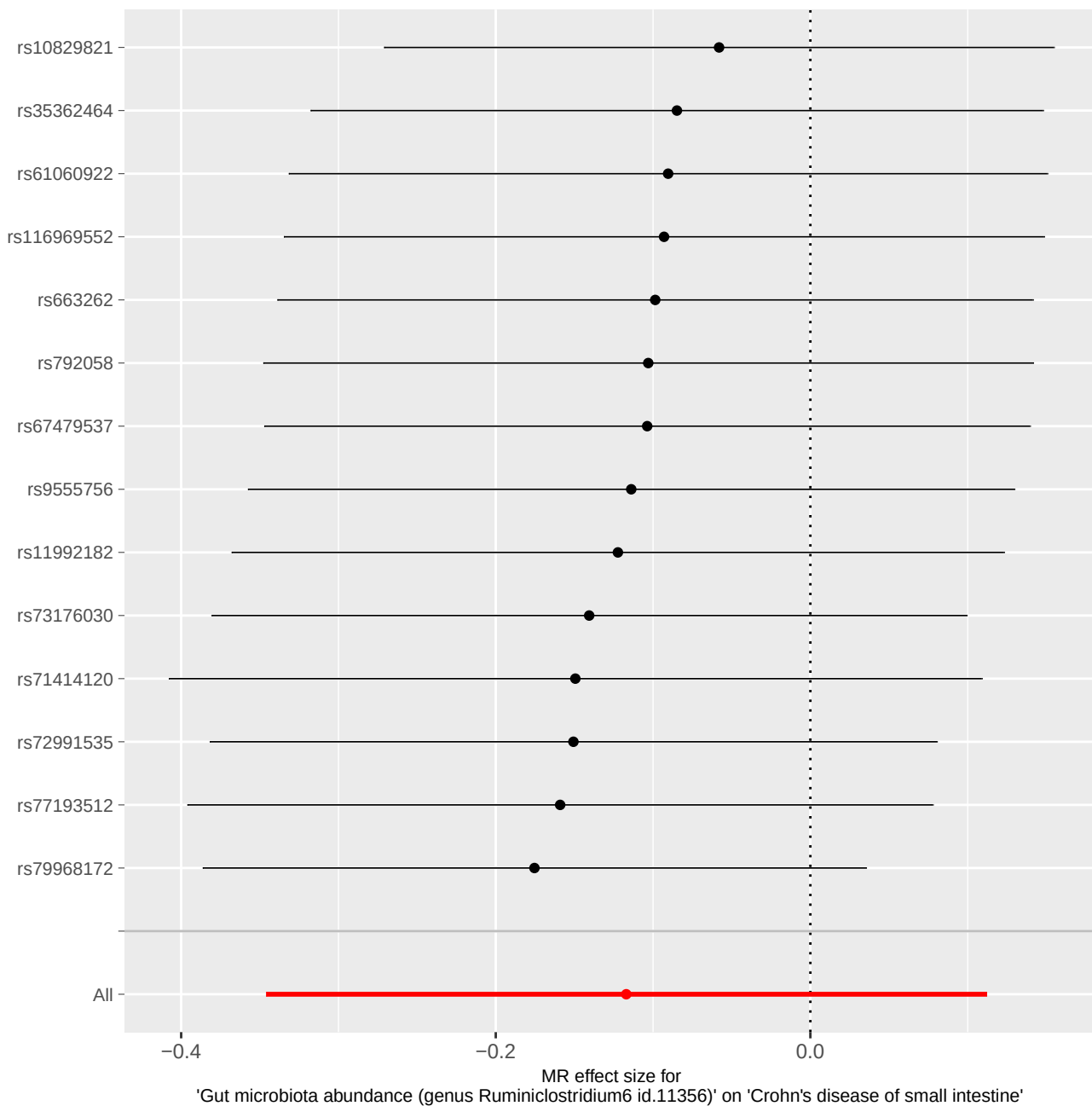


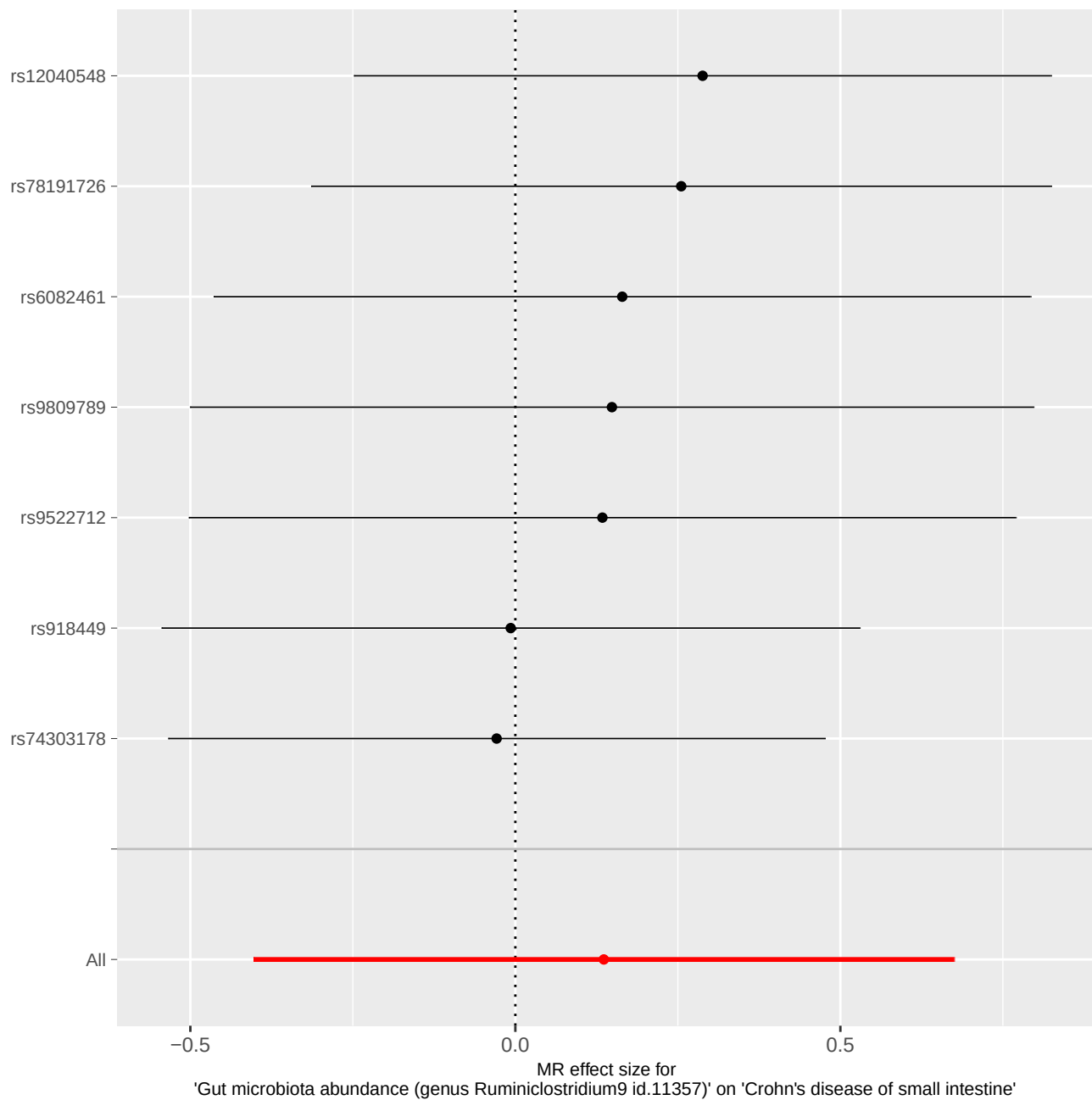




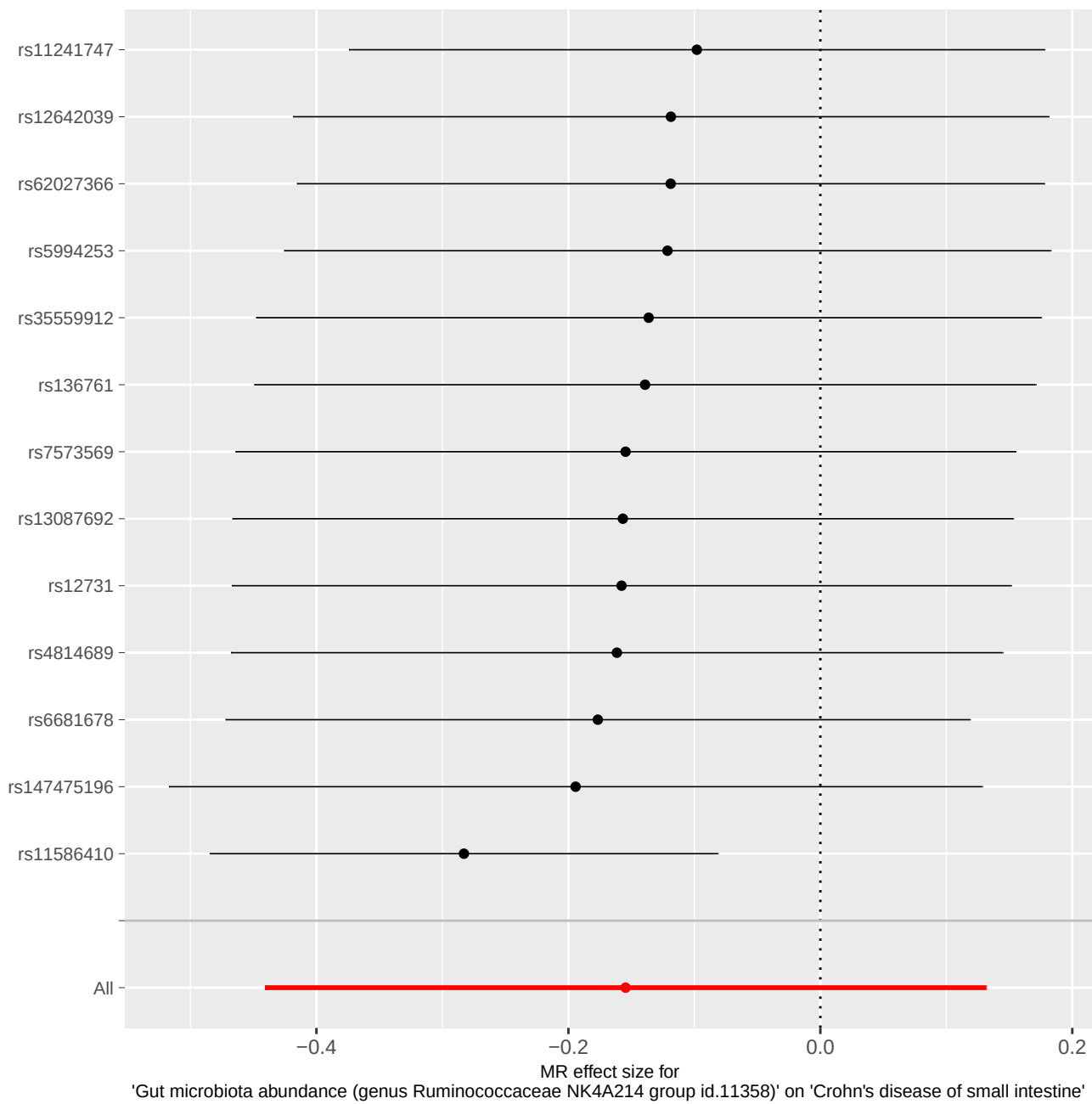


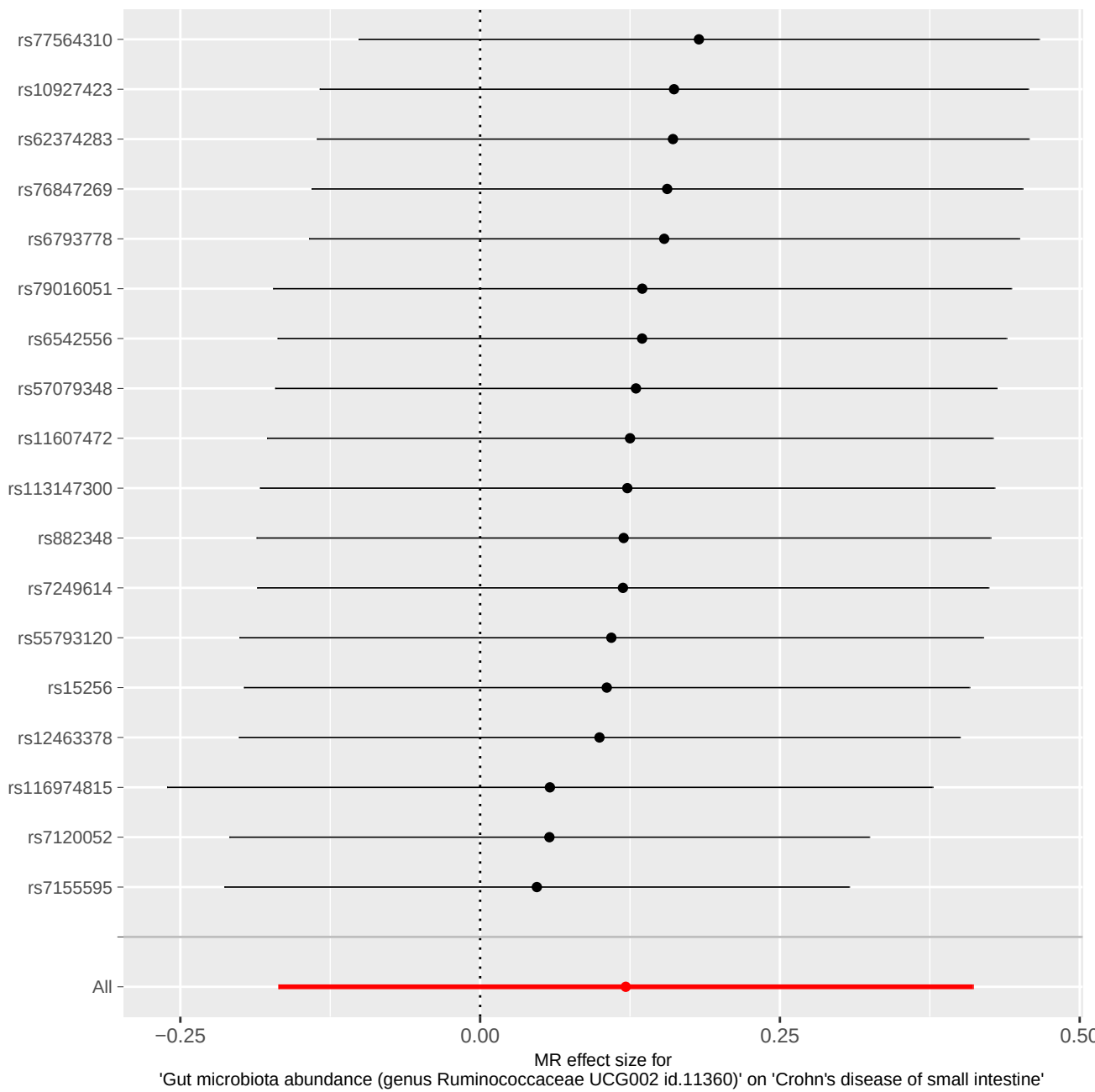


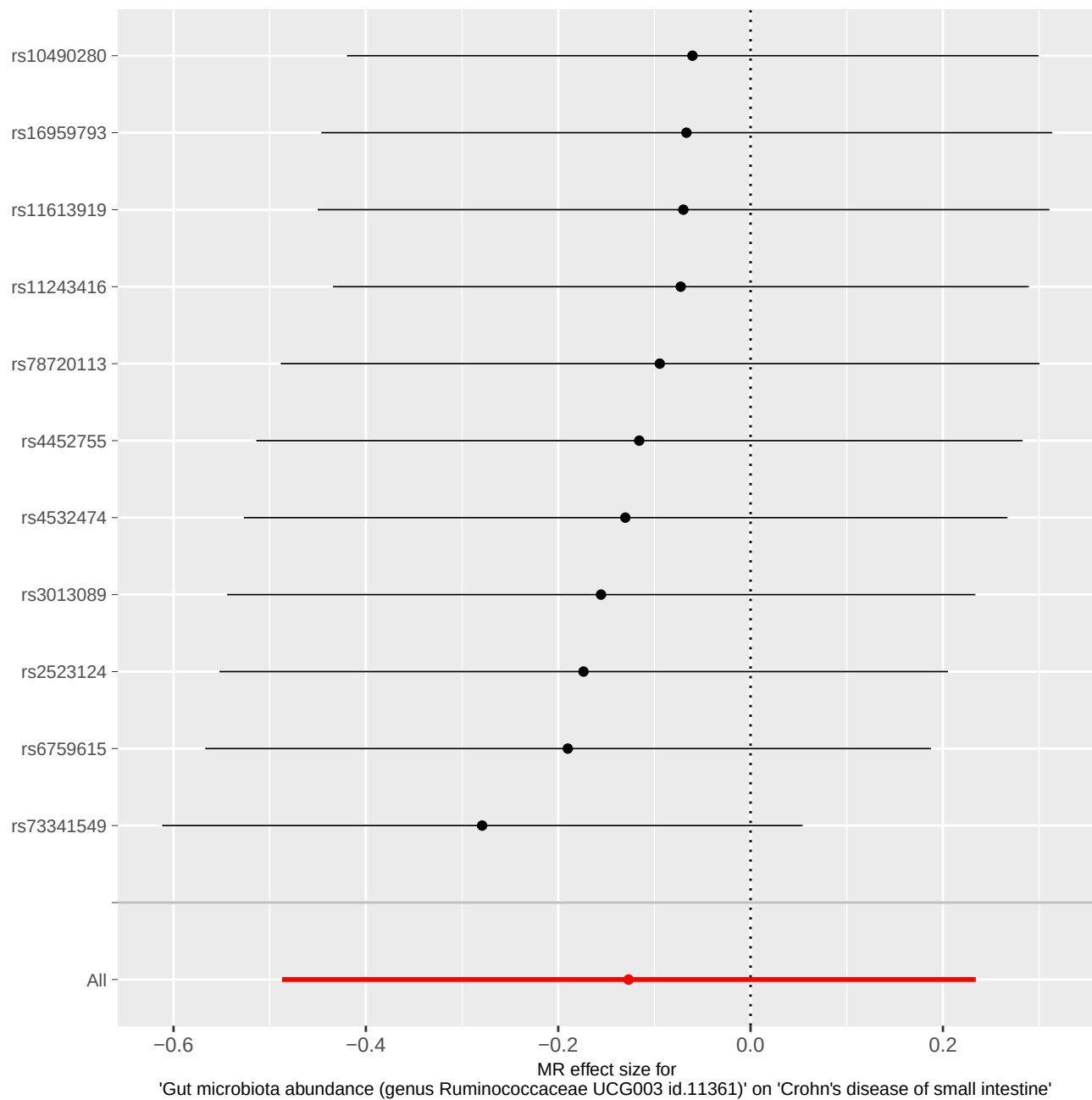


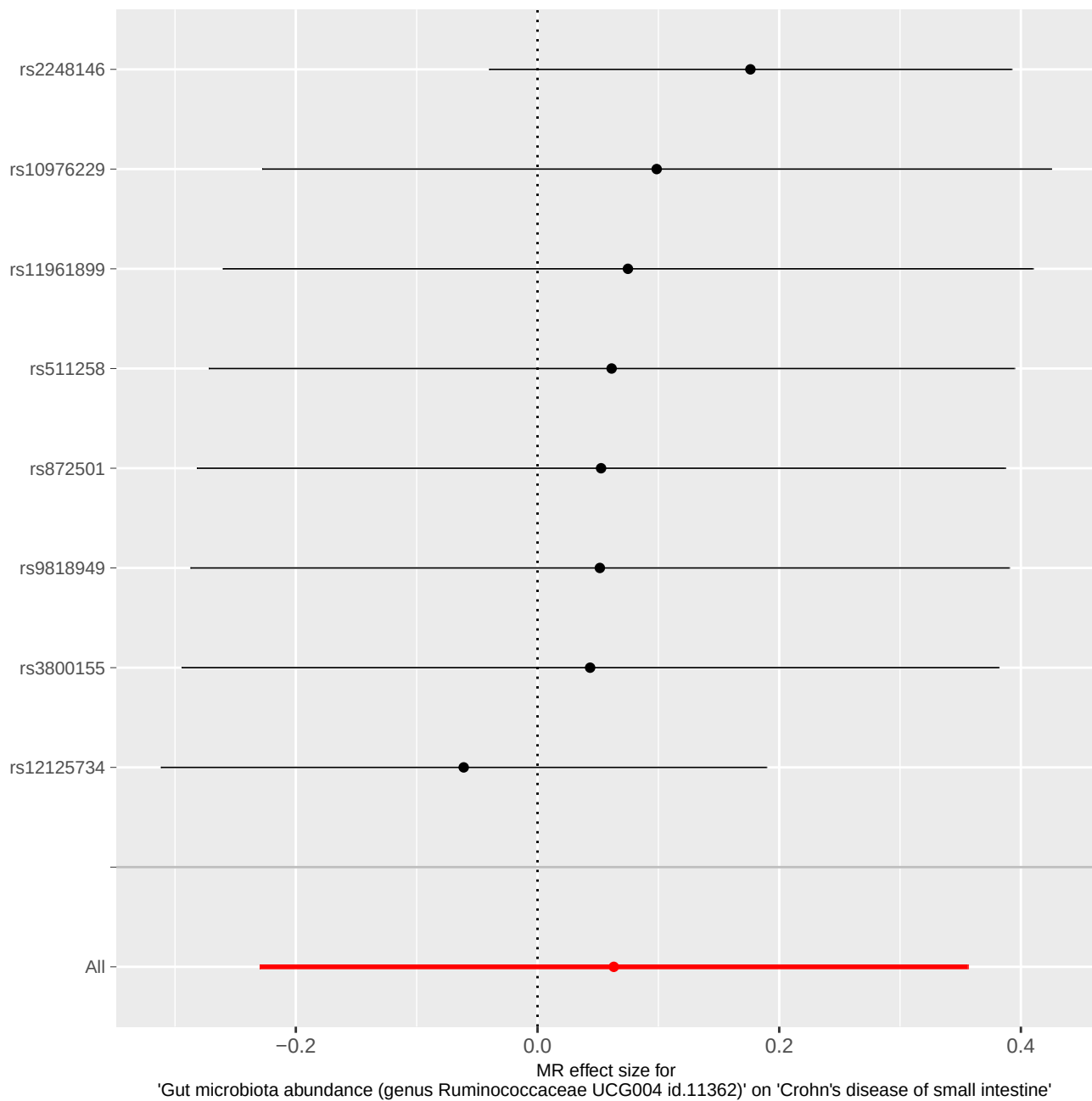


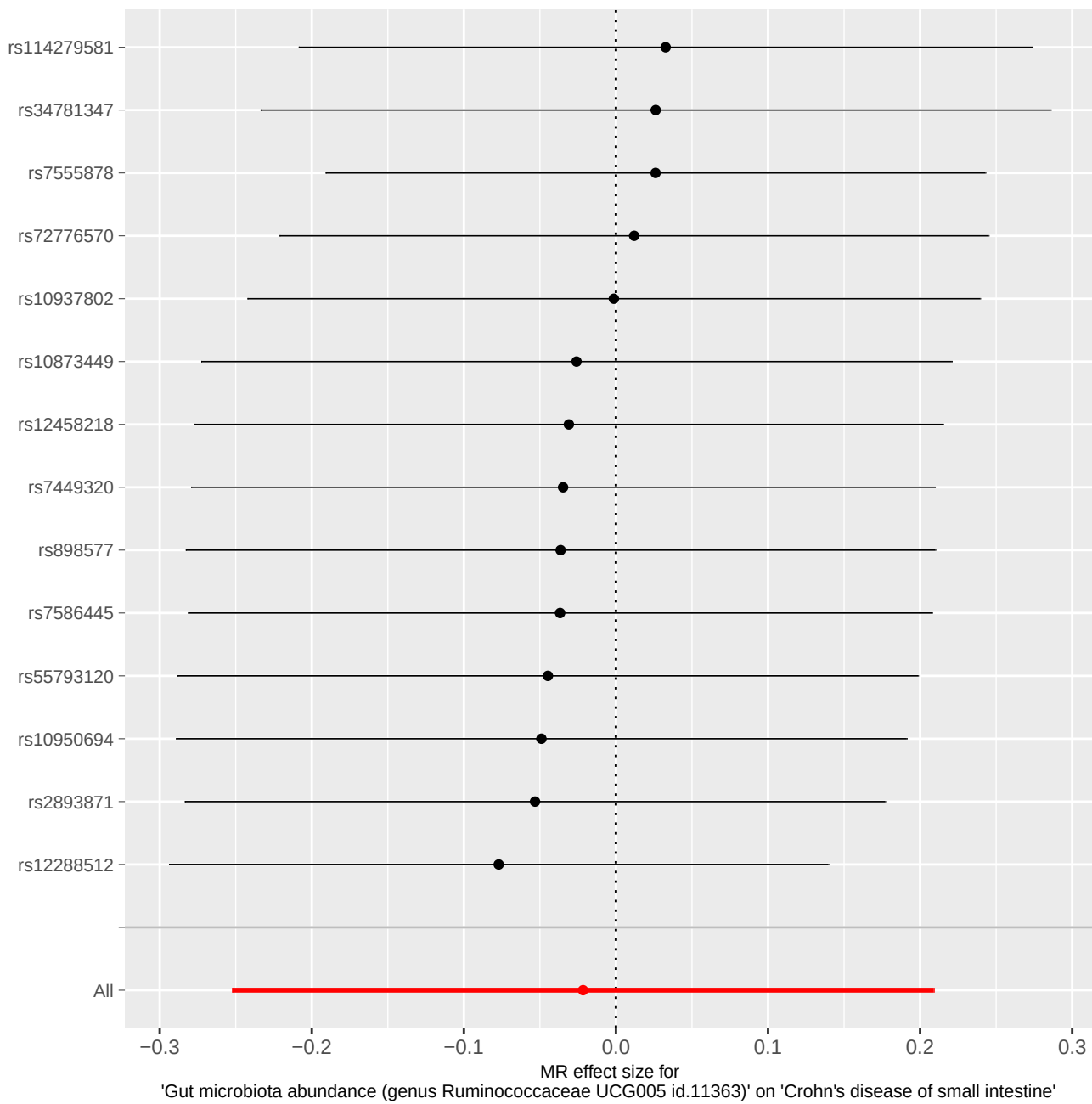
MR effect size for
'Gut microbiota abundance (genus Ruminiclostridium9 id.11357)' on 'Crohn's disease of small intestine'

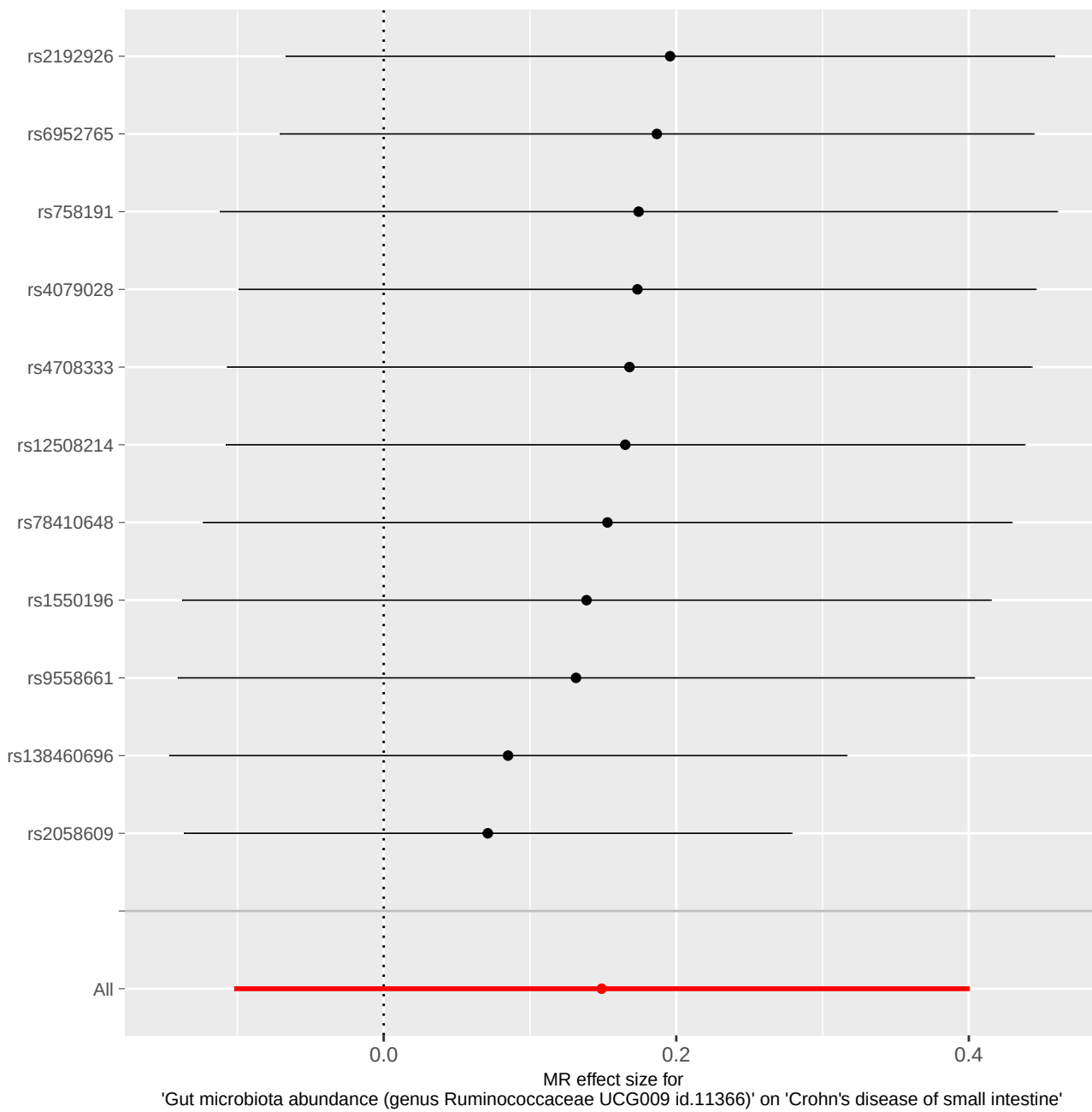


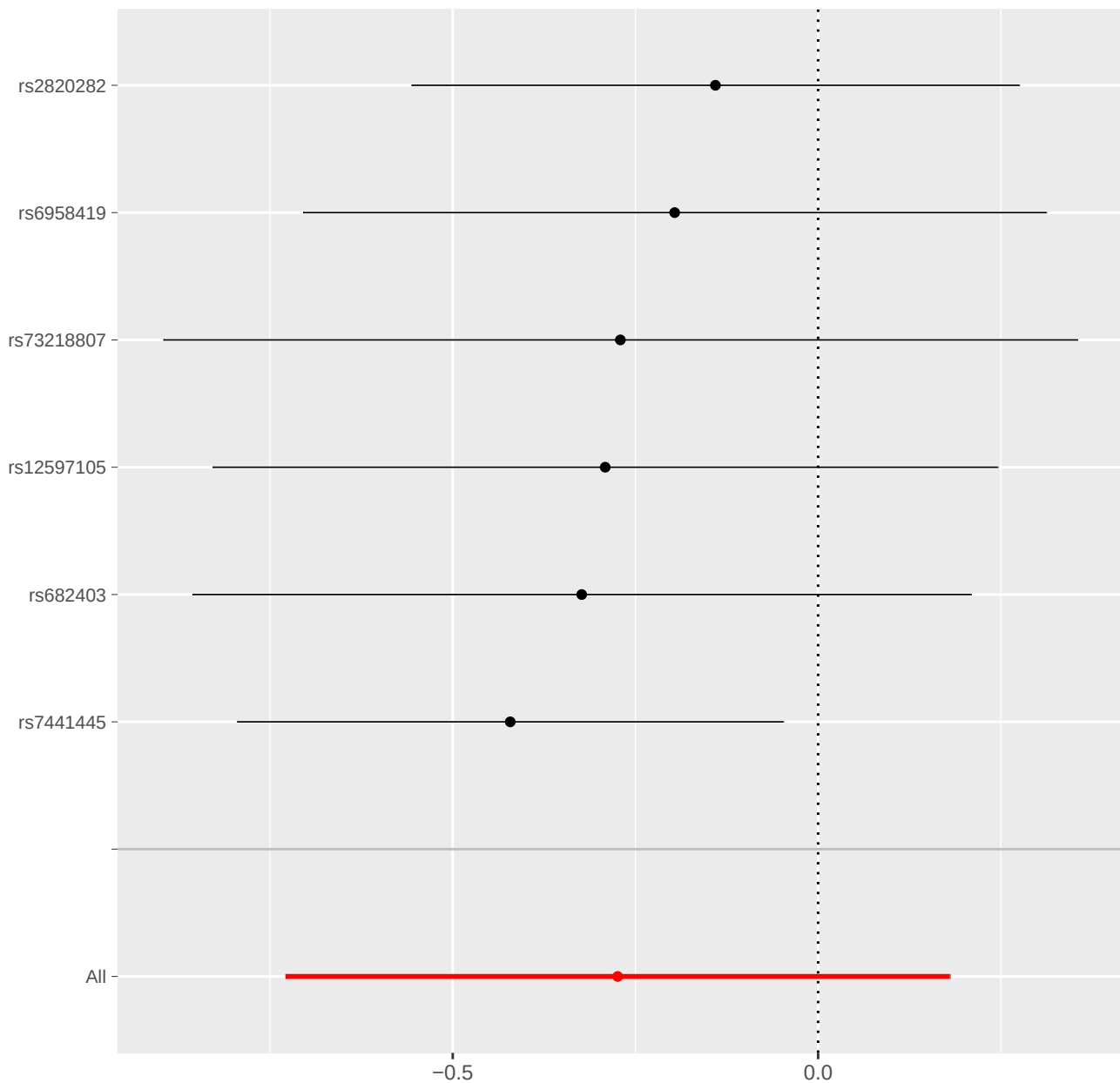


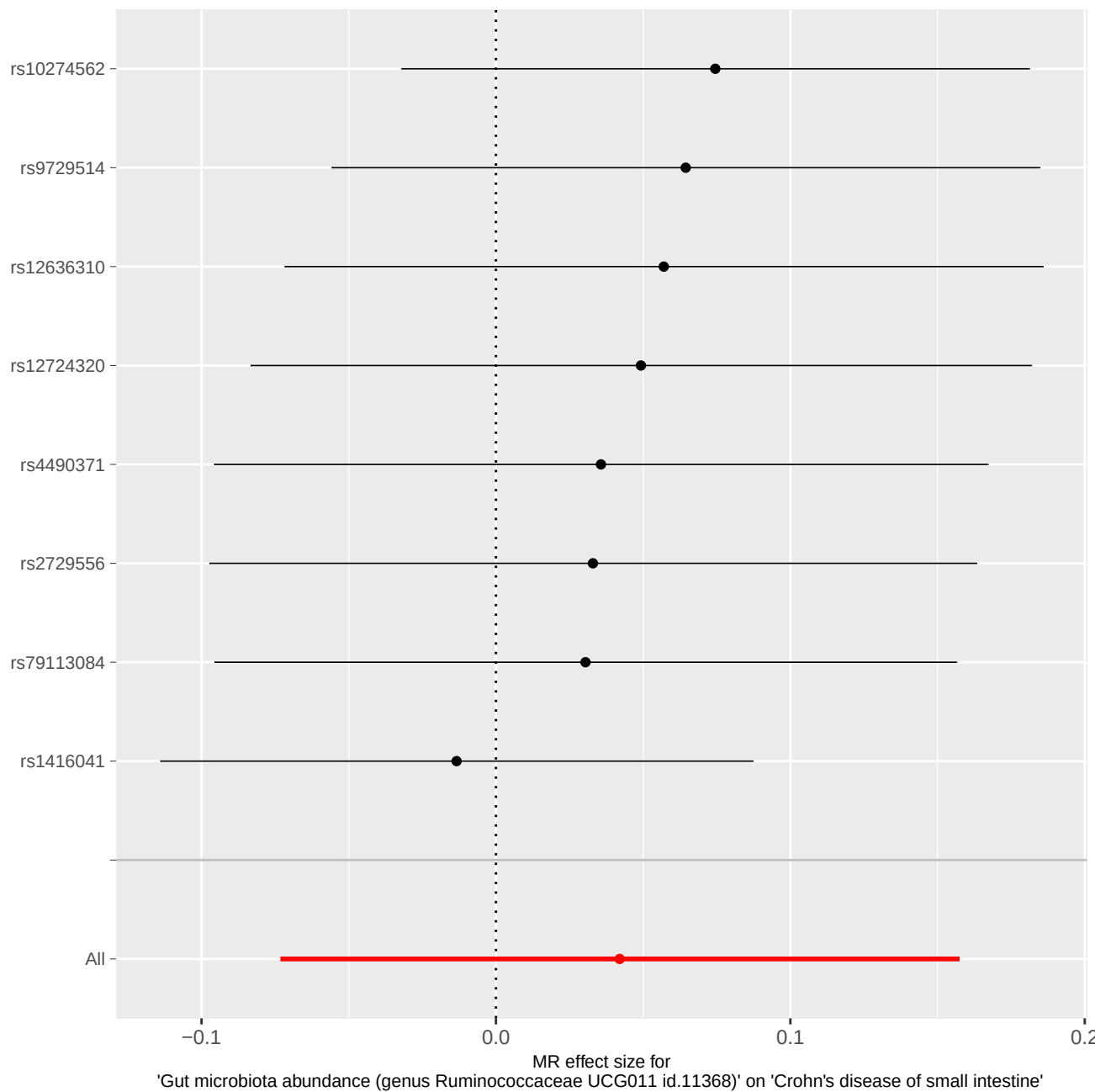


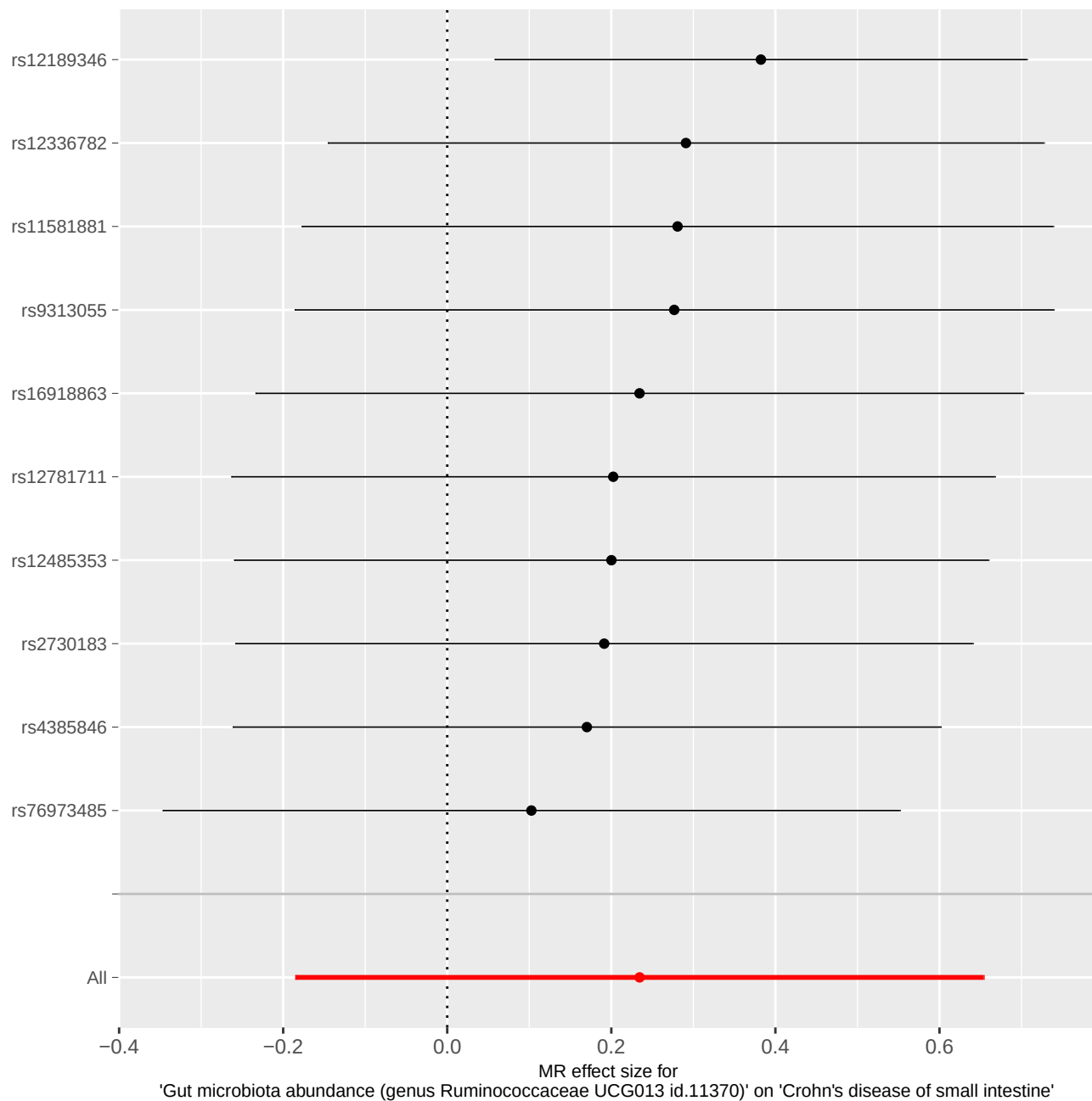


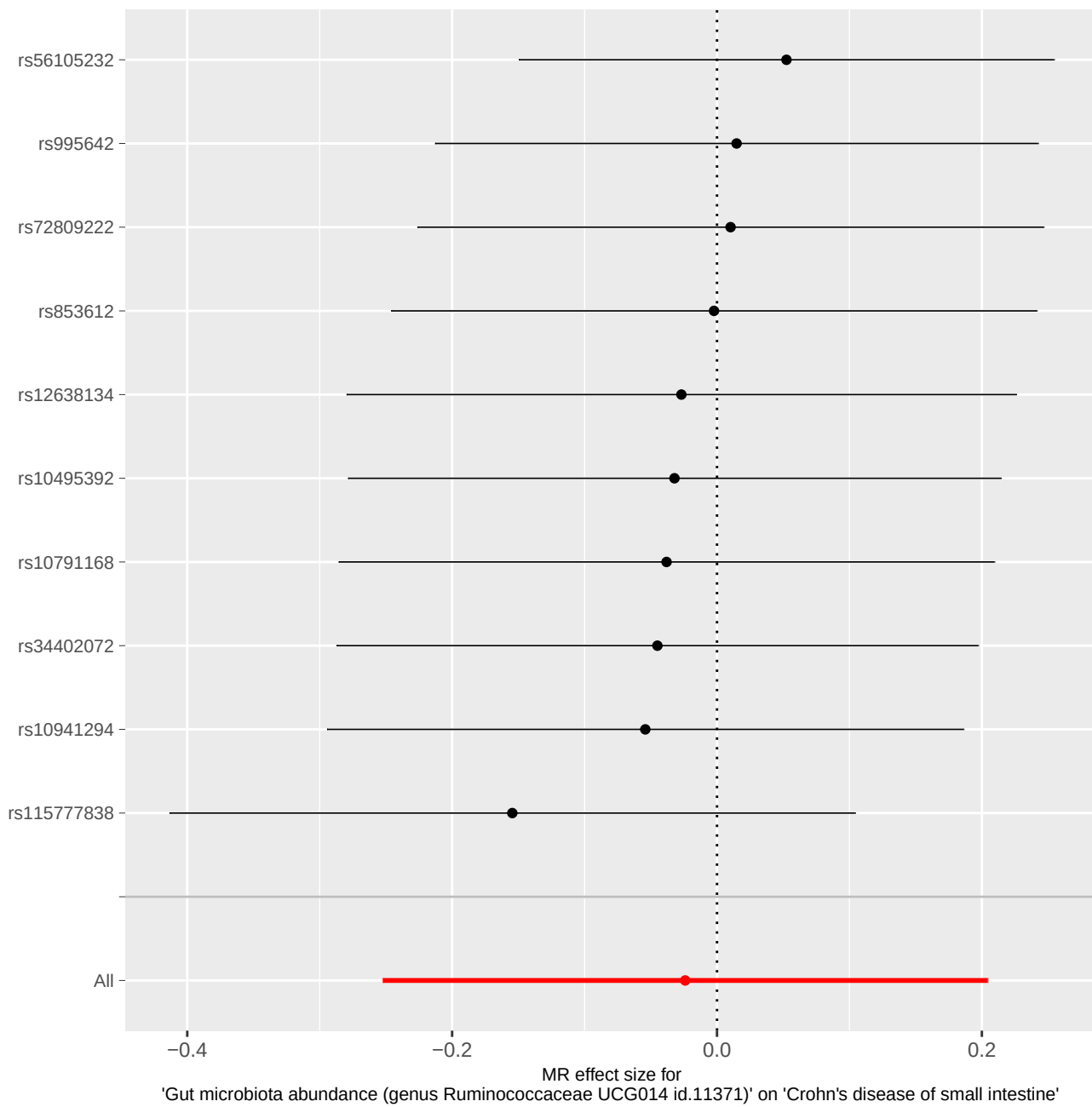


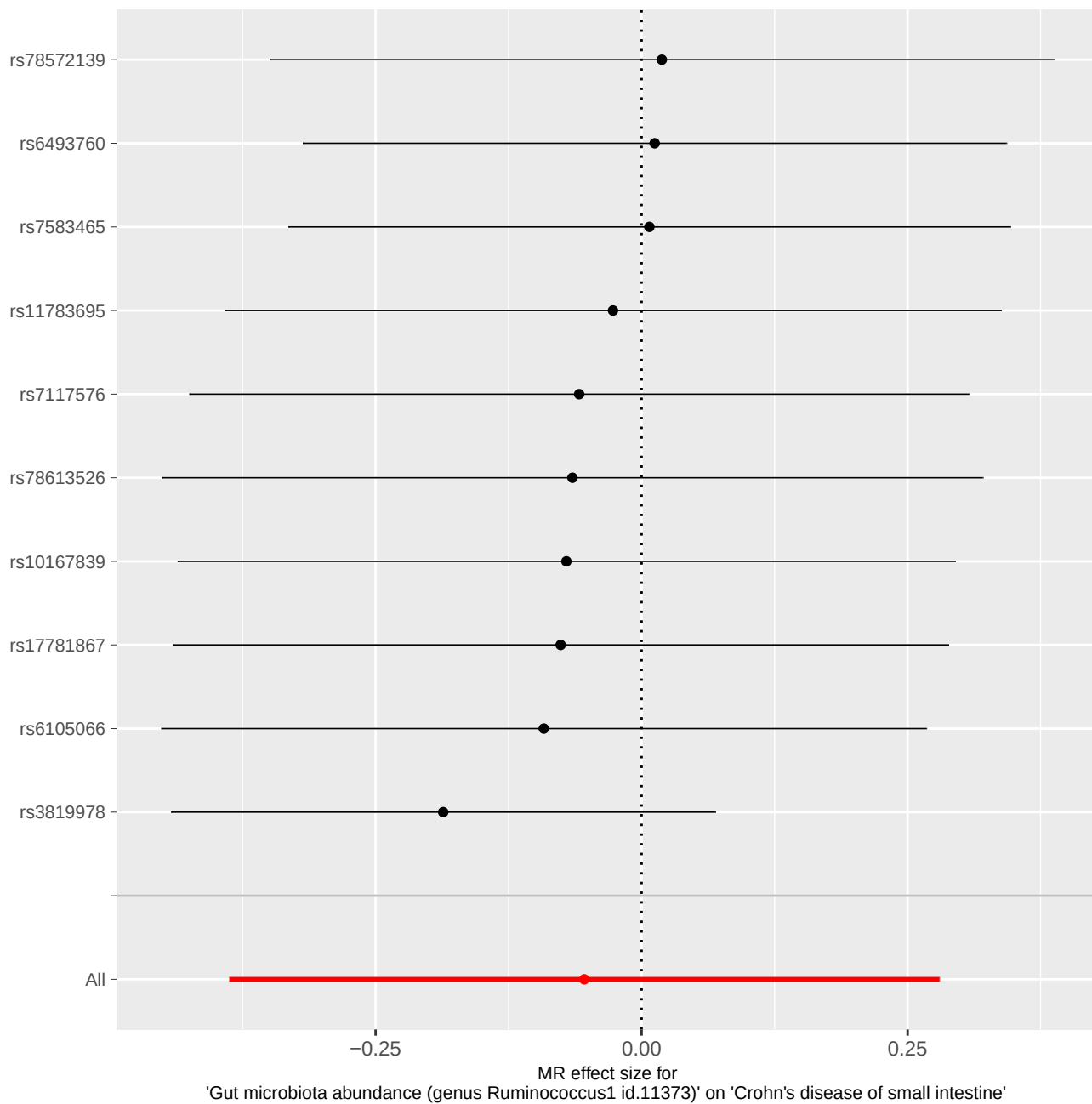


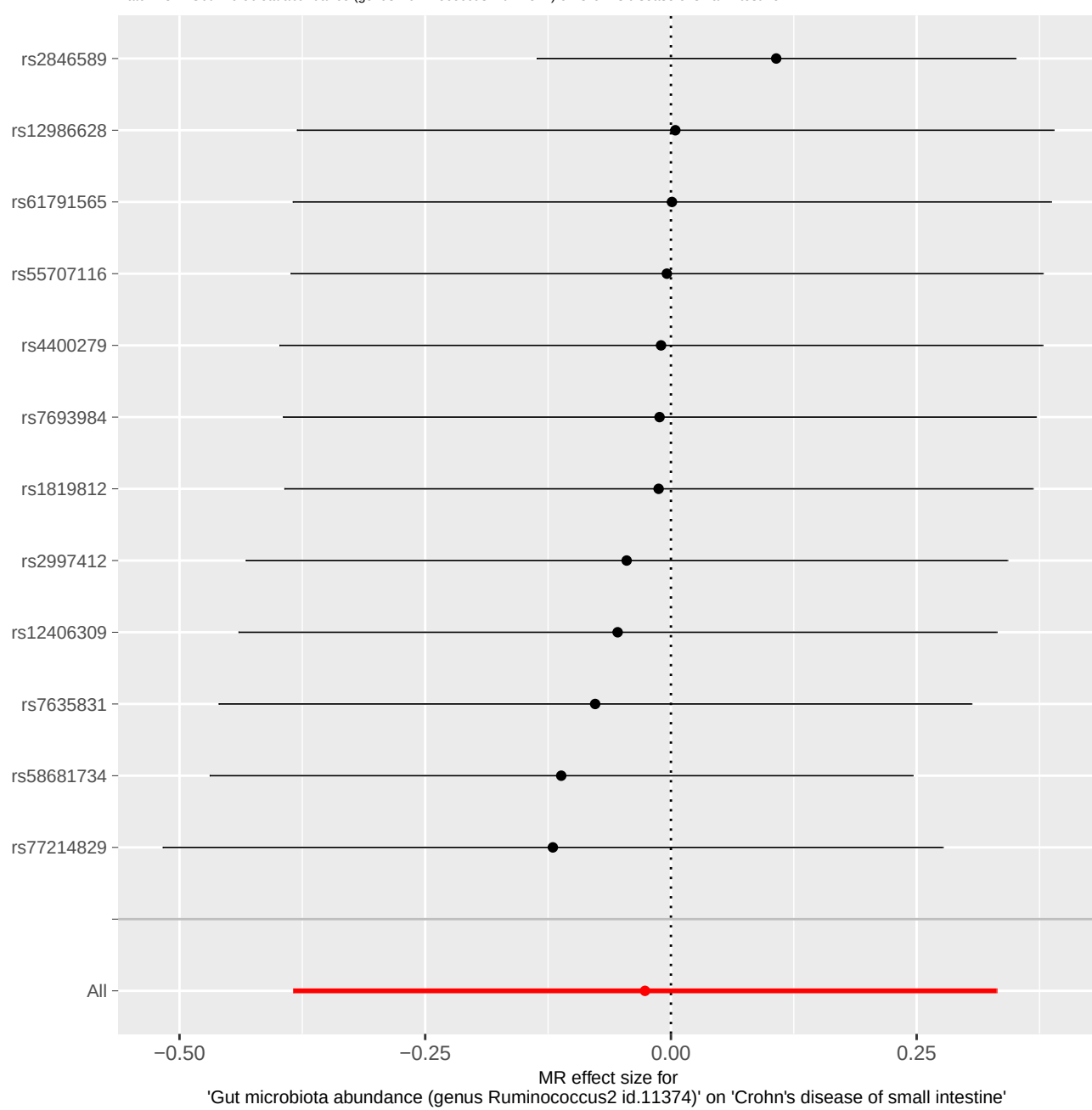


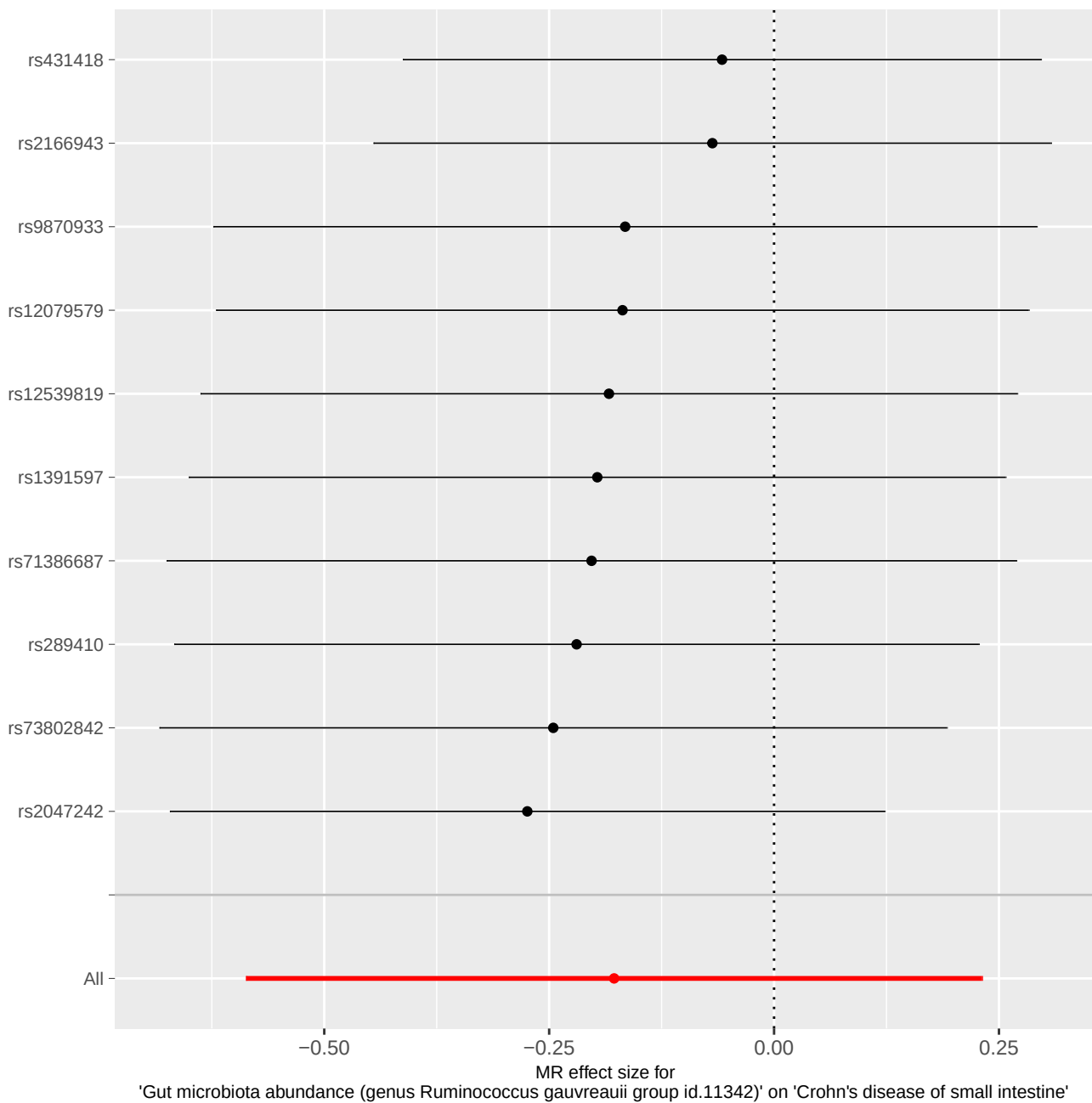


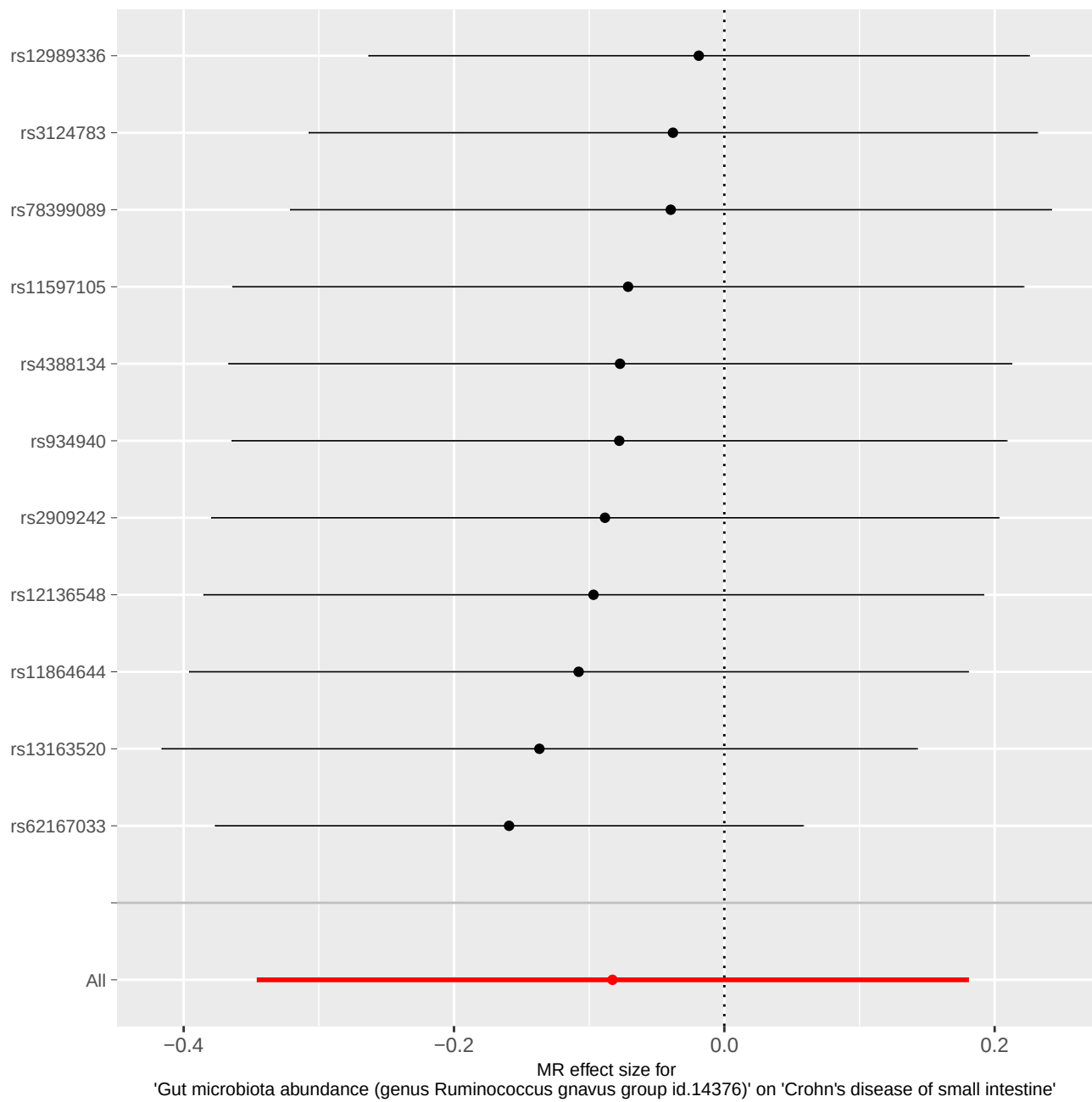


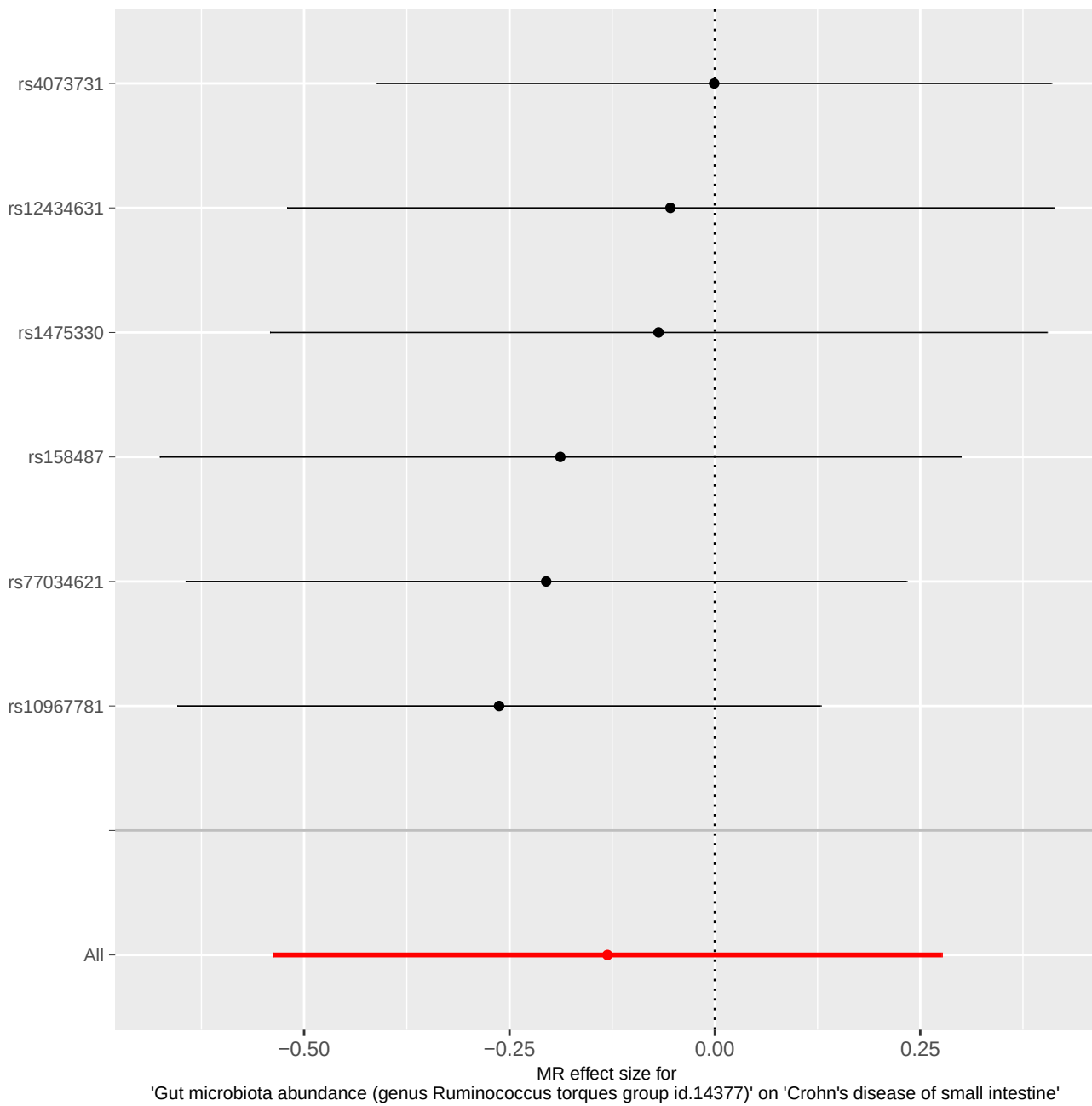


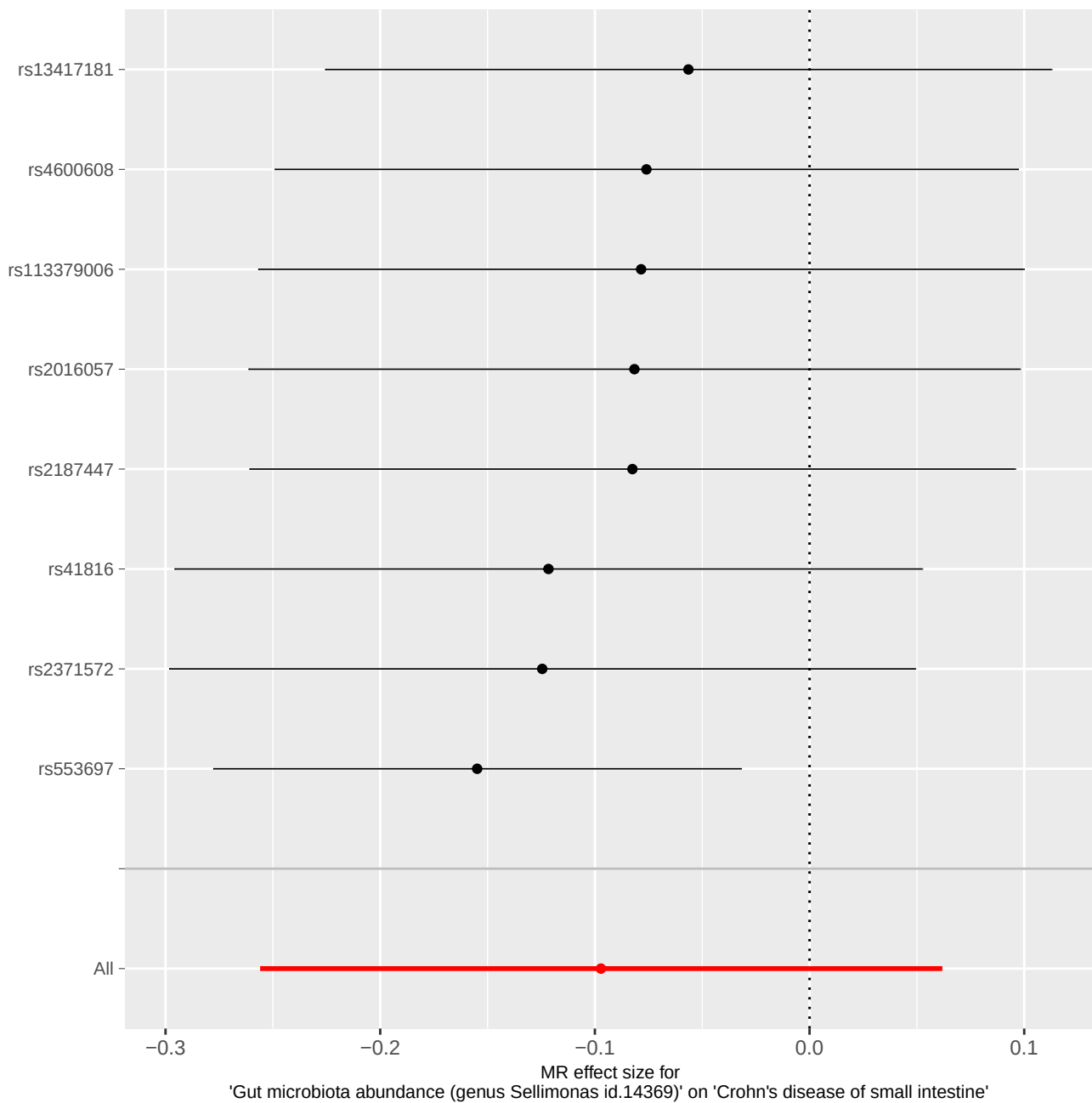


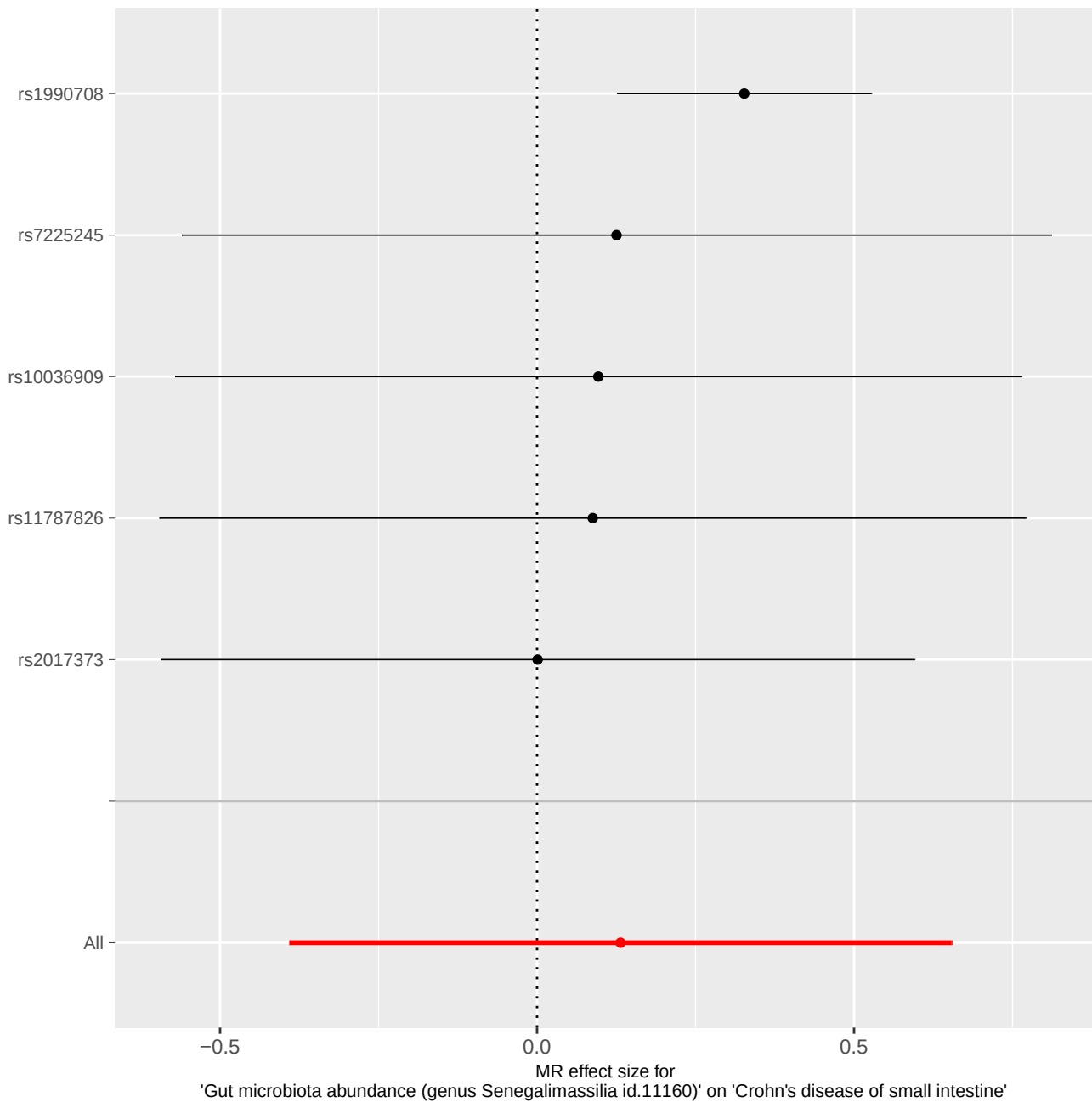


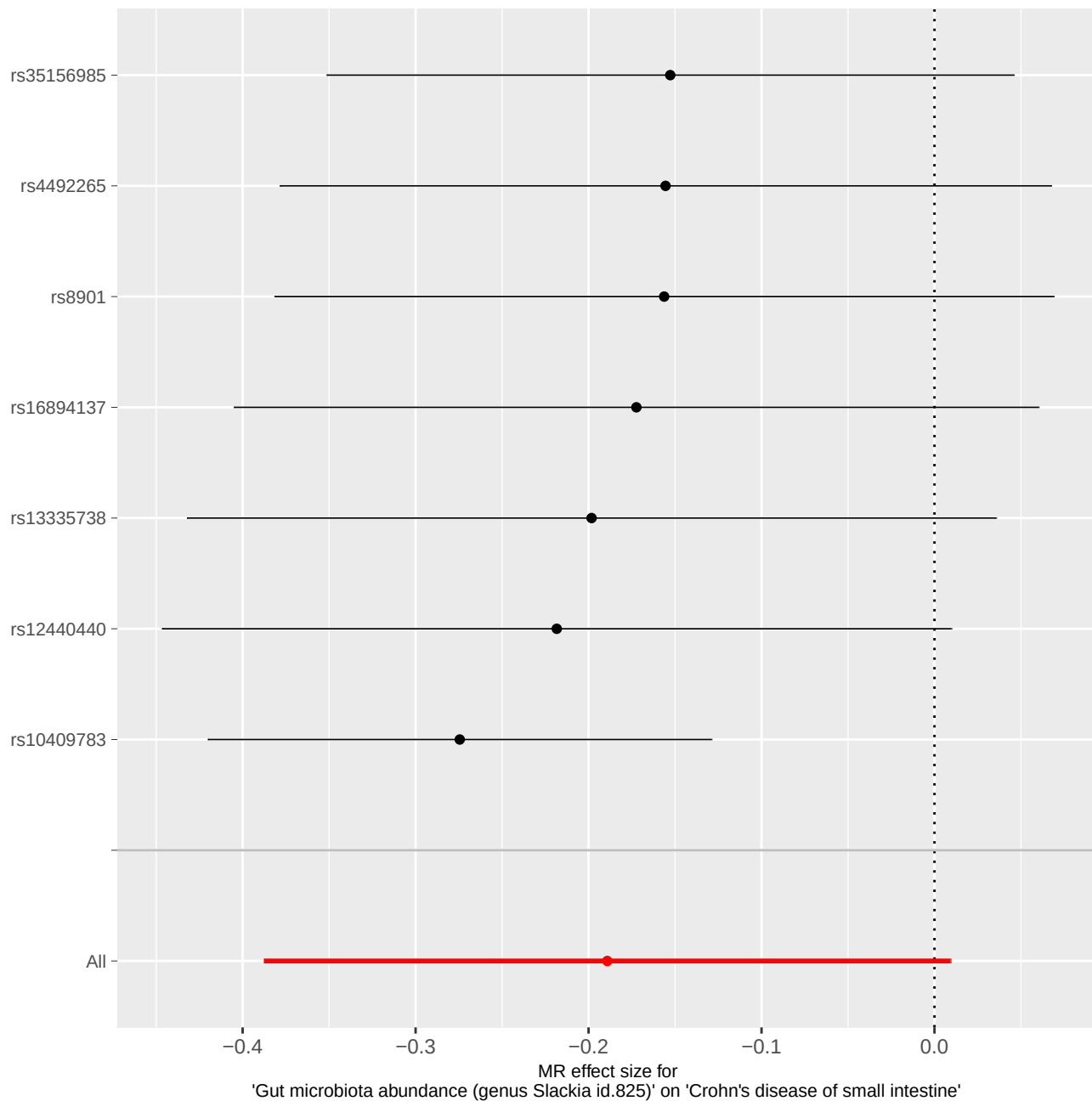


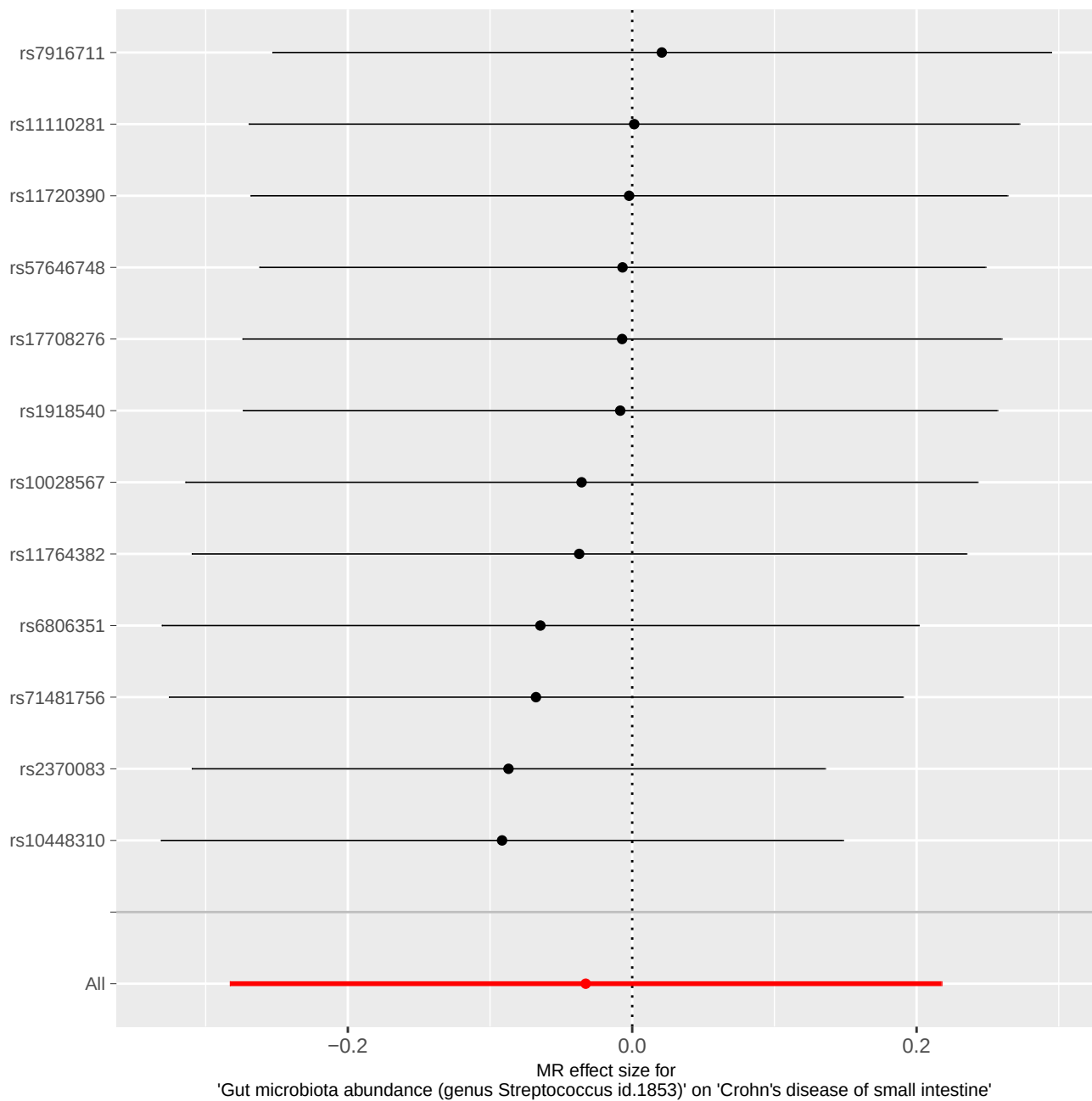


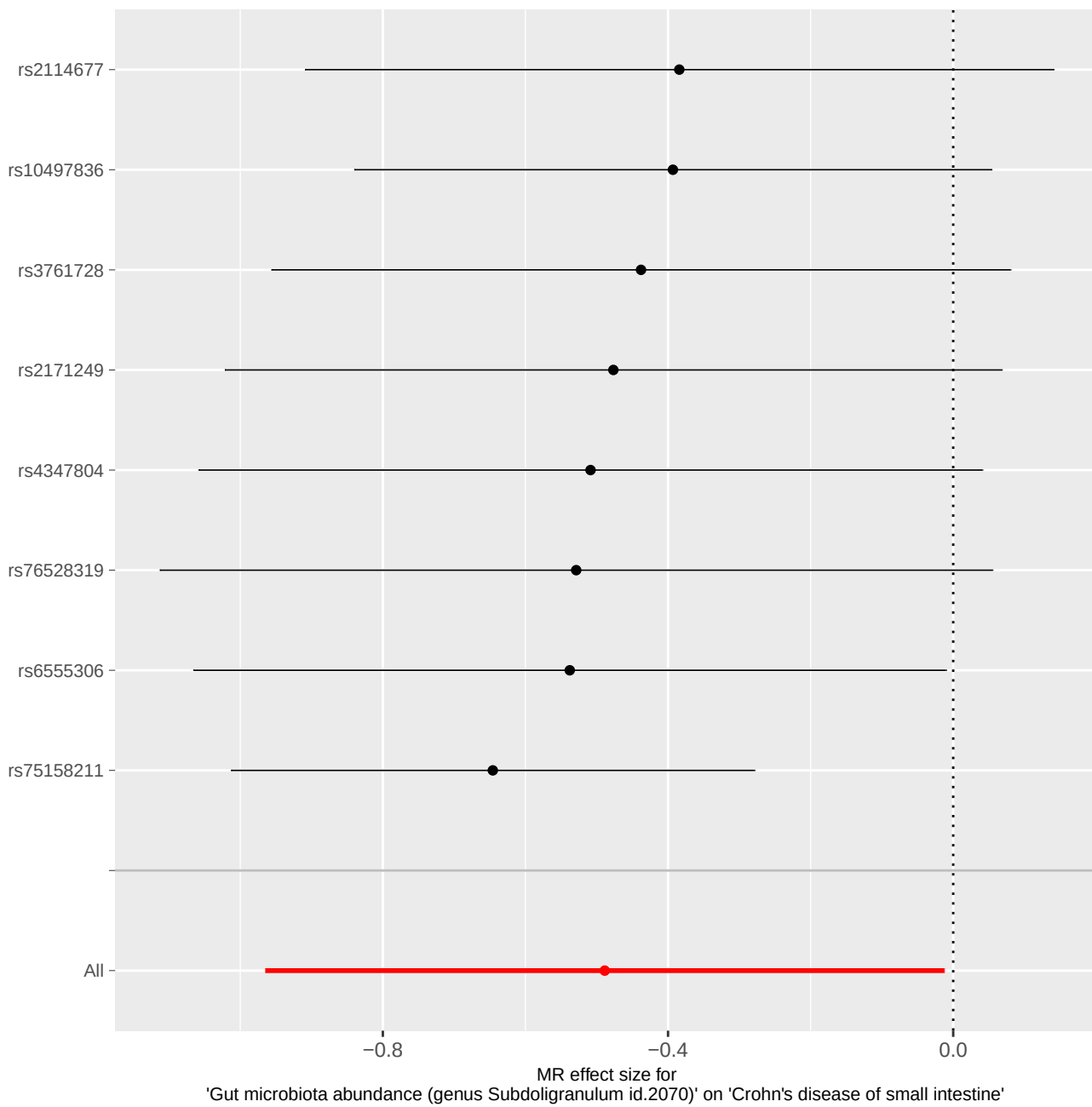


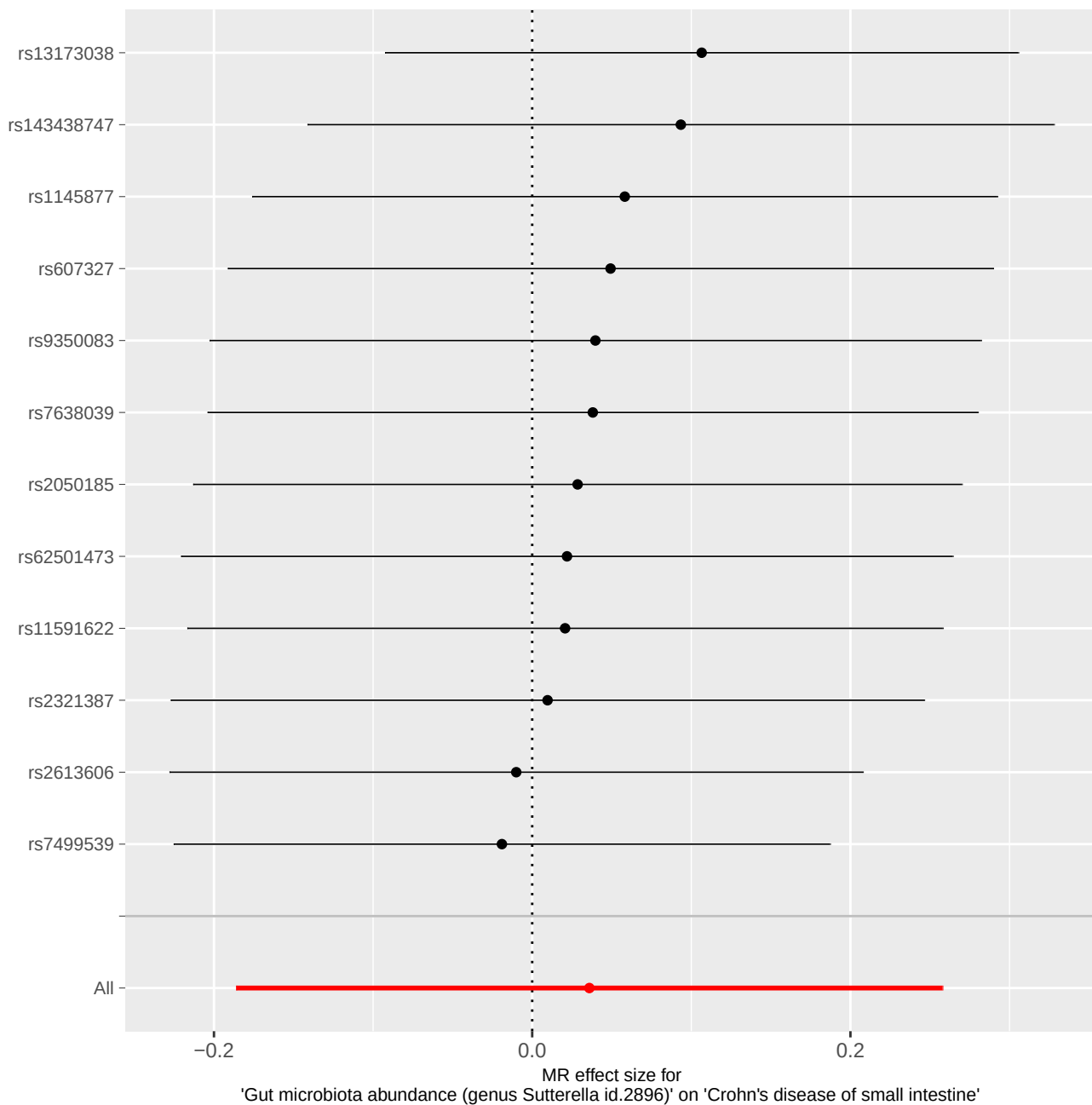


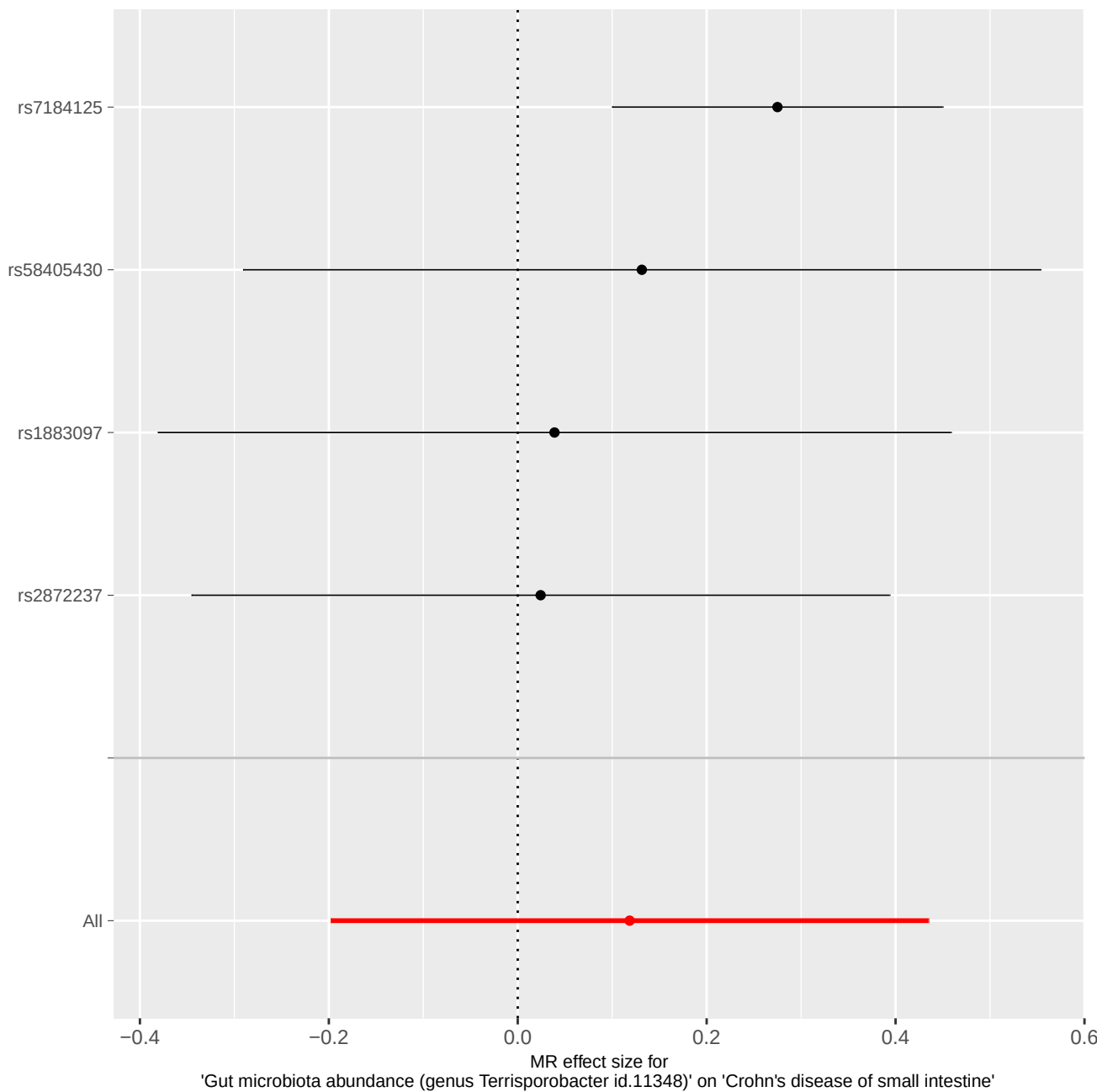


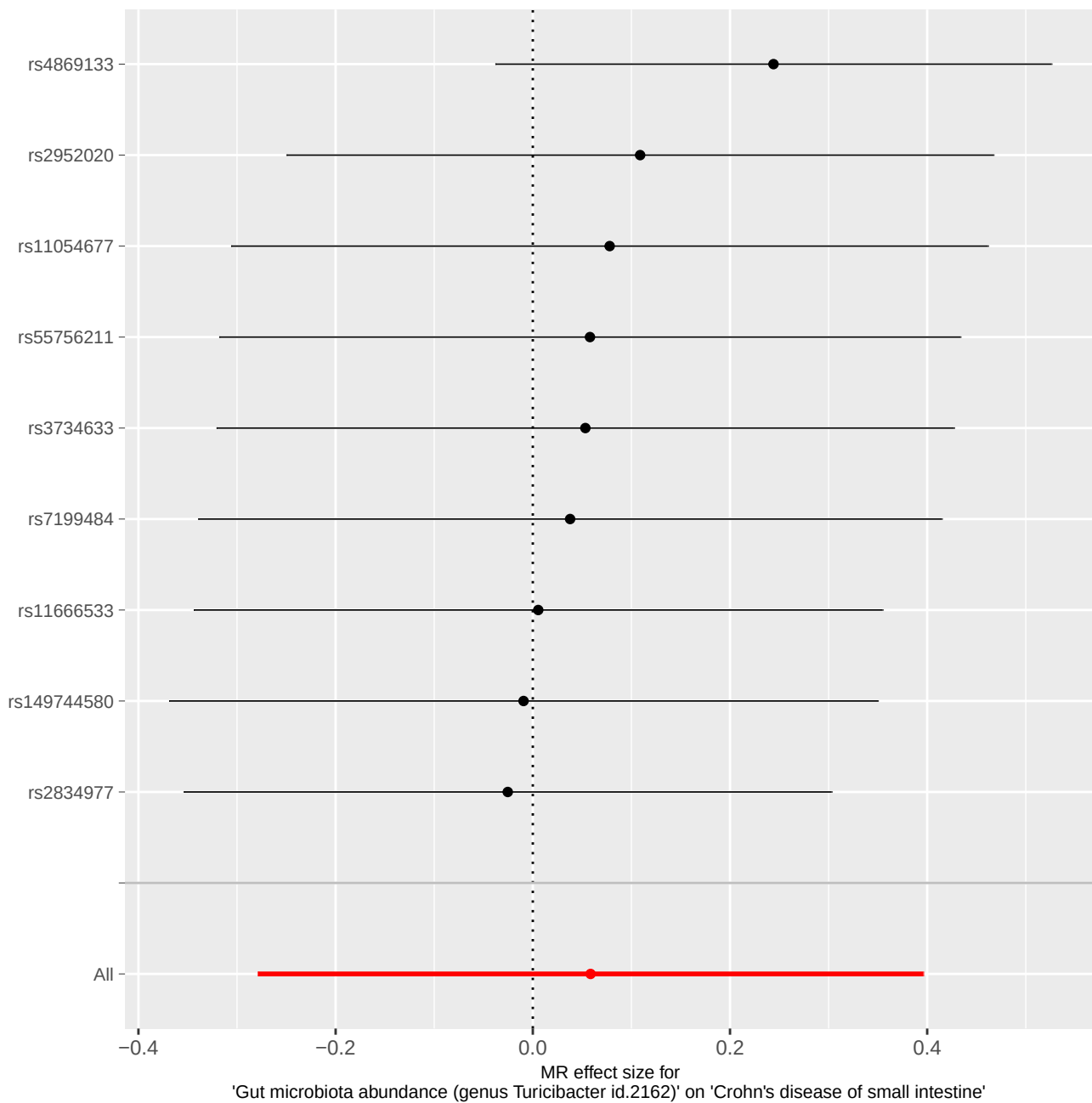


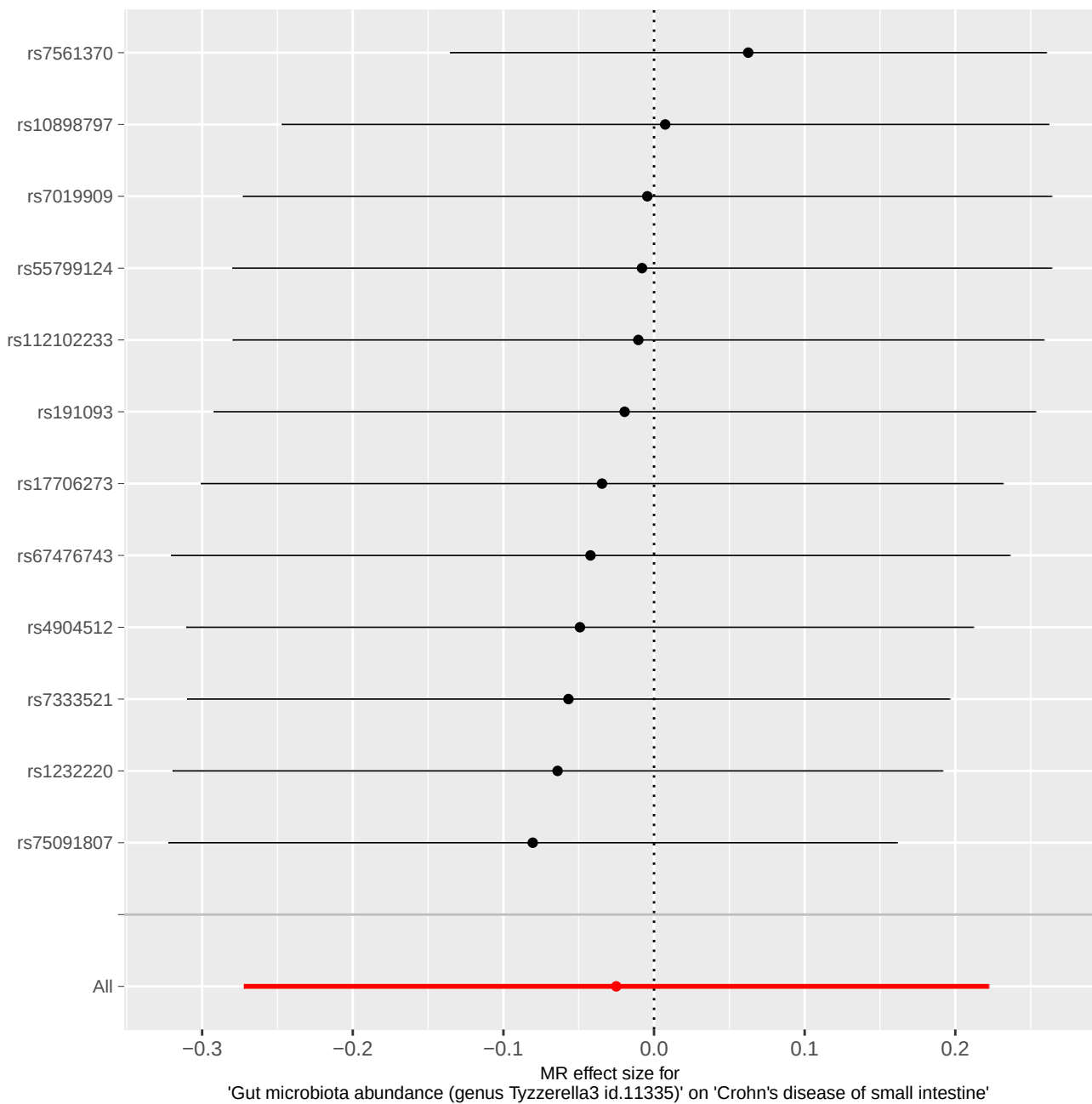


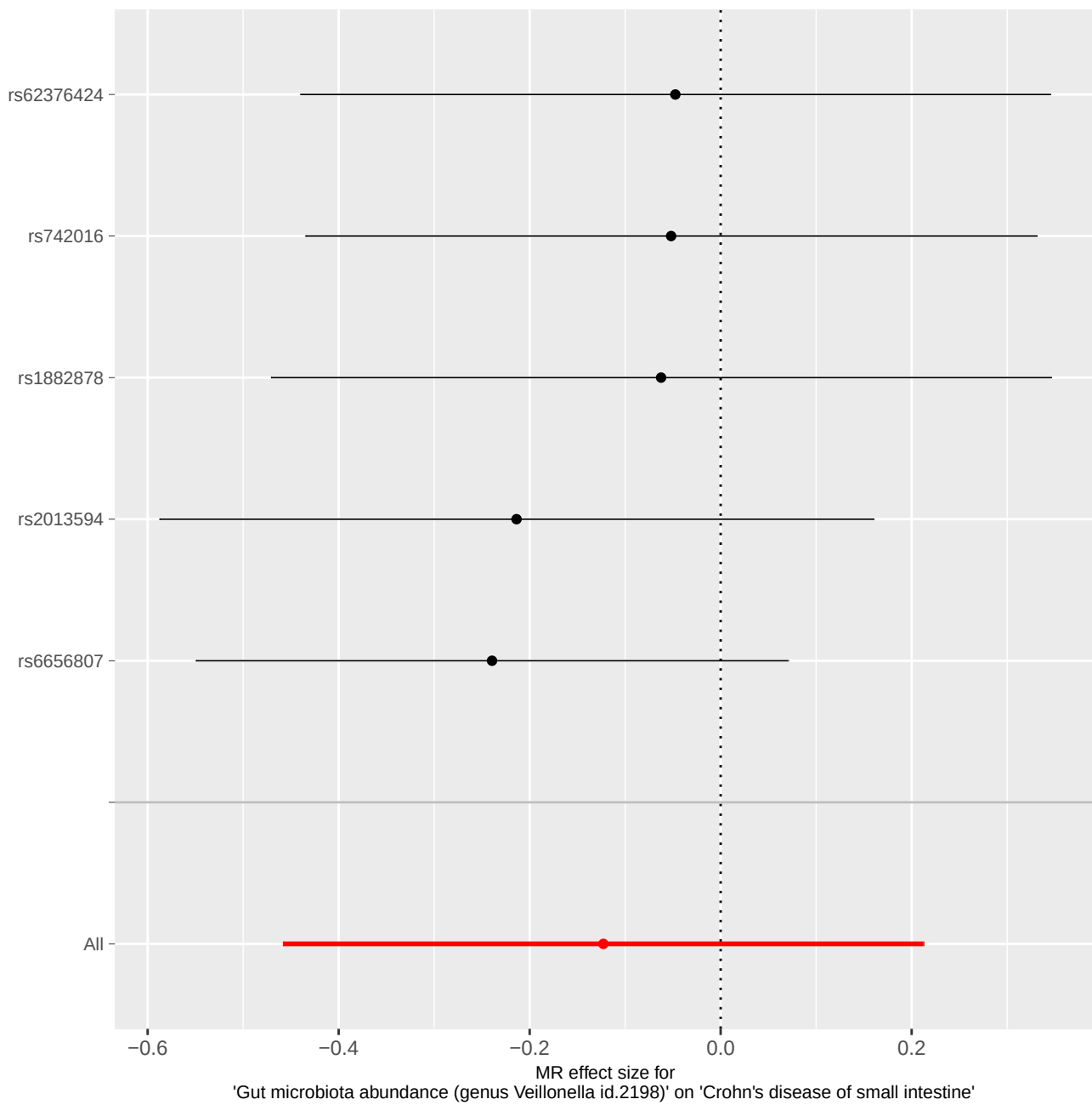


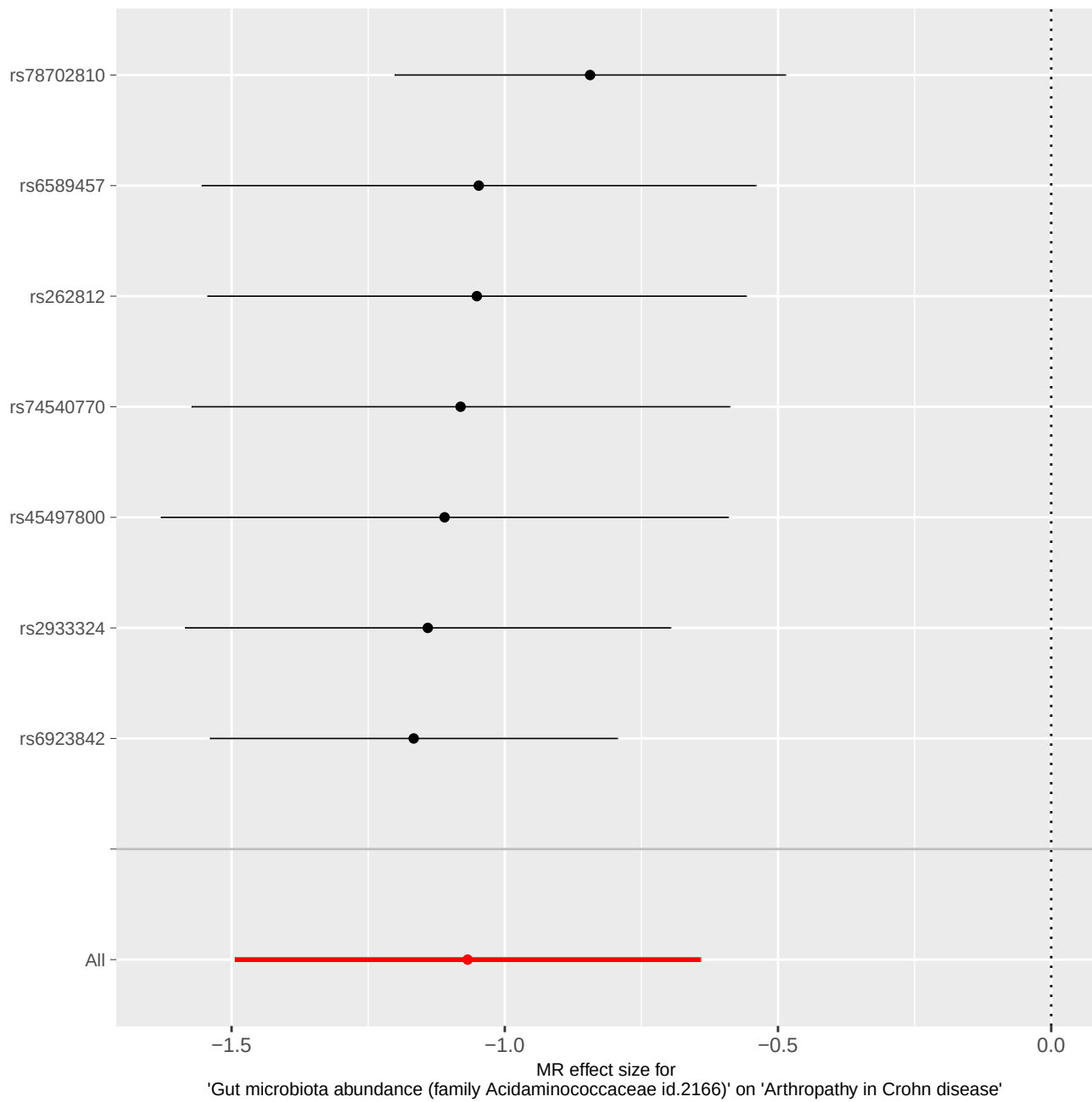


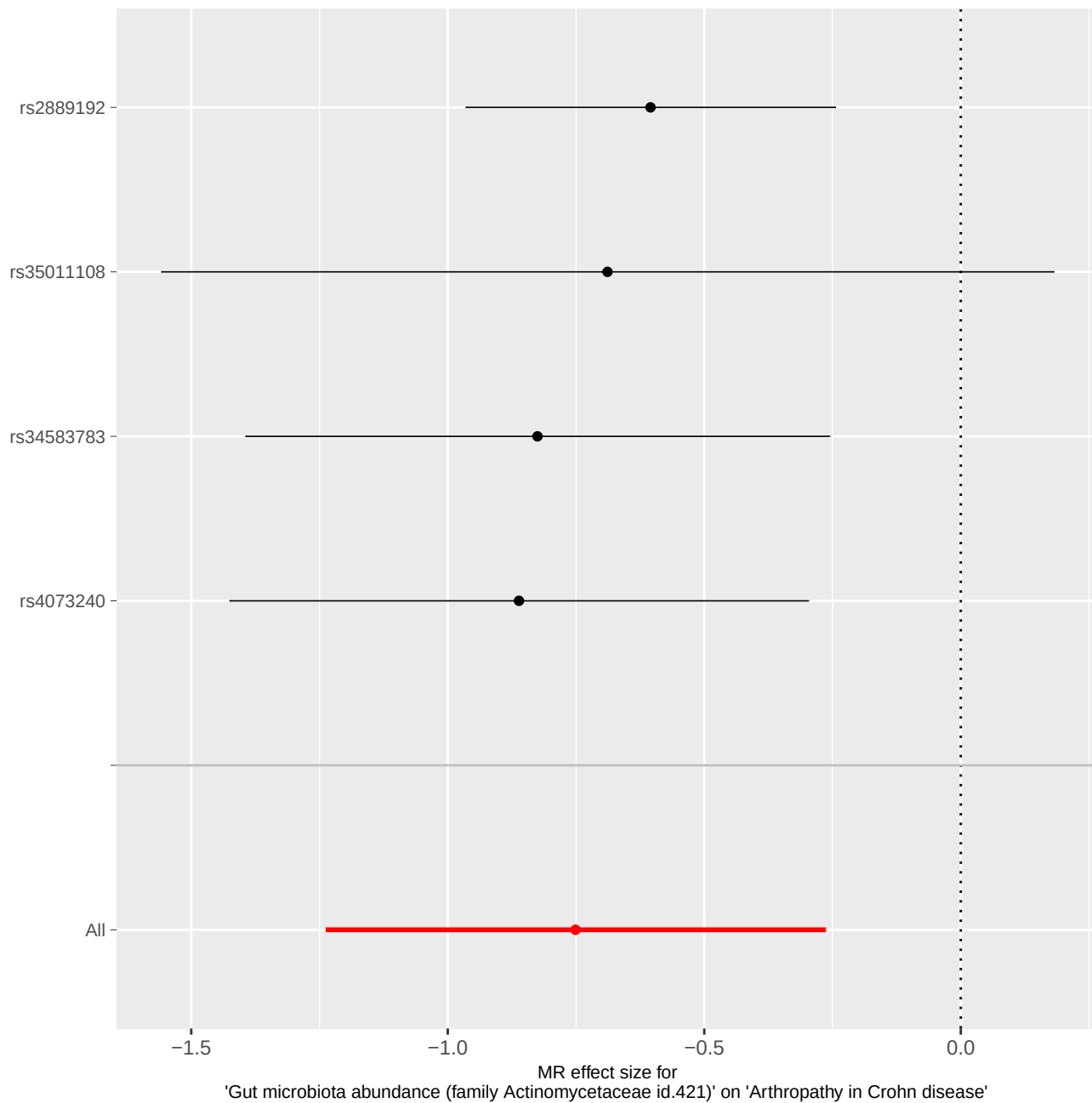


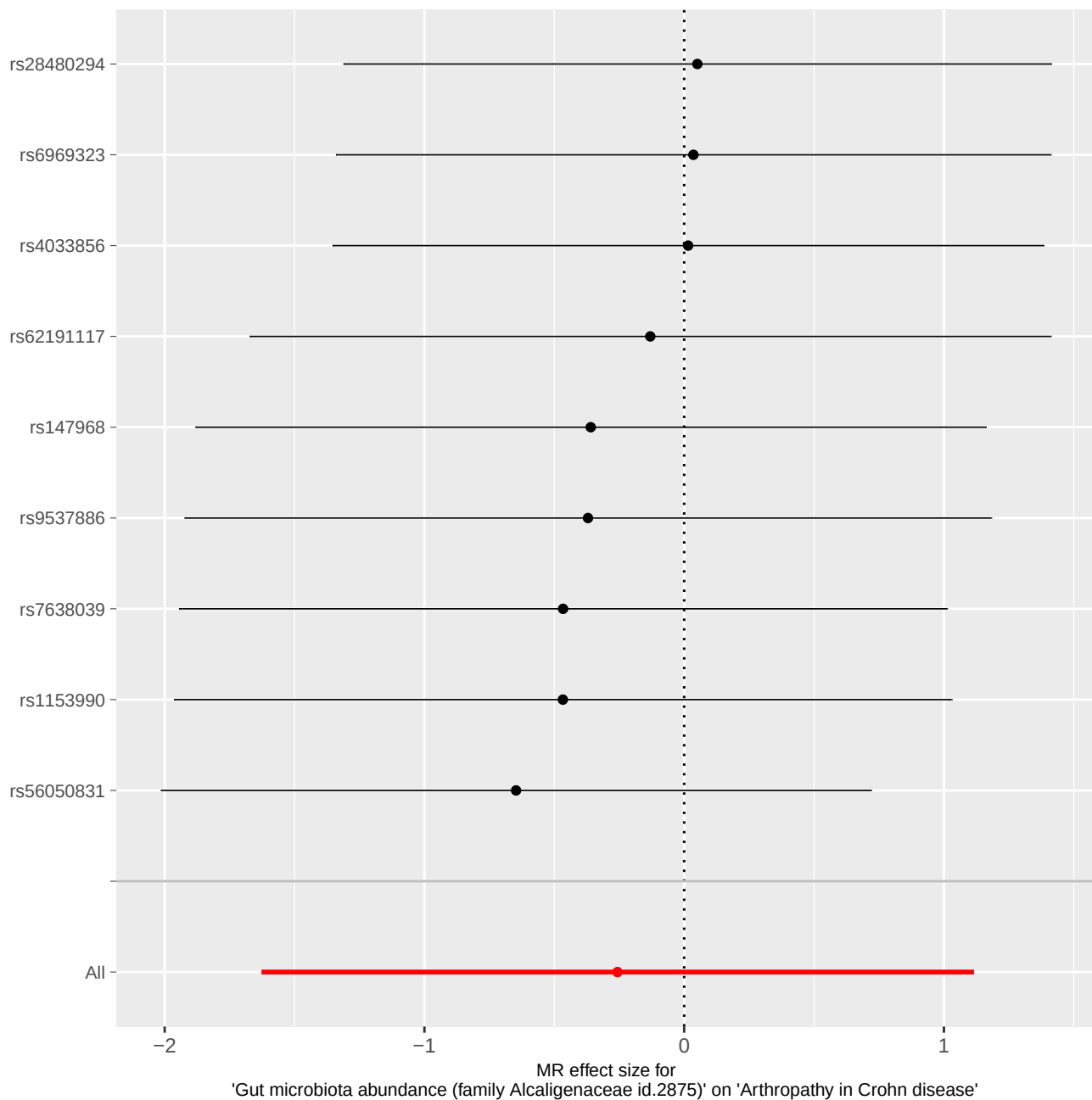


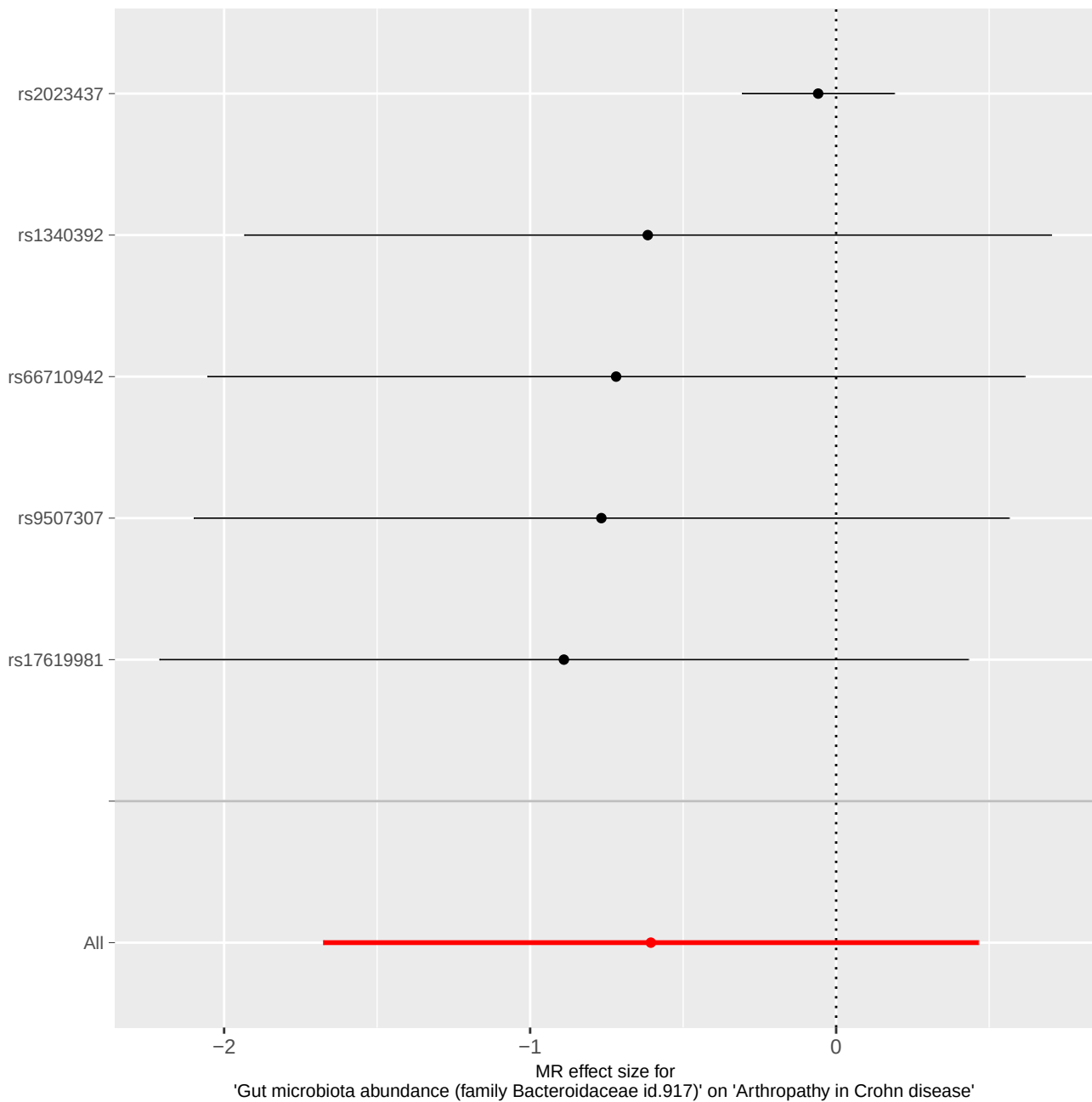


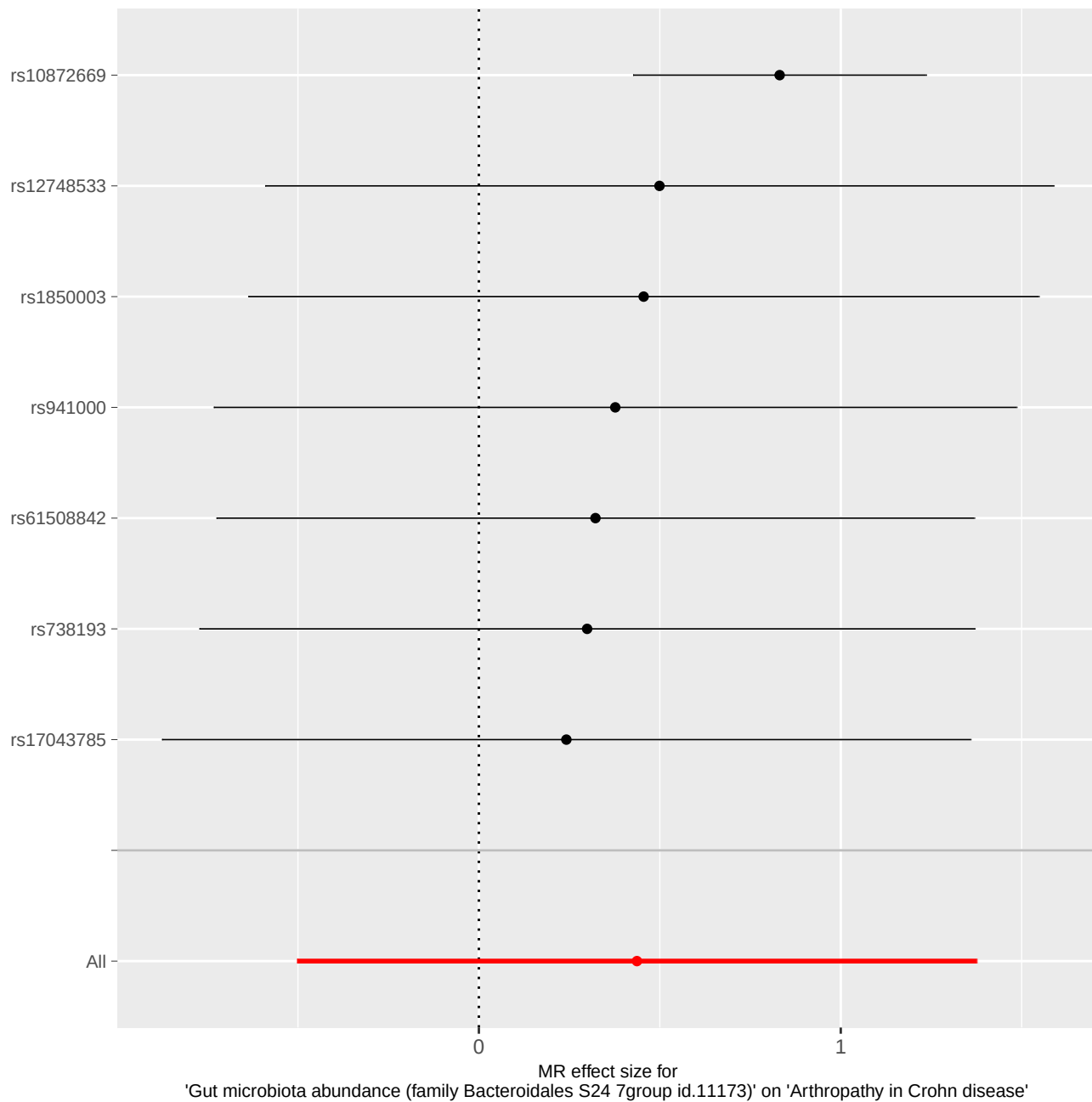


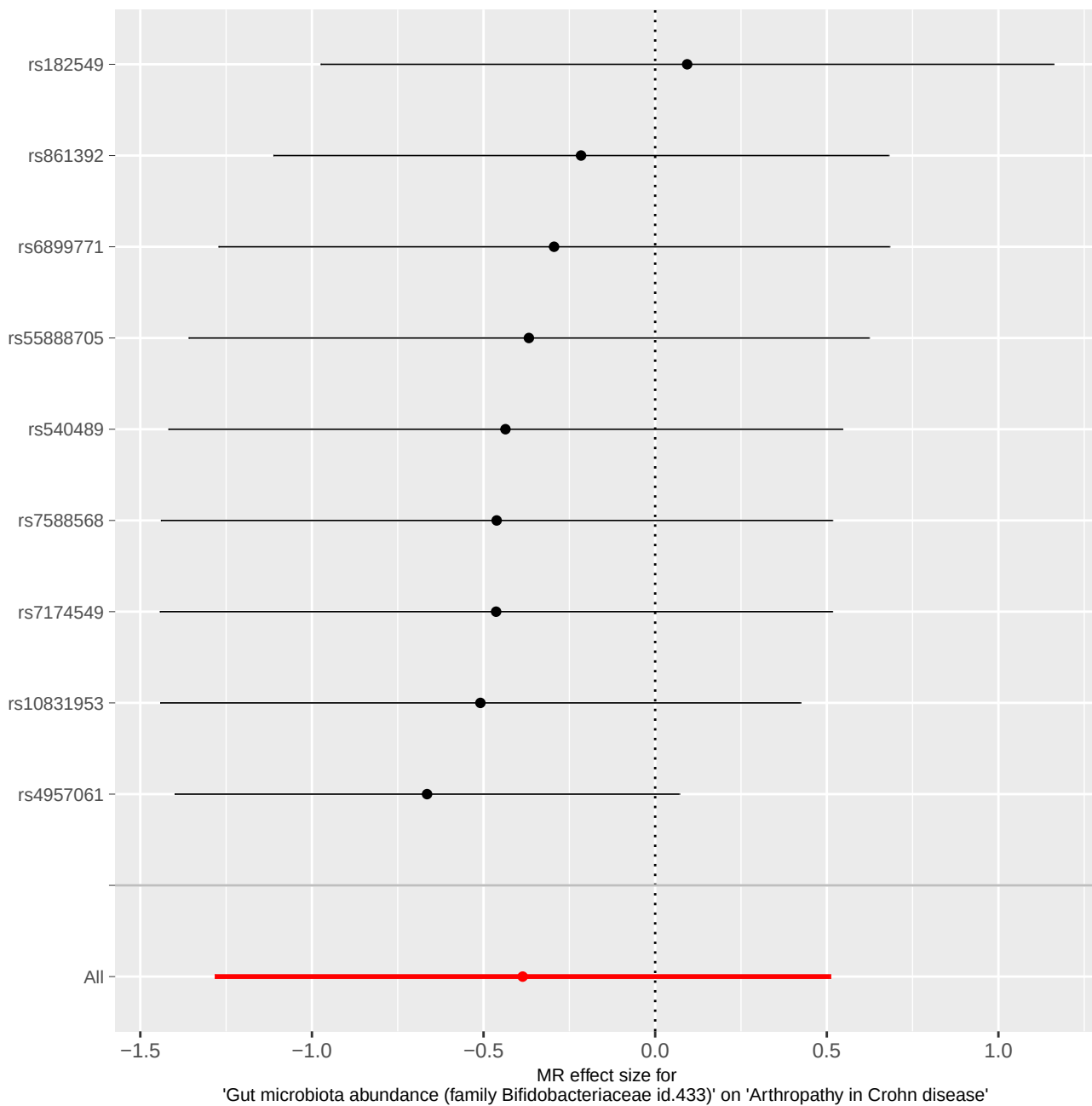


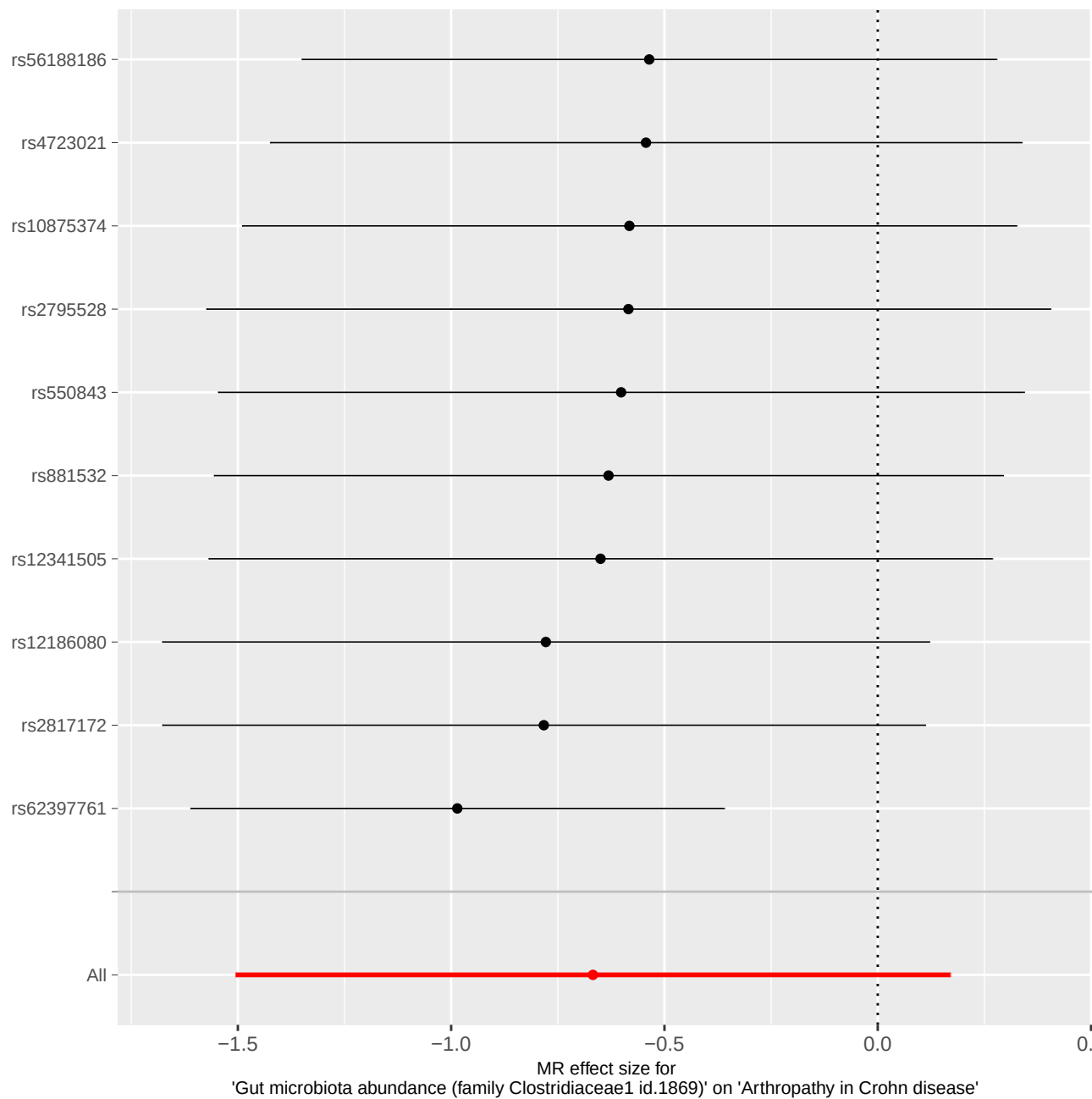


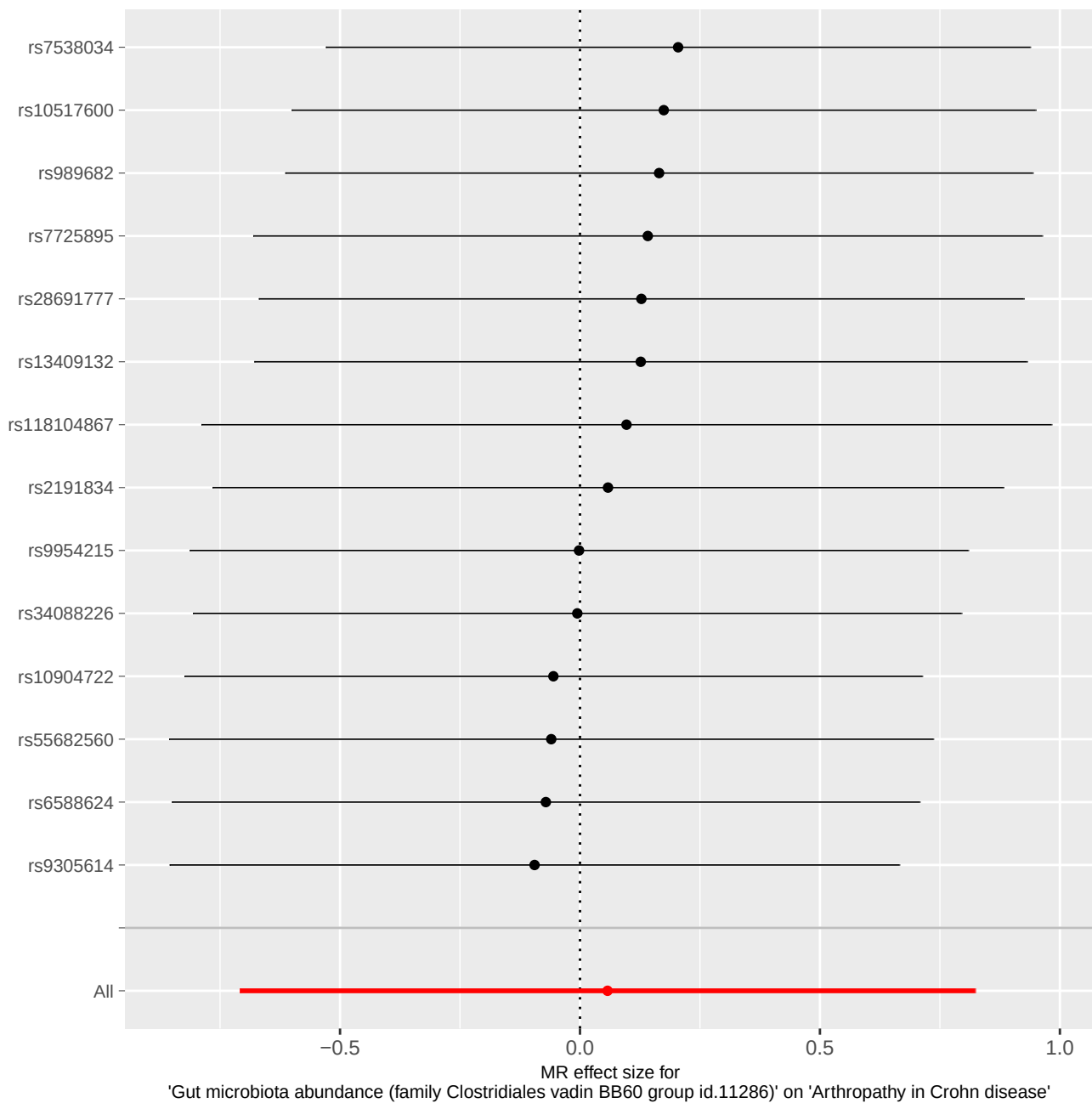


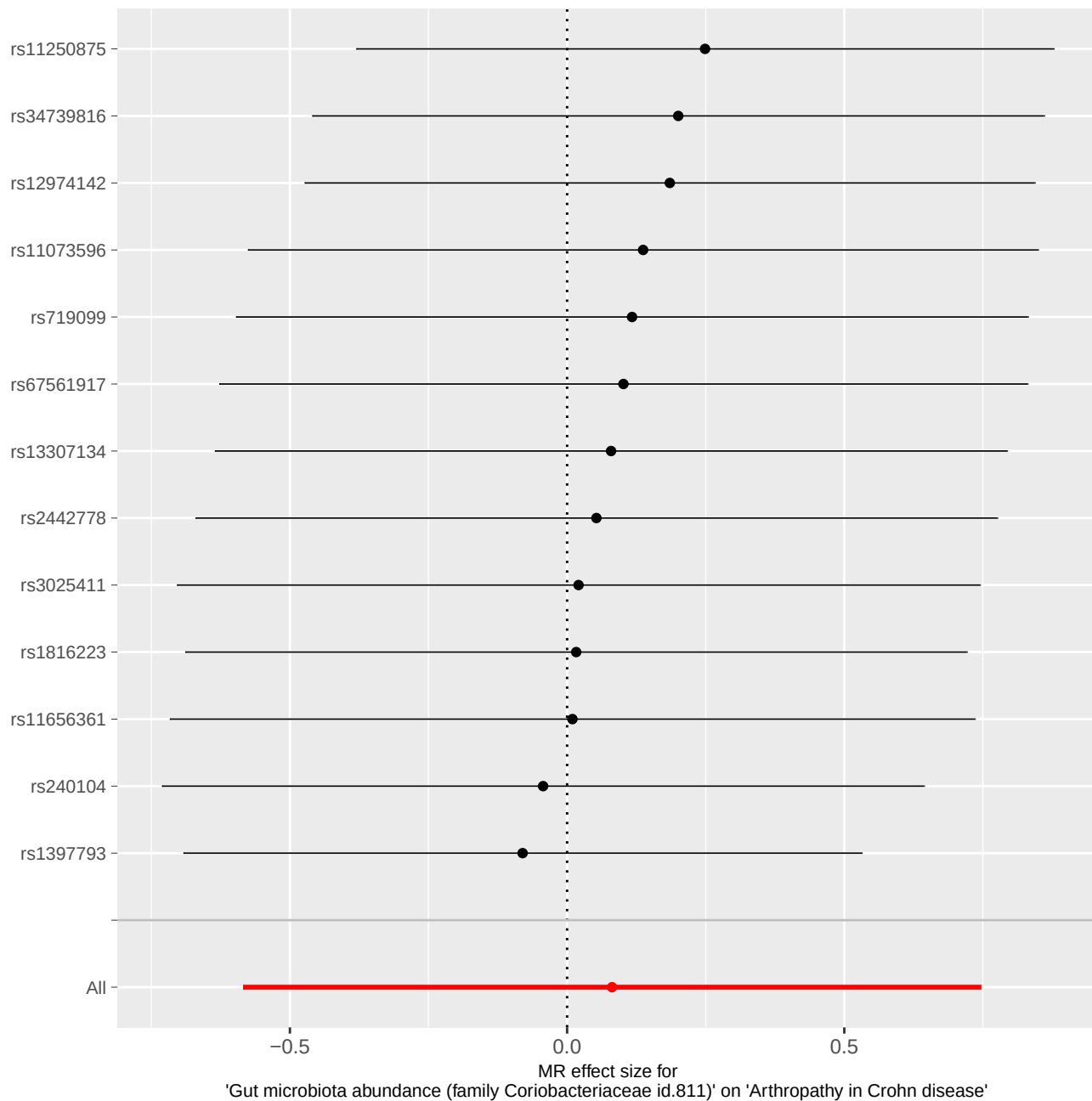


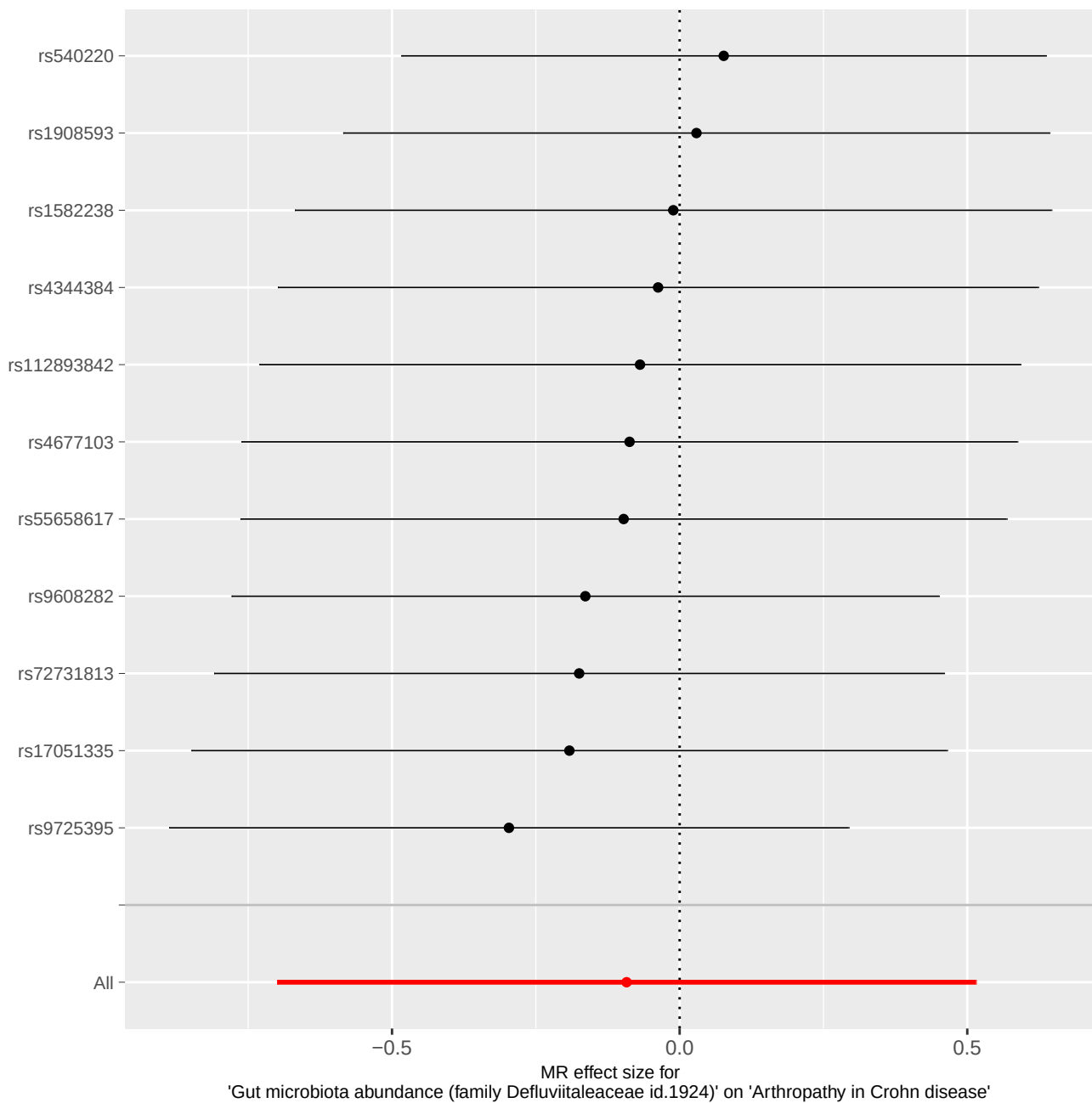


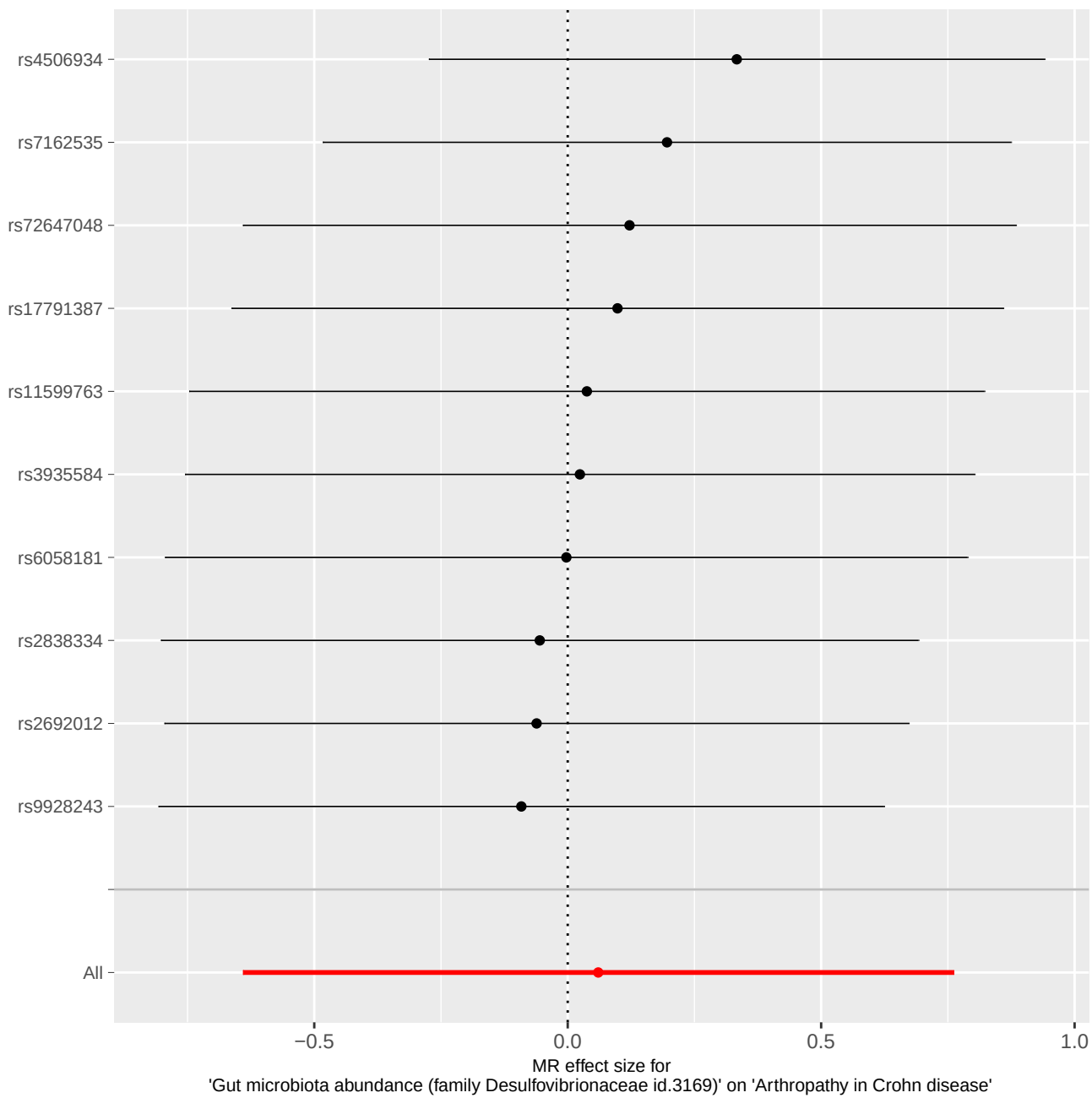


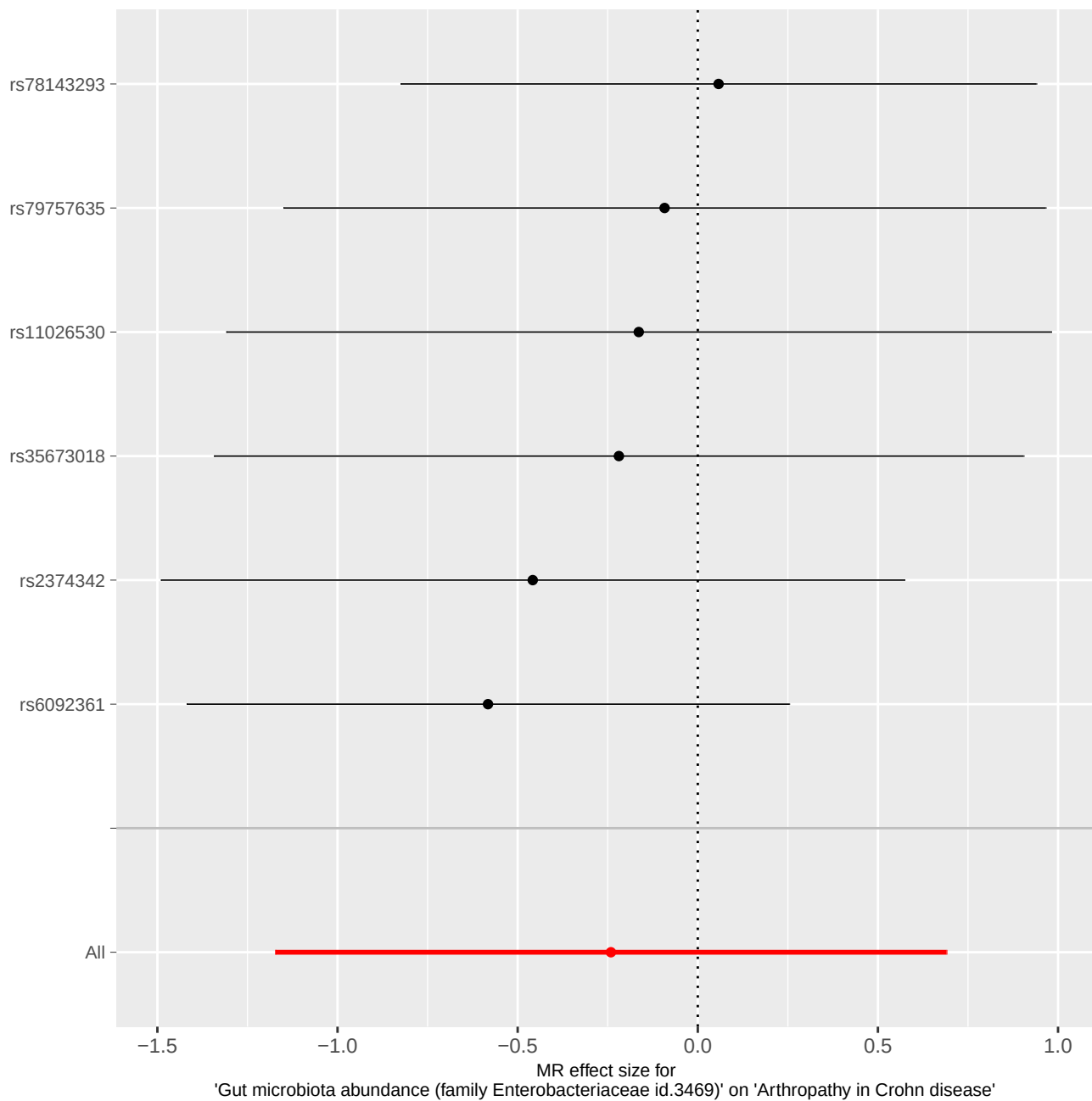


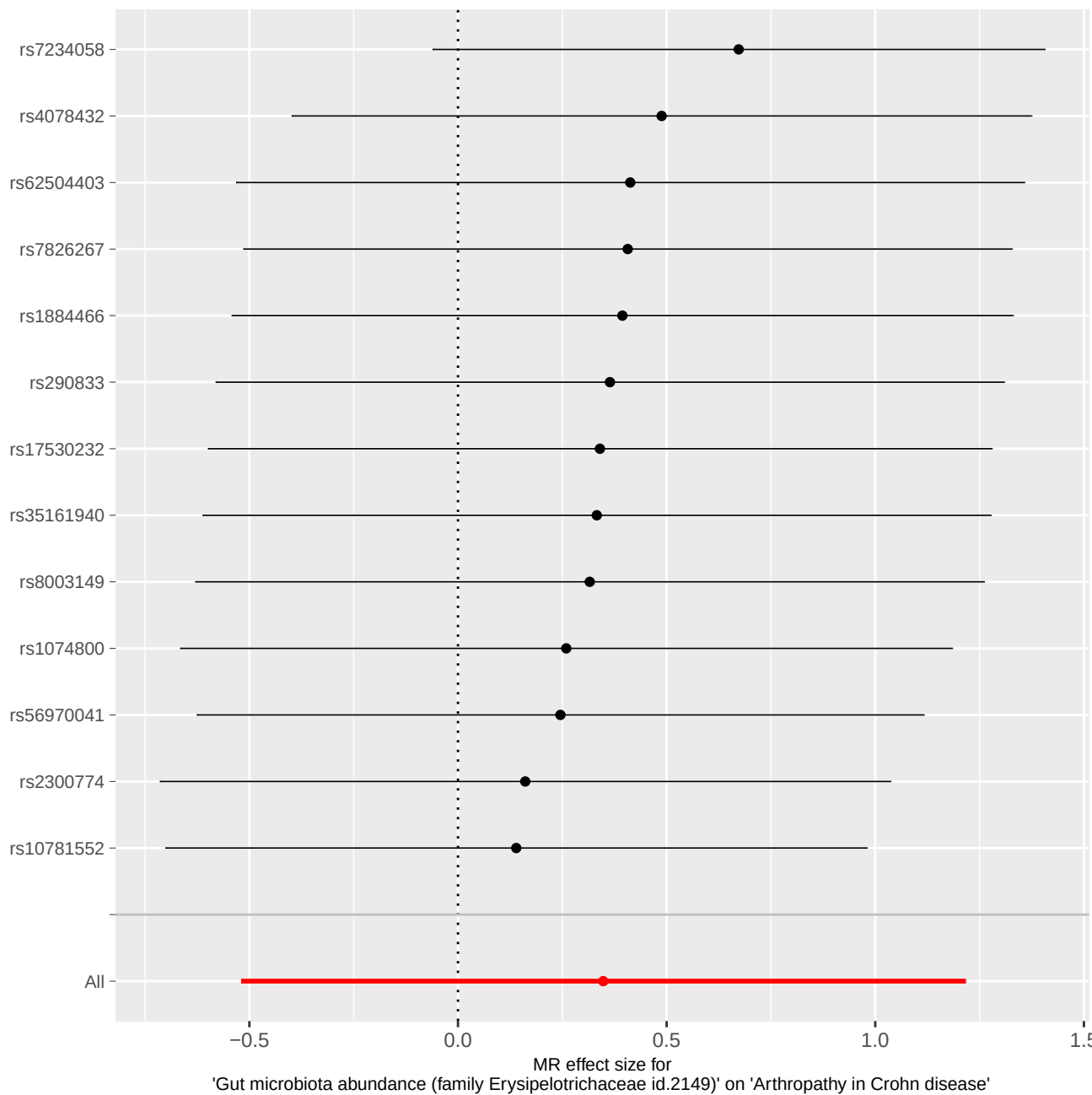


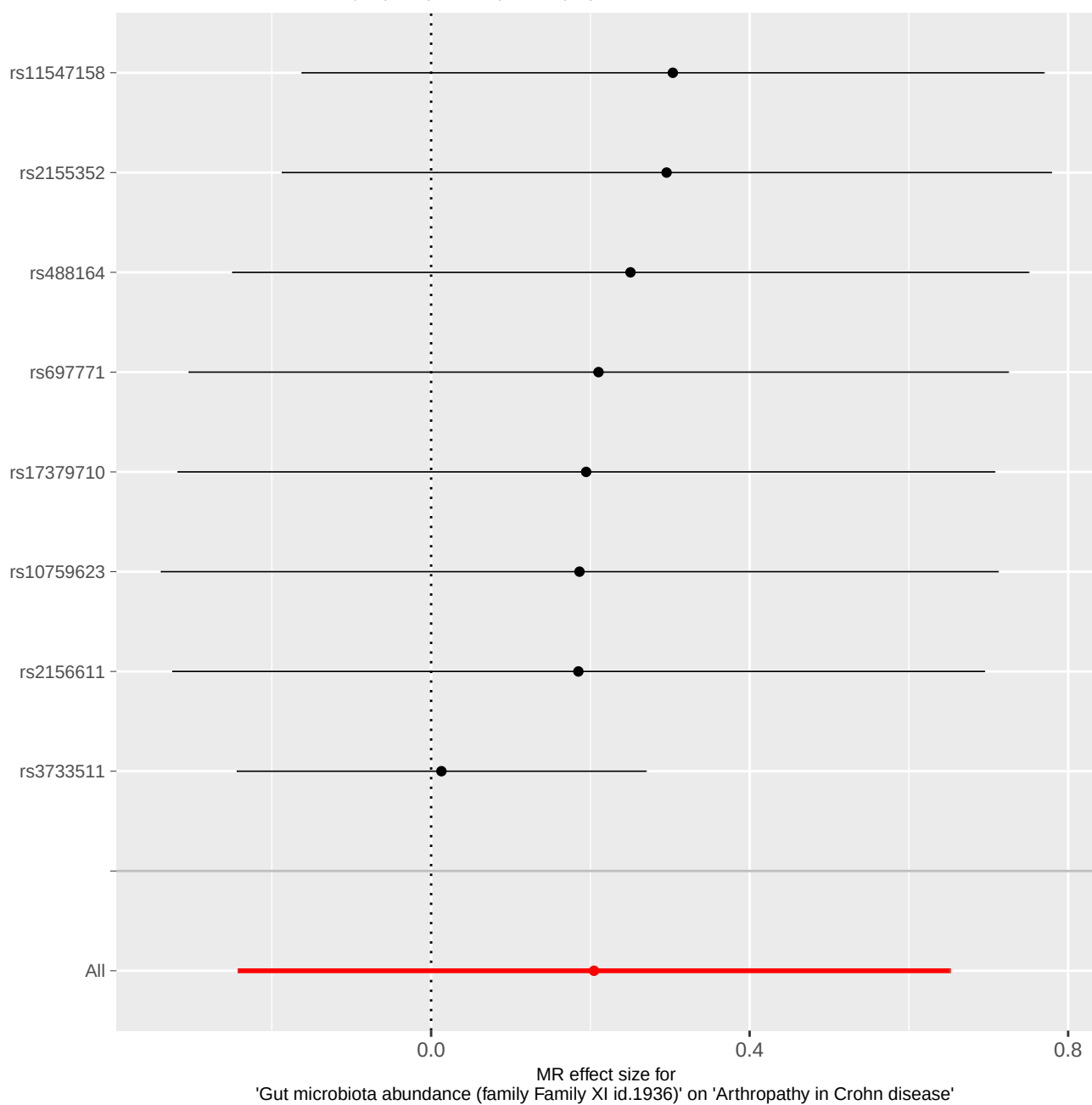


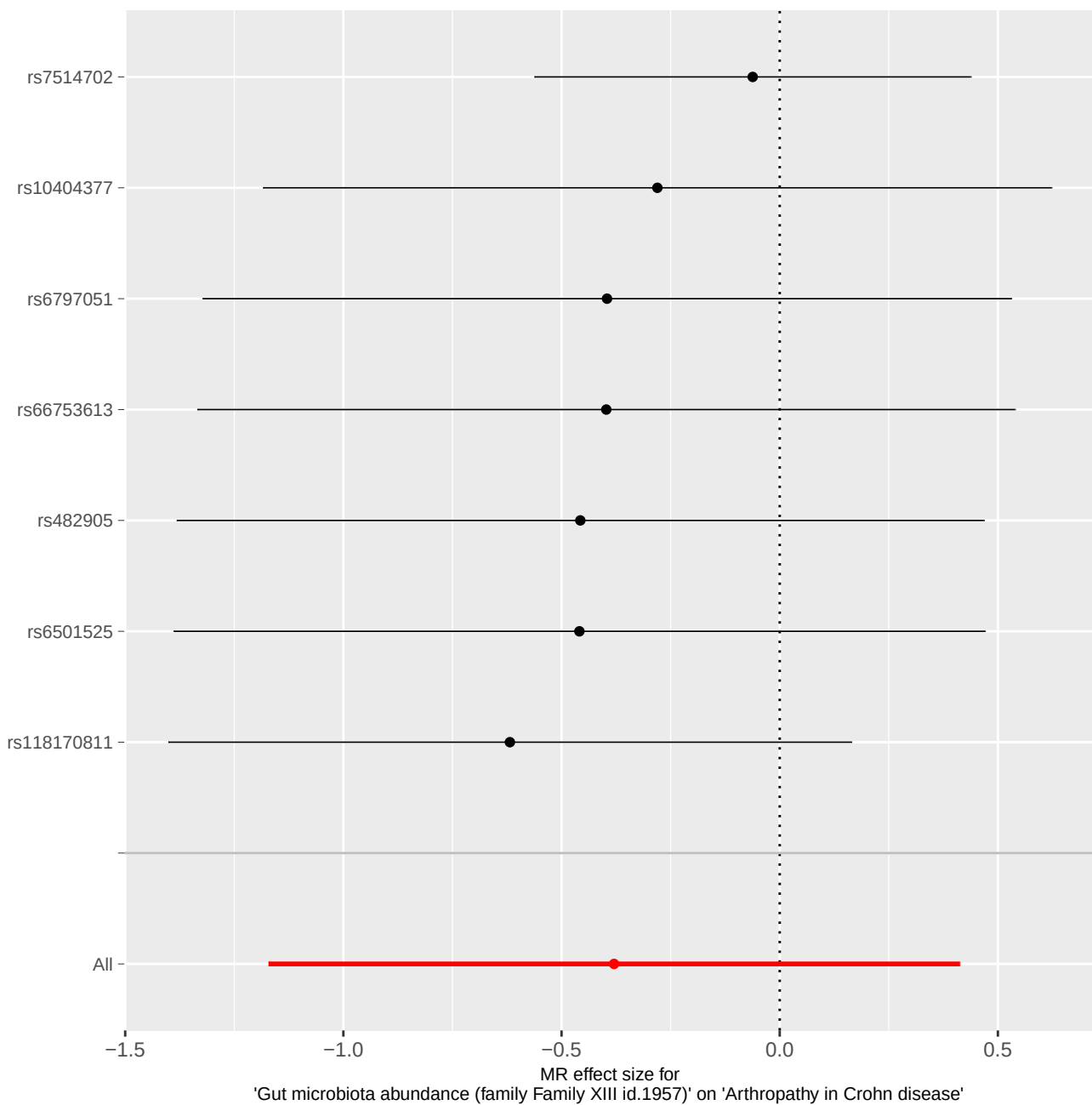


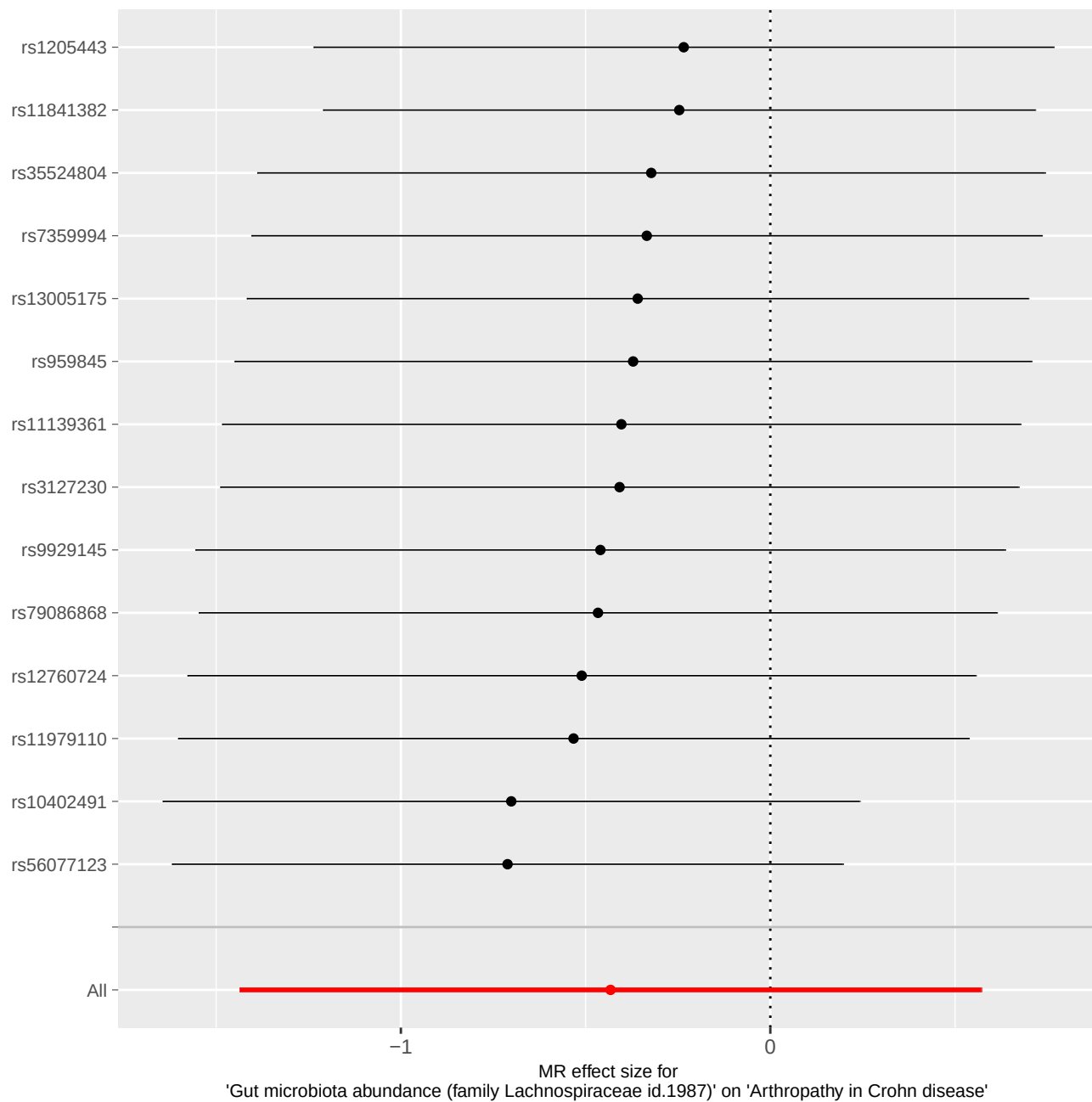










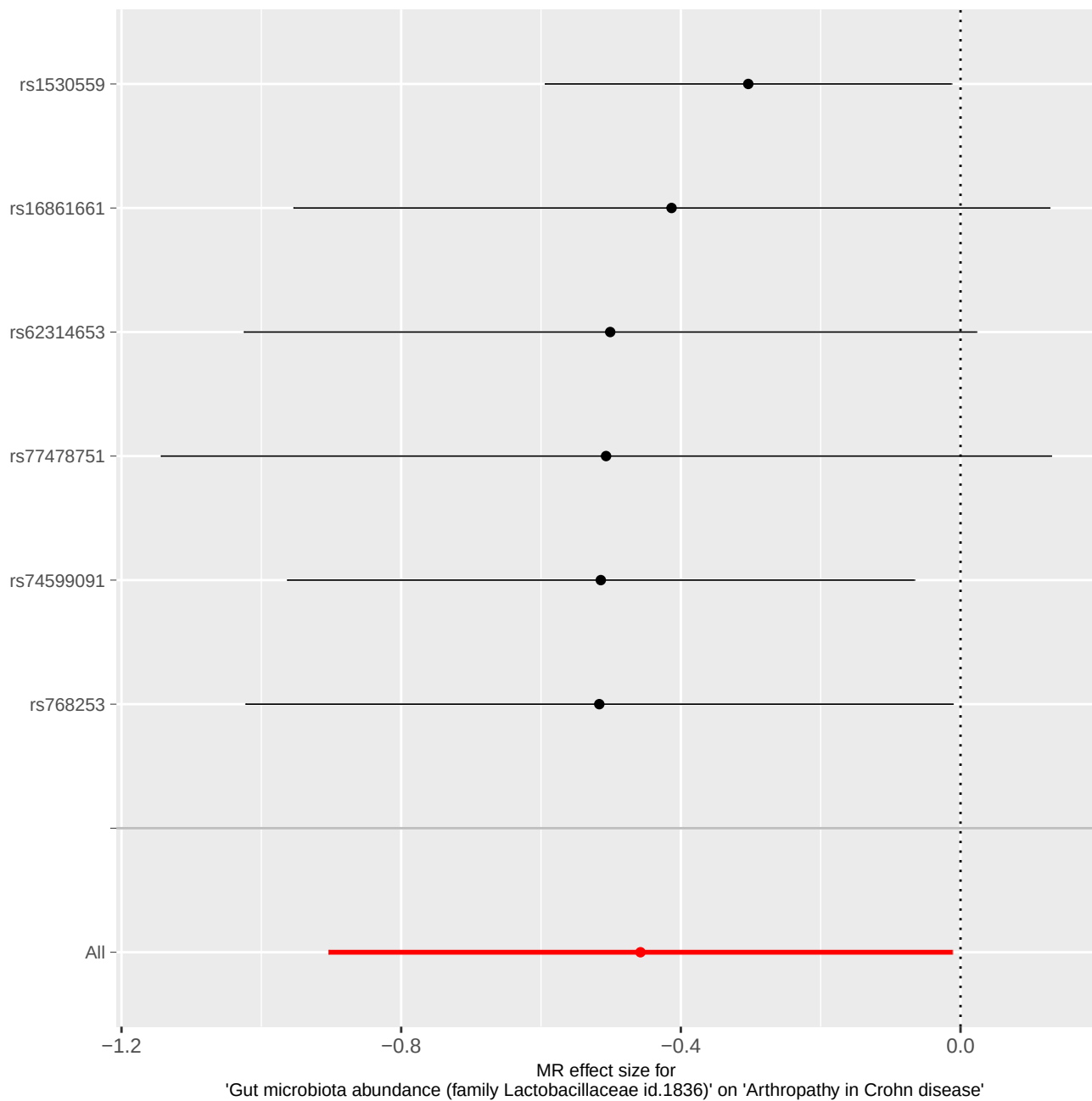


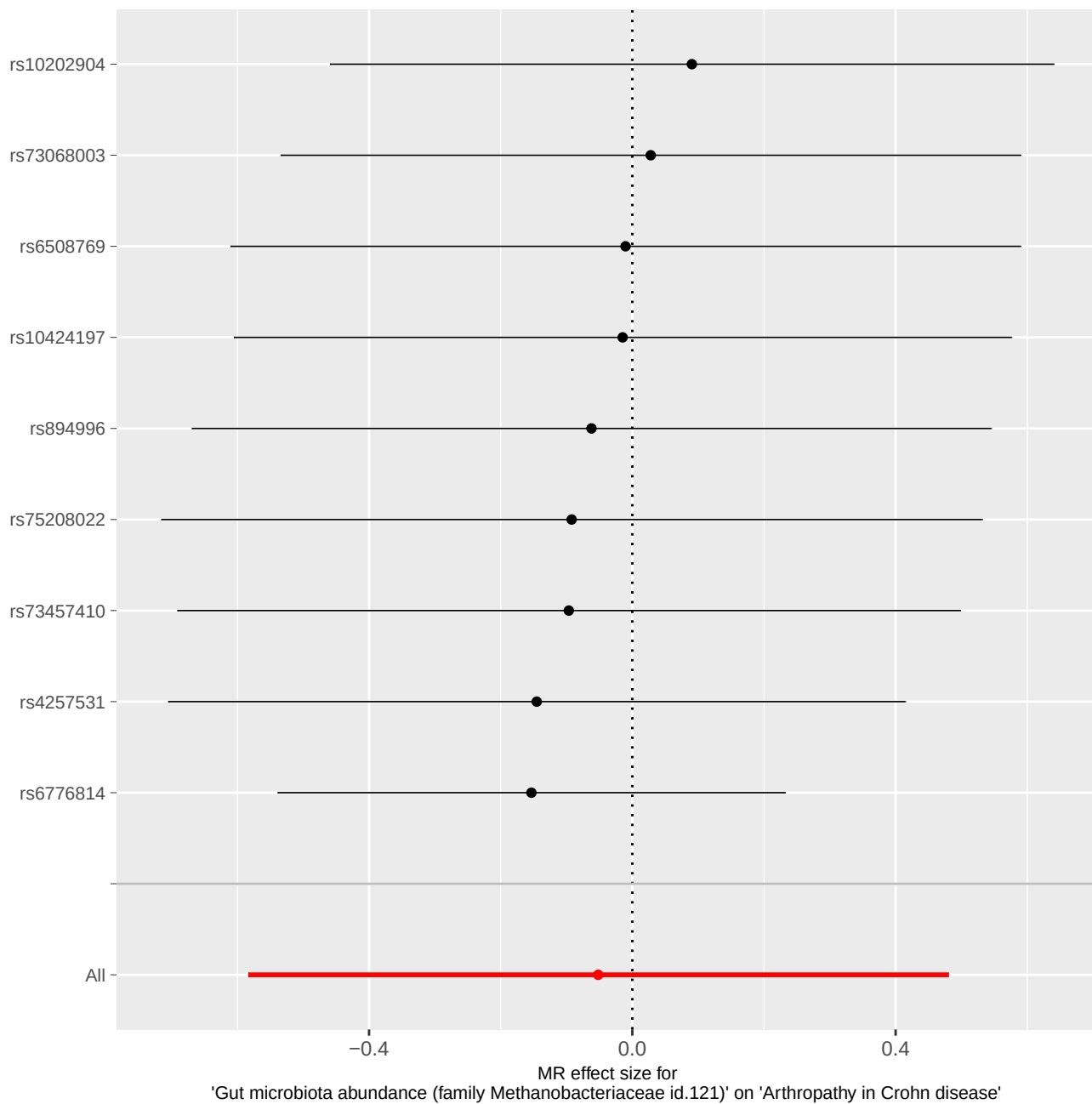
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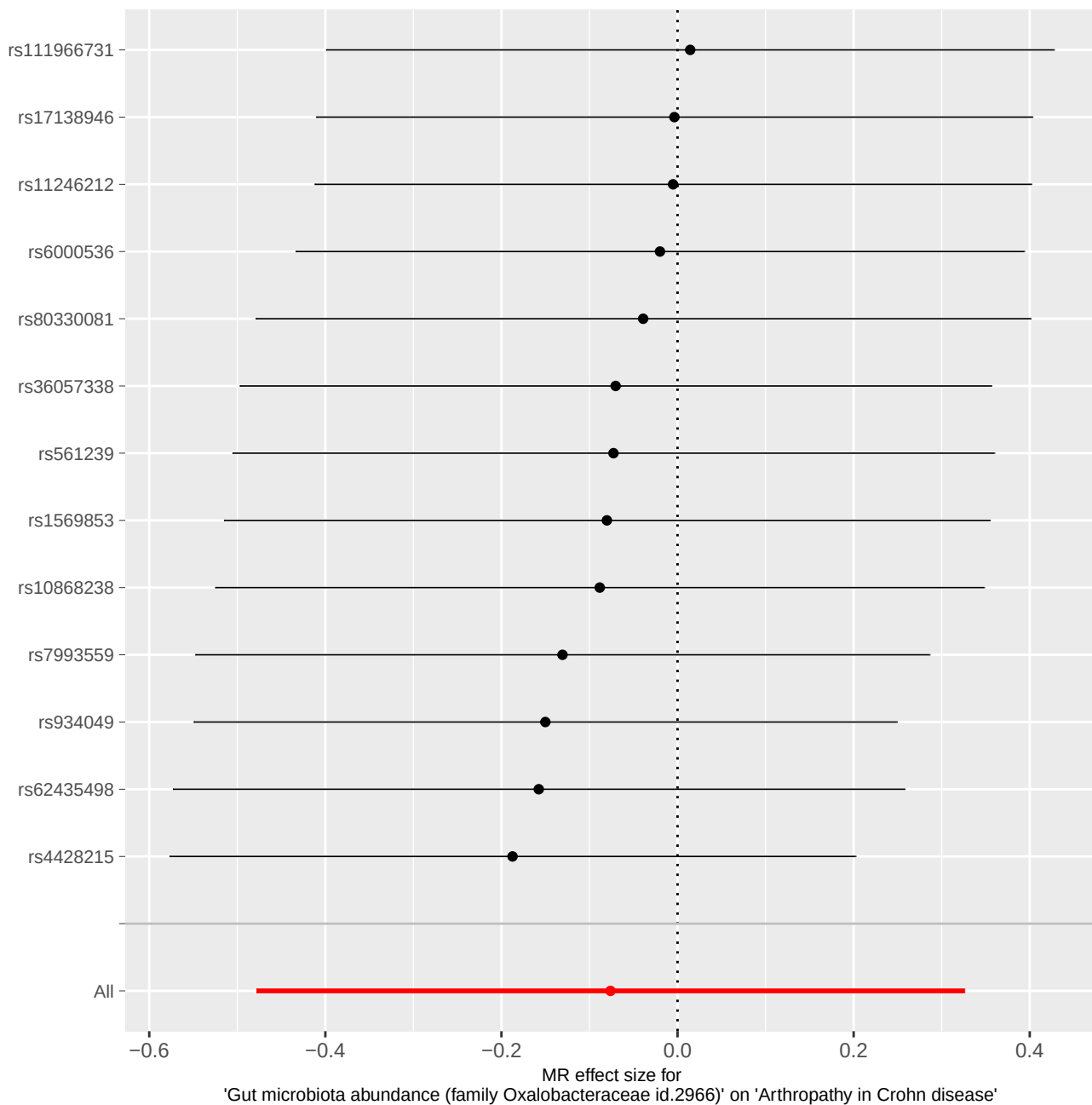
MR effect size for

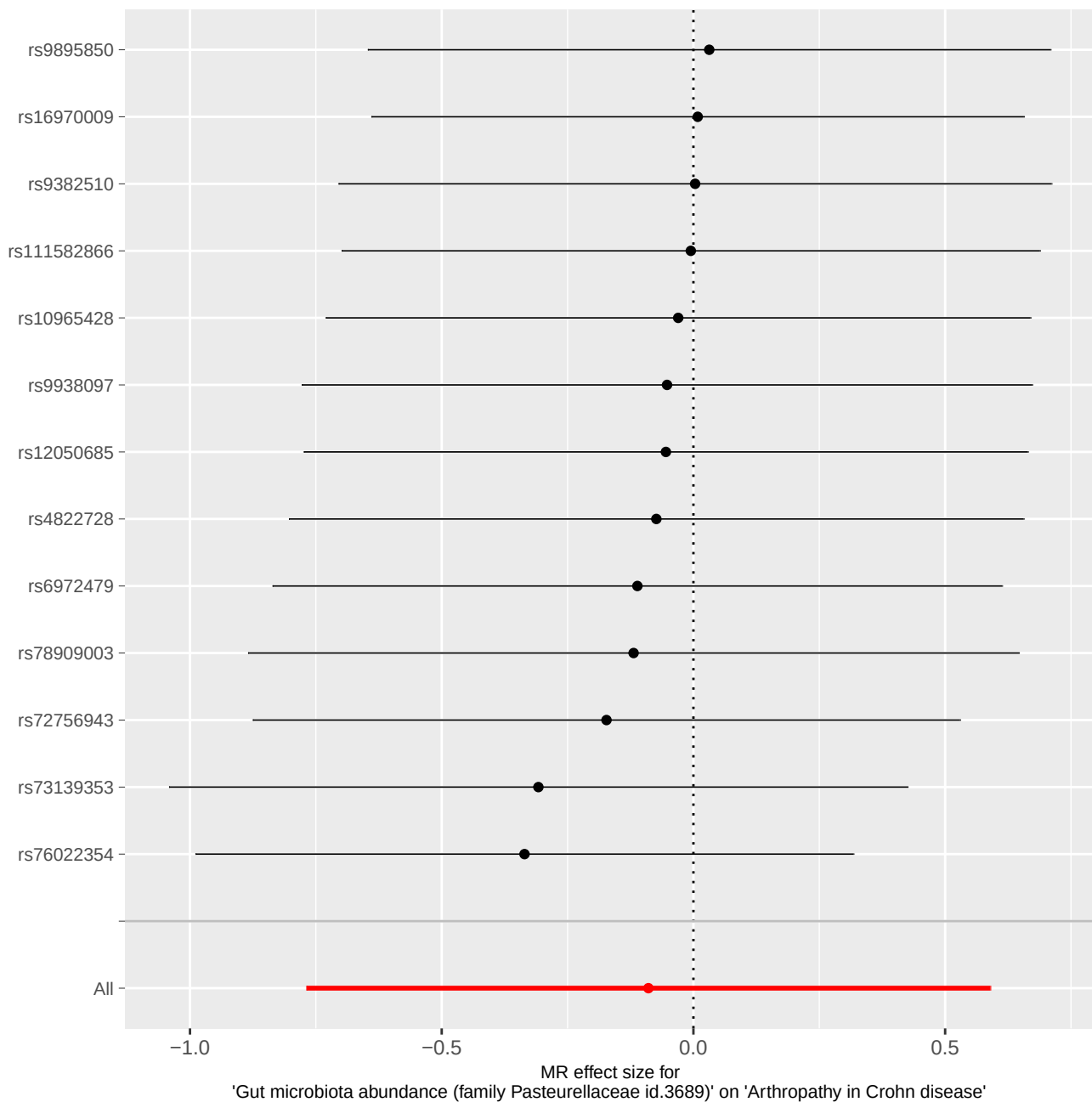
'Gut microbiota abundance (family Lachnospiraceae id.1987)' on 'Arthropathy in Crohn disease'

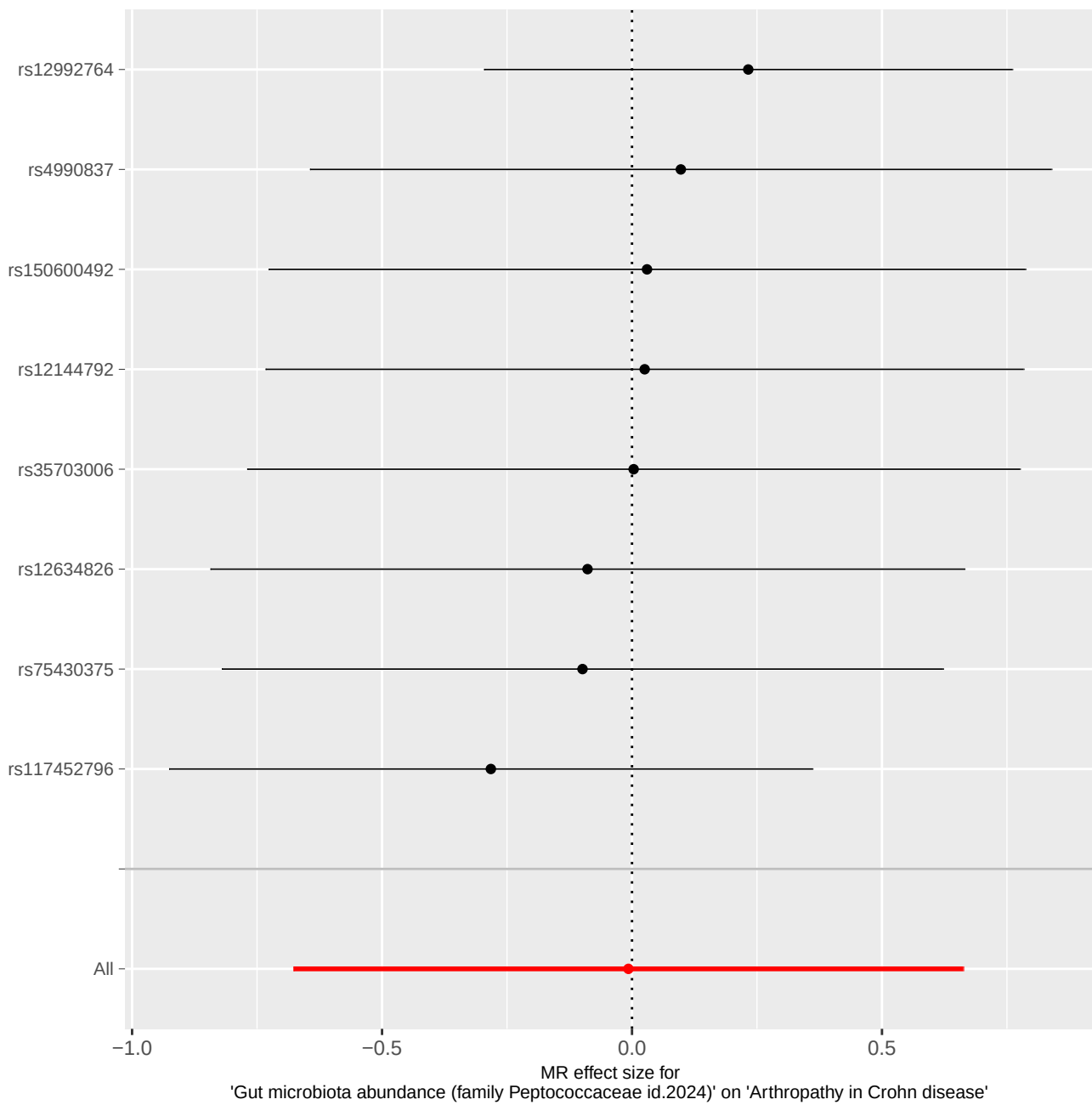


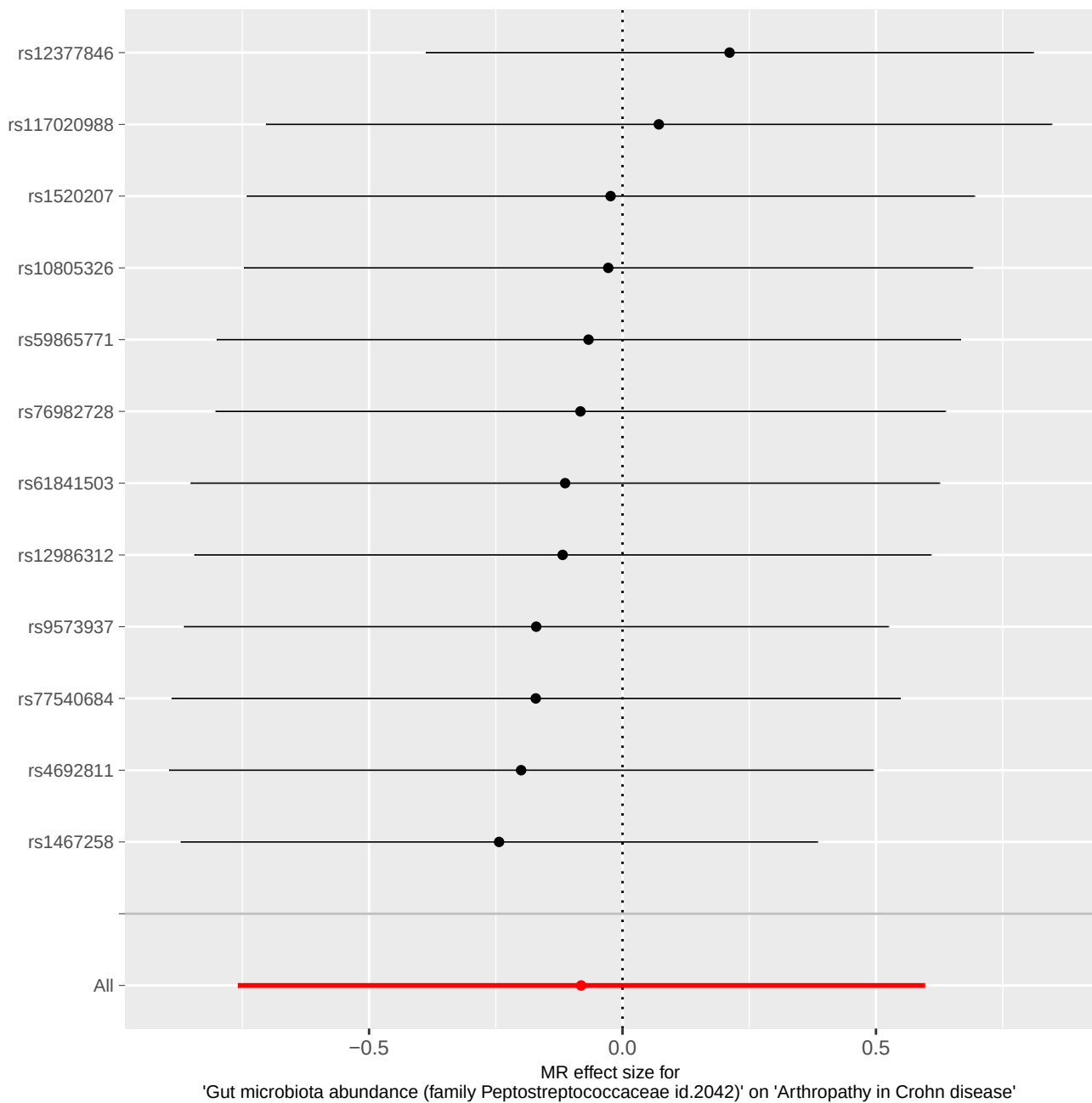


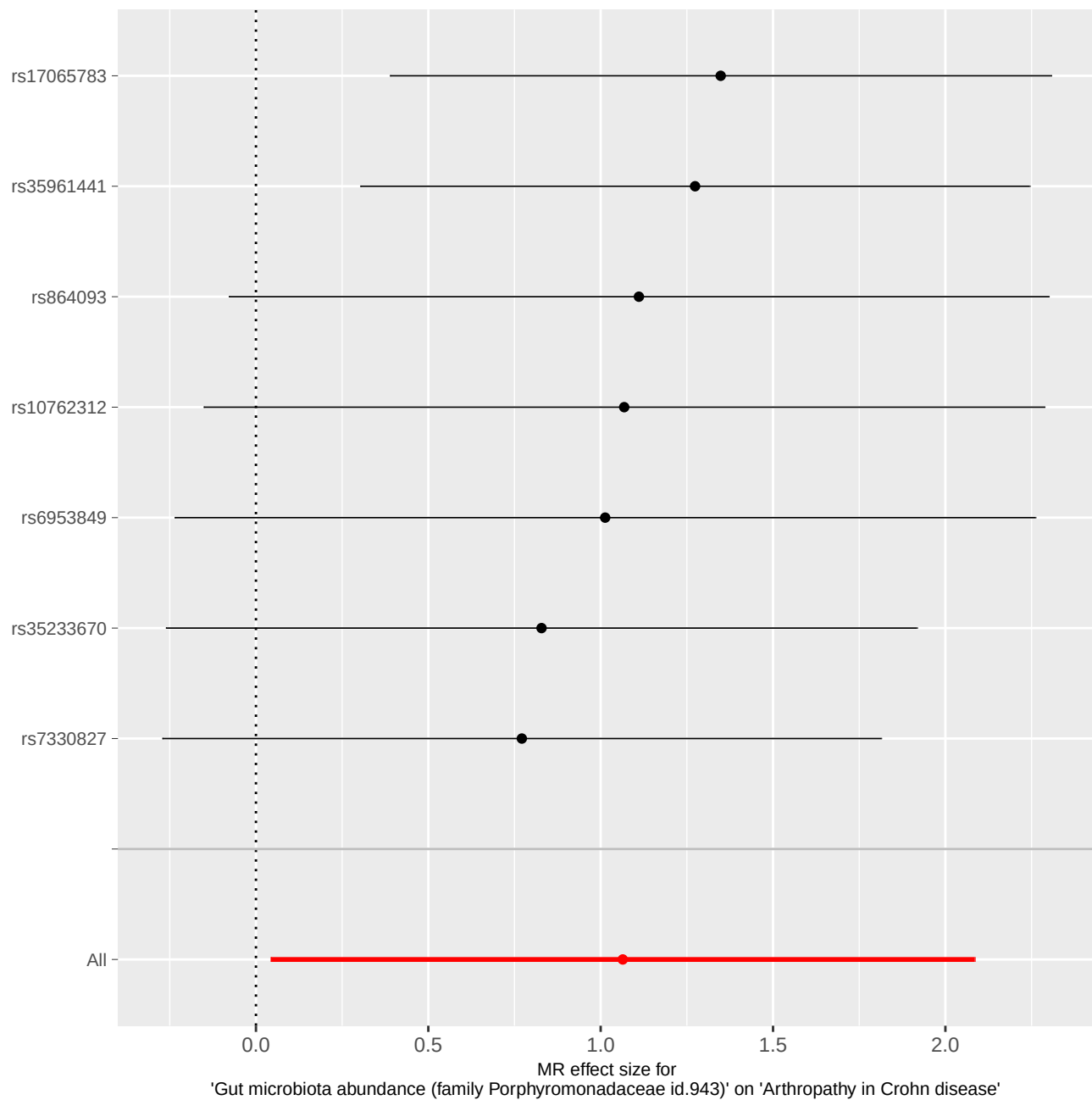
MR effect size for
'Gut microbiota abundance (family Methanobacteriaceae id.121)' on 'Arthropathy in Crohn disease'

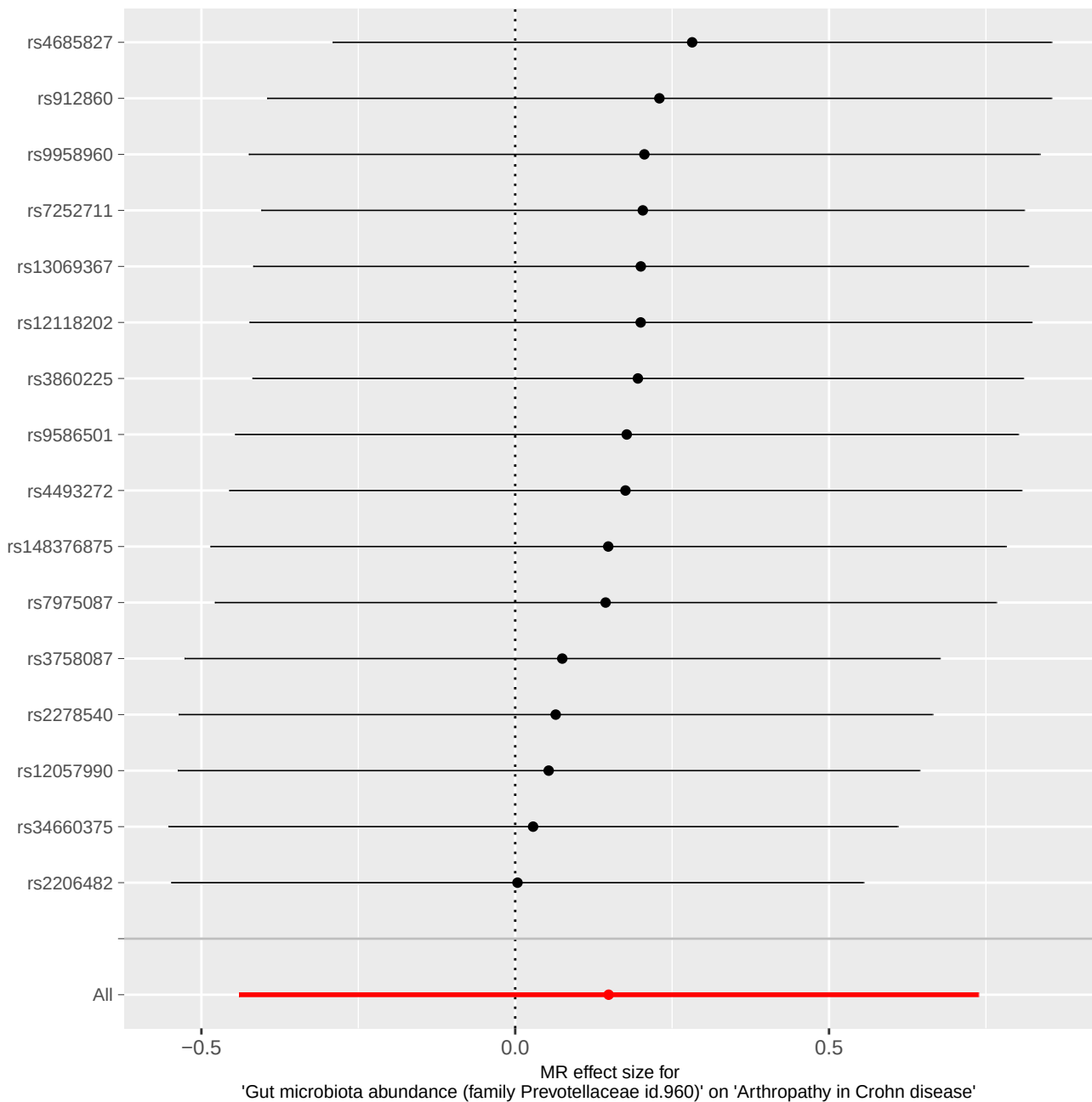


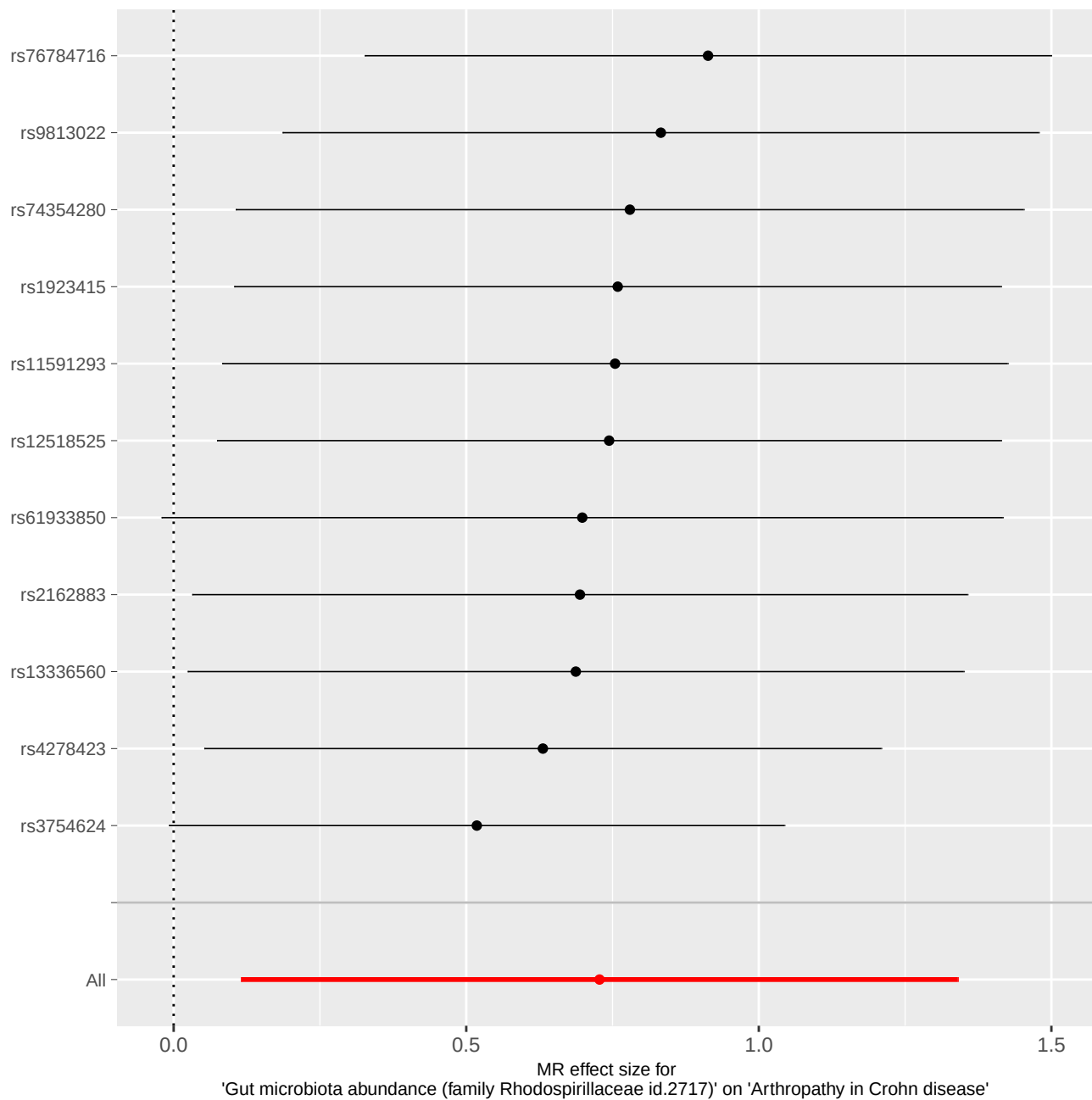




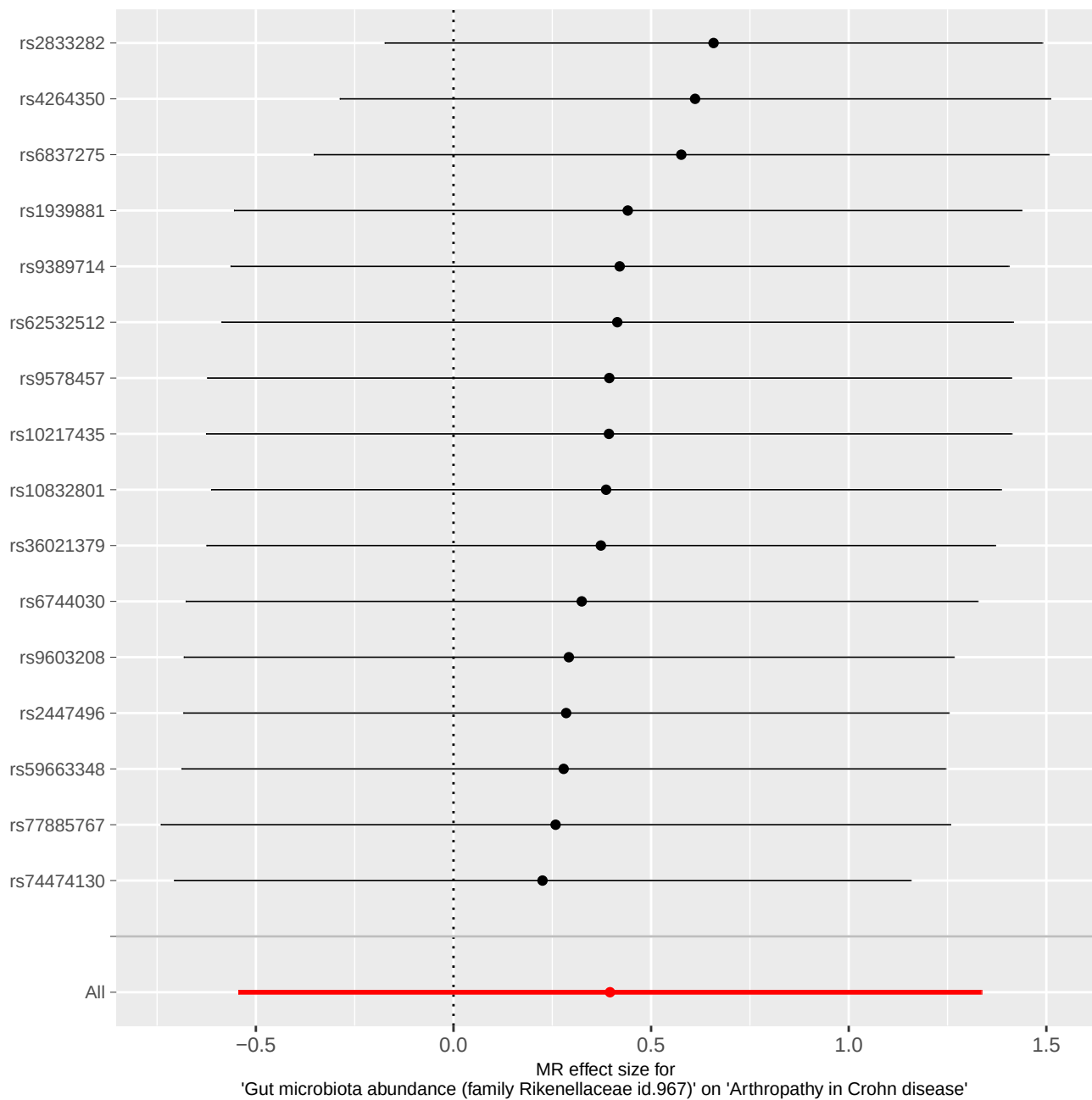


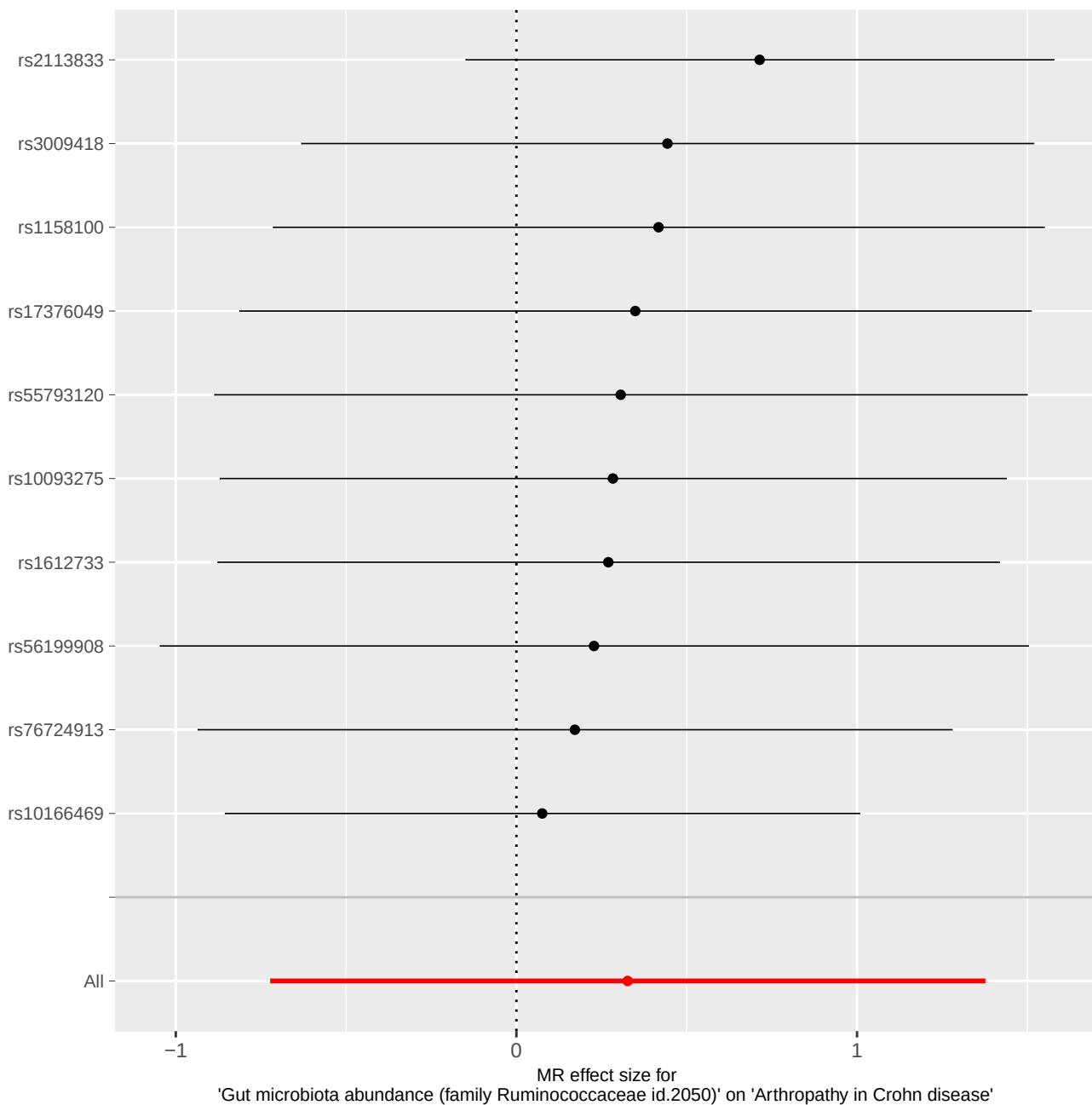


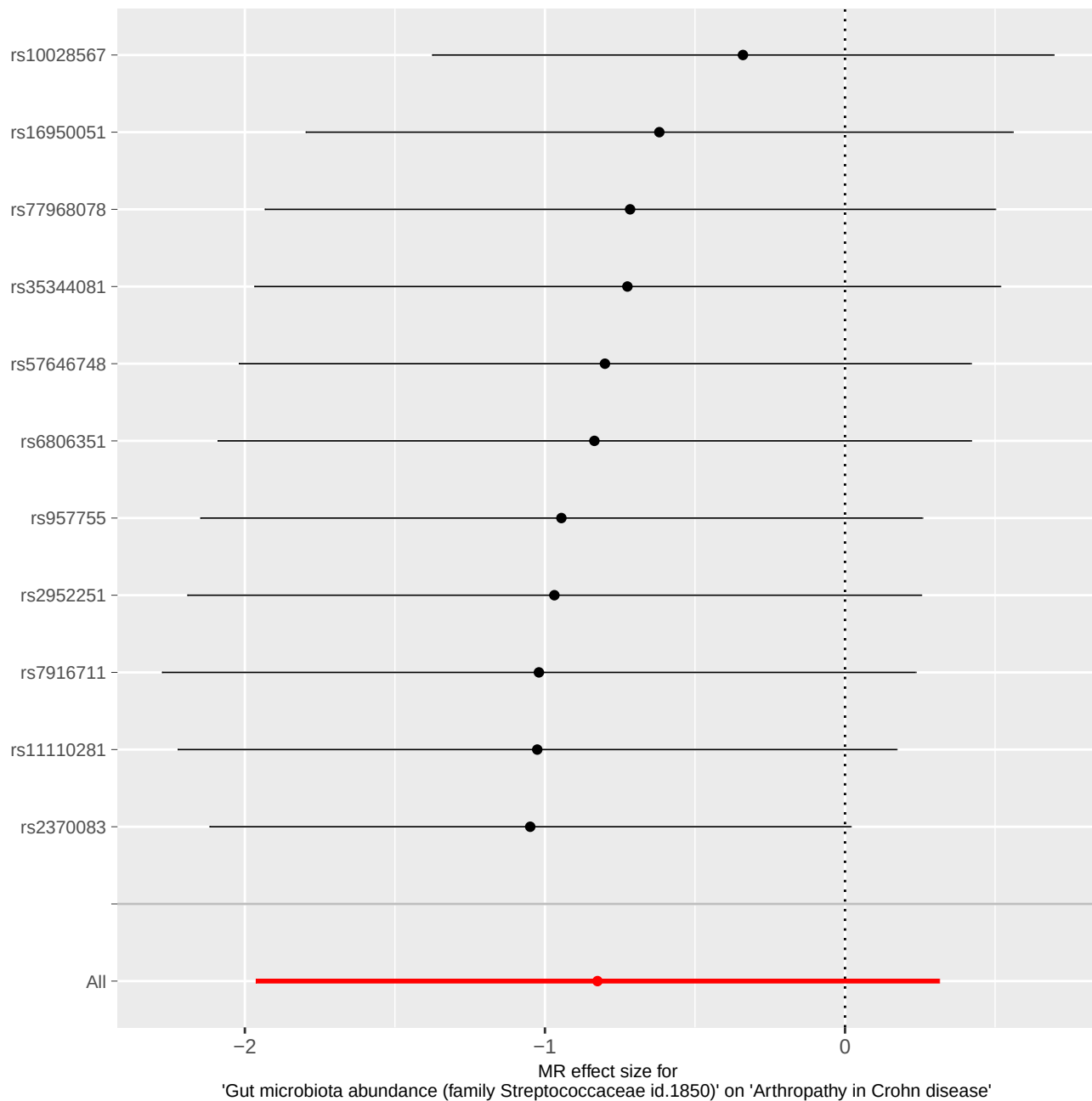


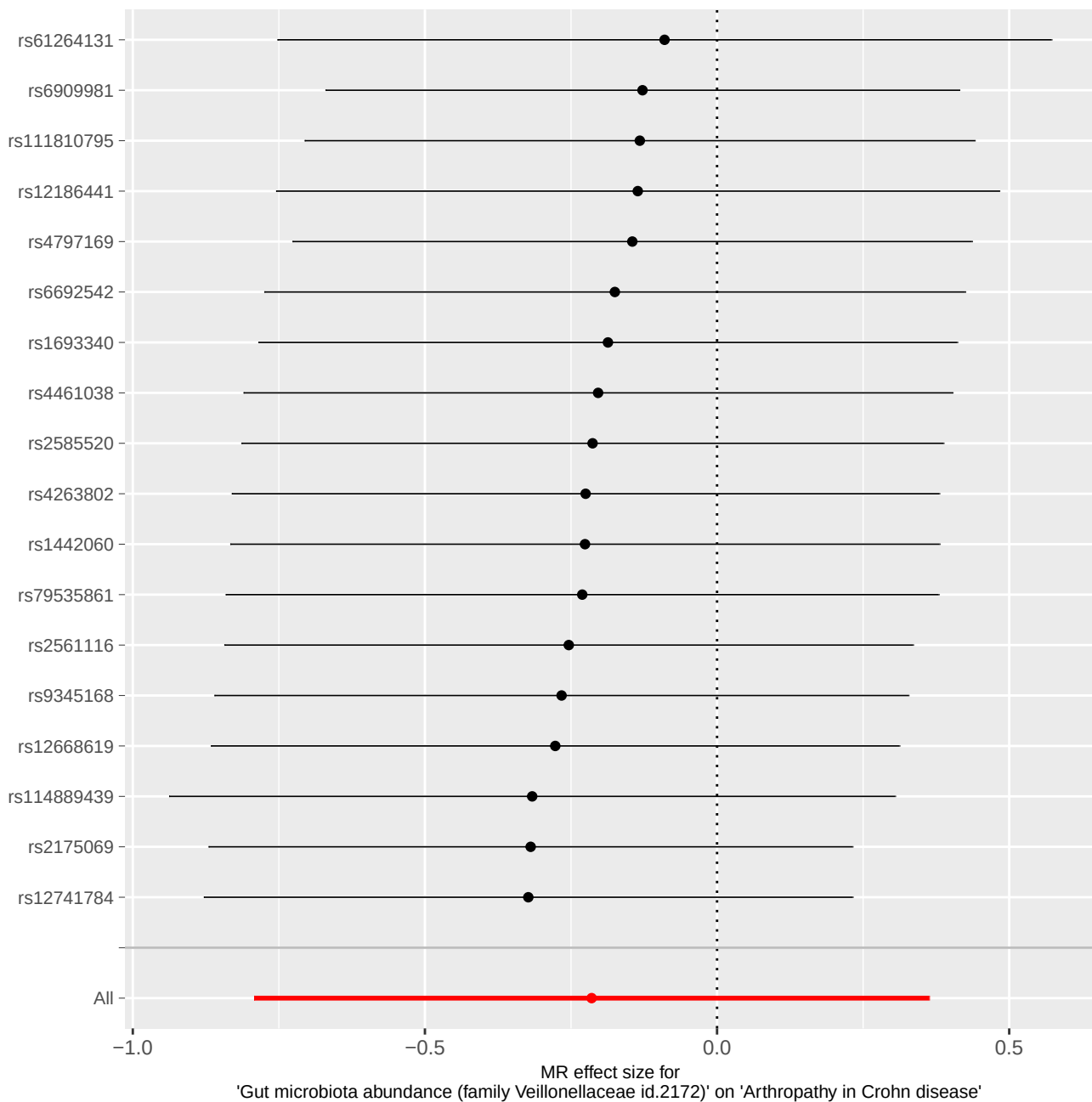


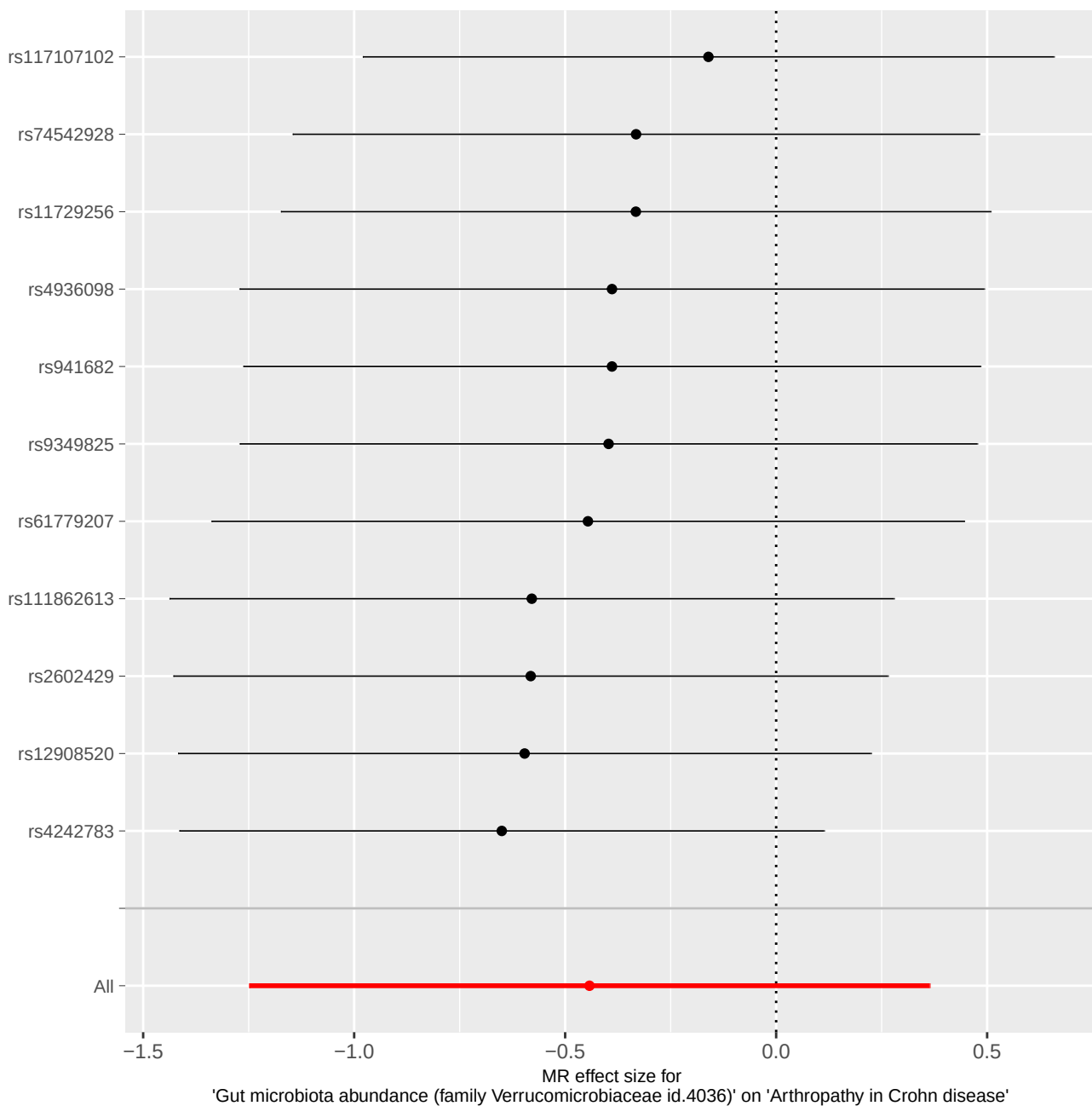
Batch 477 : Gut microbiota abundance (family Rikenellaceae id.967) on Arthropathy in Crohn disease



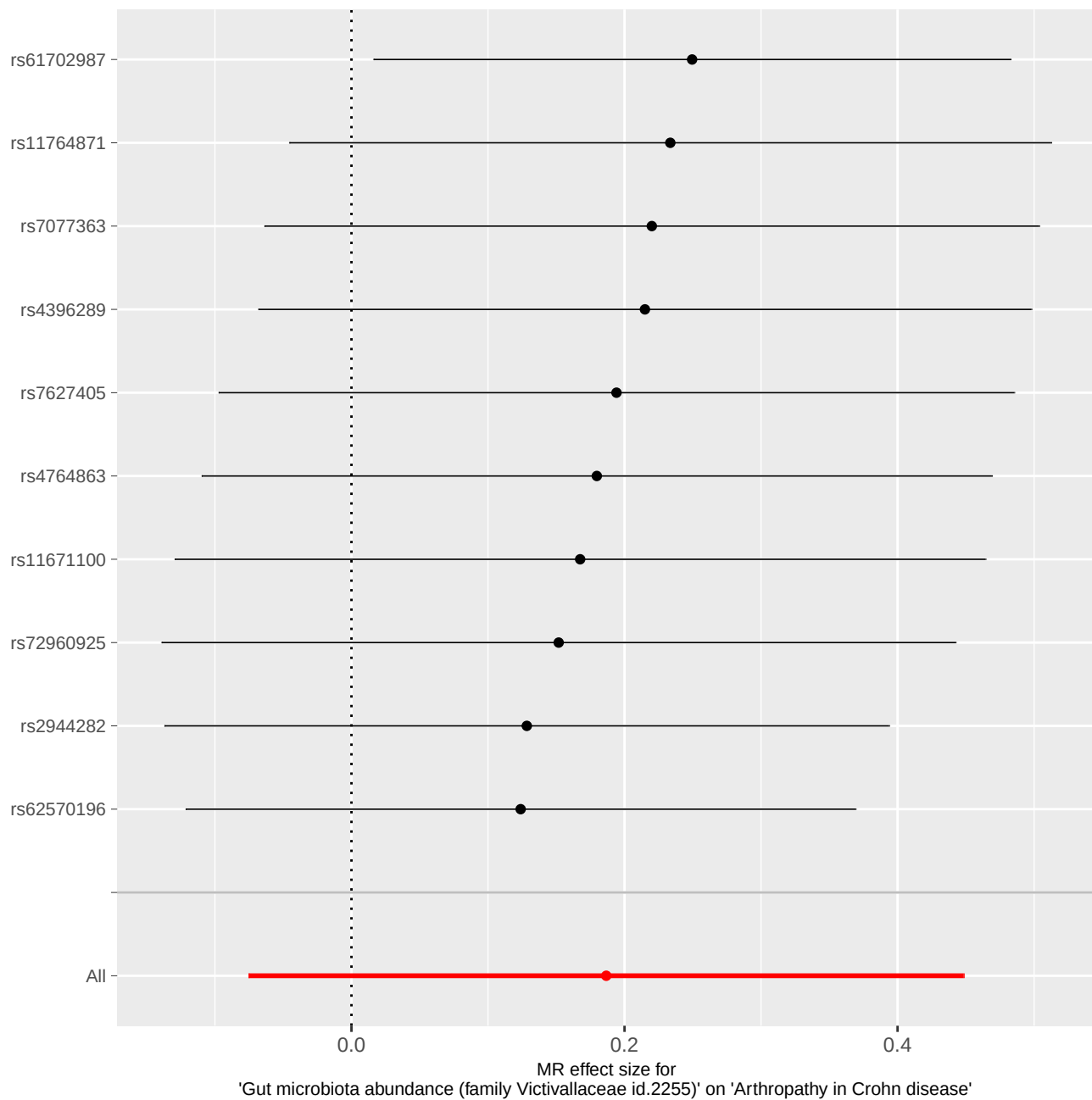


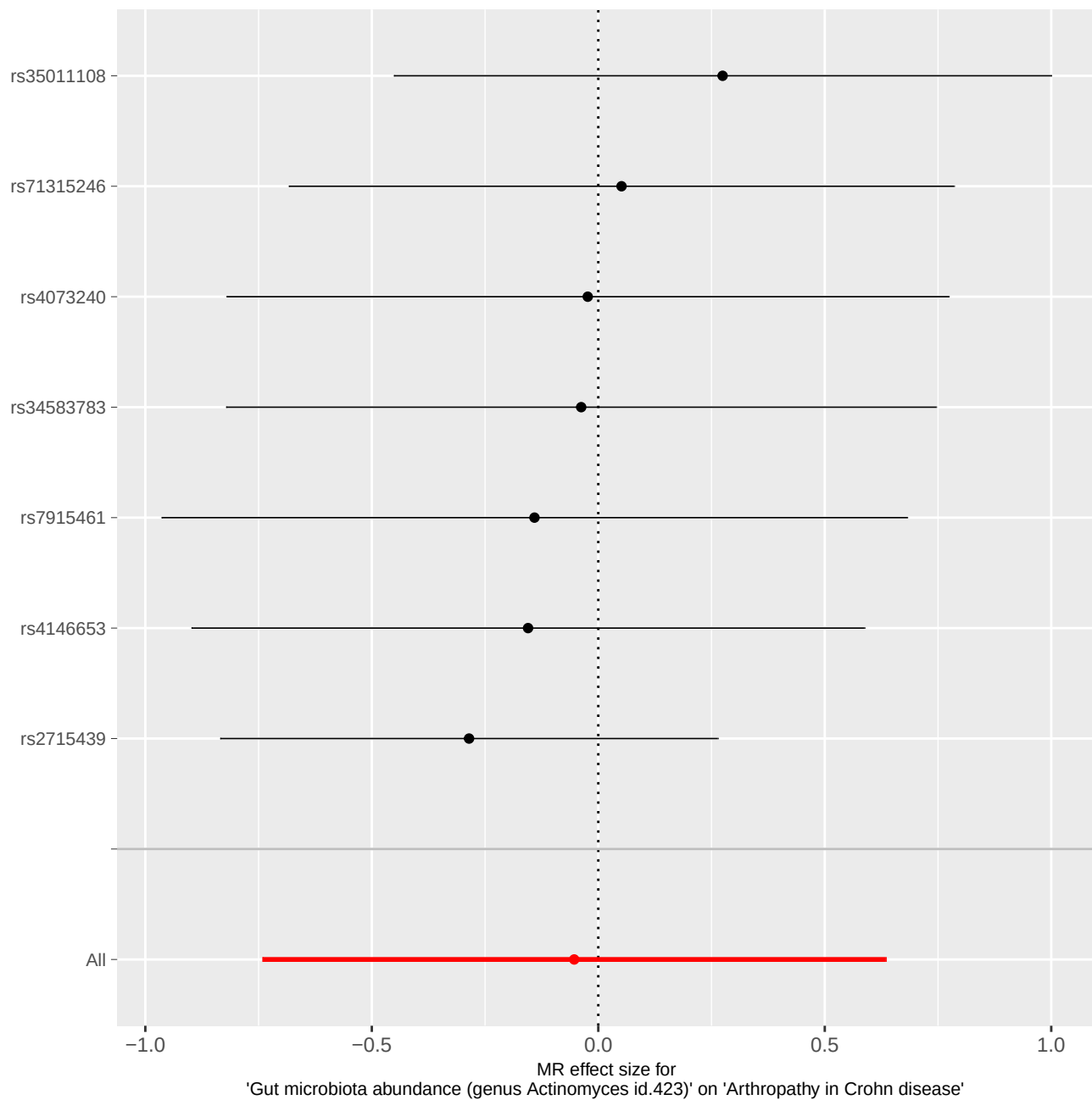


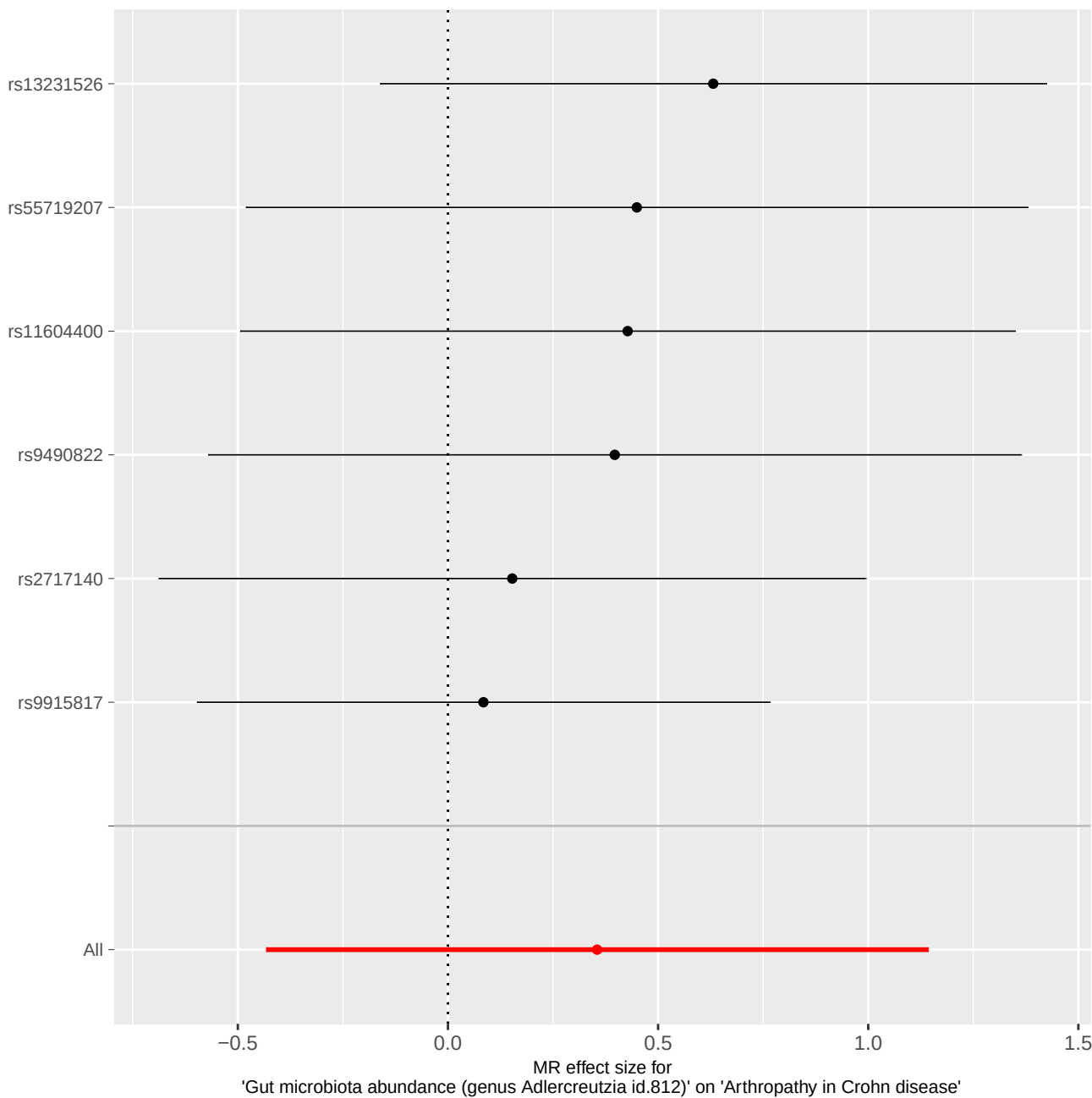


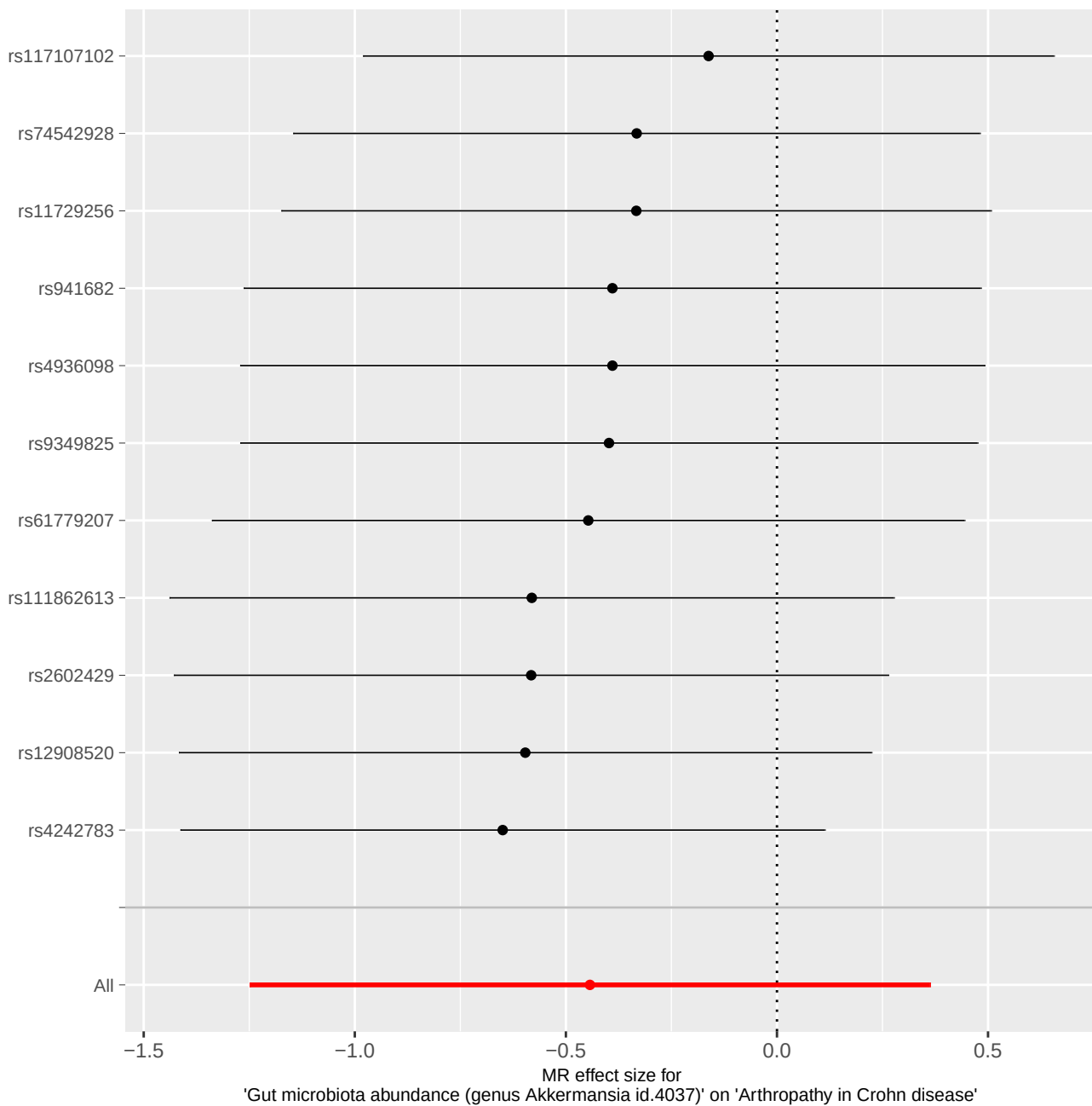


Batch 482 : Gut microbiota abundance (family Victivallaceae id.2255) on Arthropathy in Crohn disease

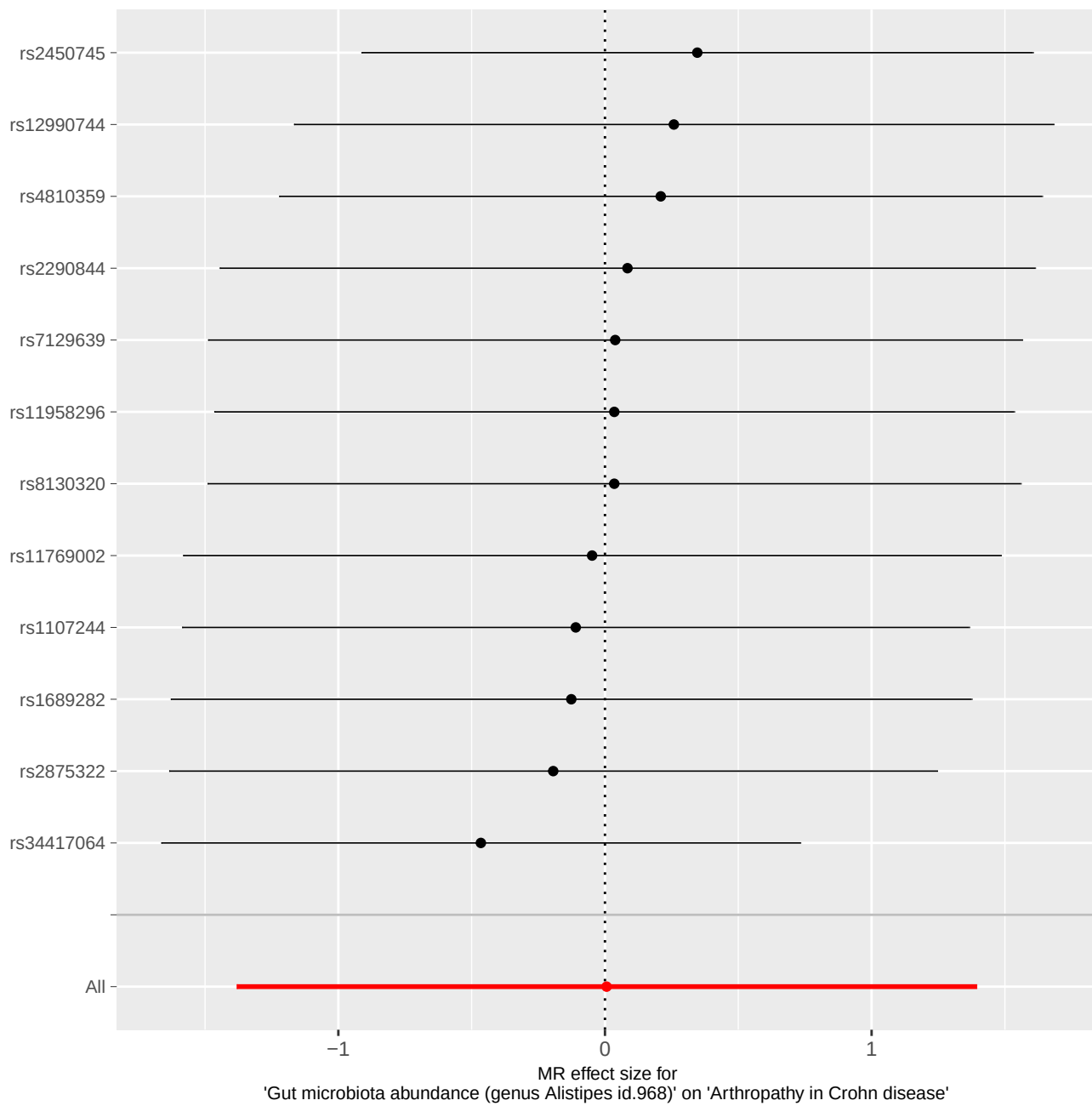


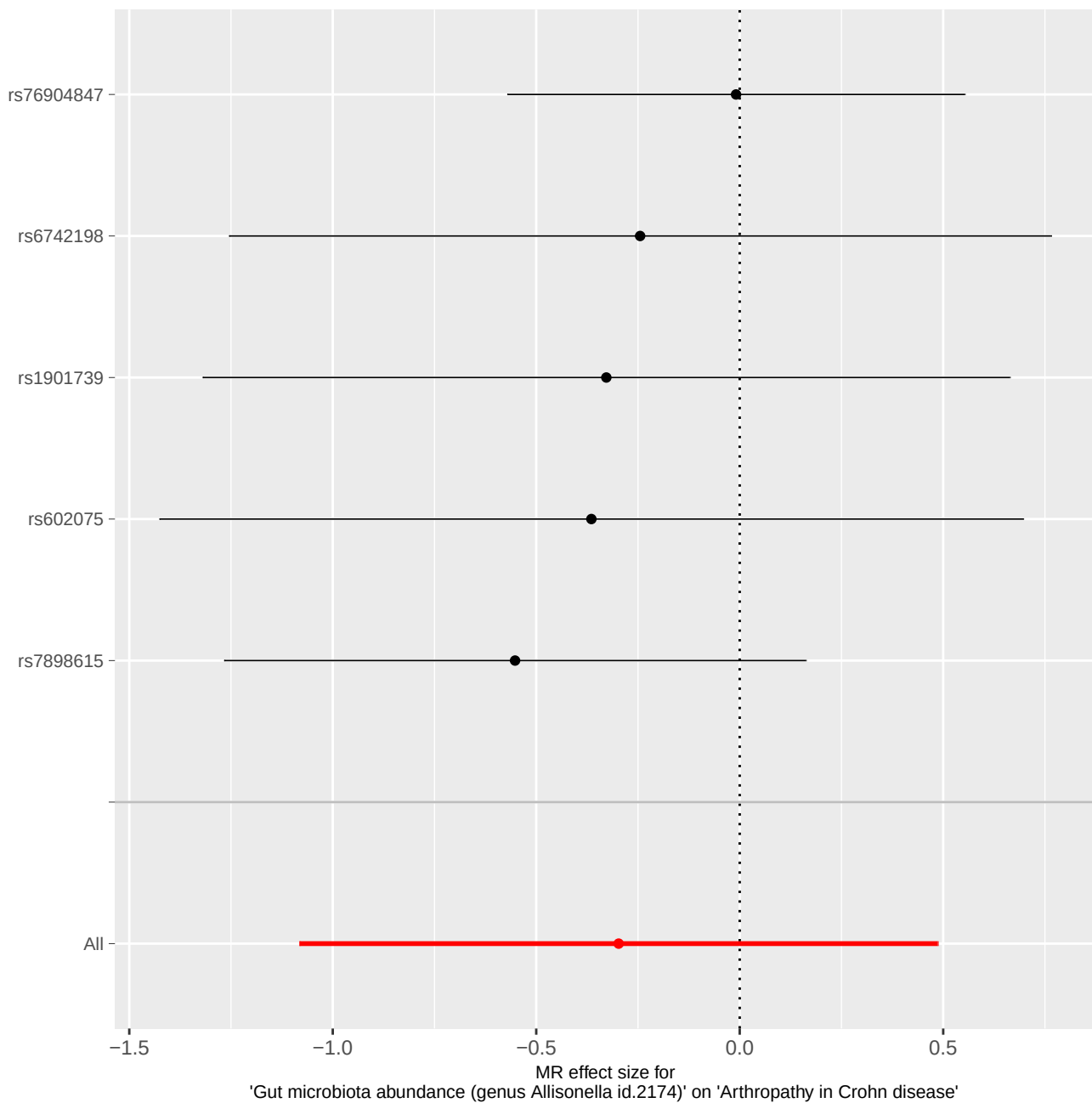




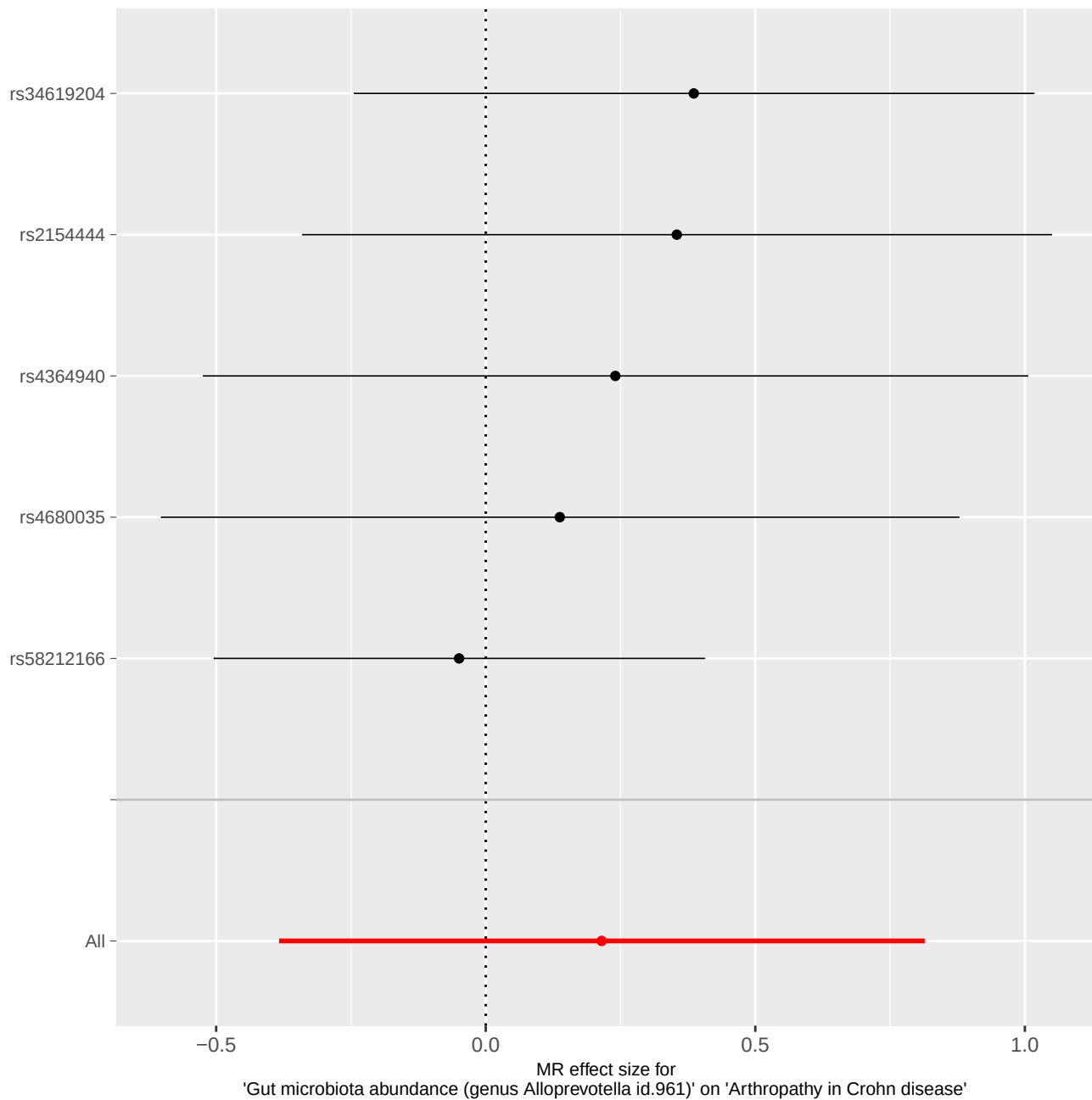


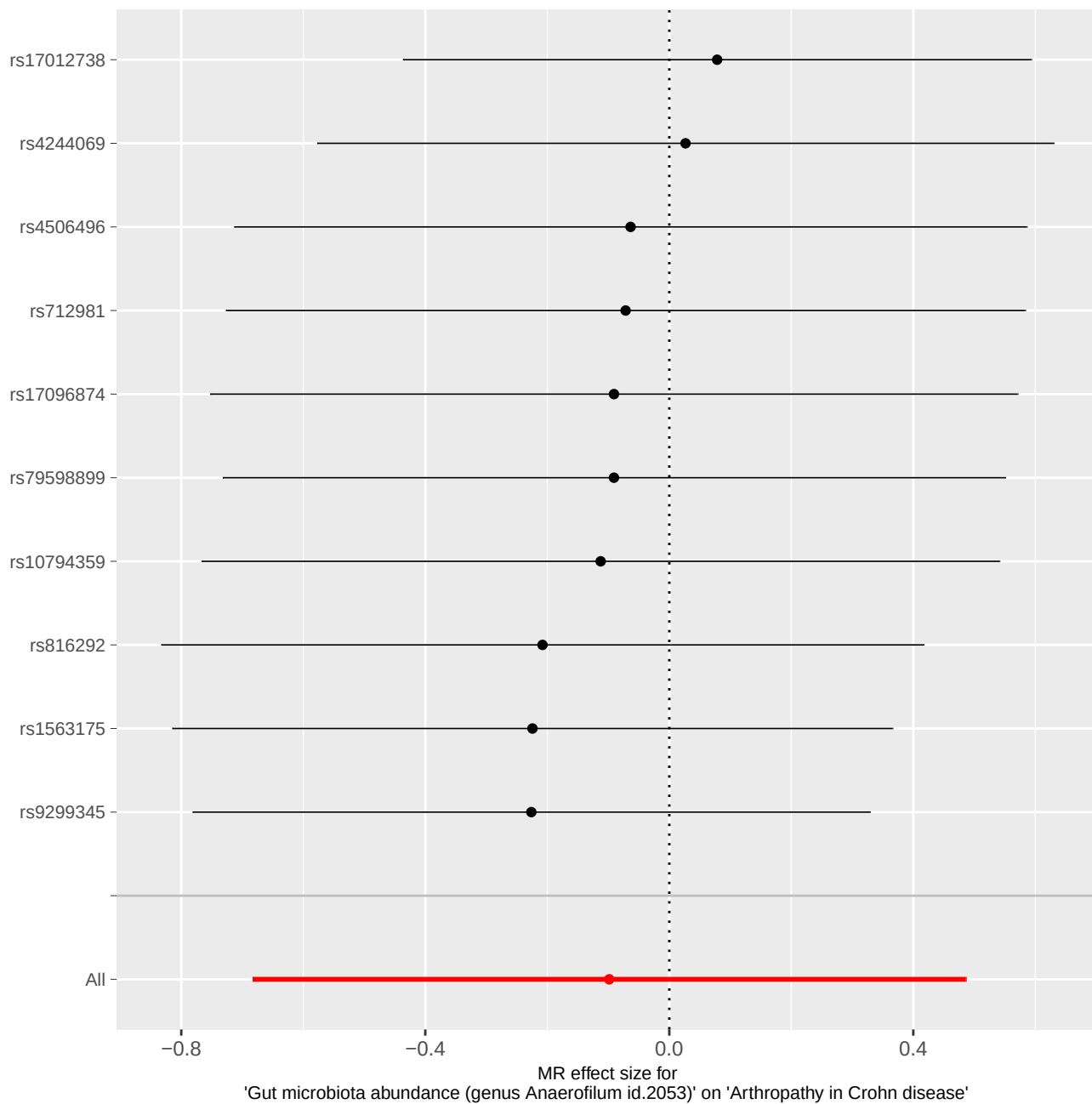
Batch 486 : Gut microbiota abundance (genus Alistipes id.968) on Arthropathy in Crohn disease

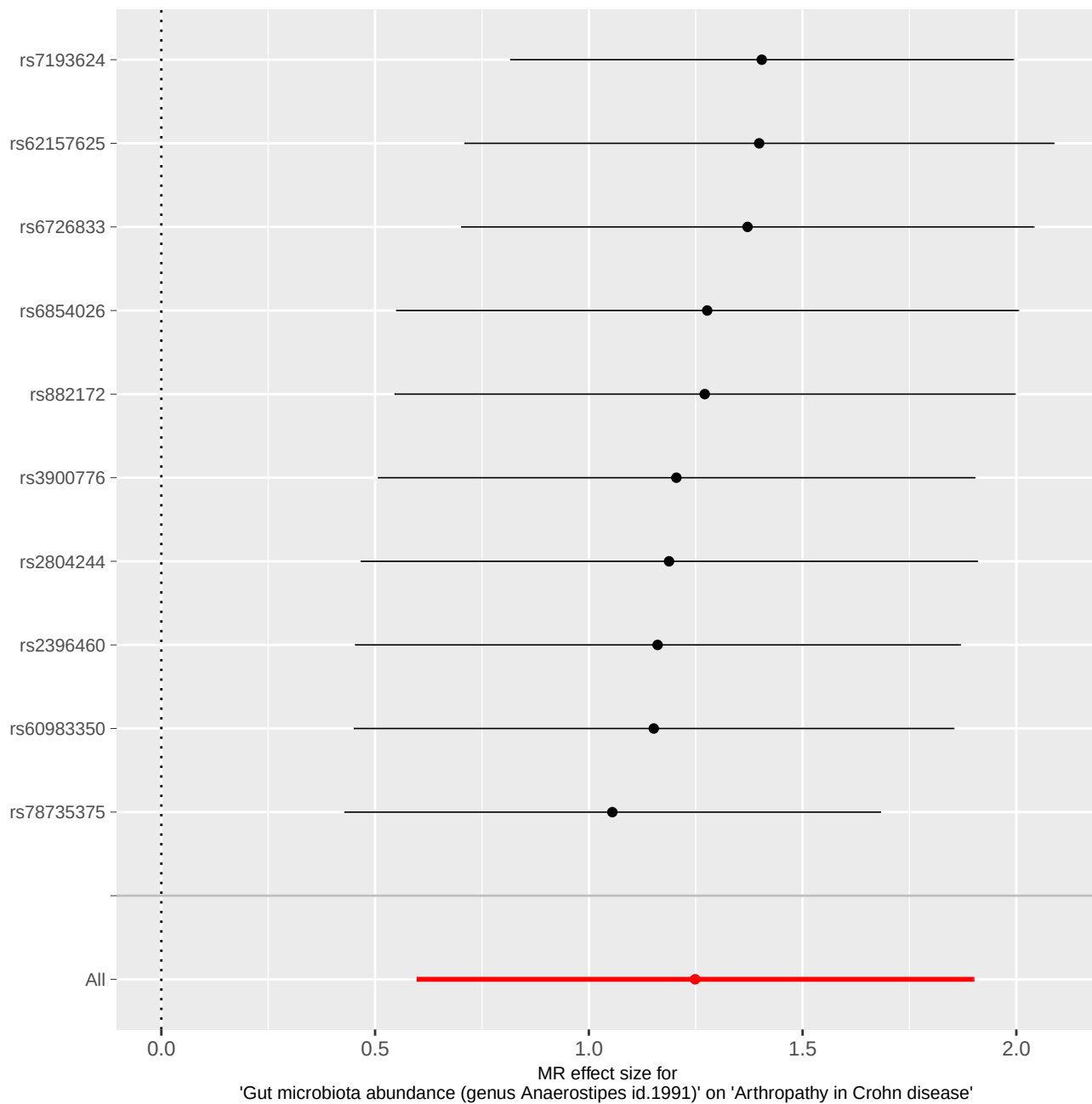


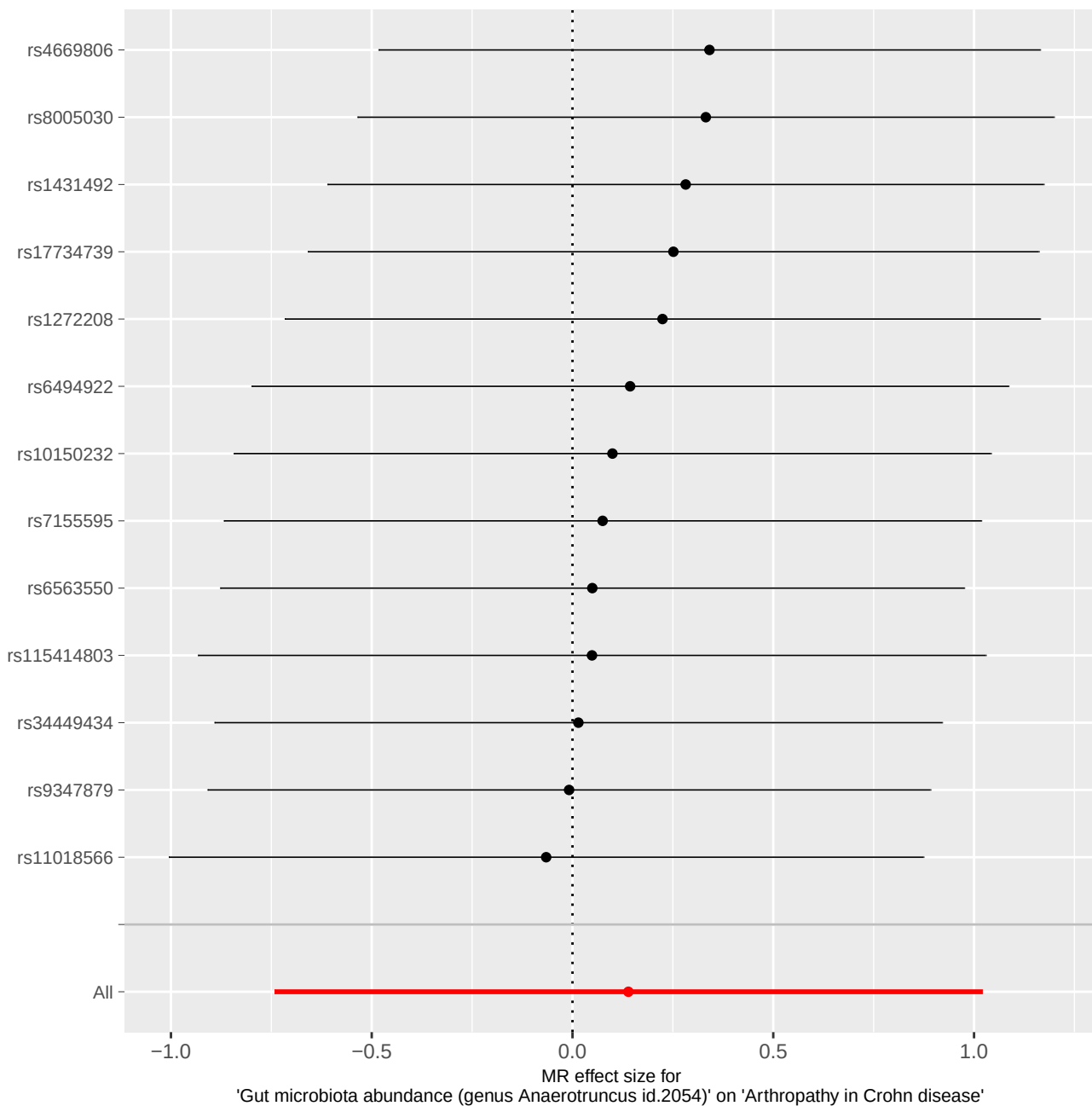


Batch 488 : Gut microbiota abundance (genus Alloprevotella id.961) on Arthropathy in Crohn disease

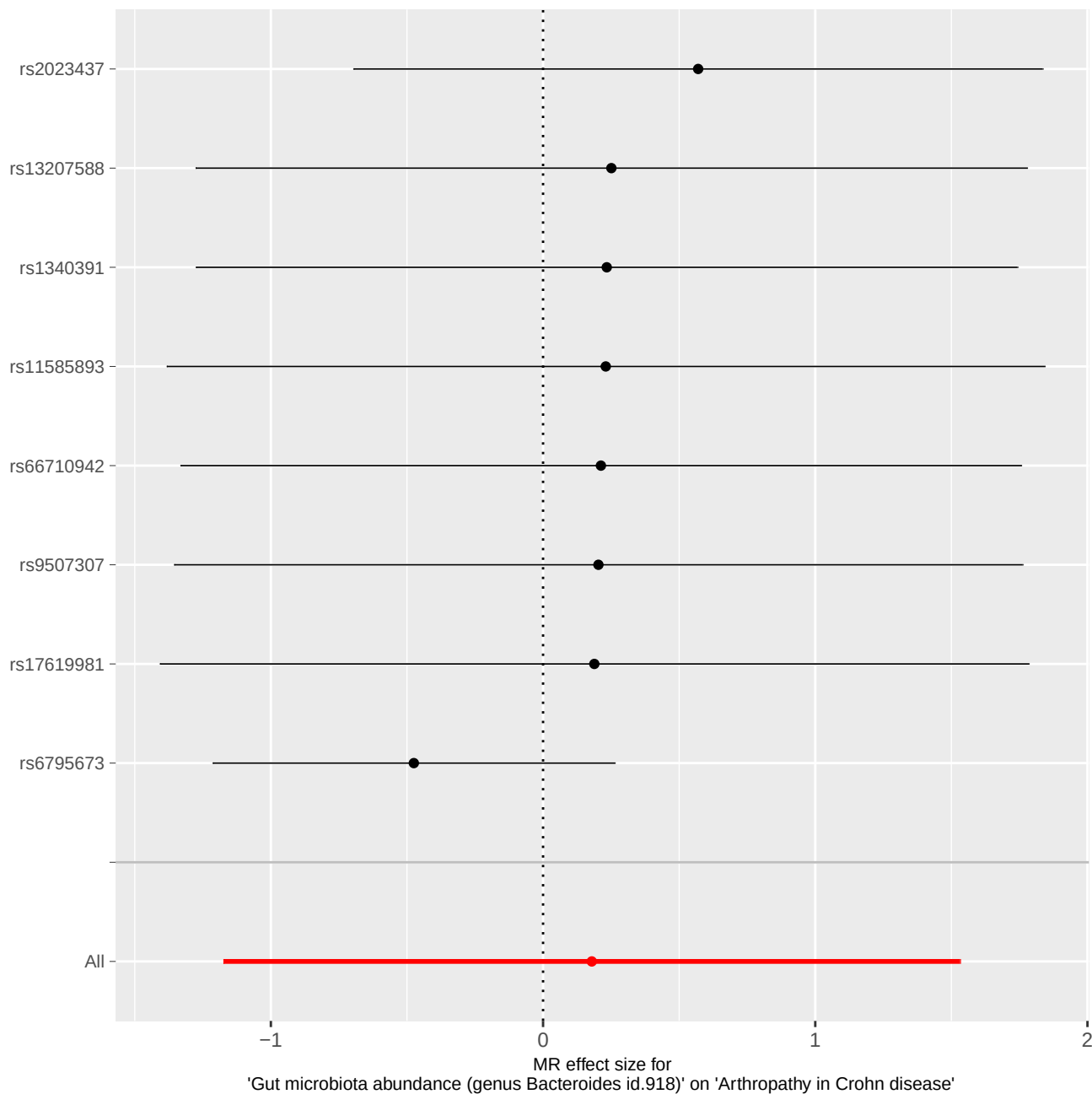


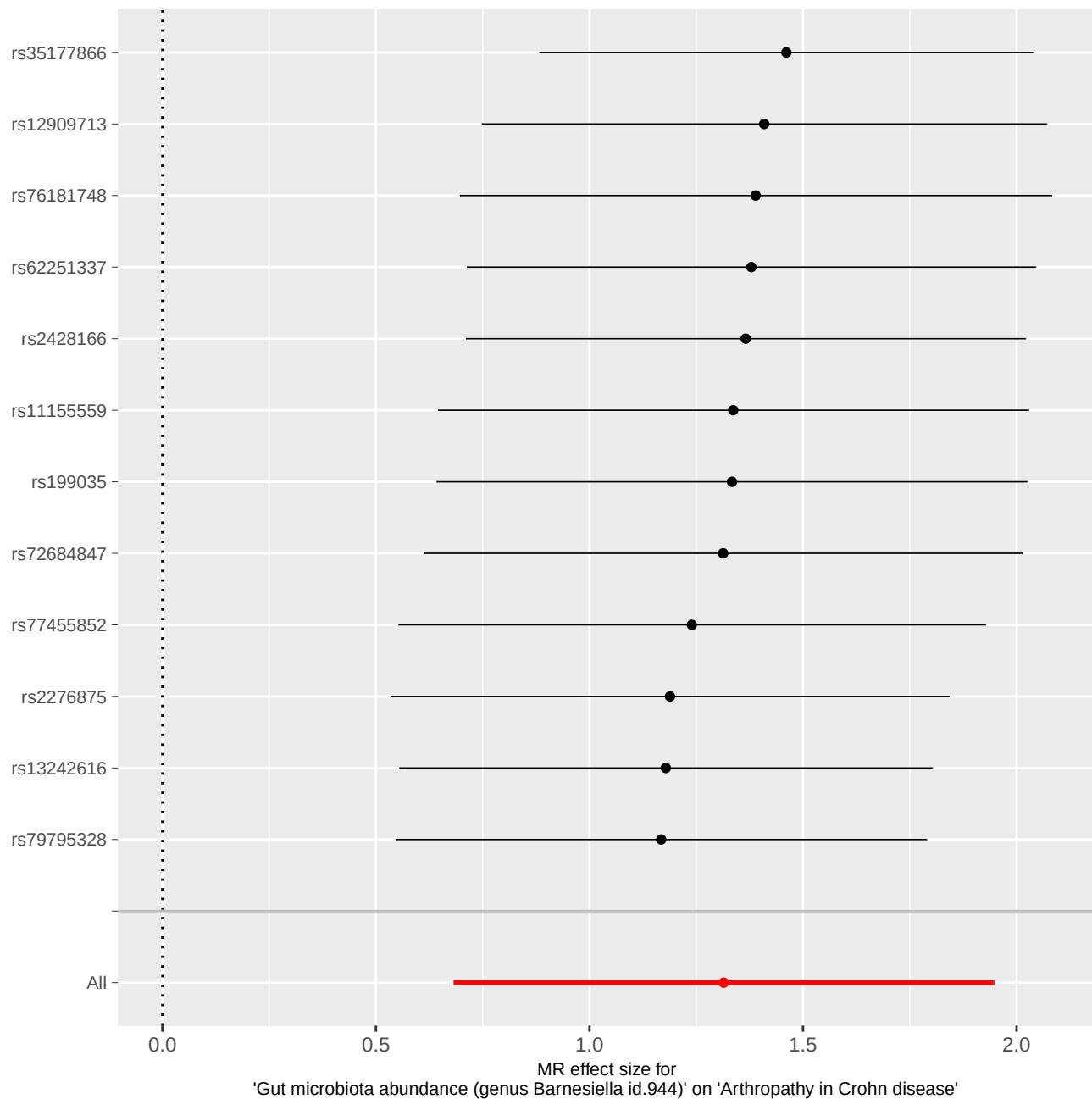


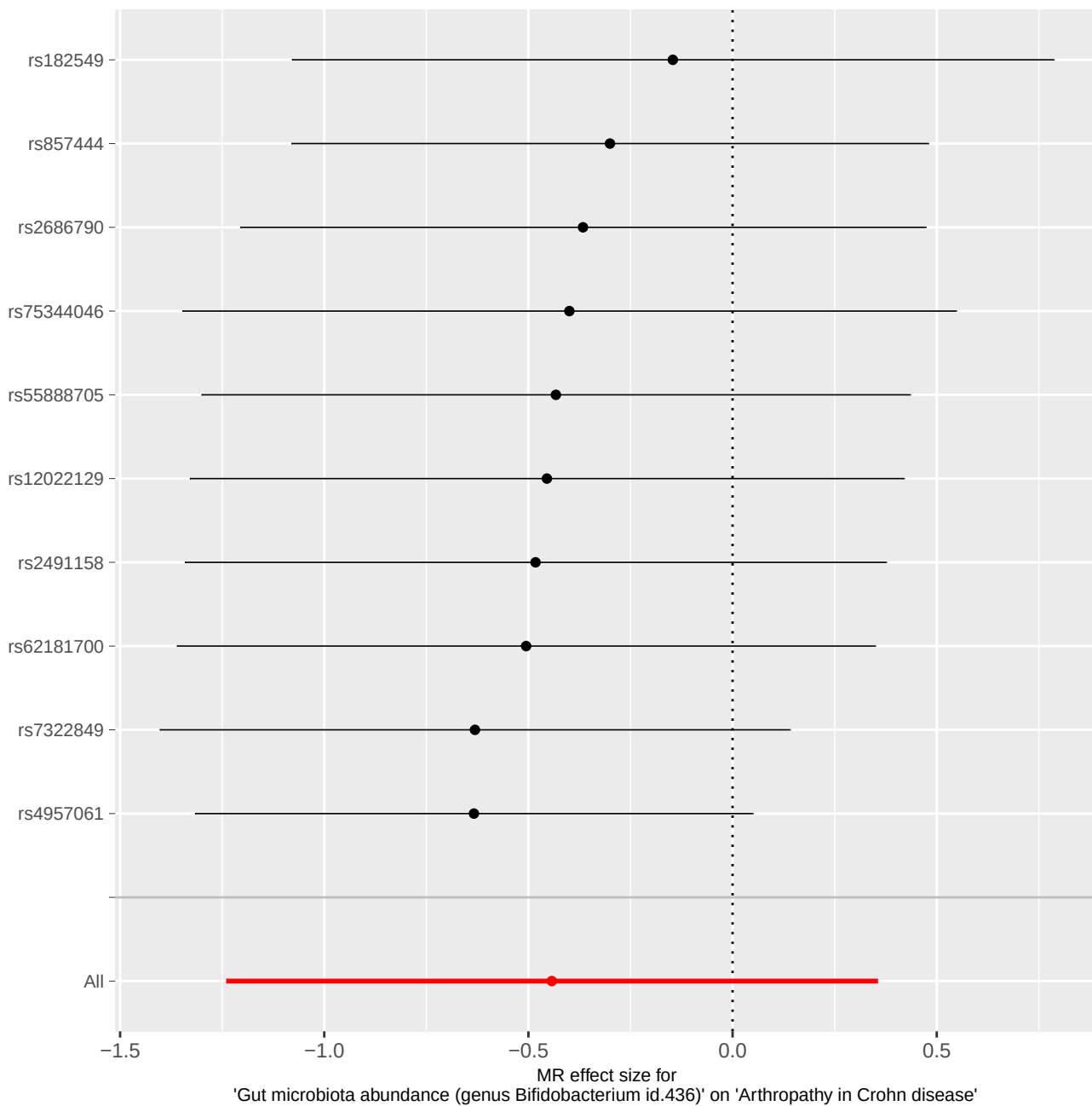


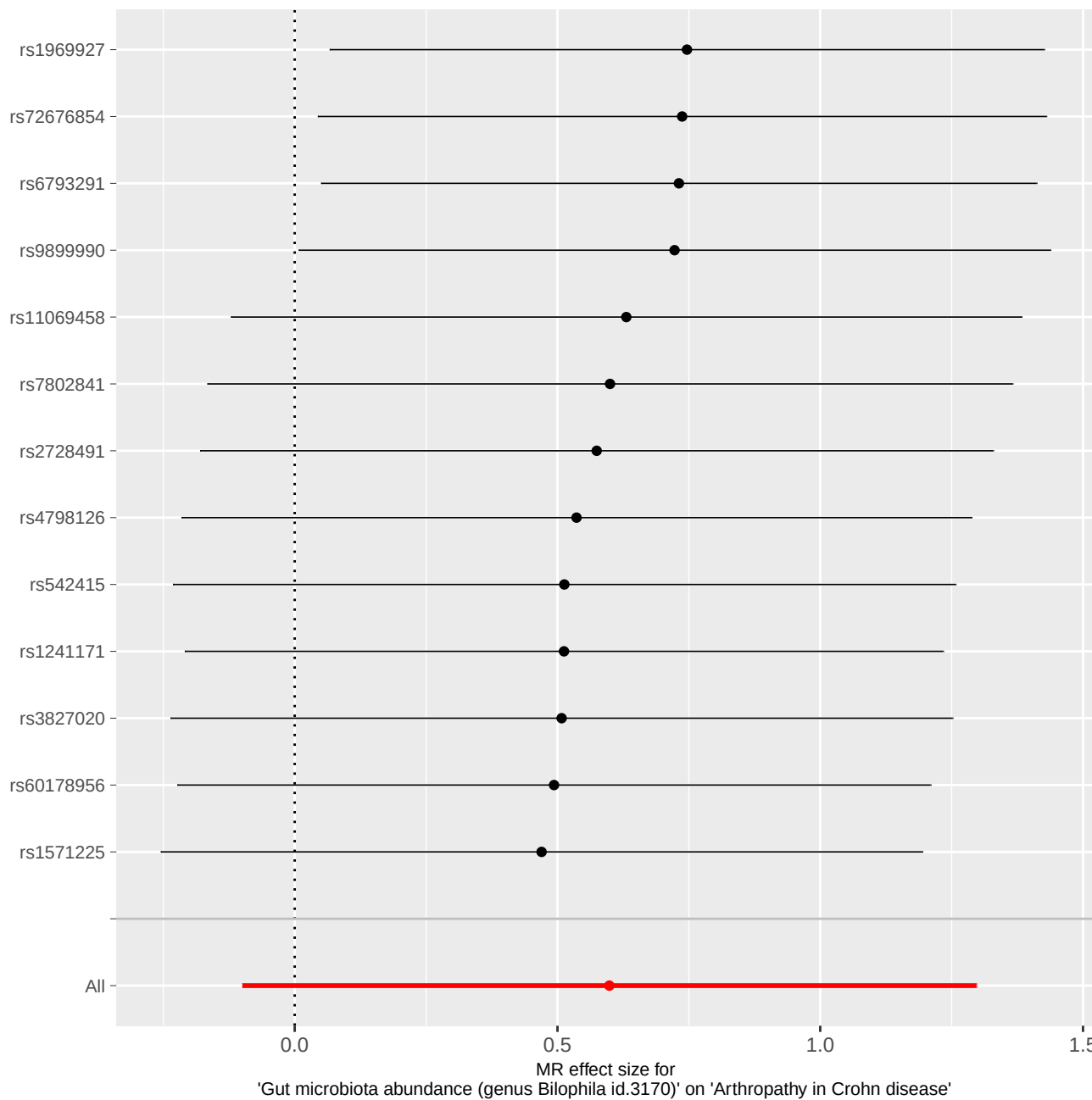


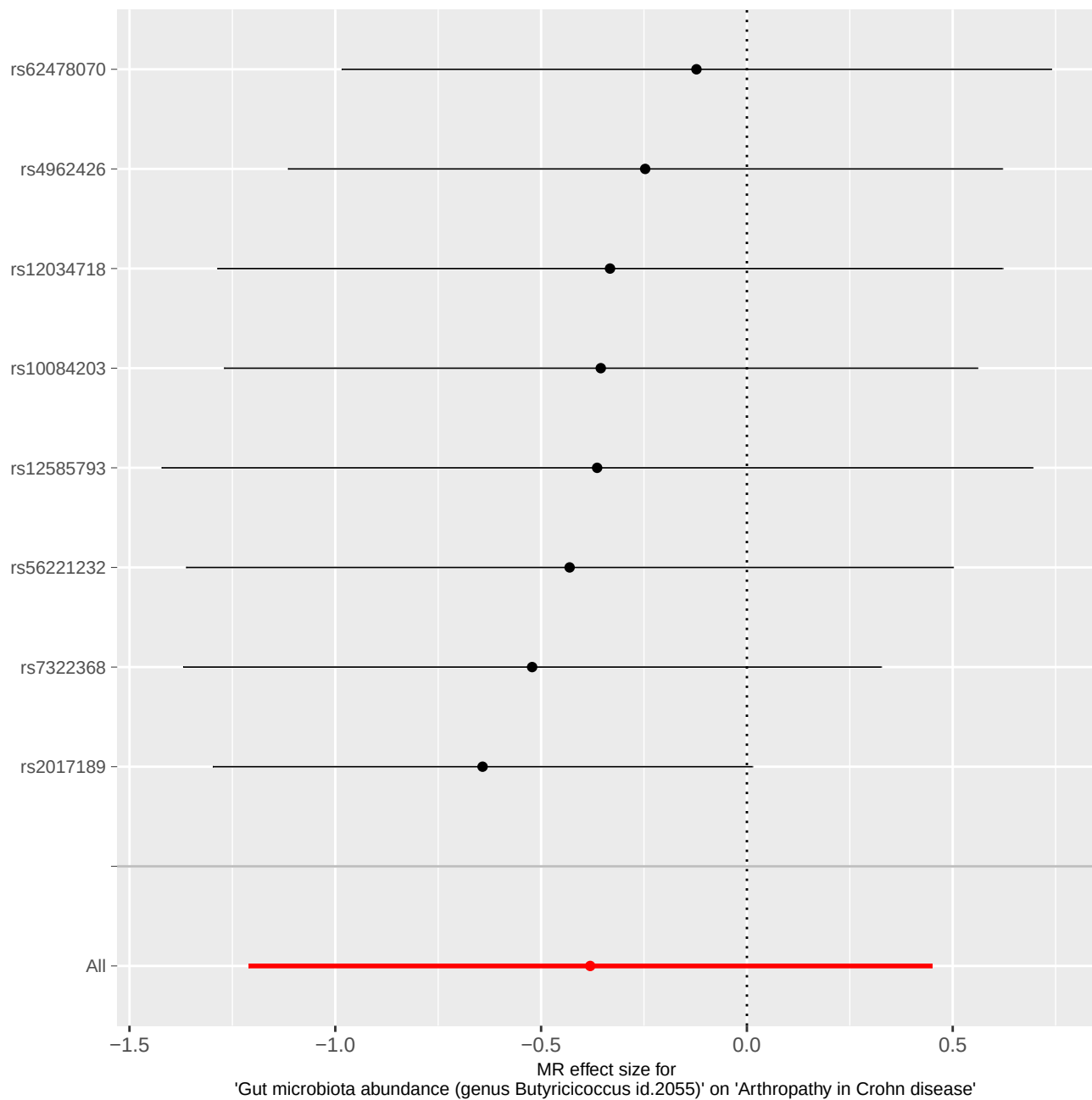
Batch 492 : Gut microbiota abundance (genus Bacteroides id.918) on Arthropathy in Crohn disease

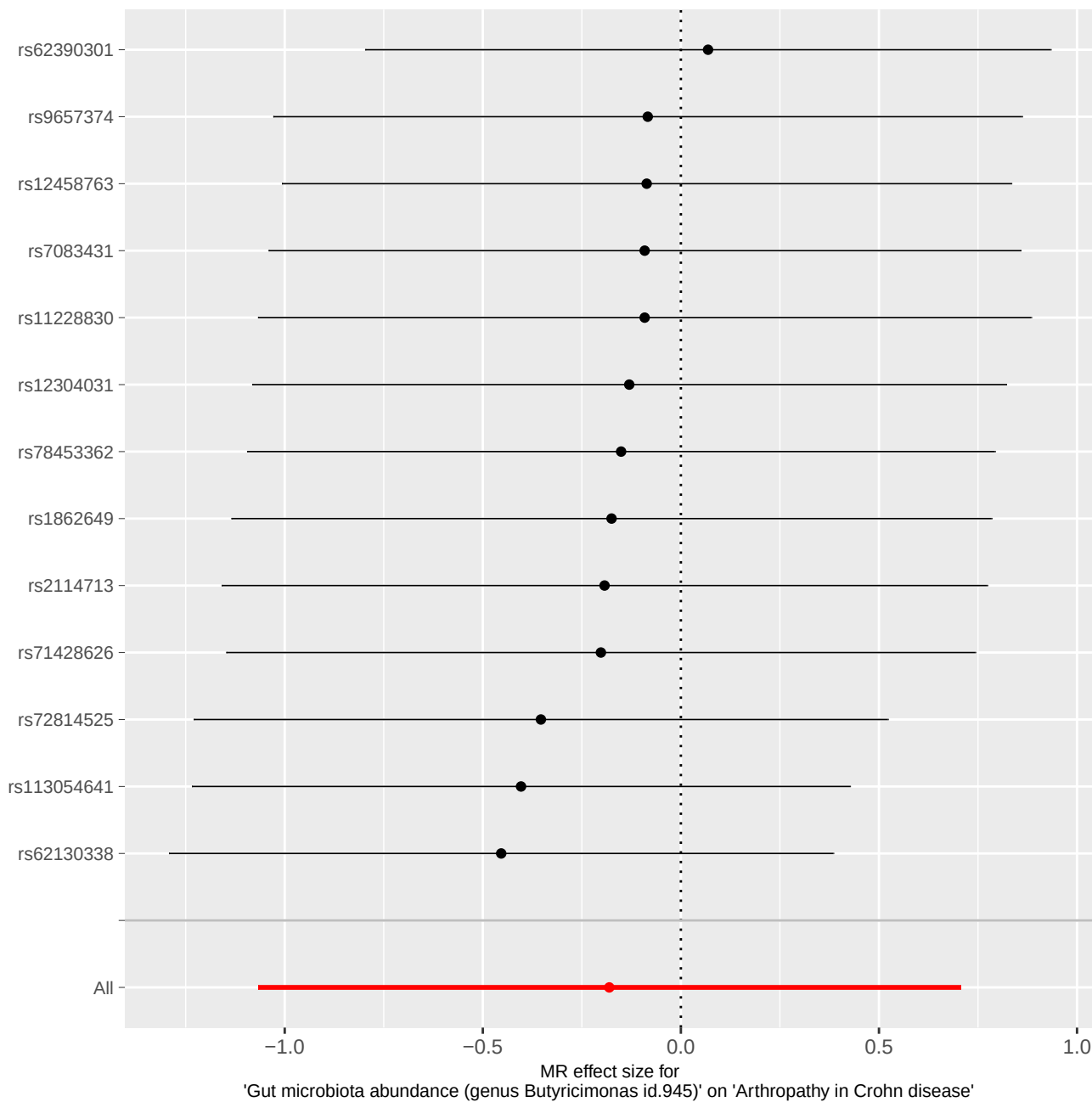


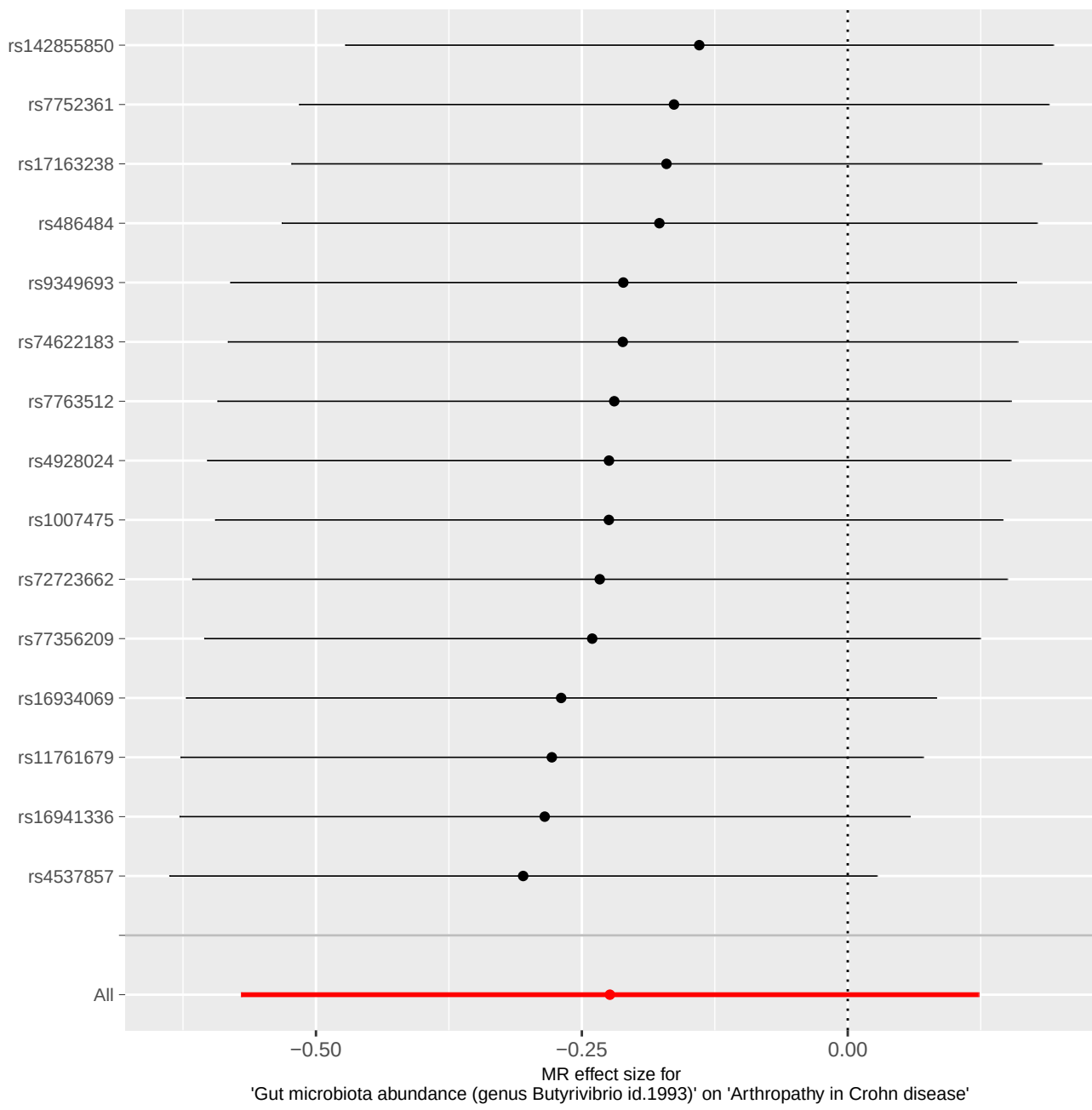


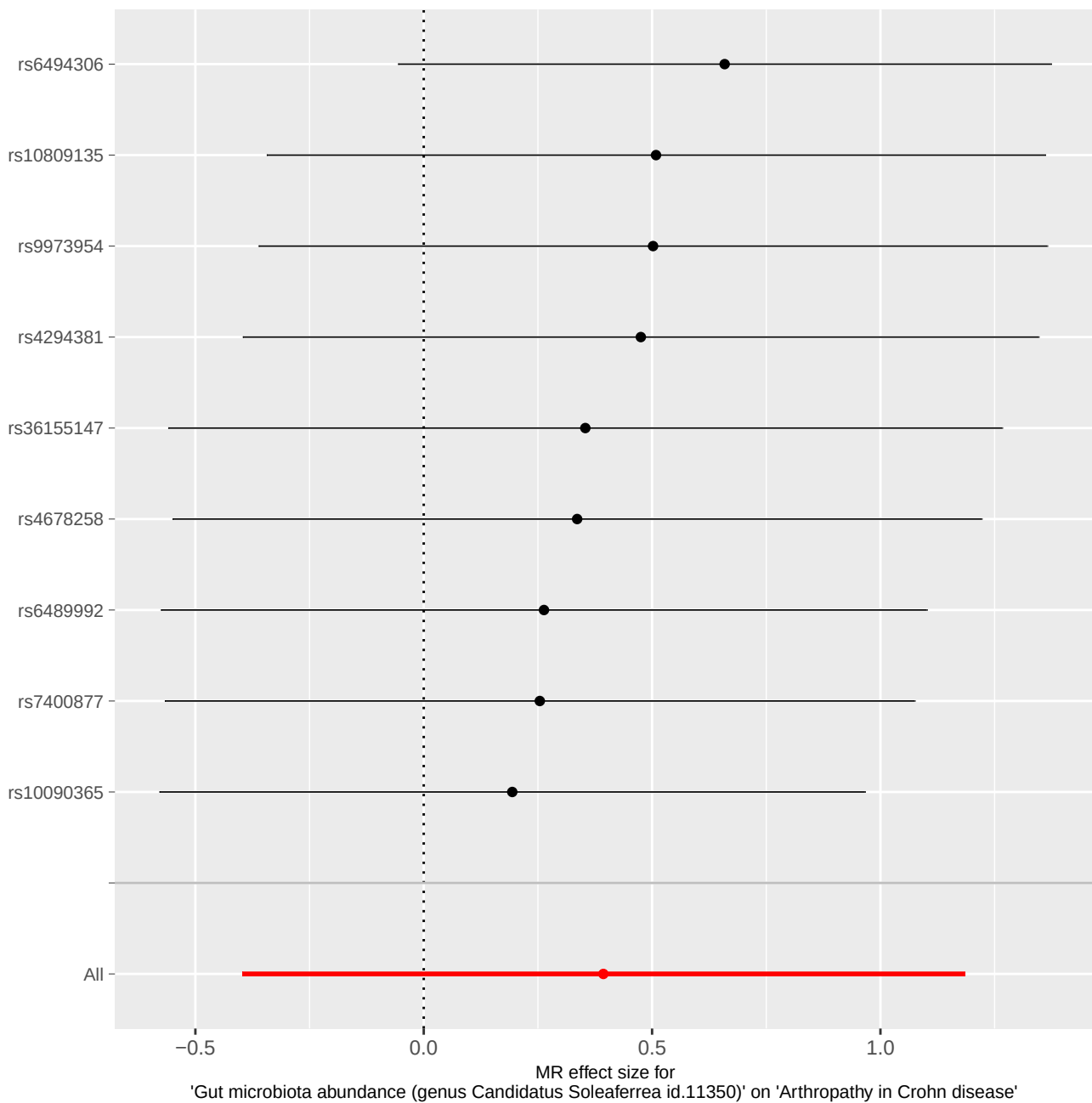


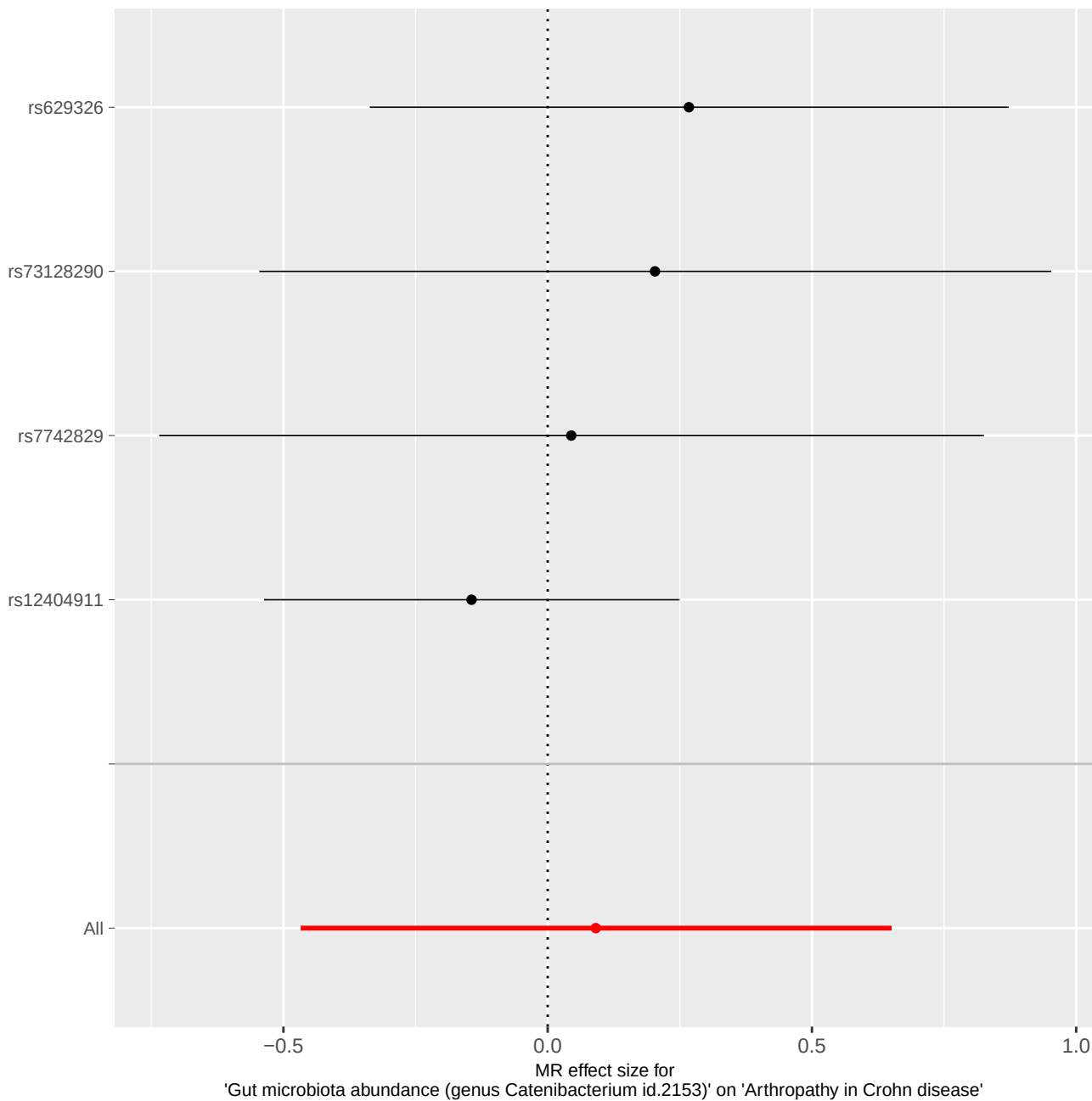


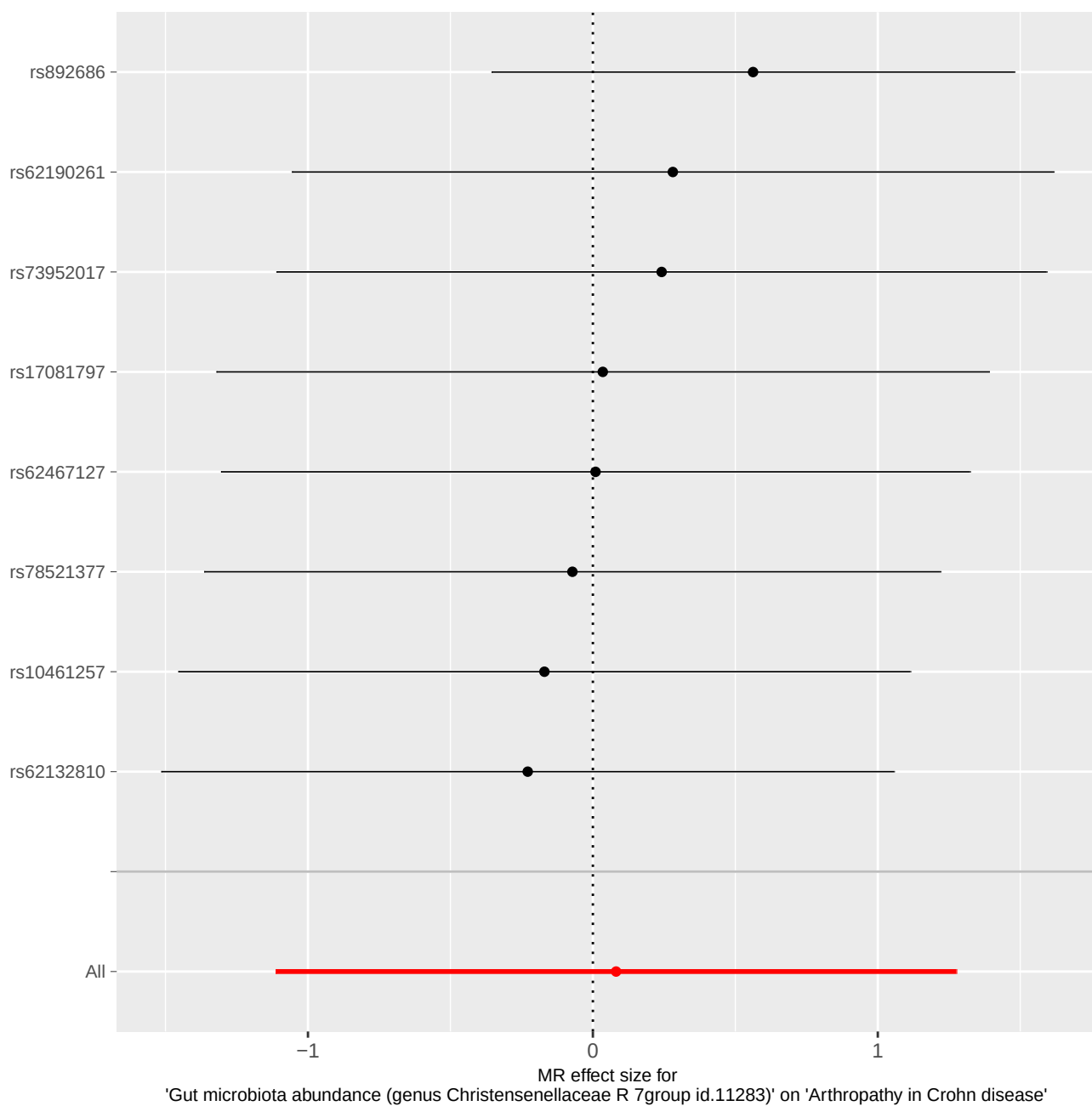




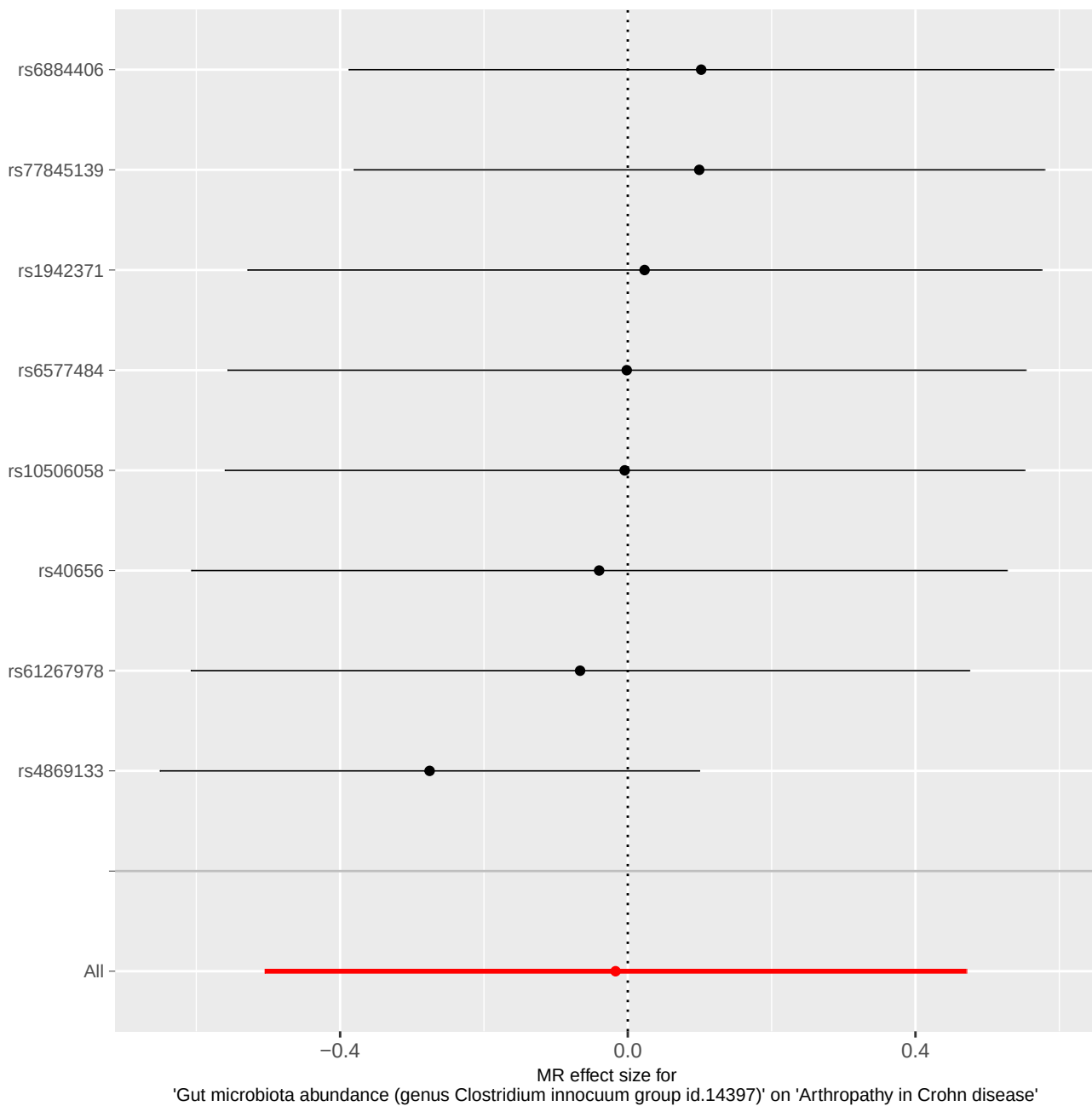


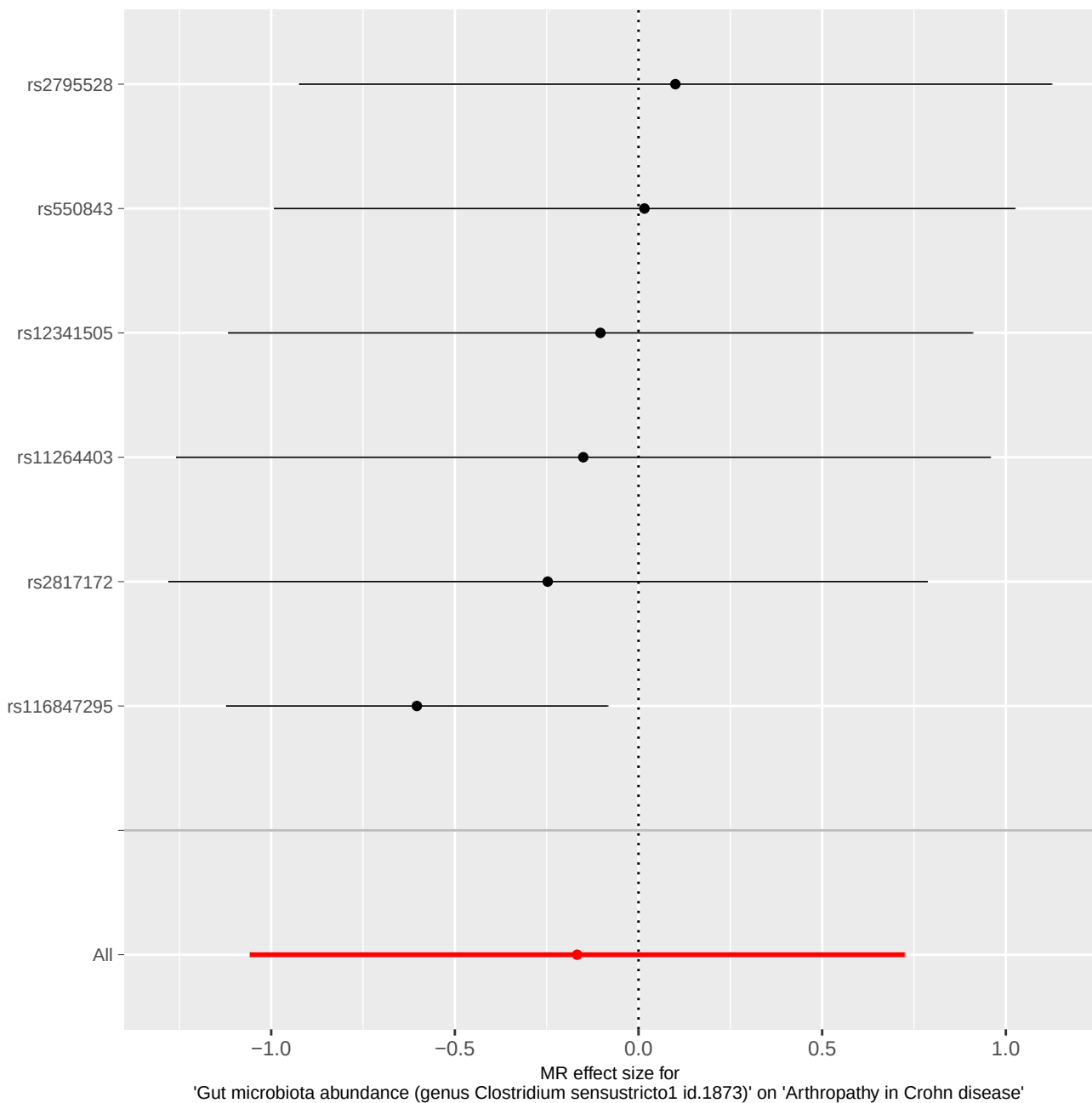


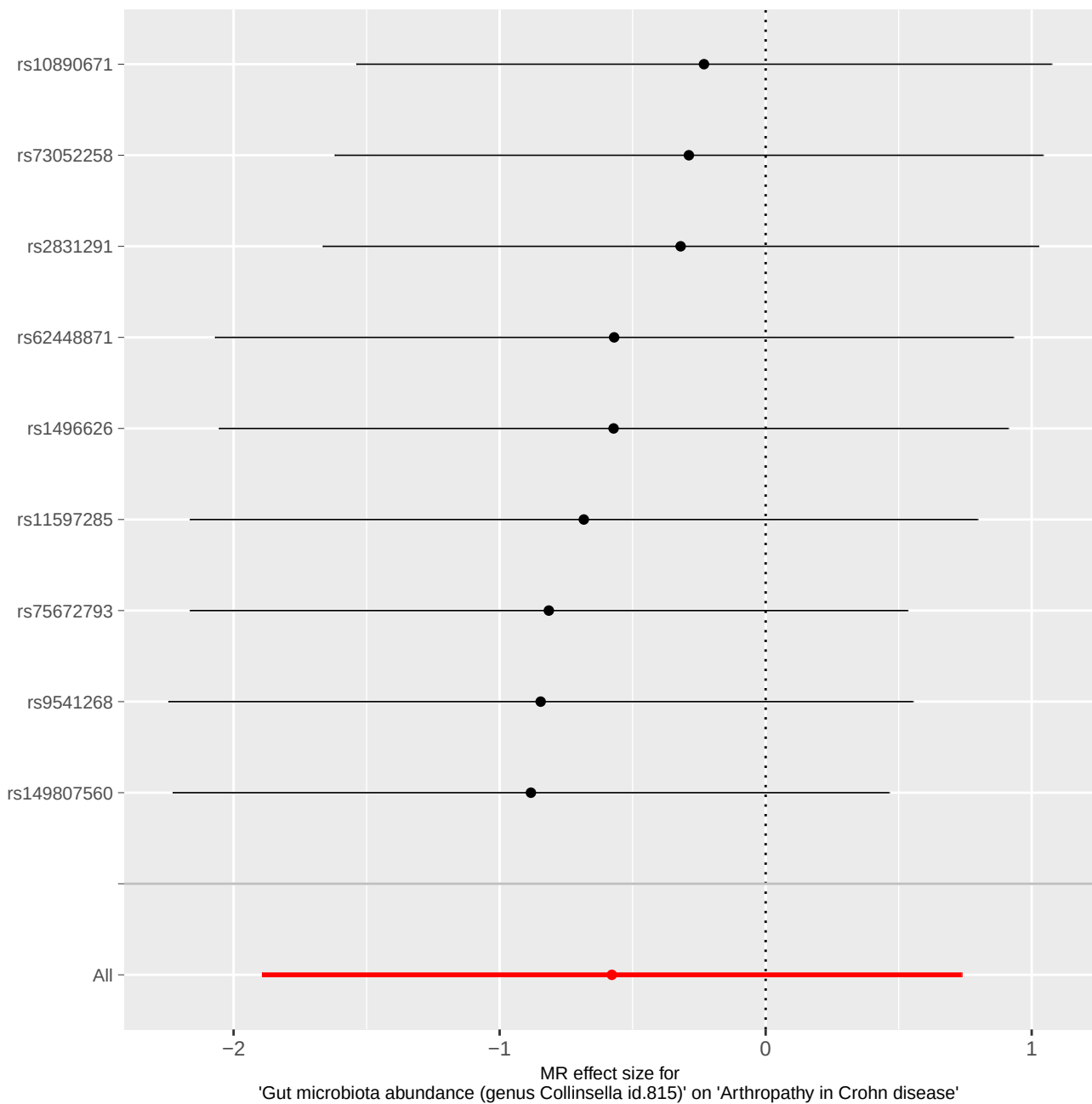


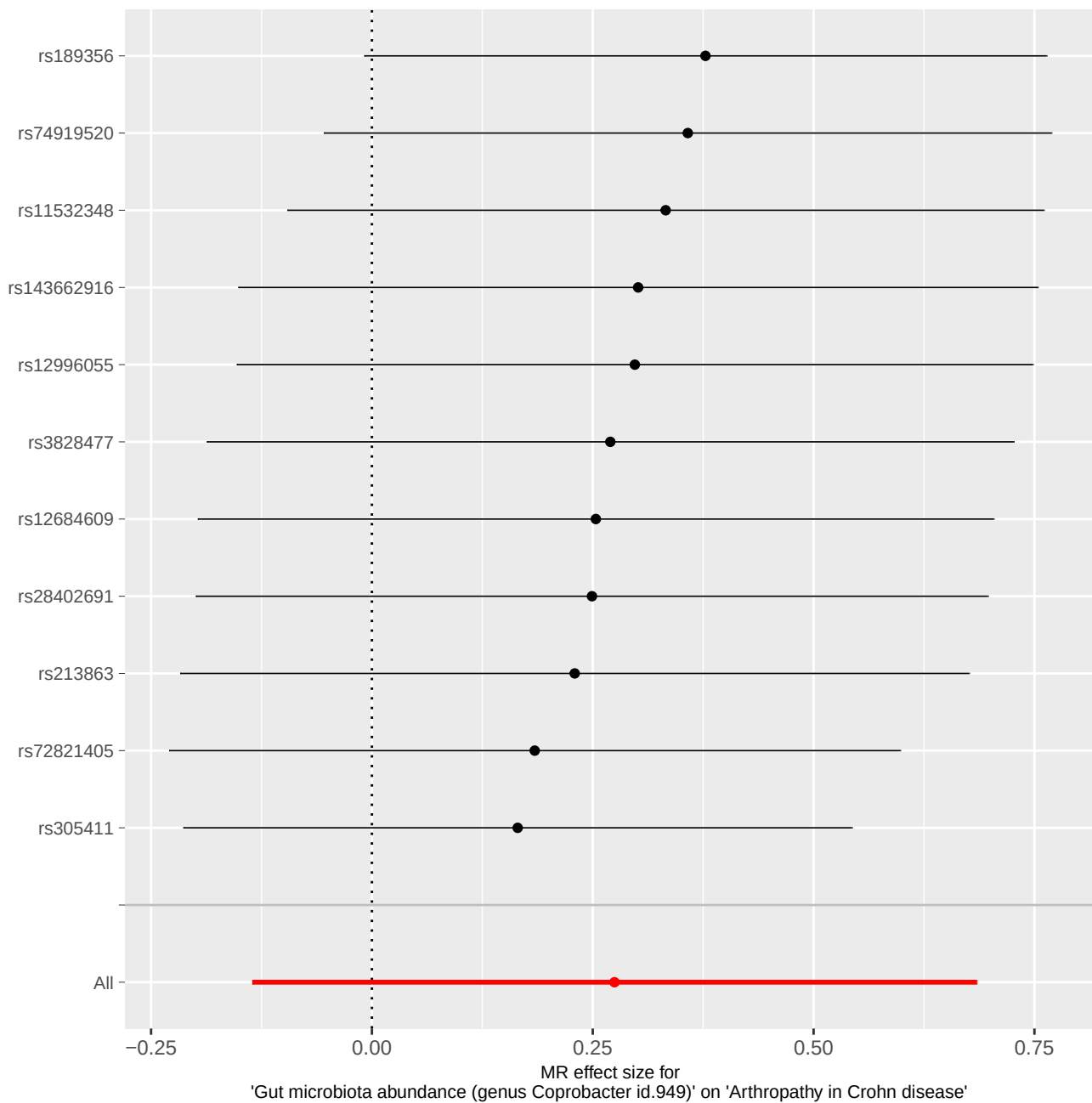


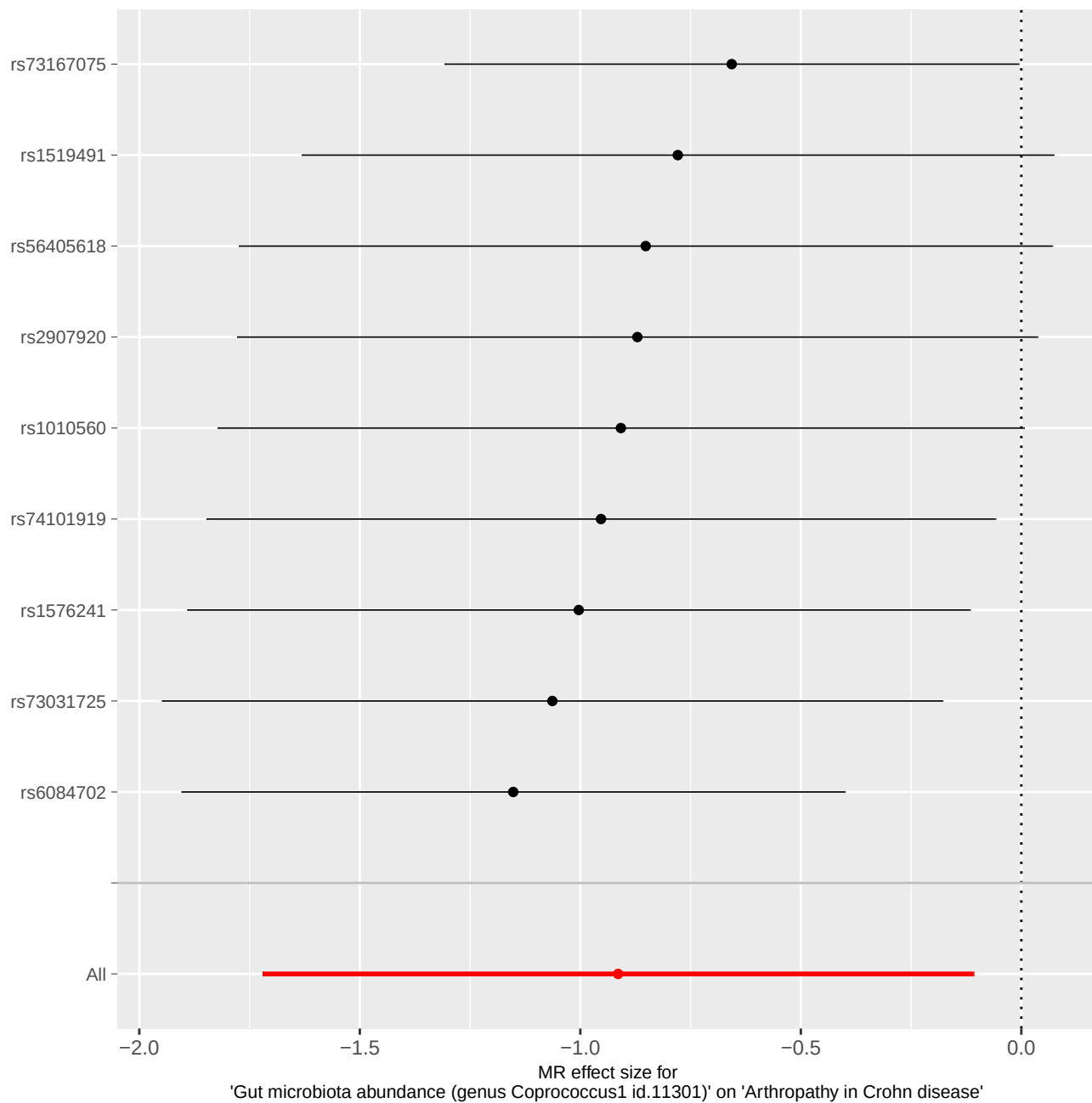
MR effect size for
'Gut microbiota abundance (genus Christensenellaceae R 7group id.11283)' on 'Arthropathy in Crohn disease'



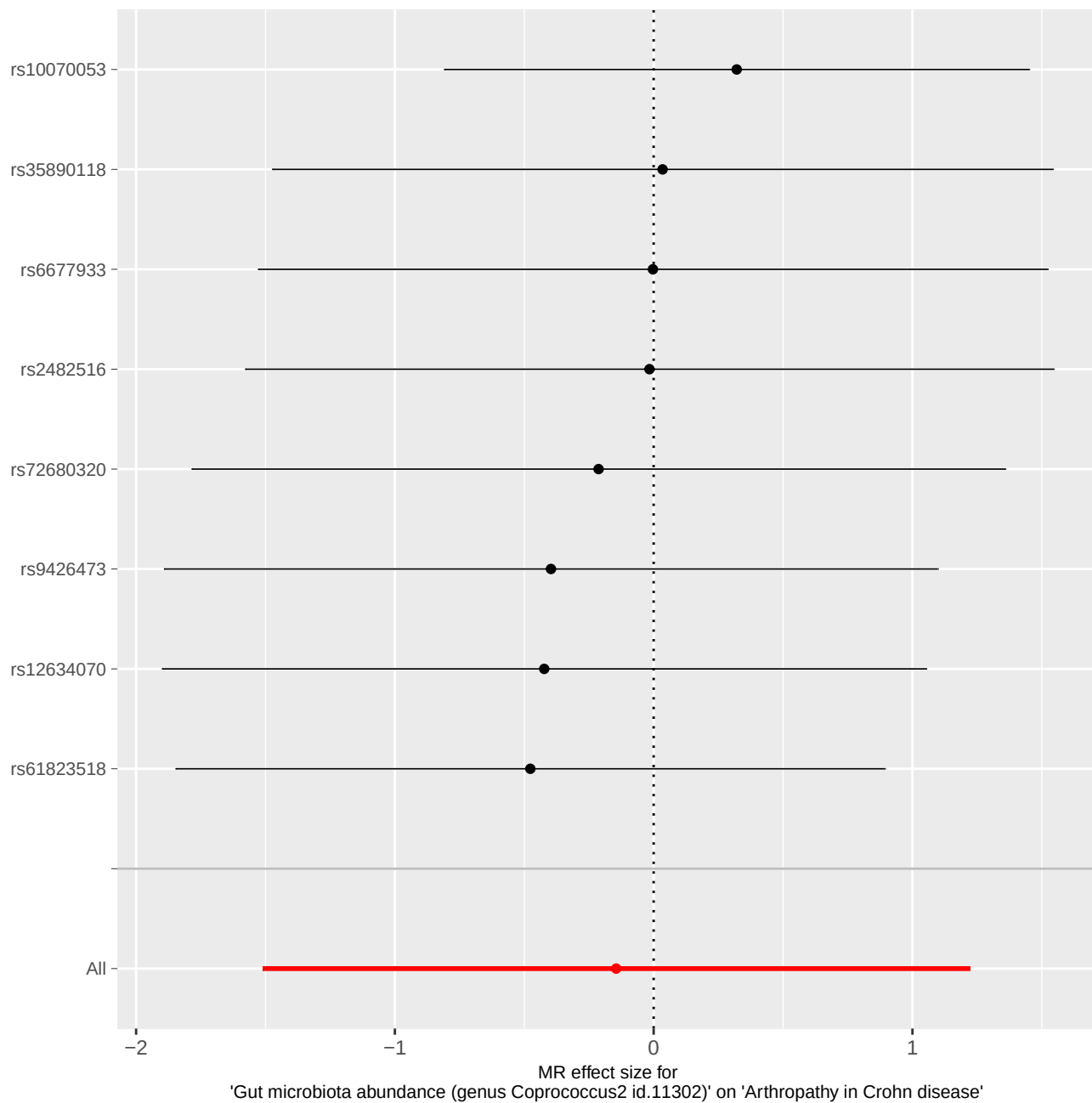


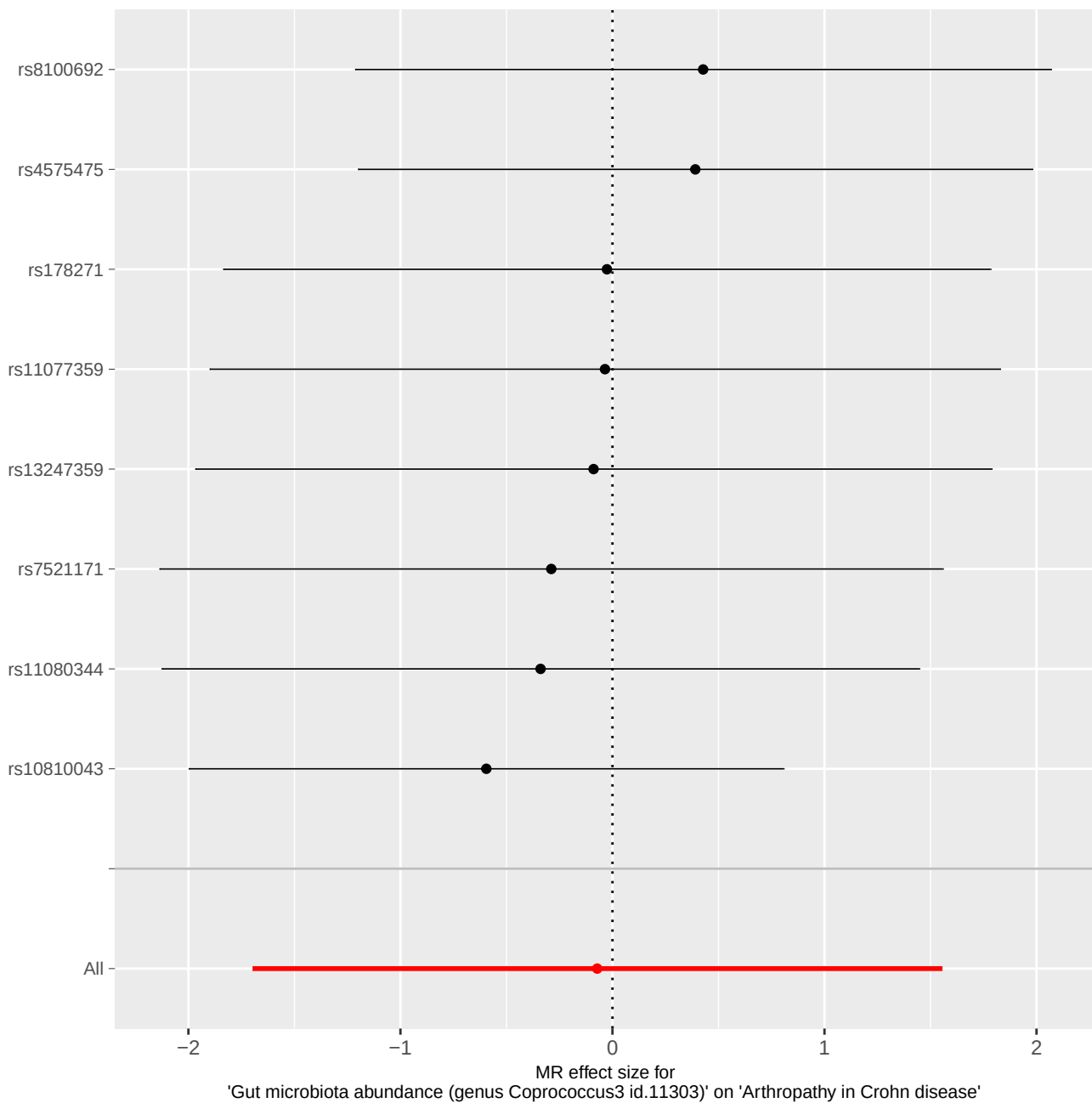


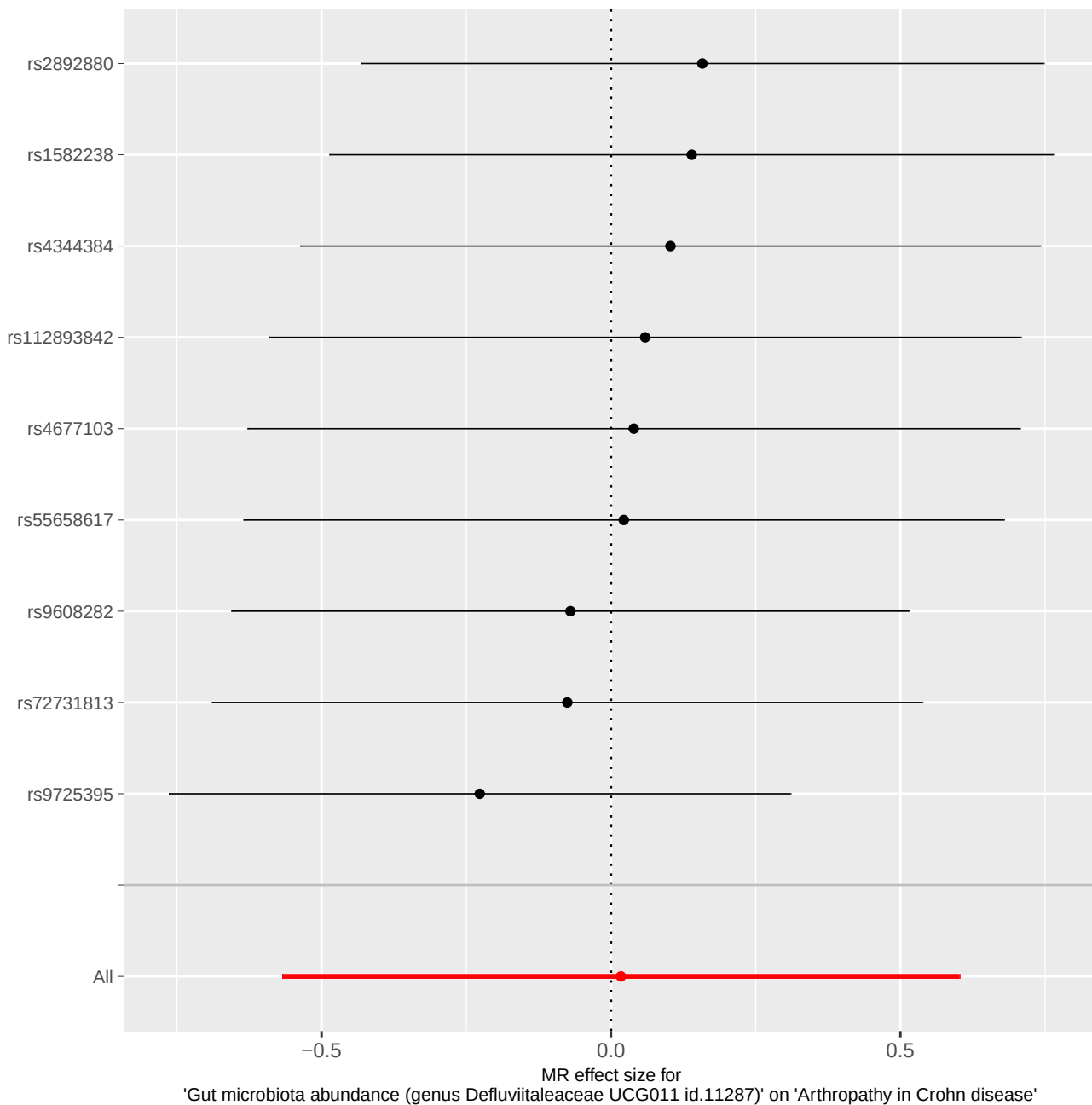


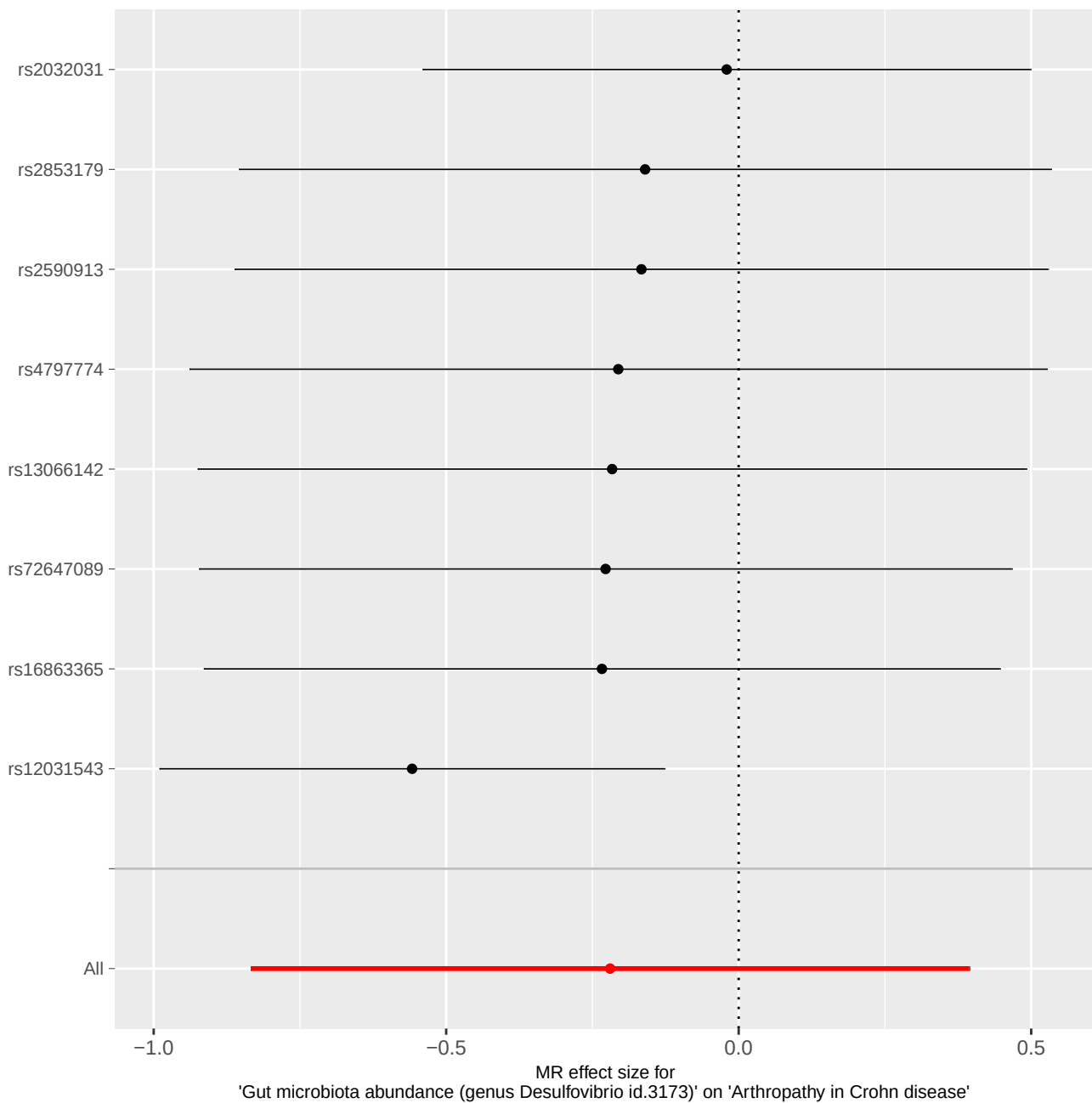


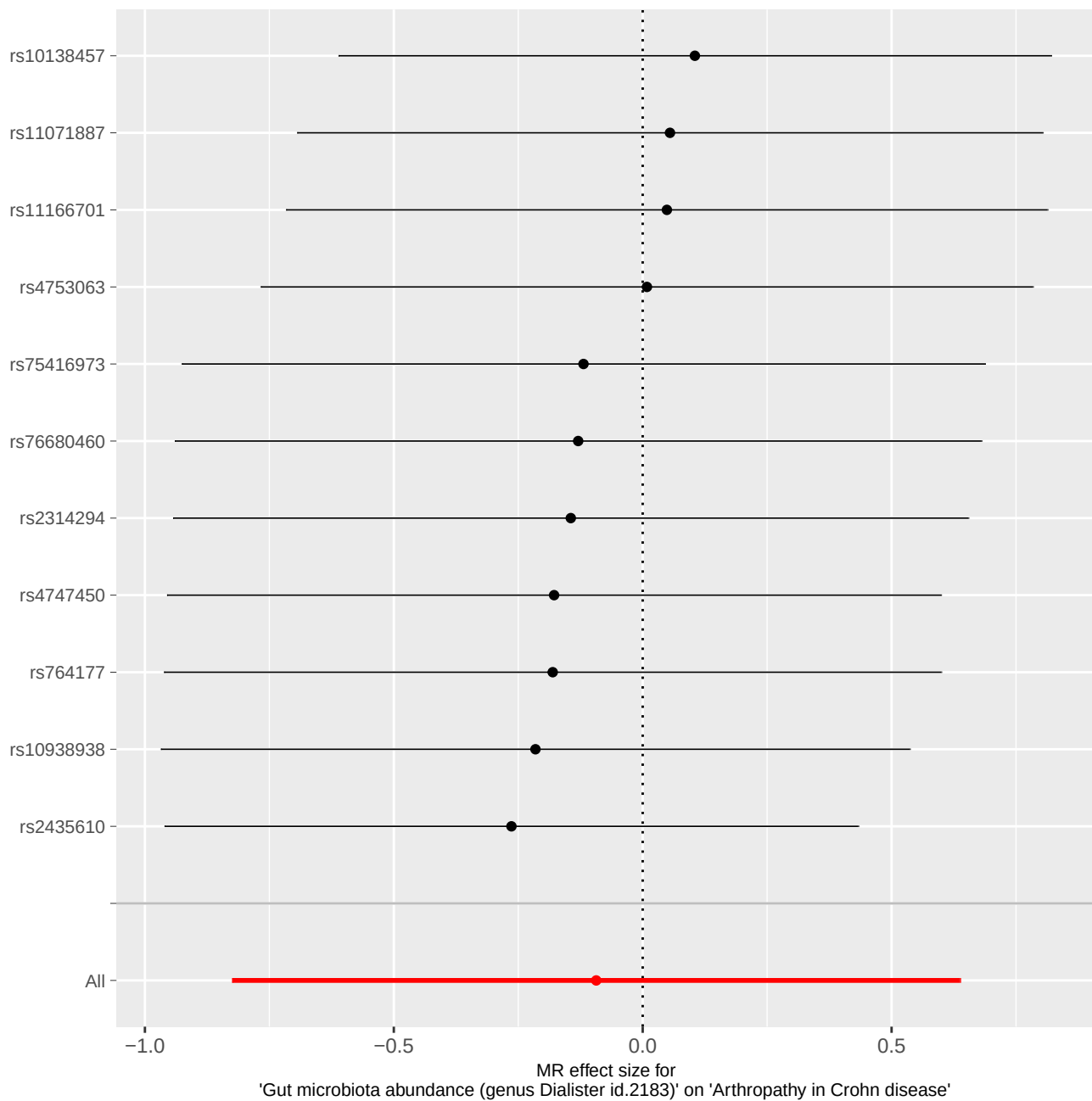
Batch 508 : Gut microbiota abundance (genus Coprococcus2 id.11302) on Arthropathy in Crohn disease

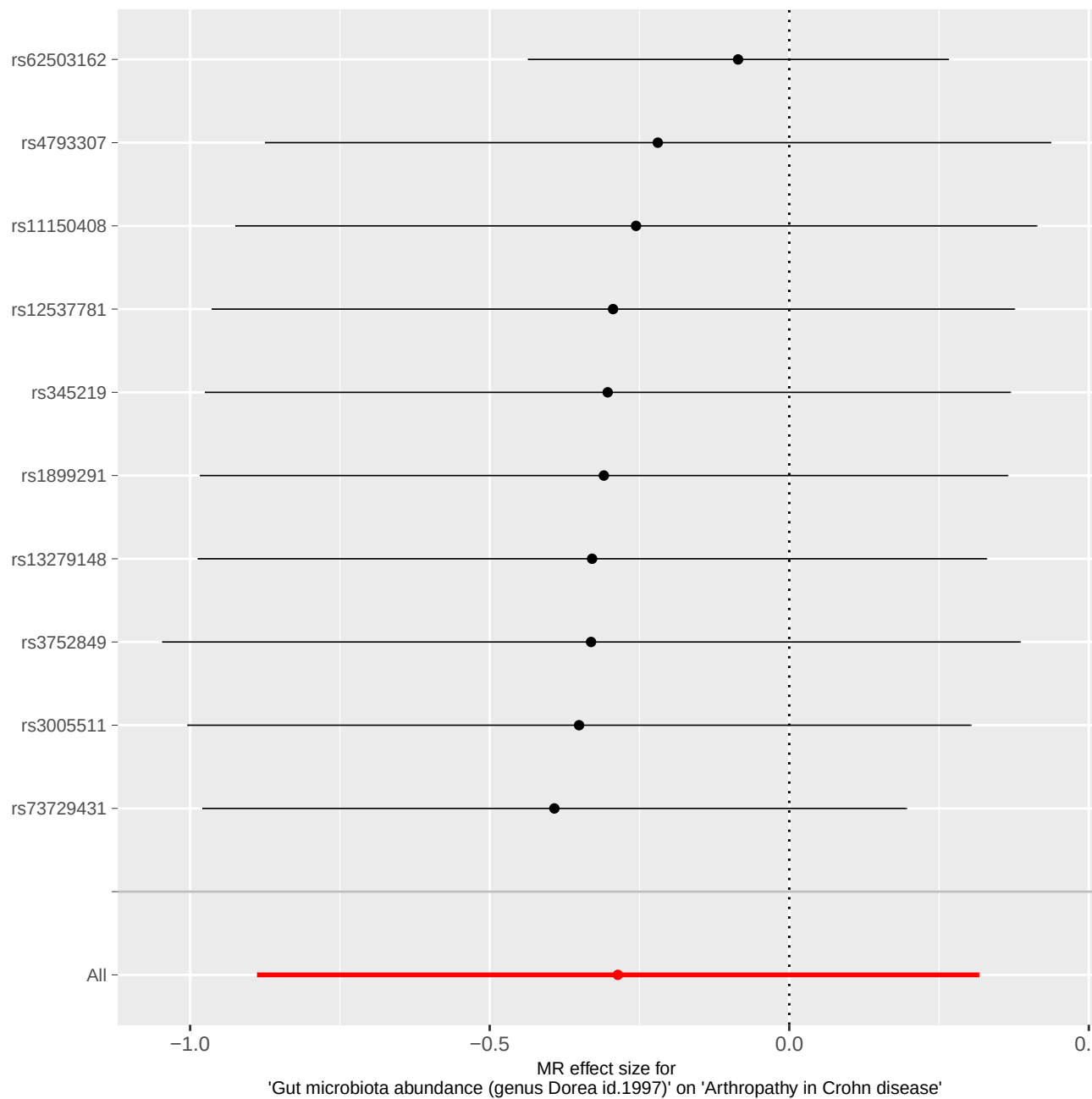


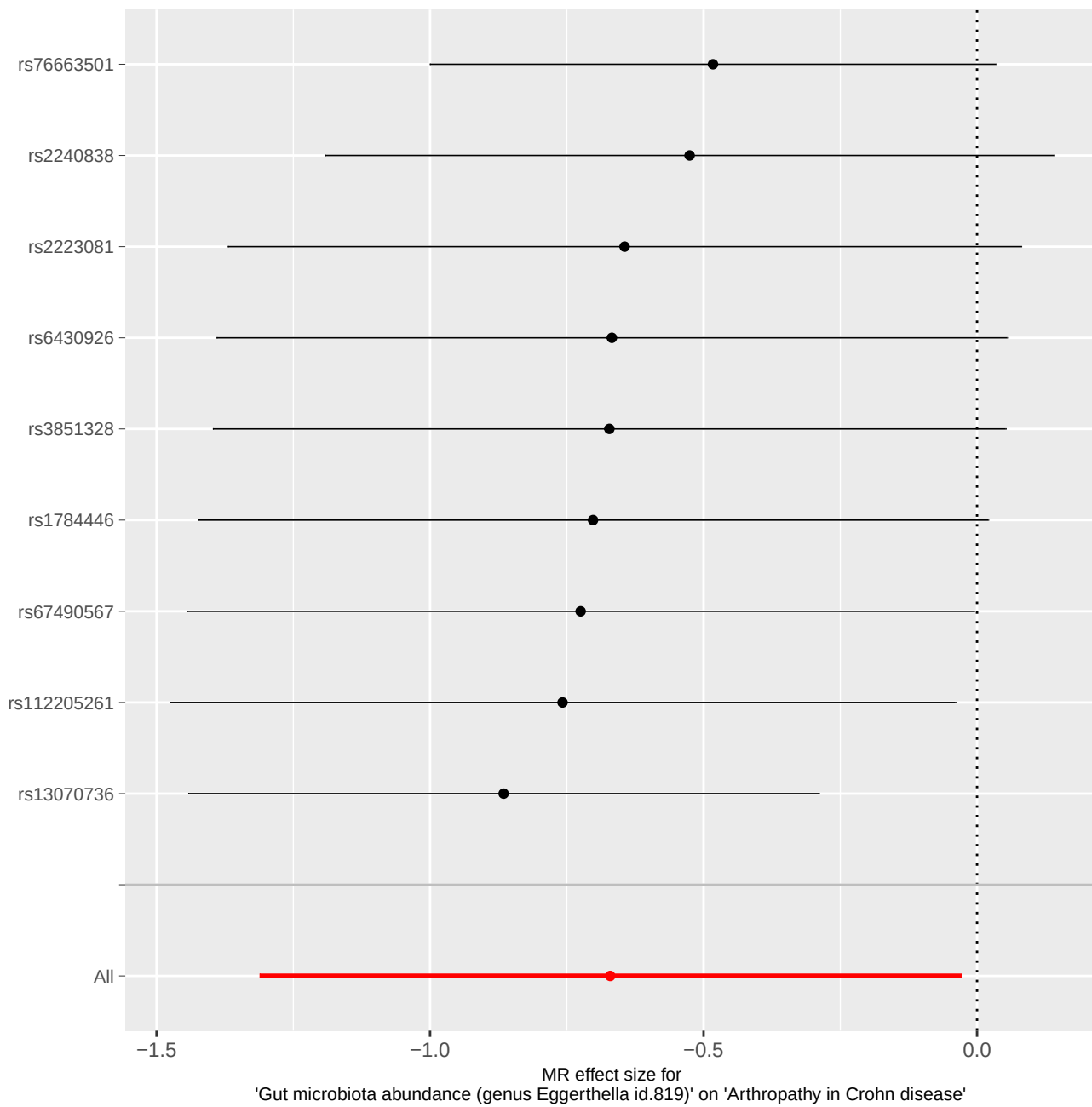


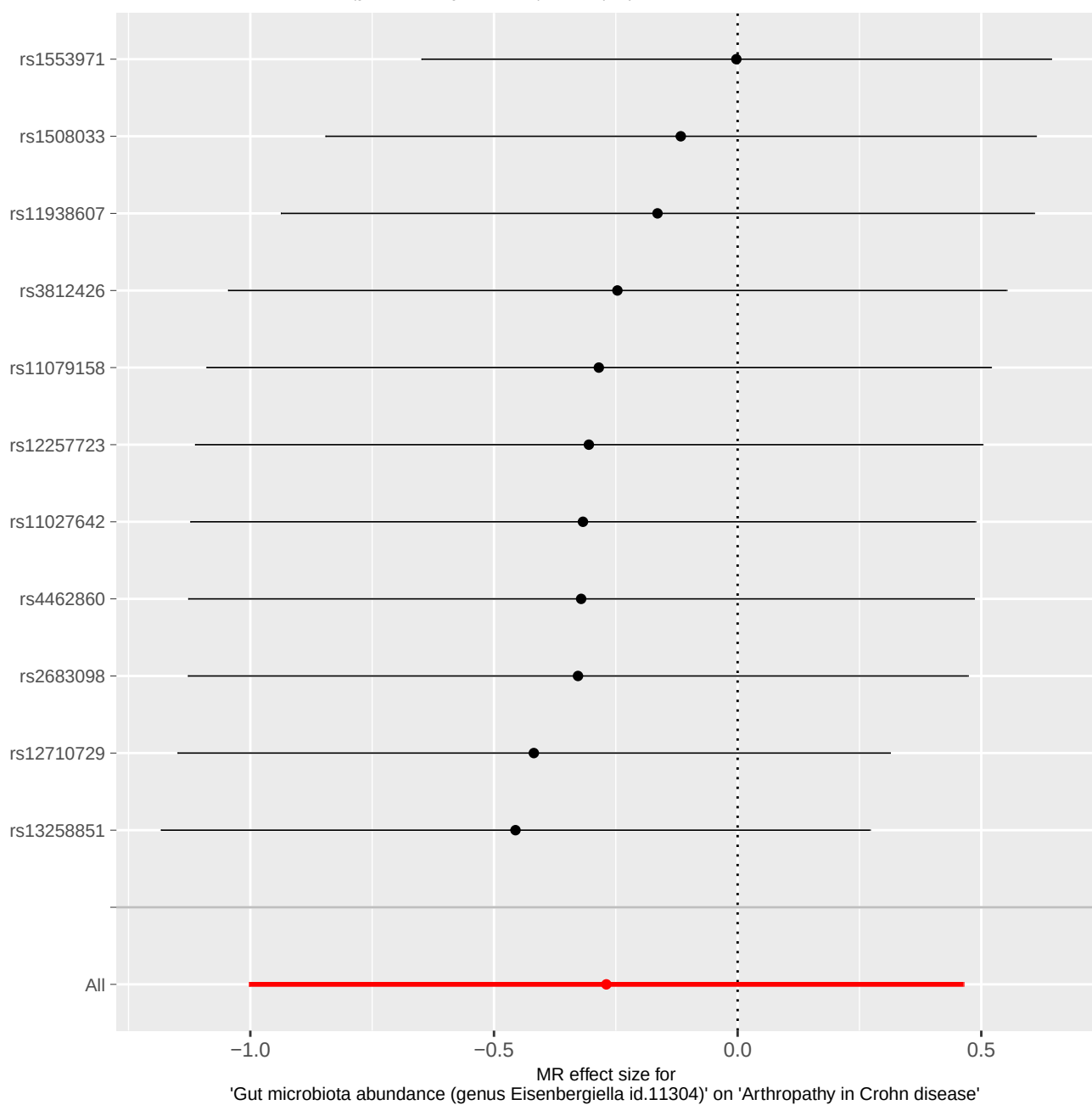




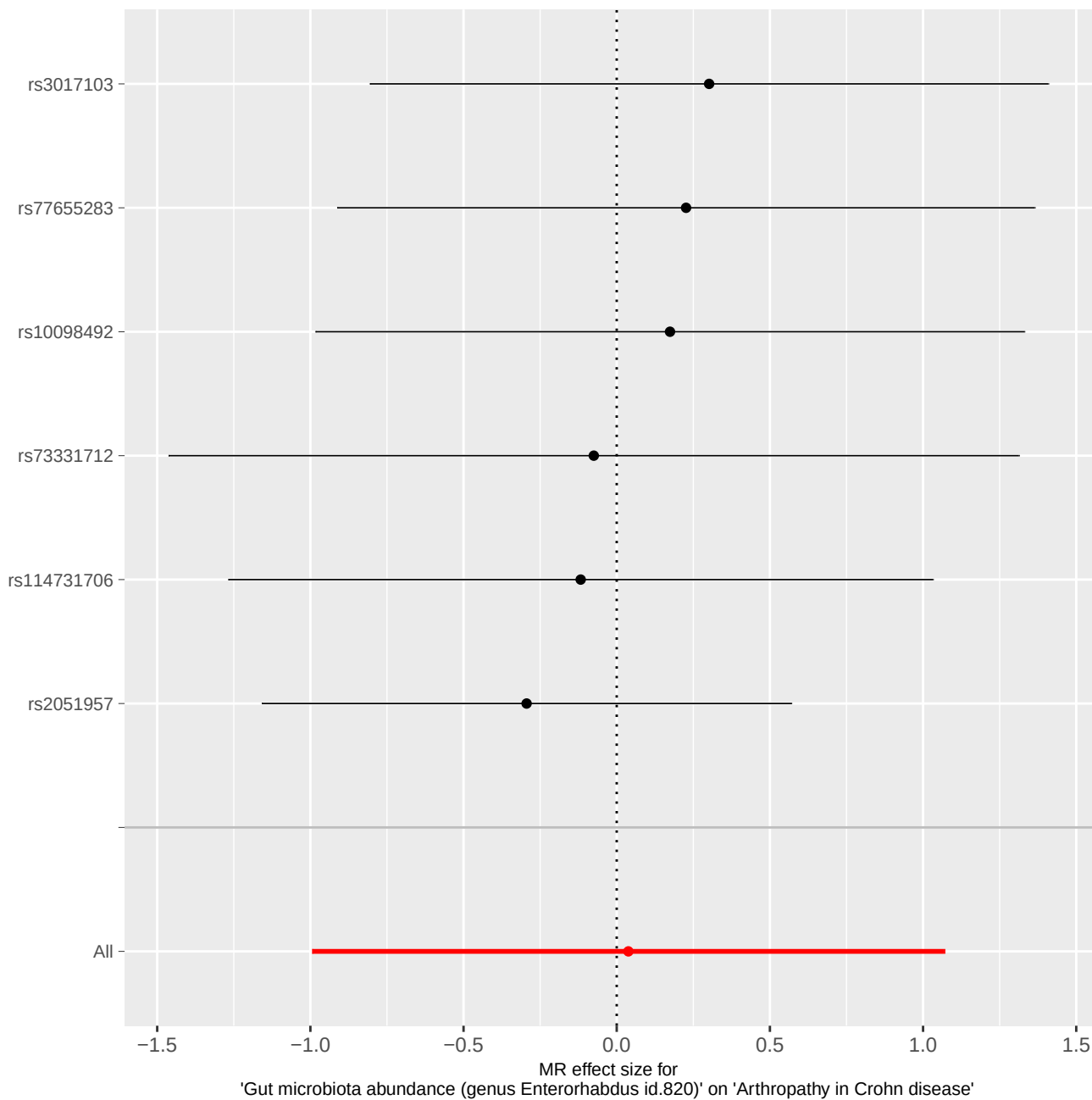


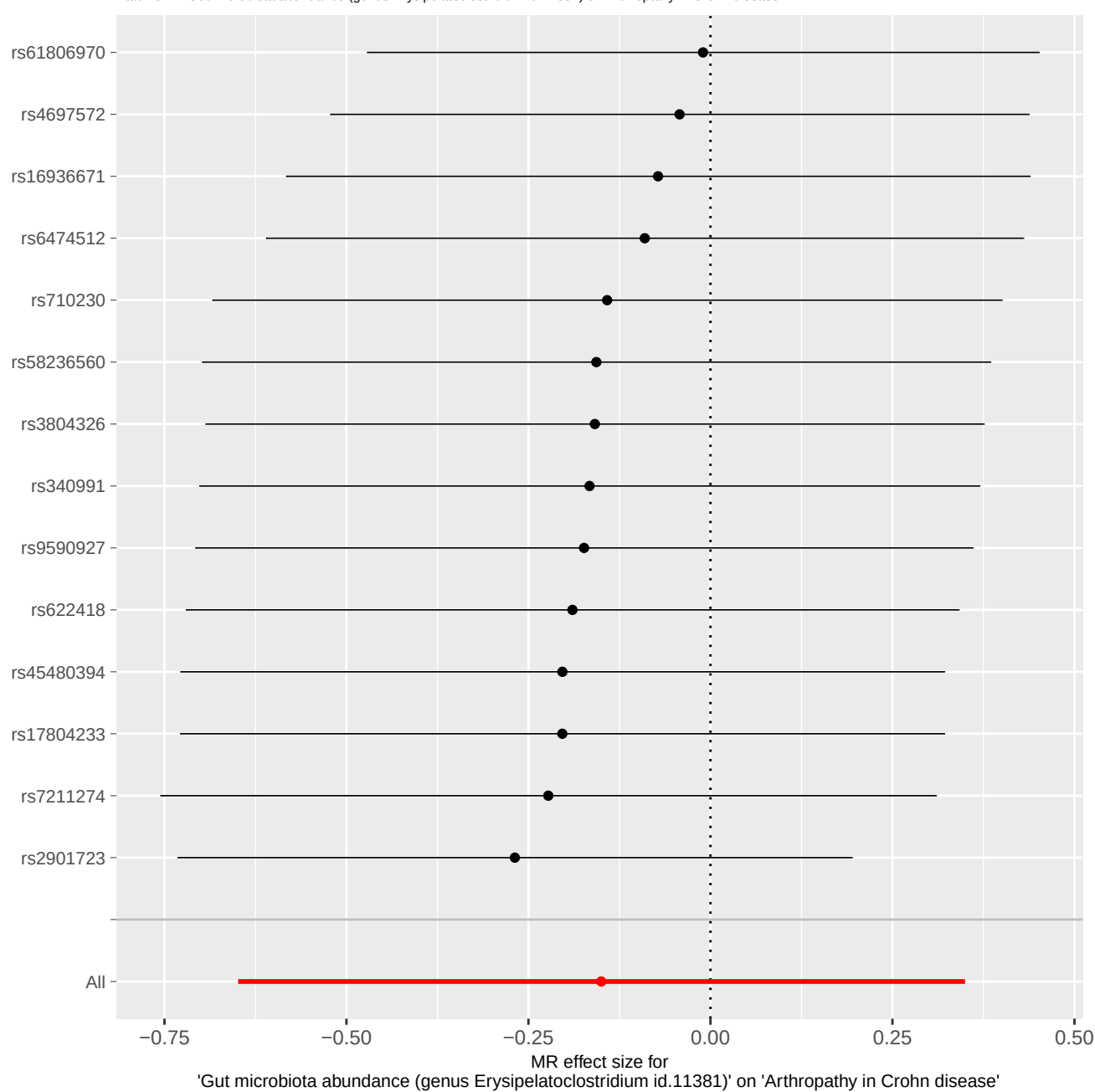


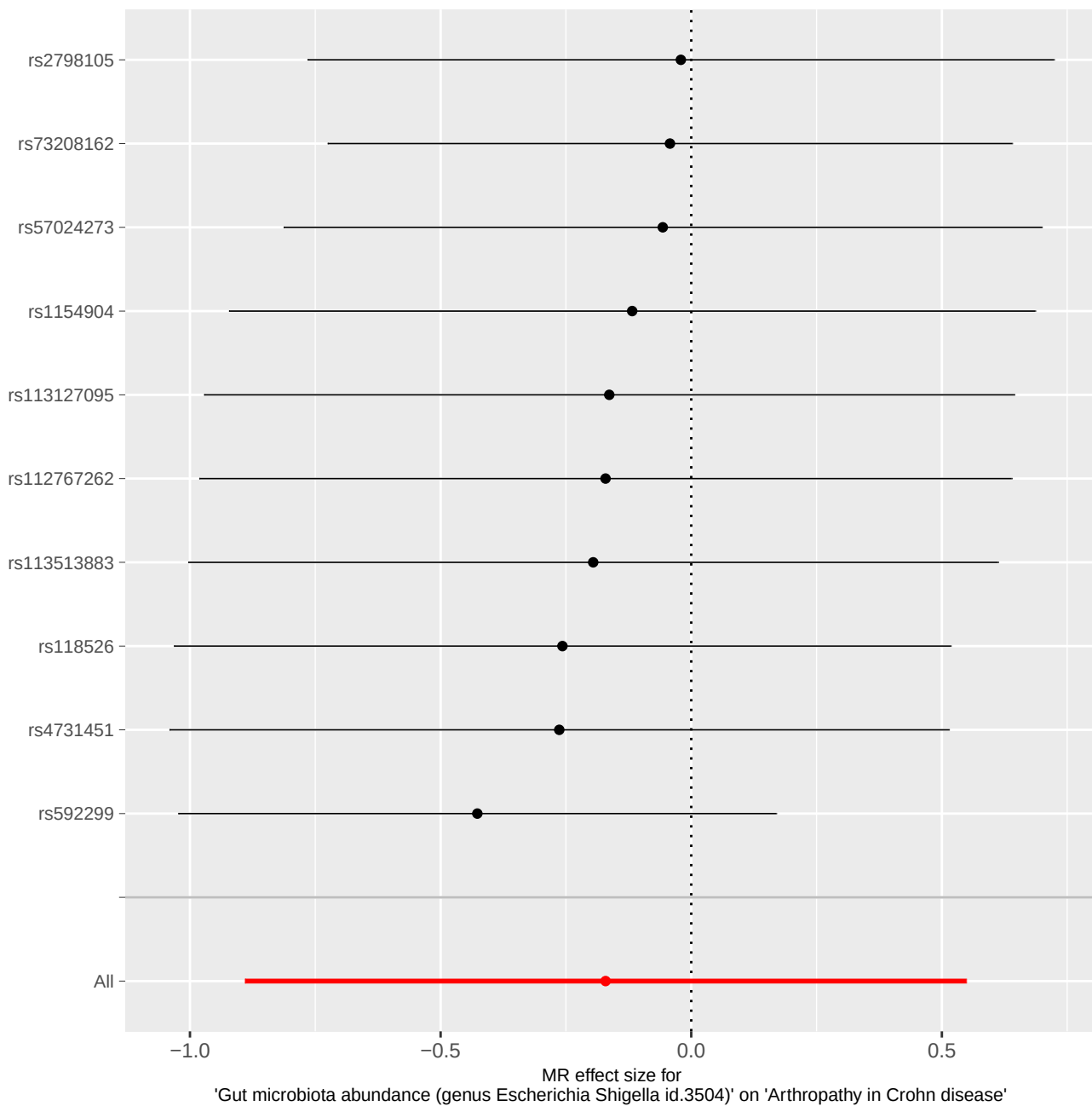


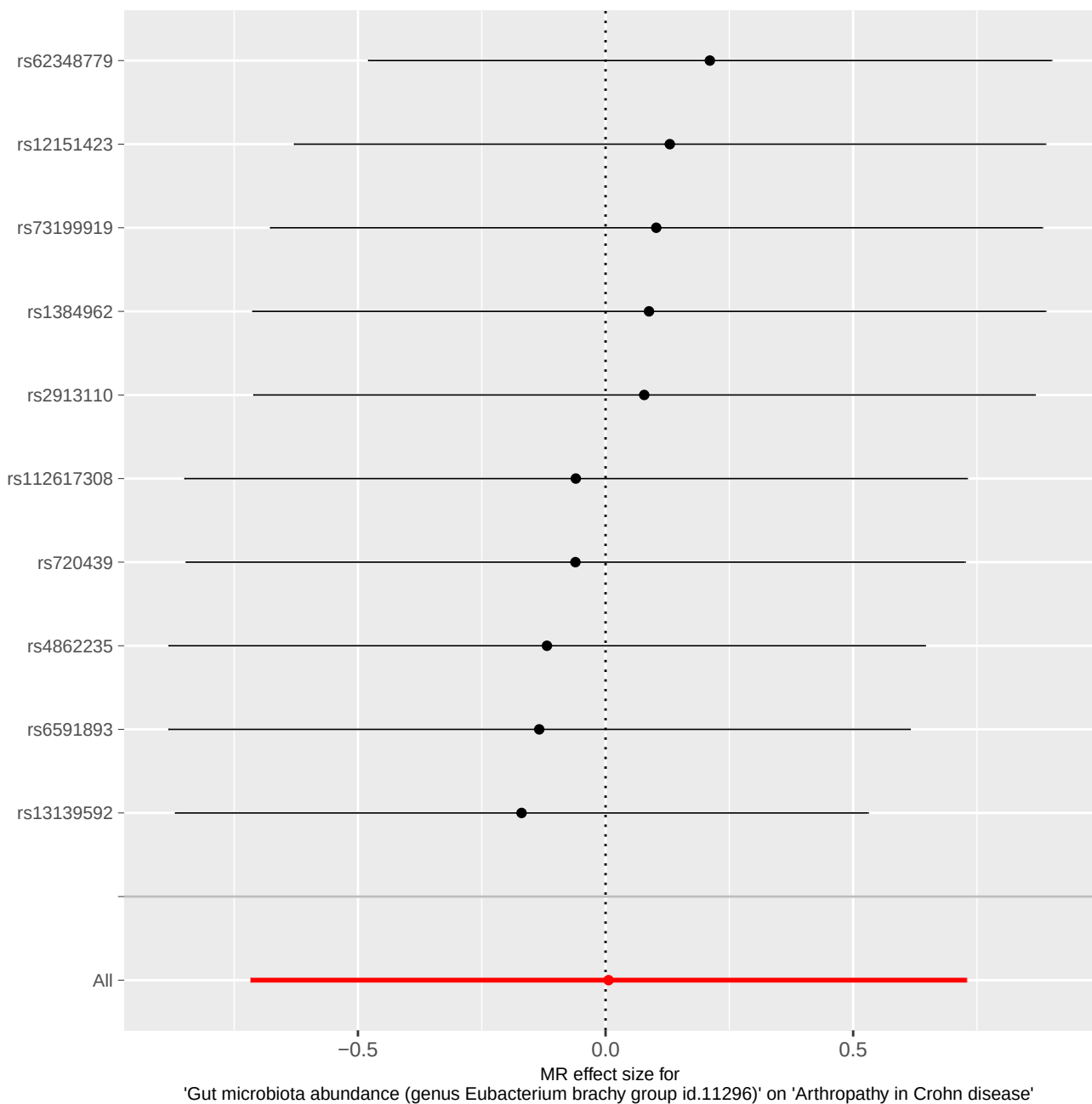


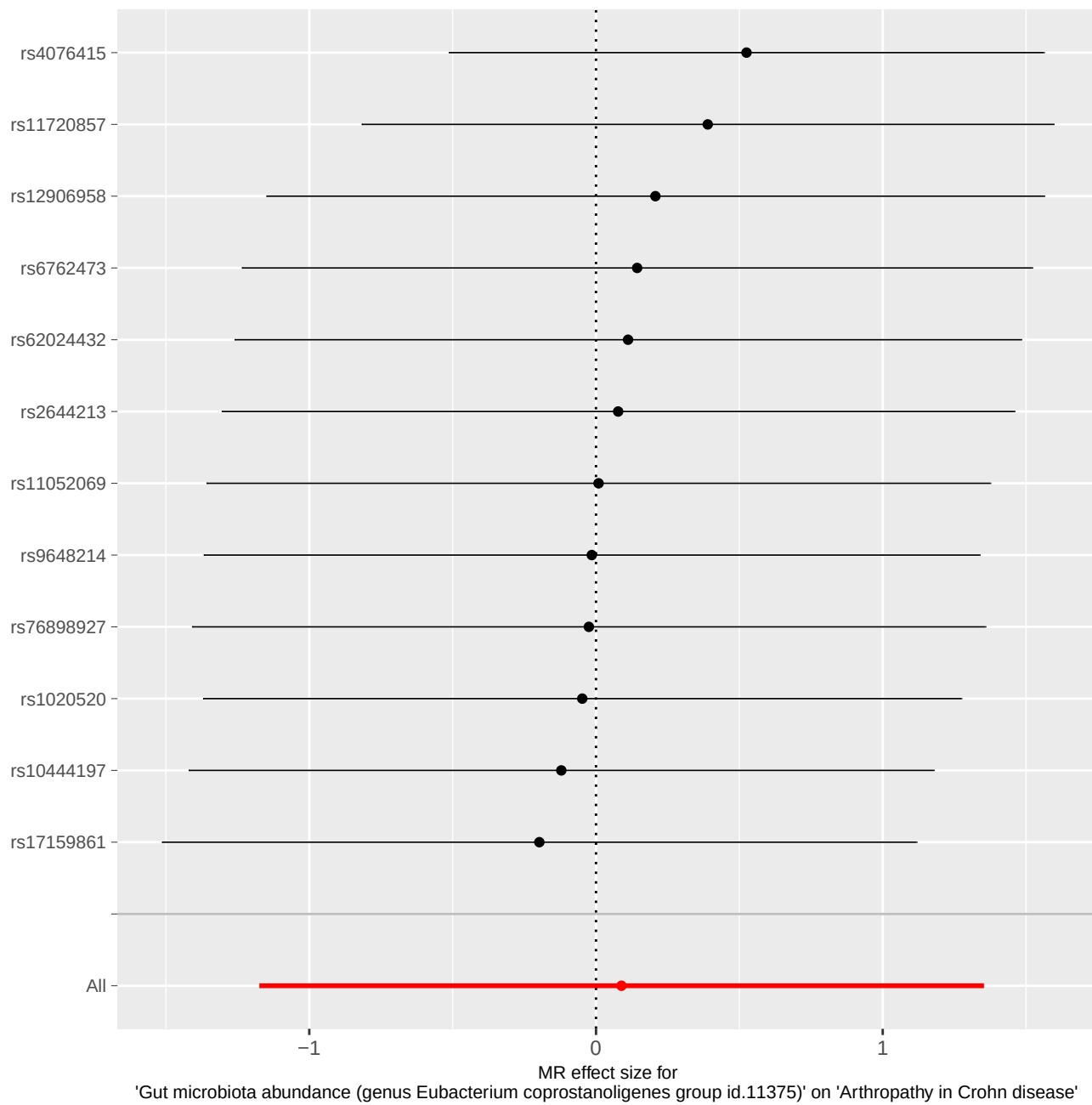
Batch 516 : Gut microbiota abundance (genus Enterorhabdus id.820) on Arthropathy in Crohn disease

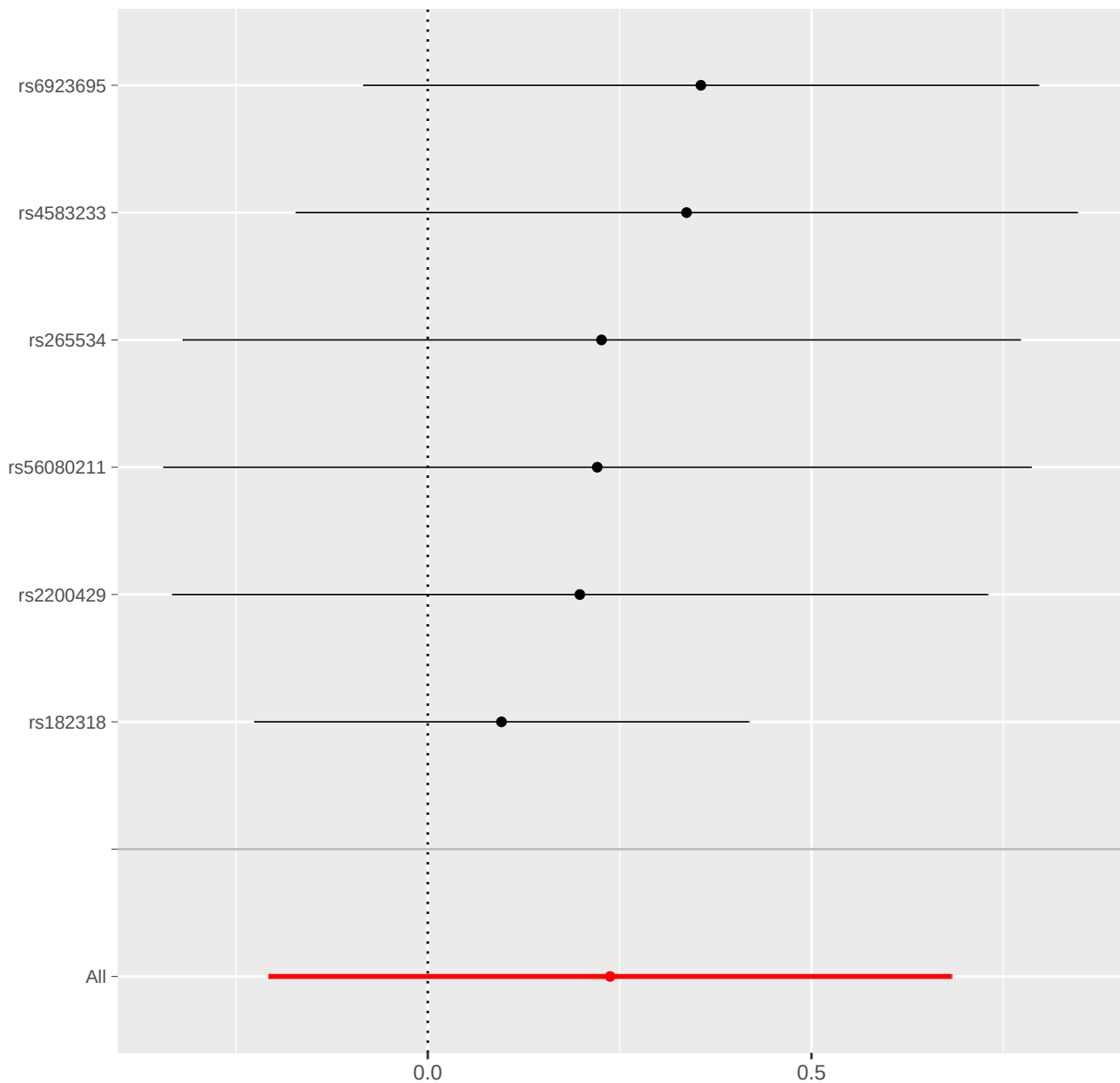


MR effect size for
'Gut microbiota abundance (genus Erysipelatoclostridium id.11381)' on 'Arthropathy in Crohn disease'

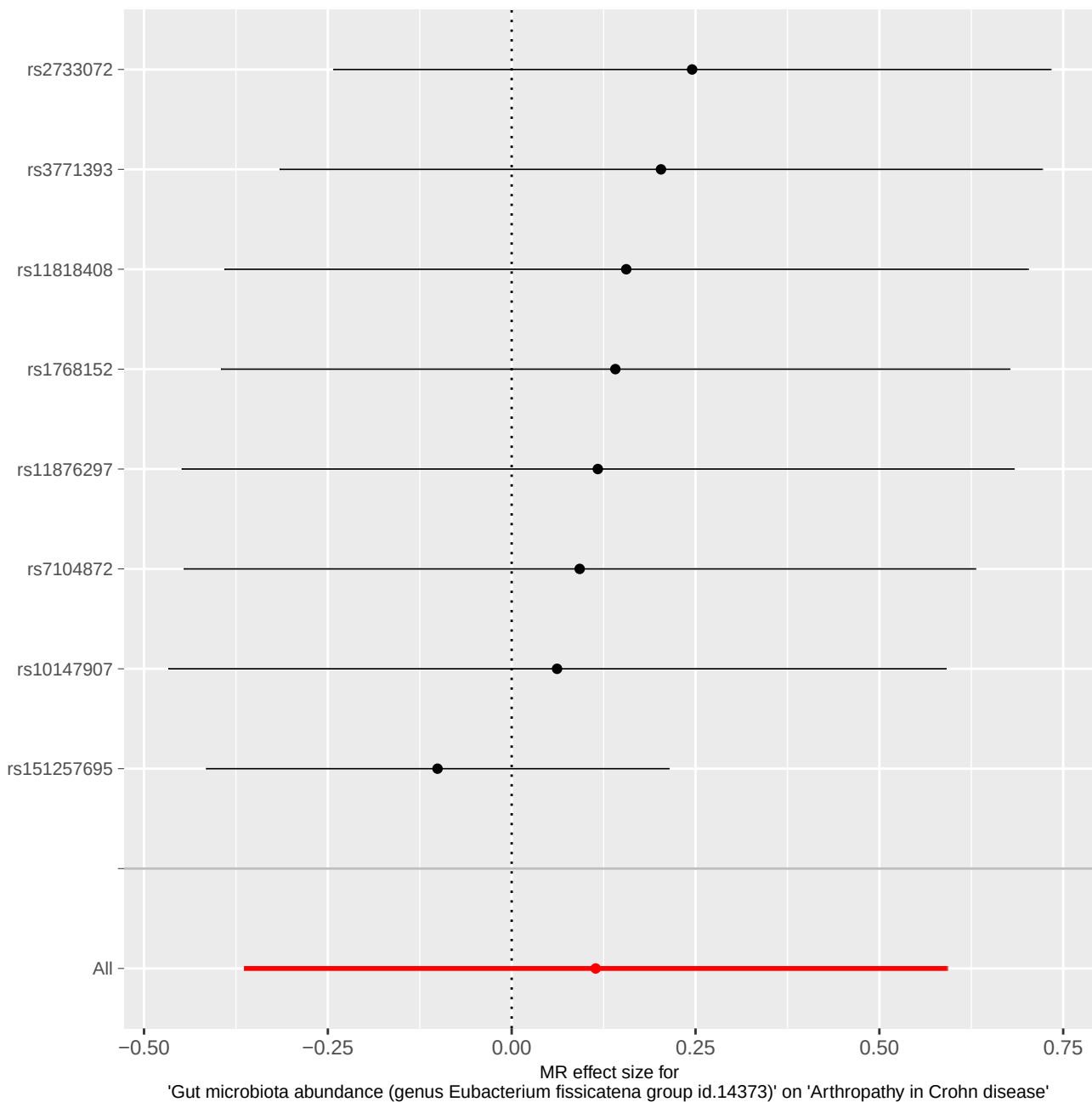


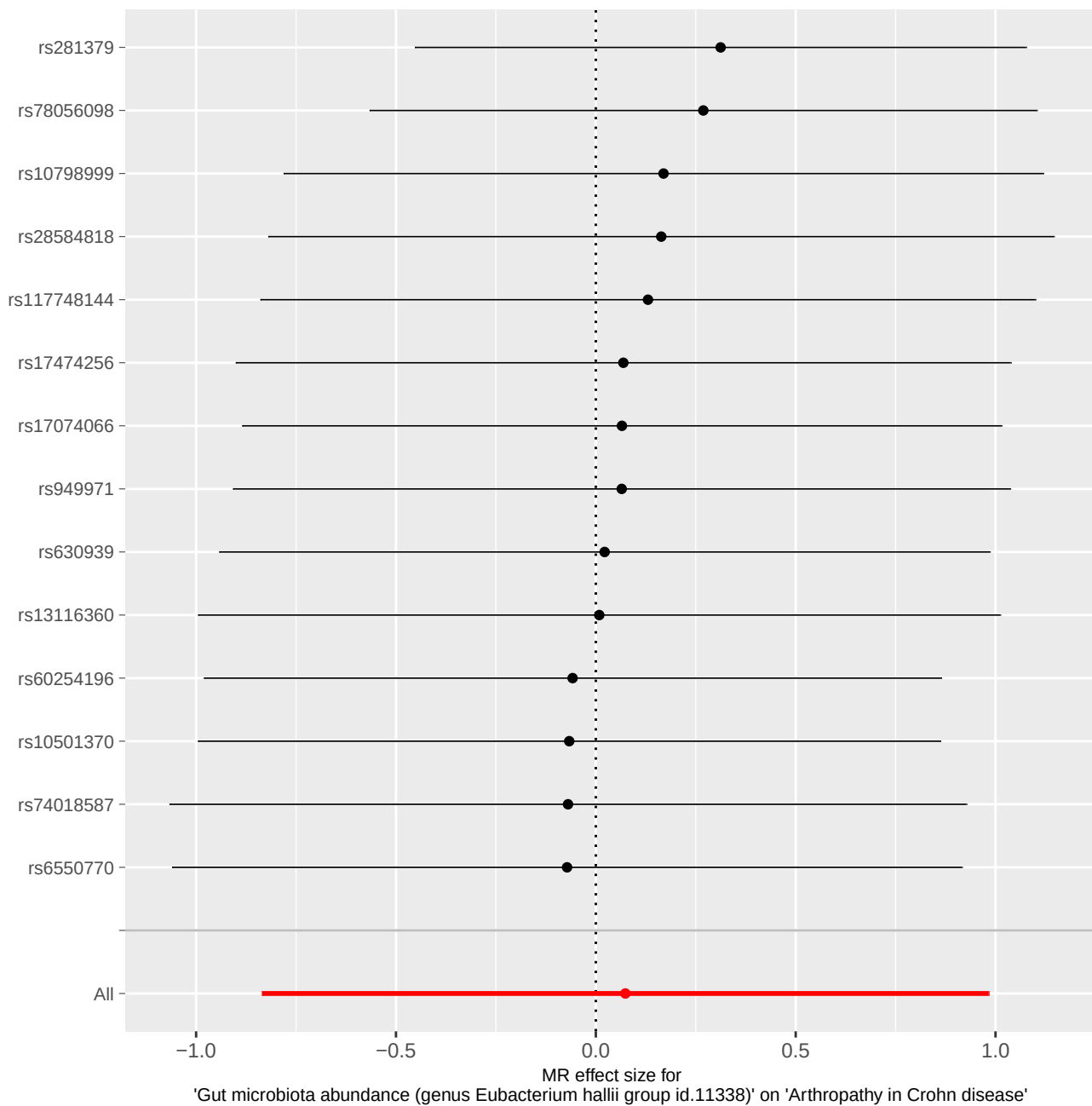


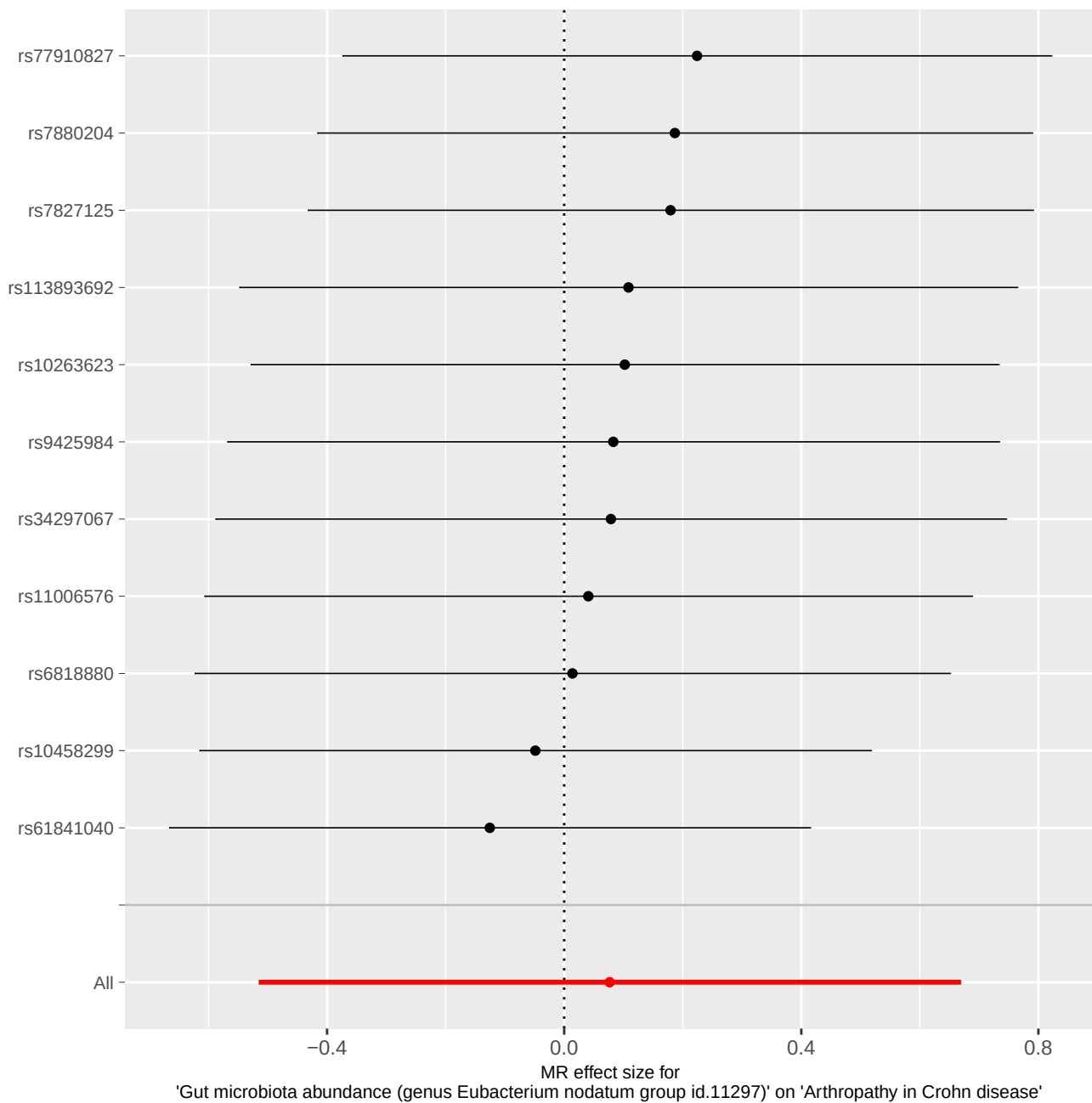


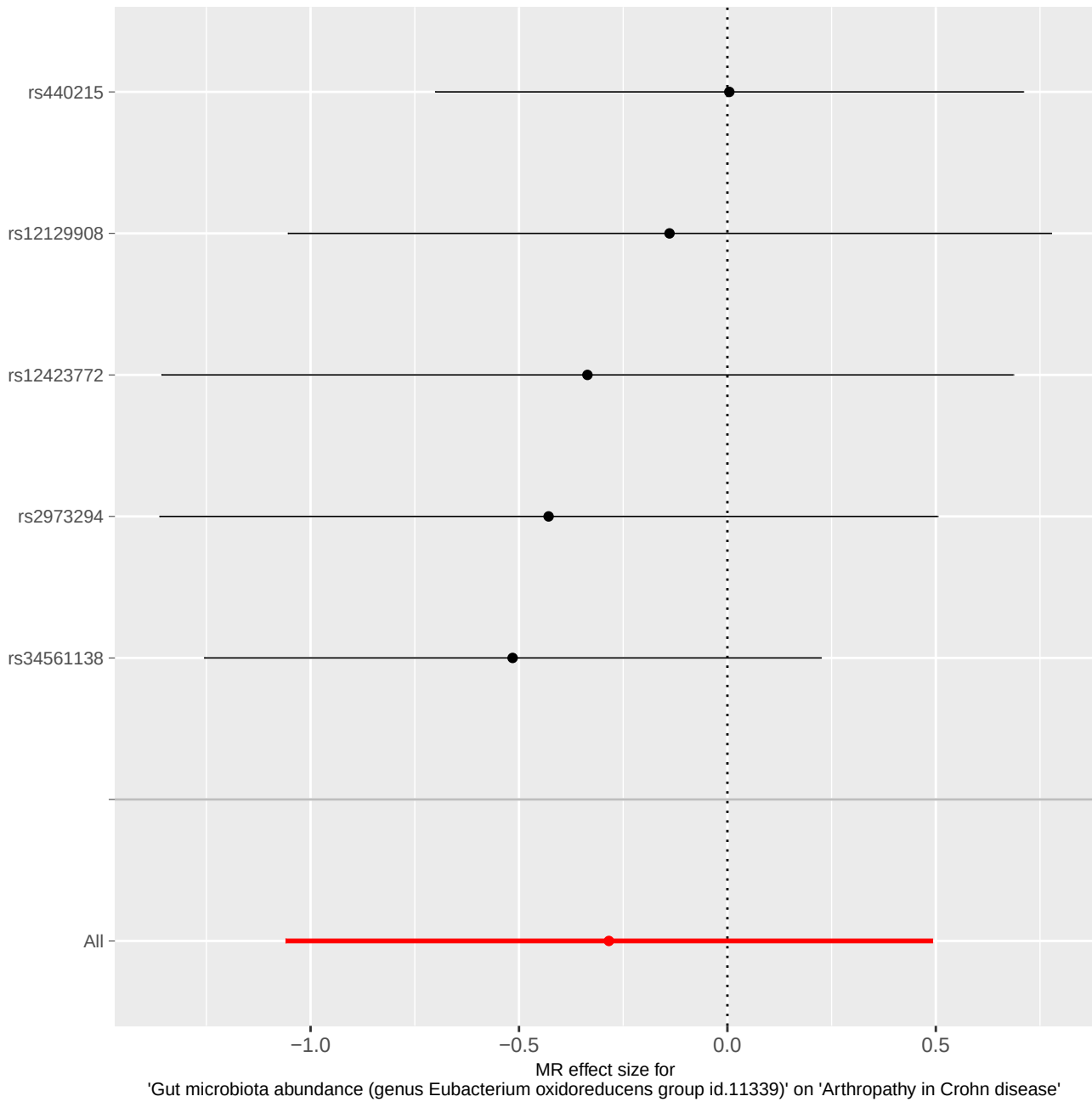


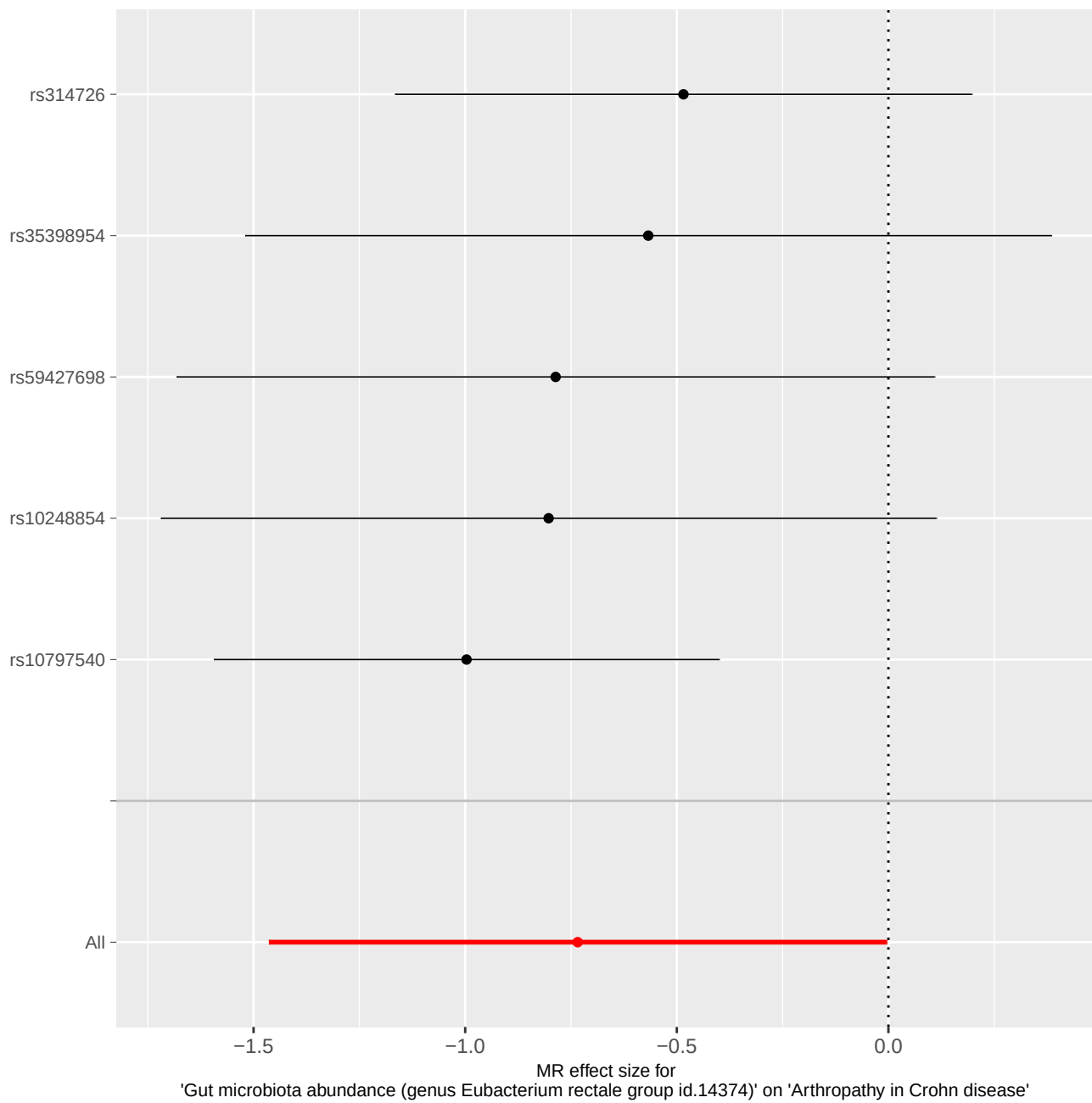
MR effect size for
'Gut microbiota abundance (genus Eubacterium eligens group id.14372)' on 'Arthropathy in Crohn disease'

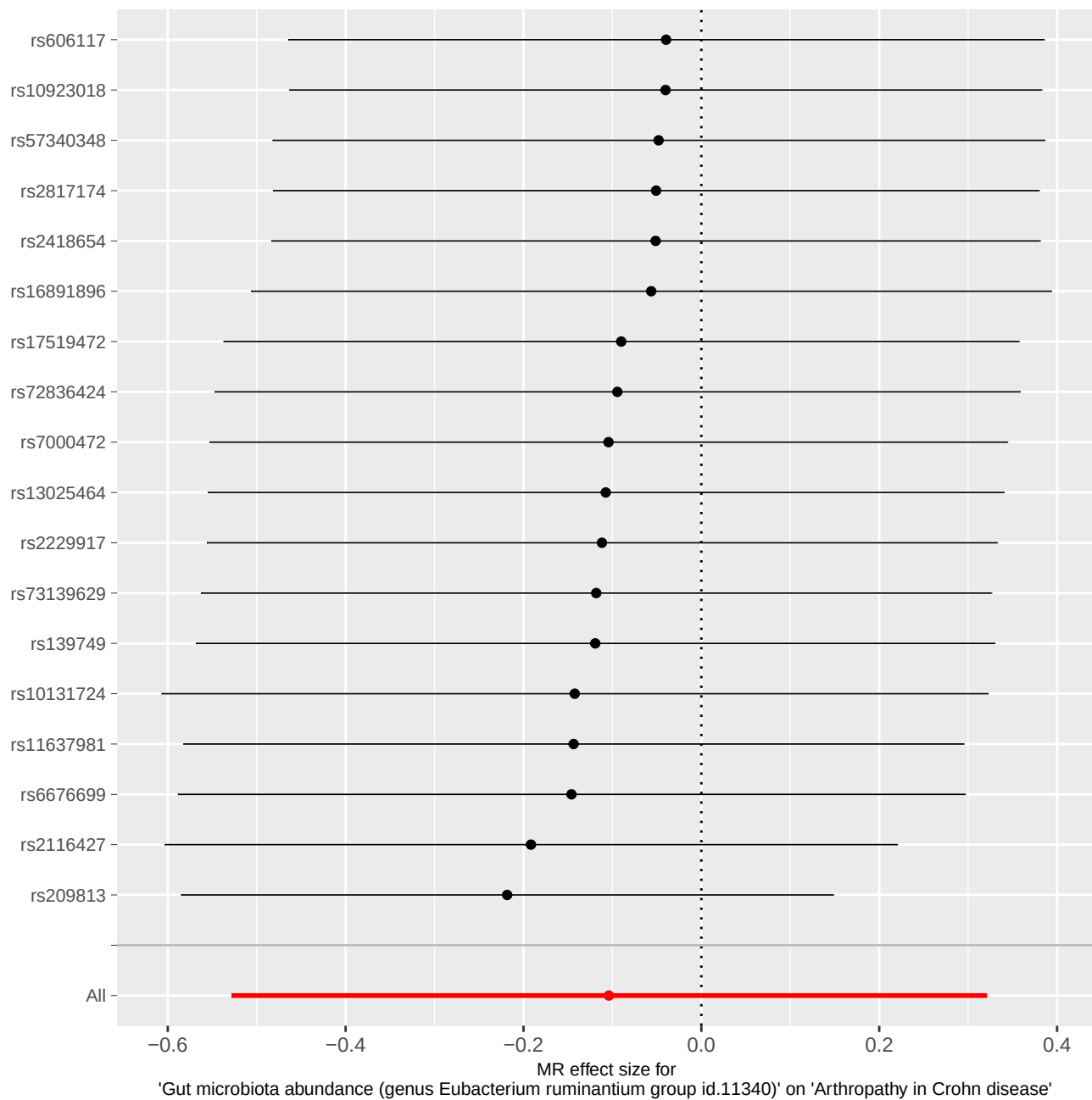


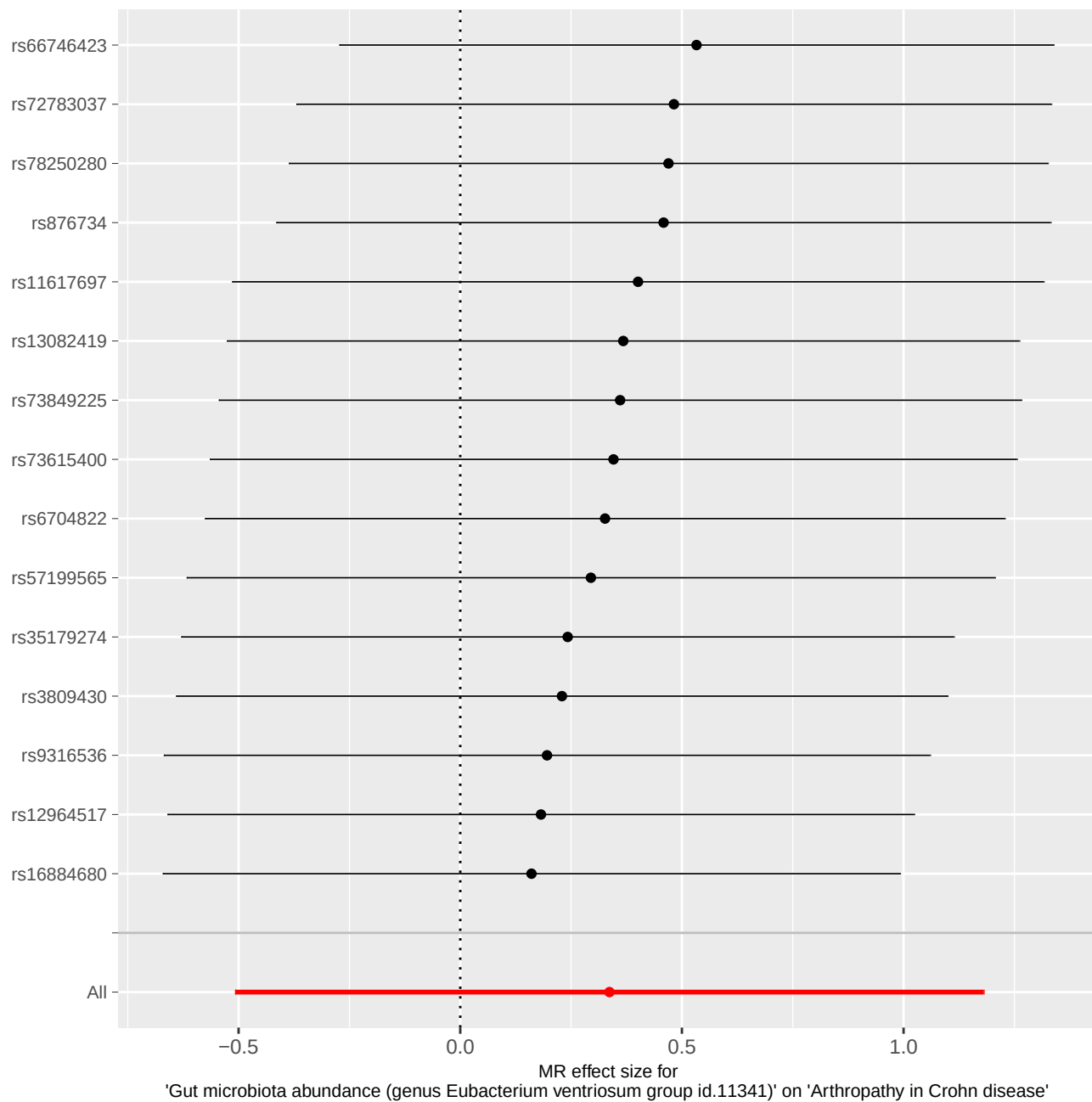


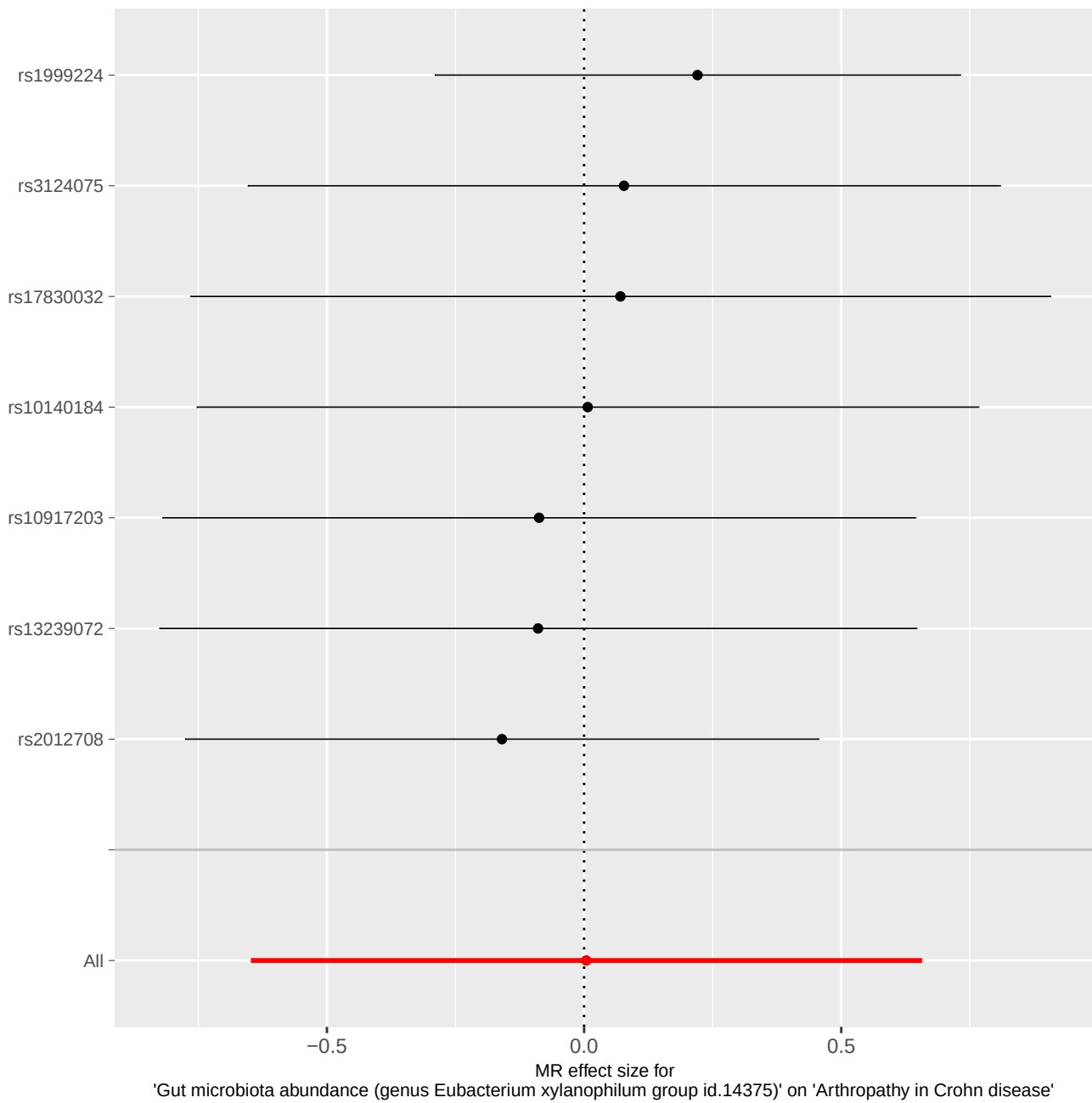


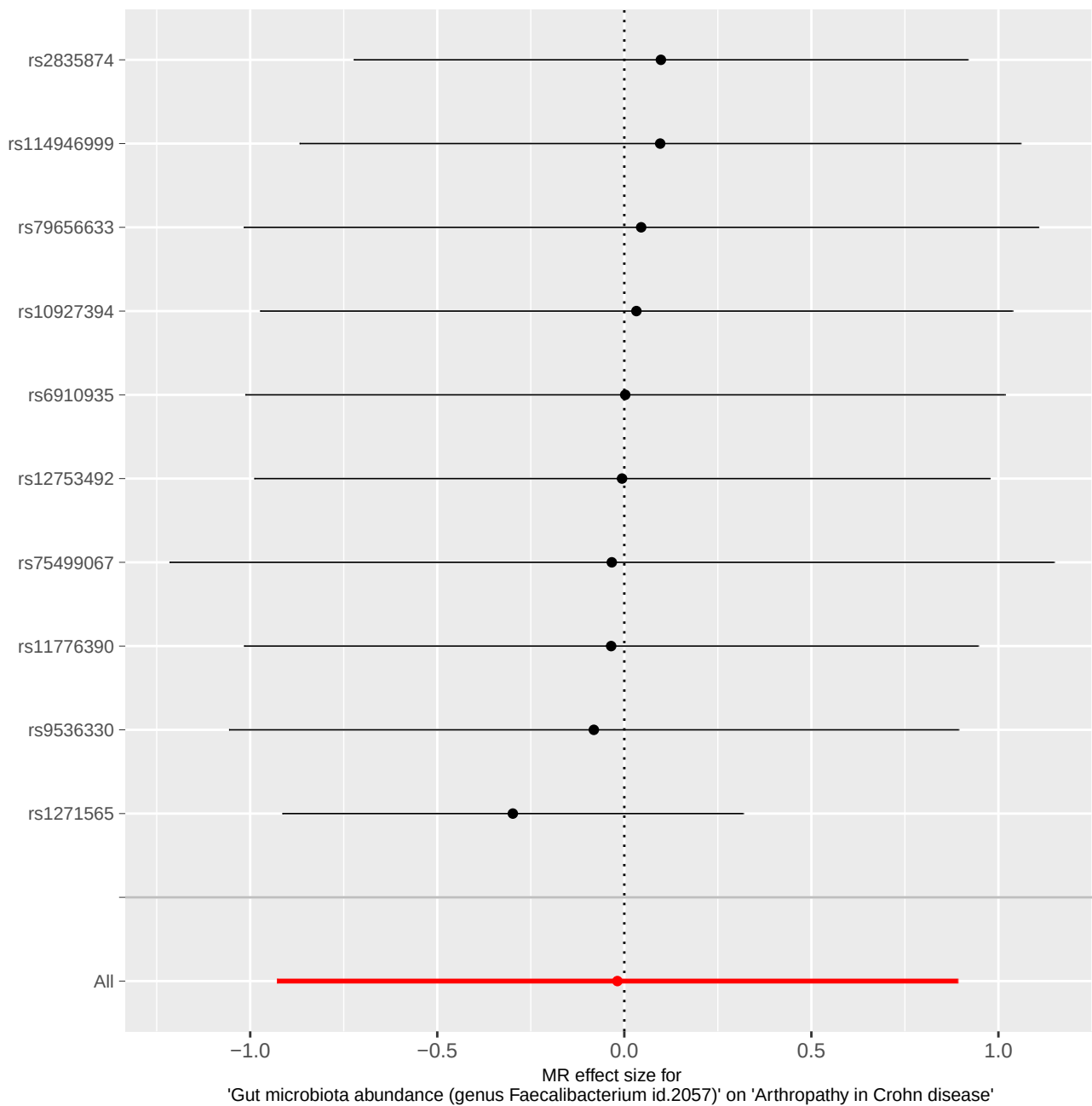


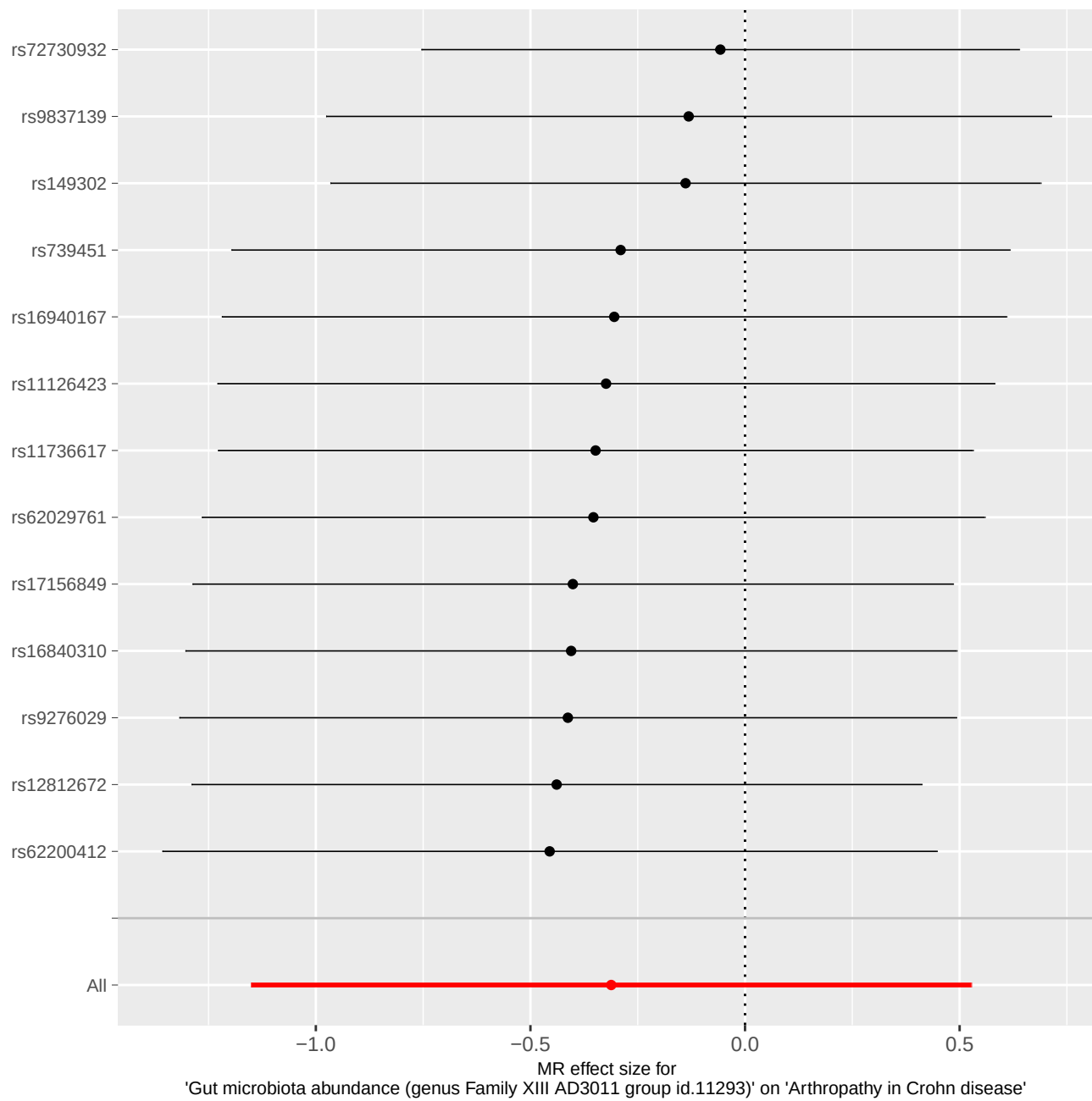


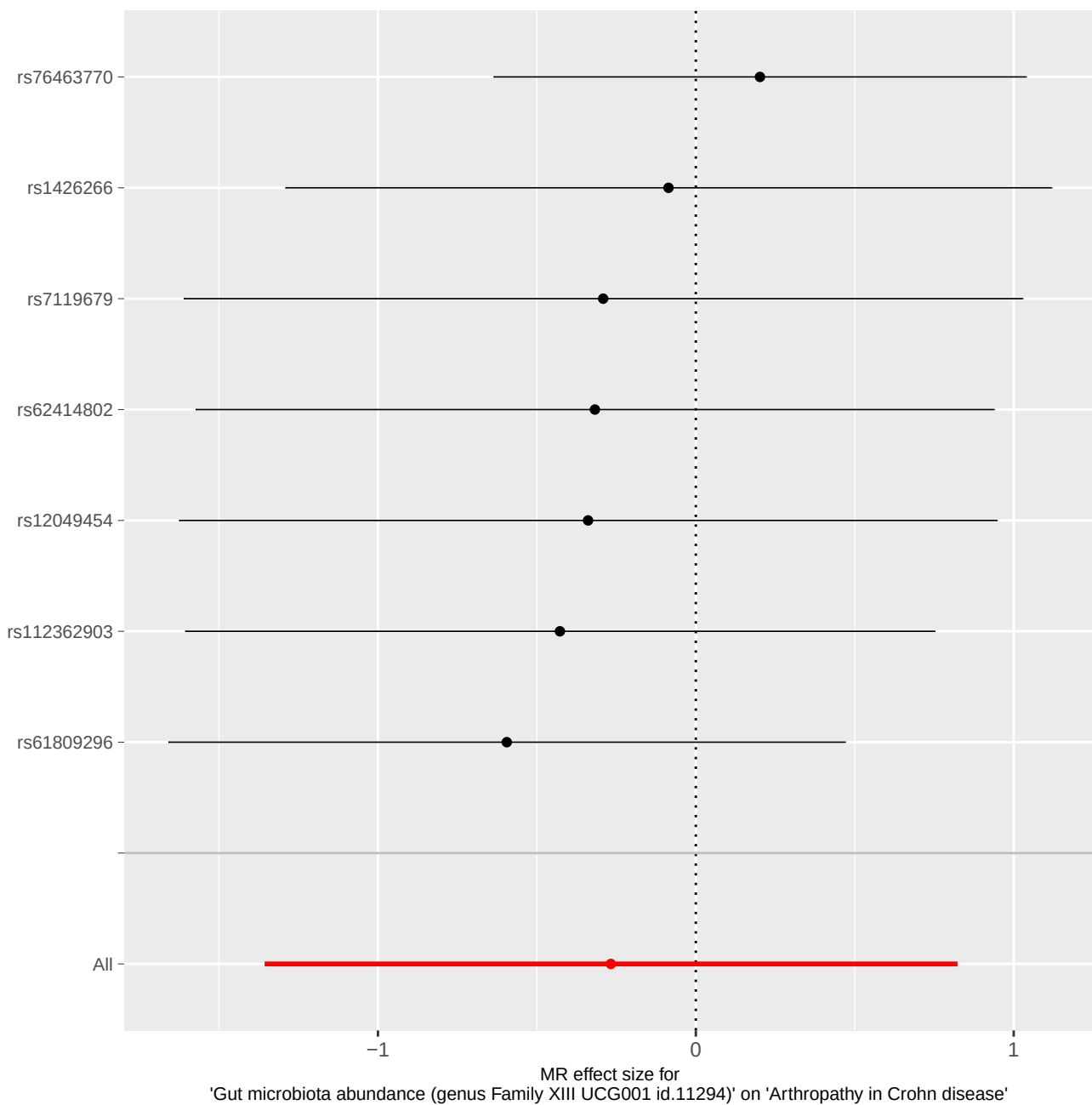


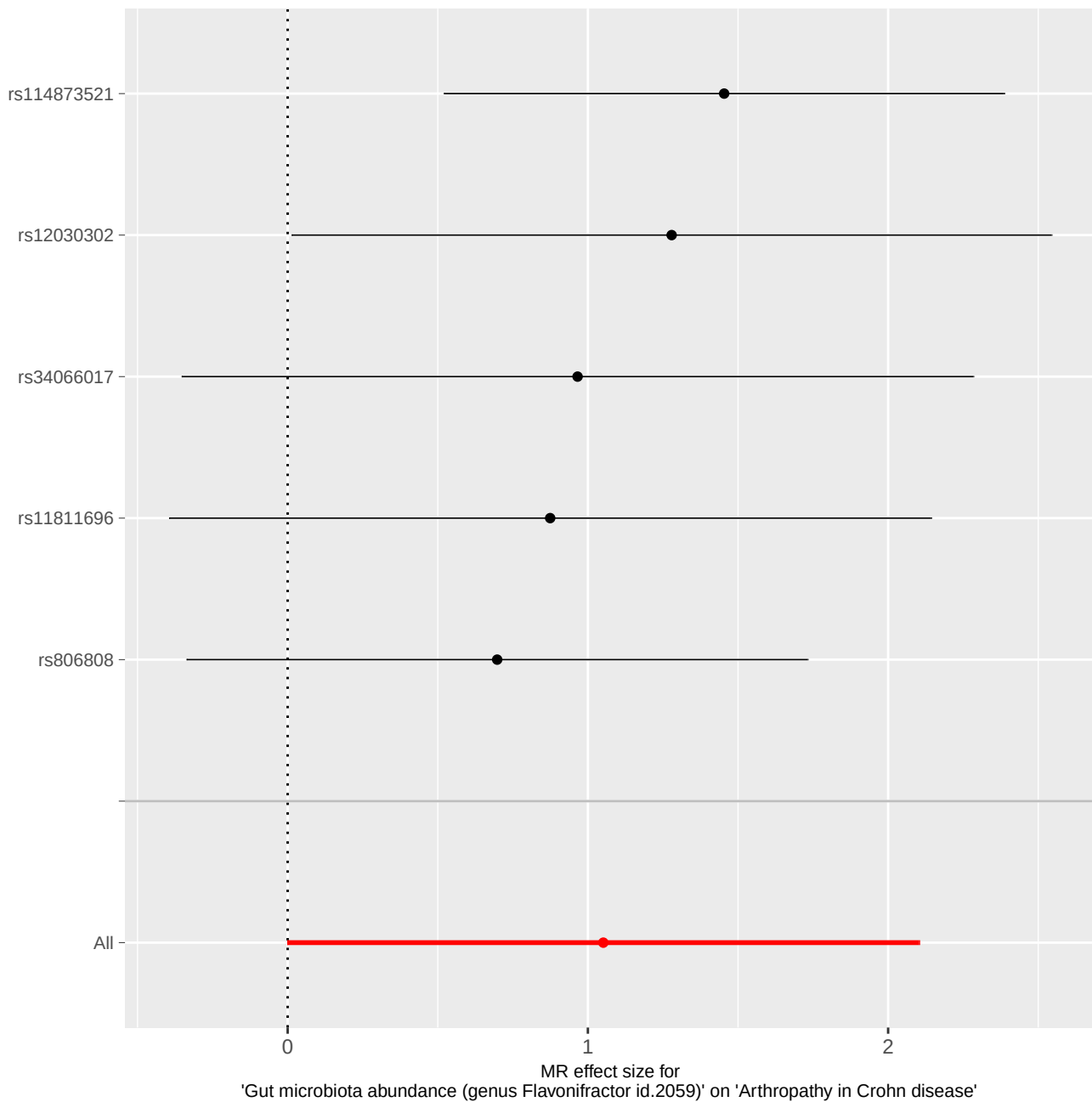


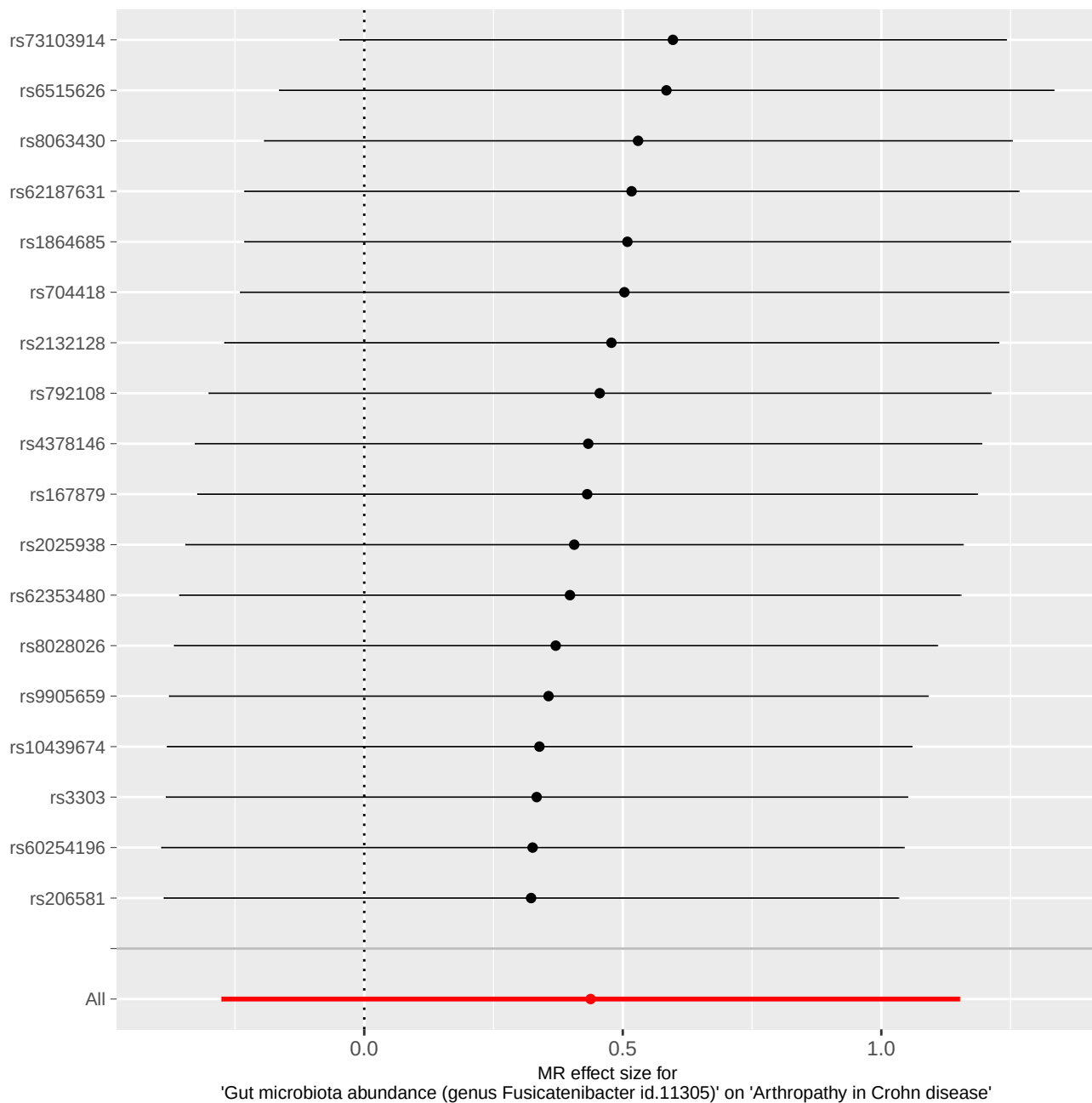


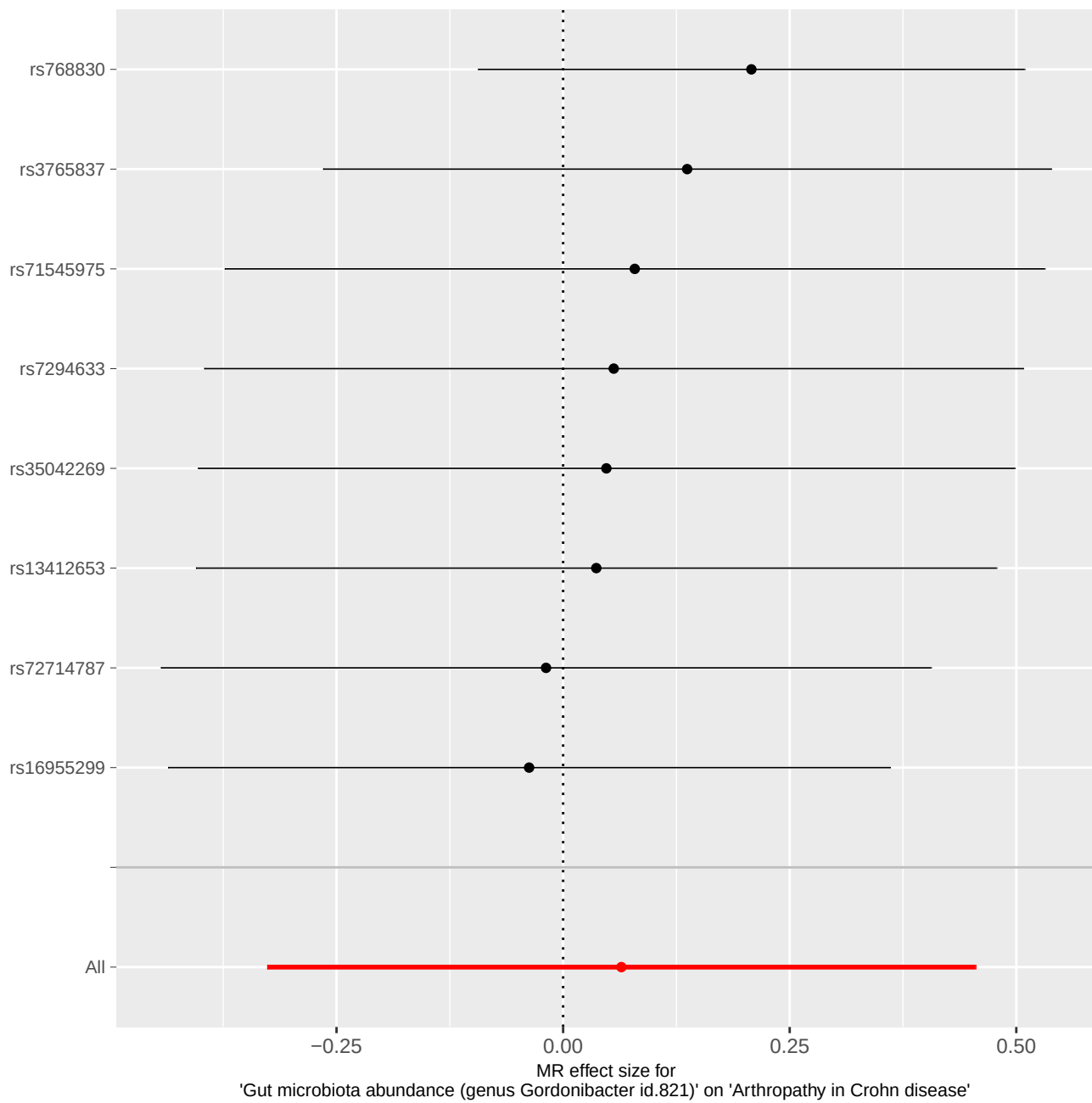


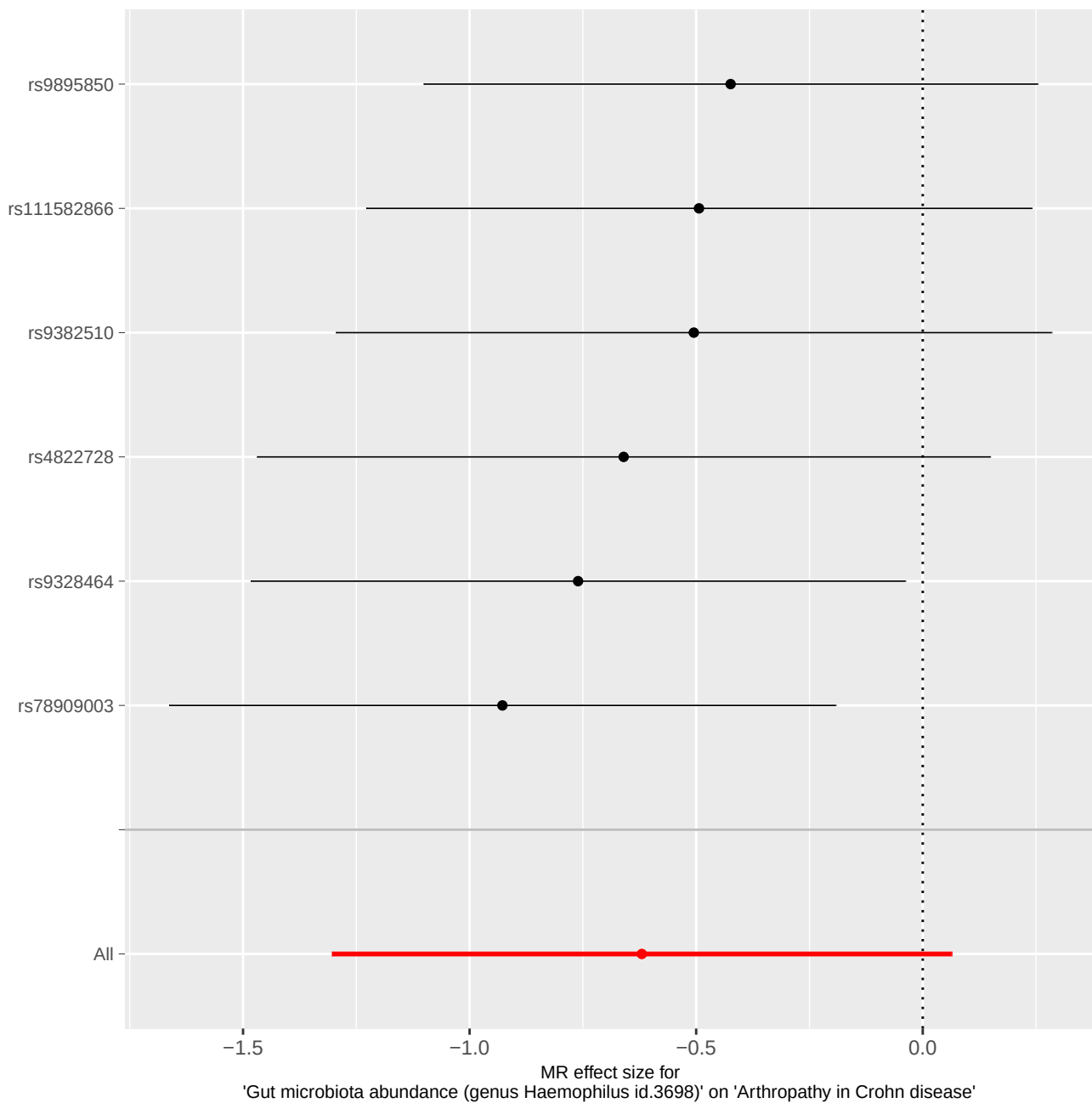


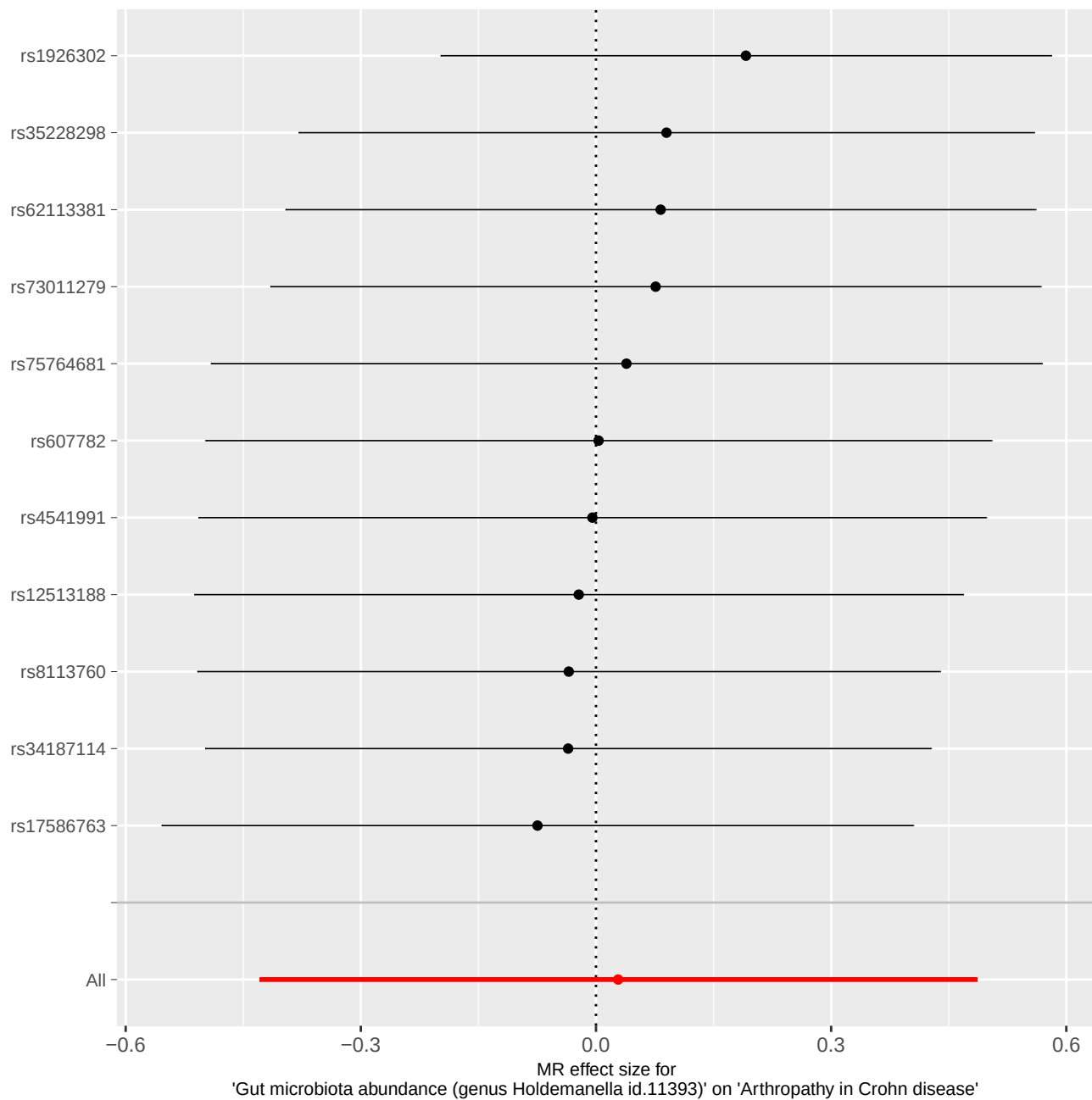


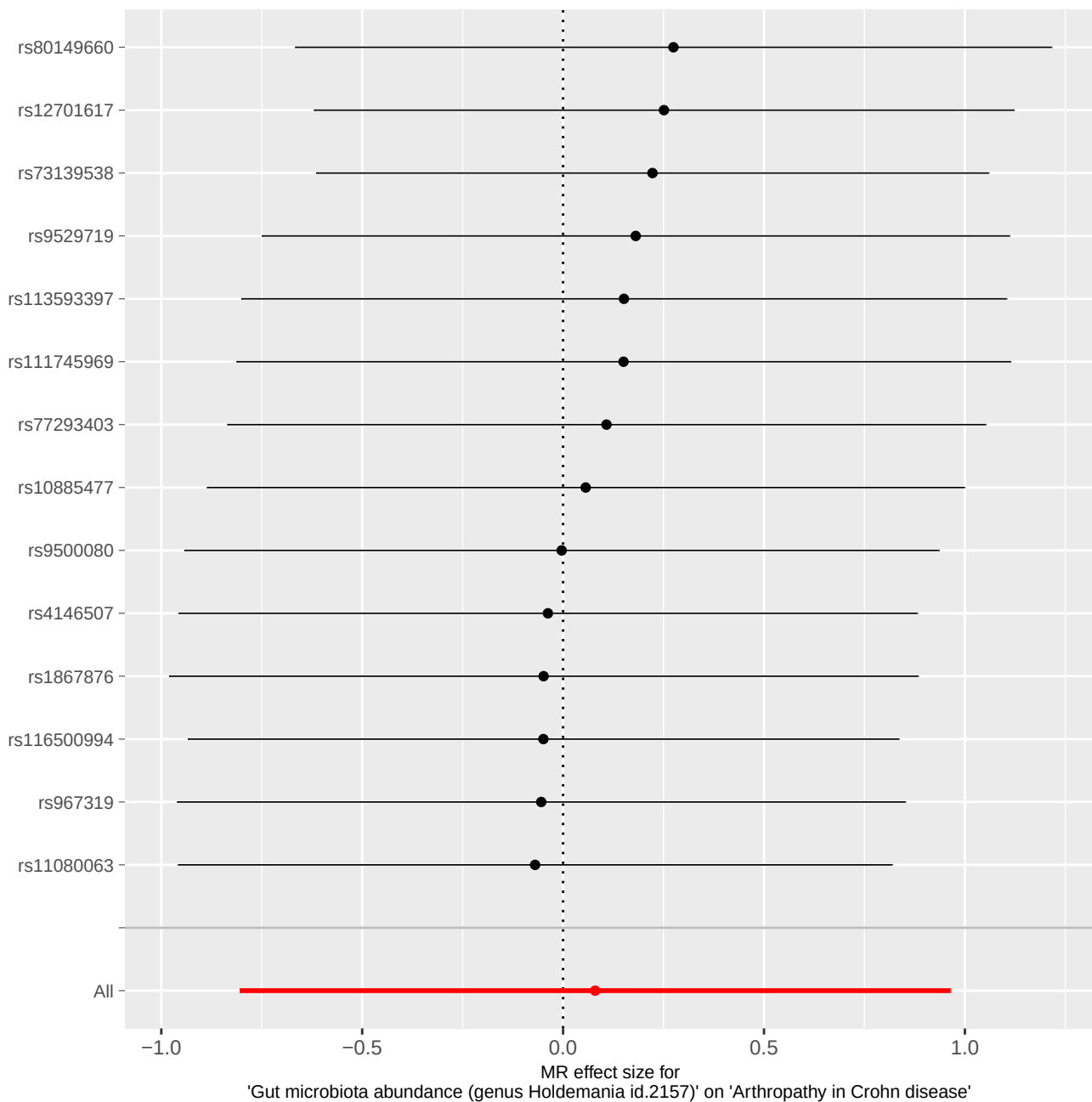


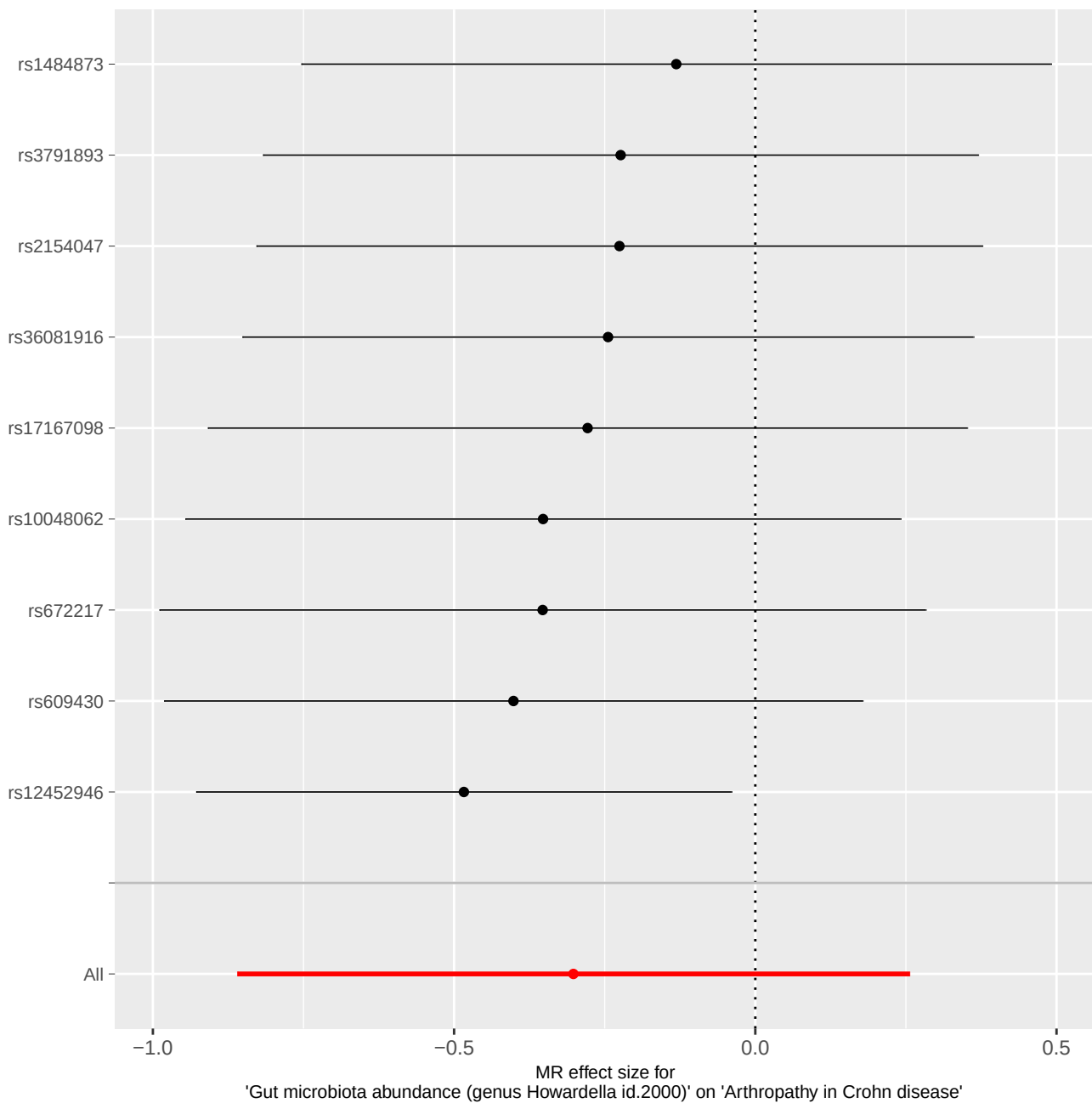


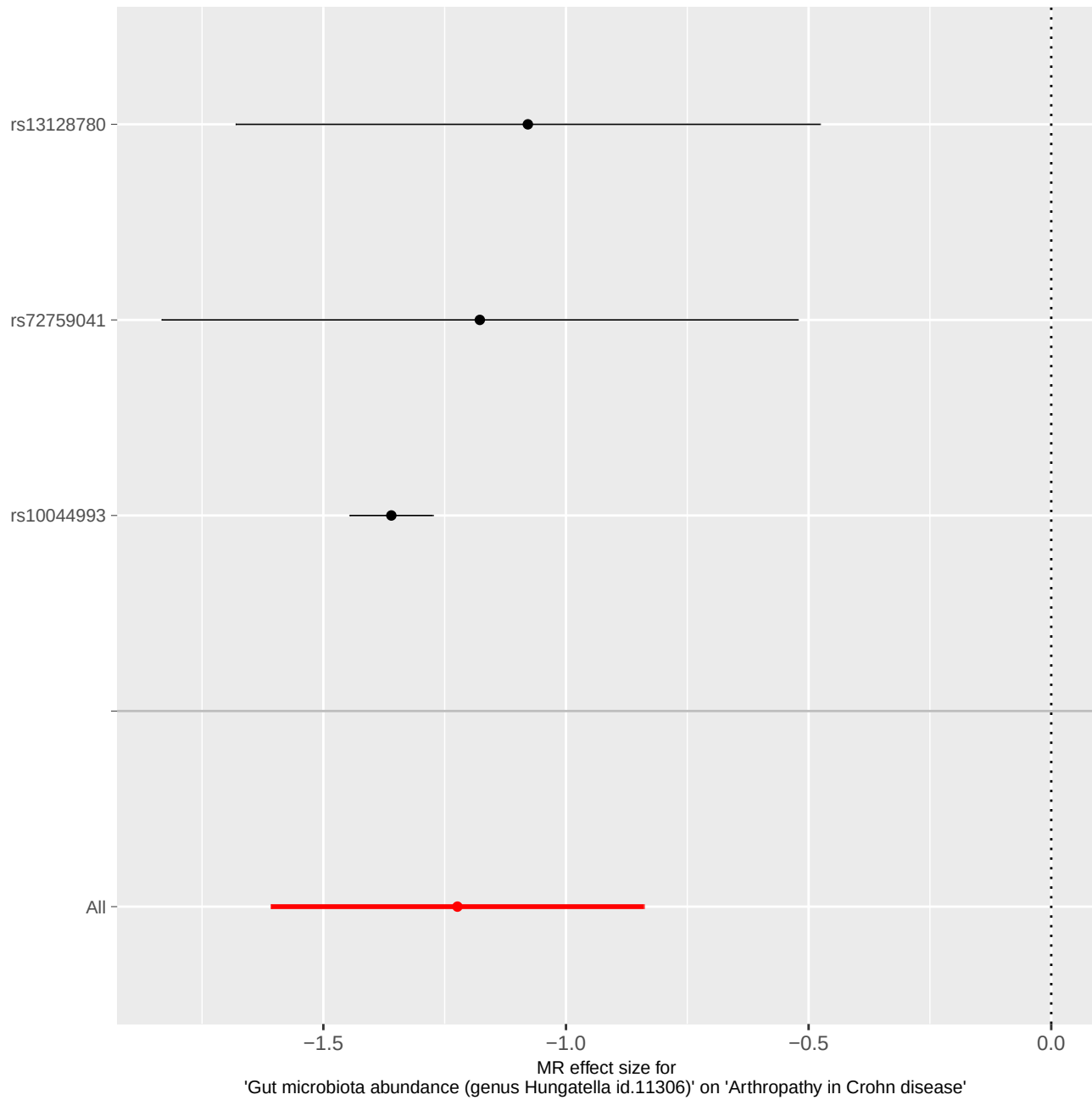


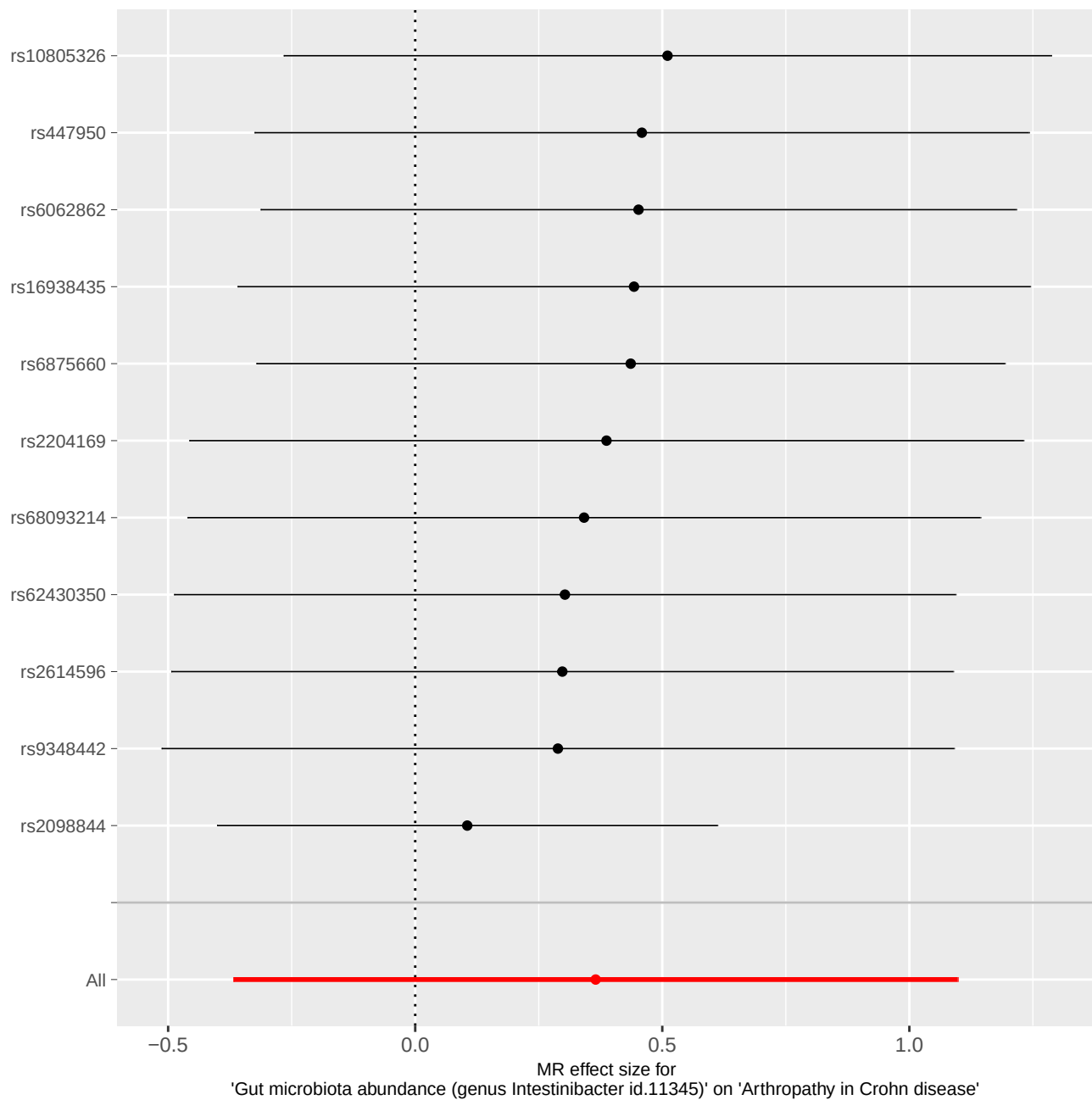


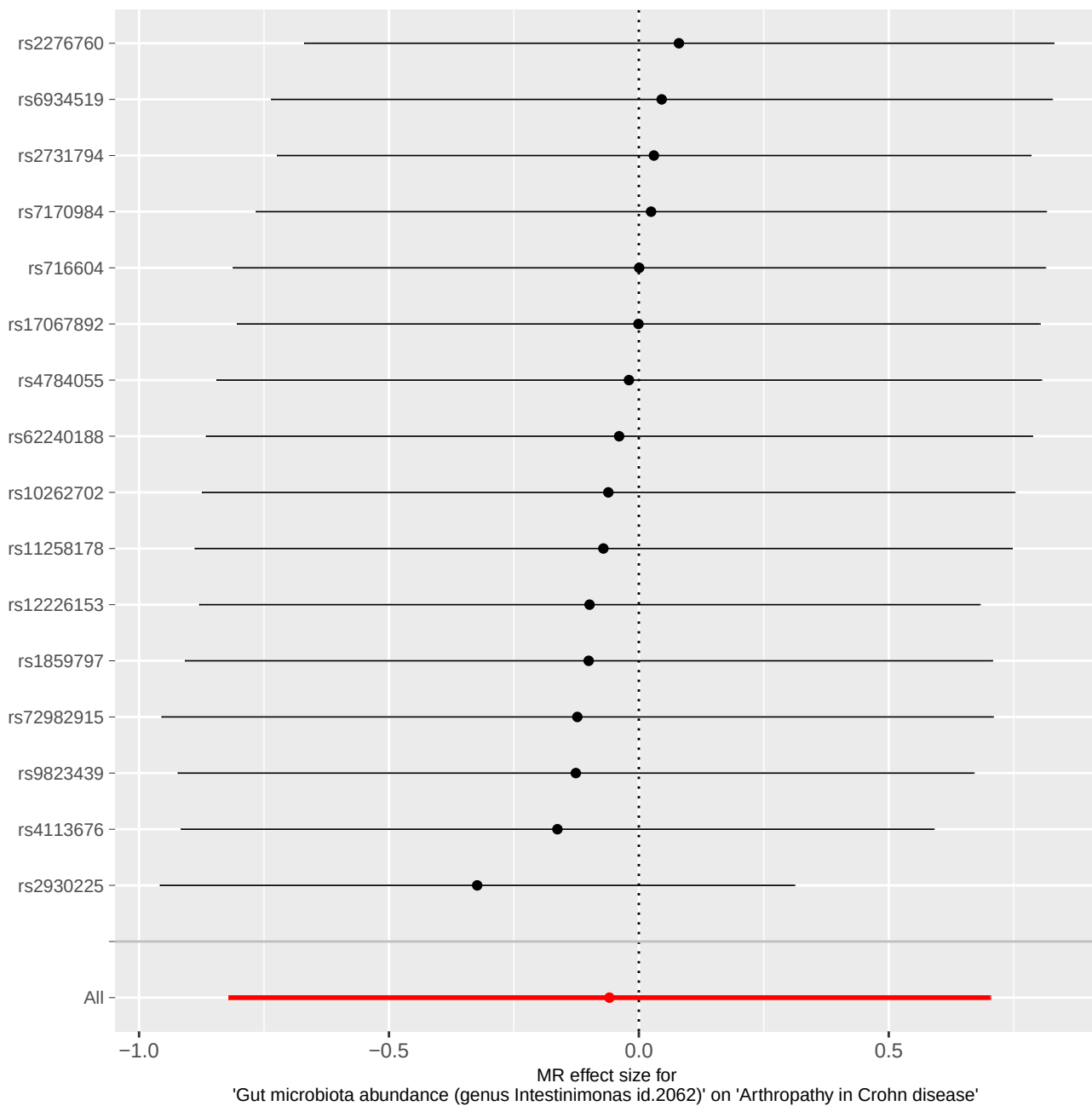


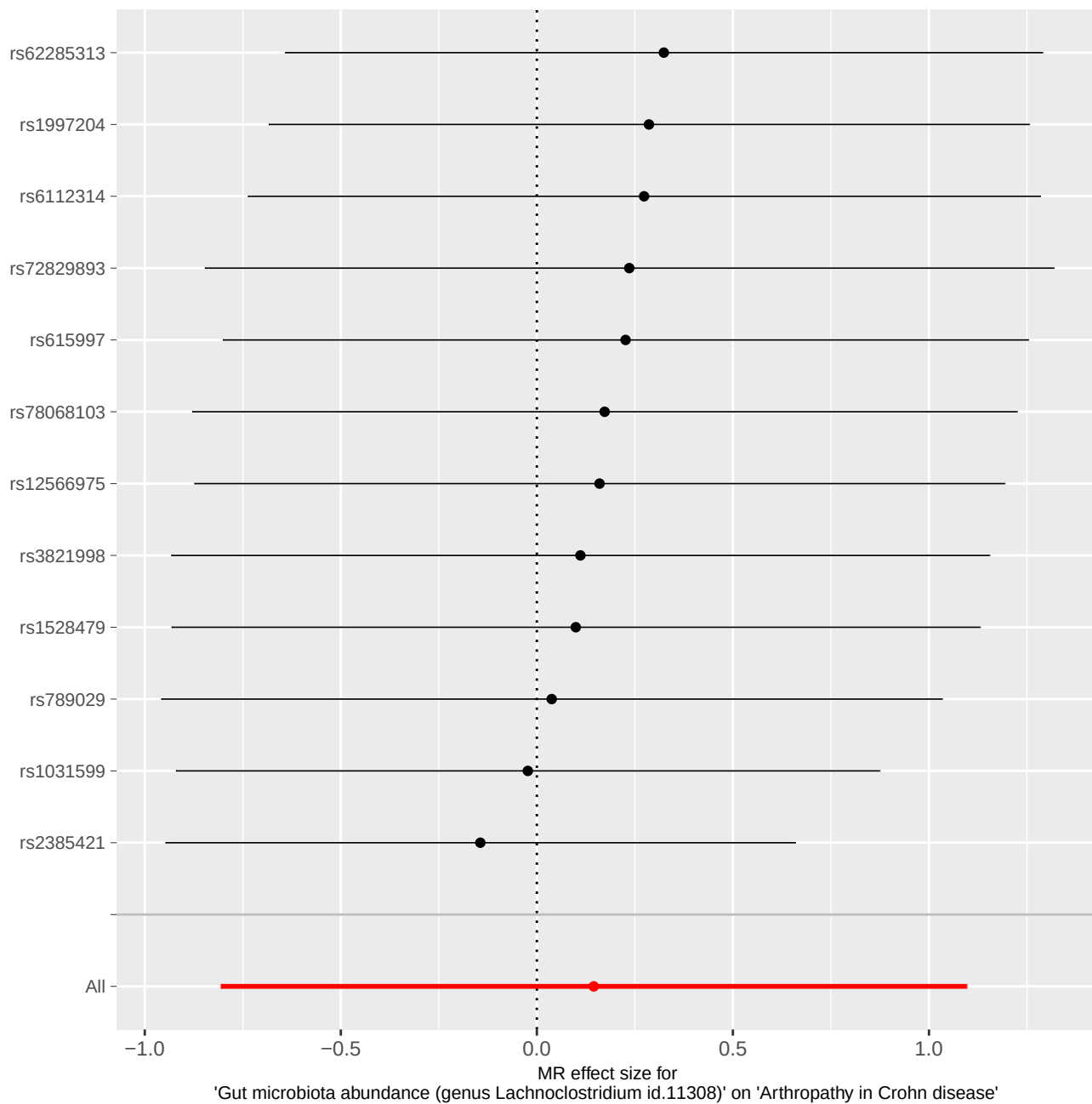


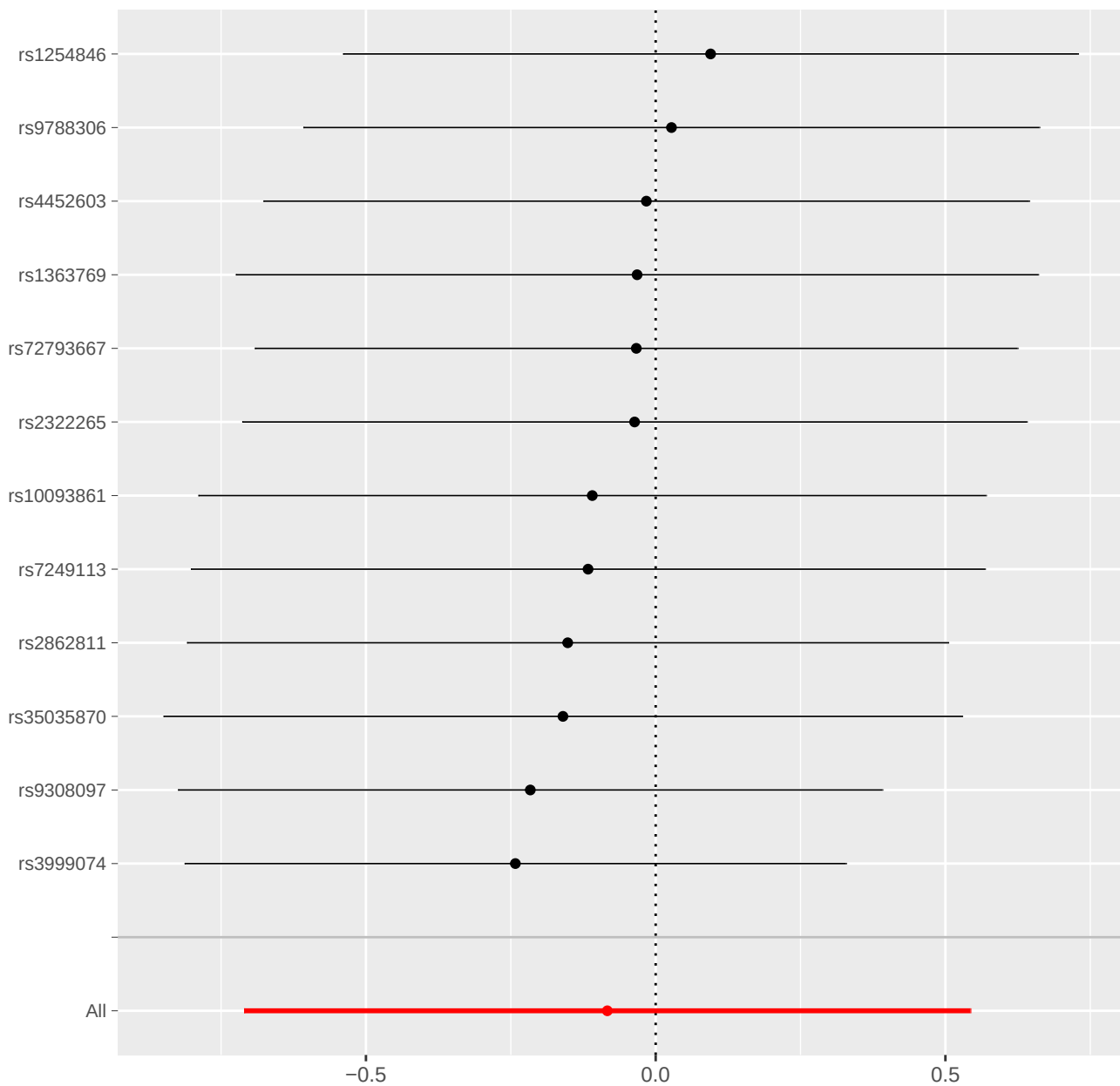




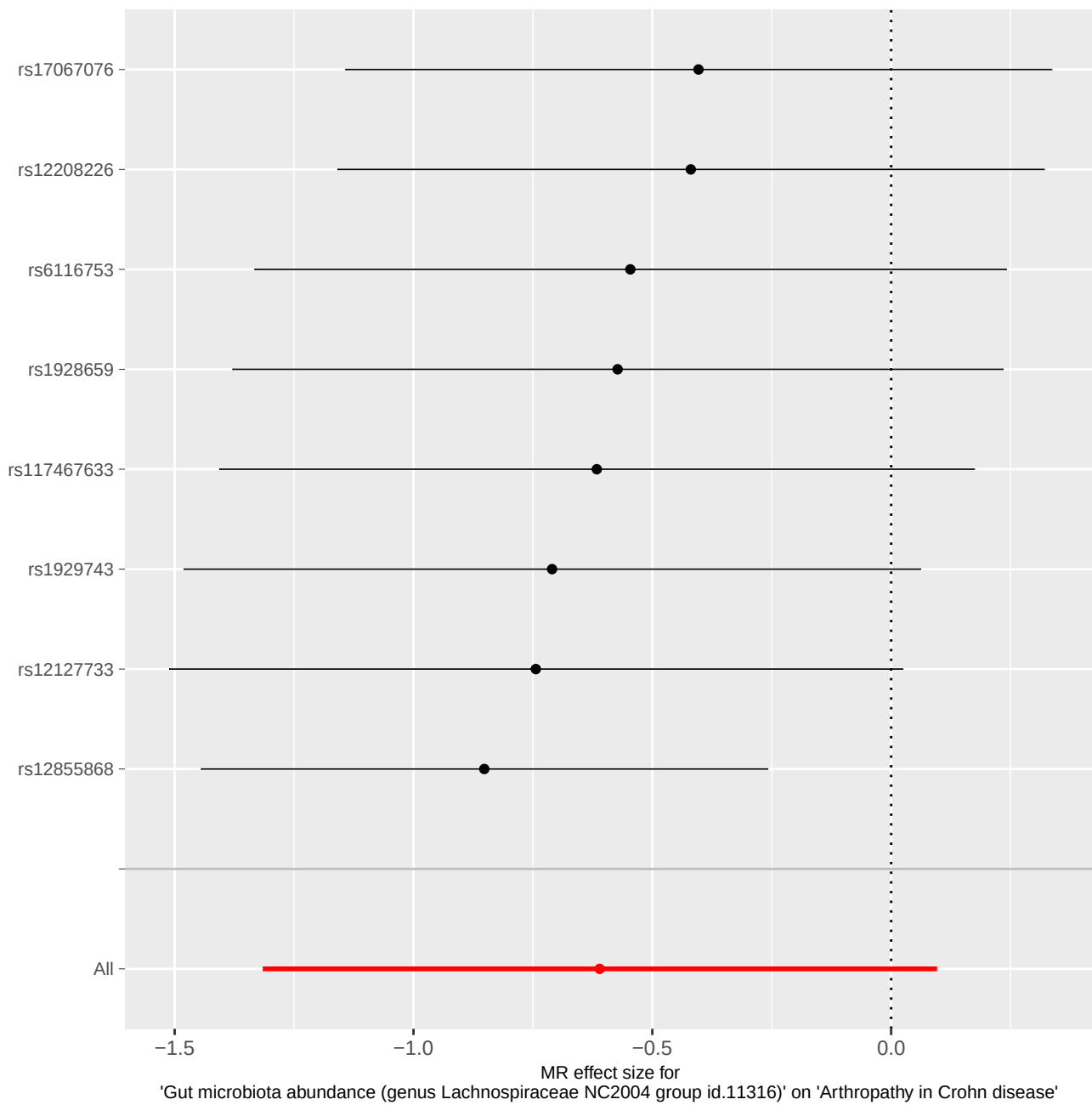


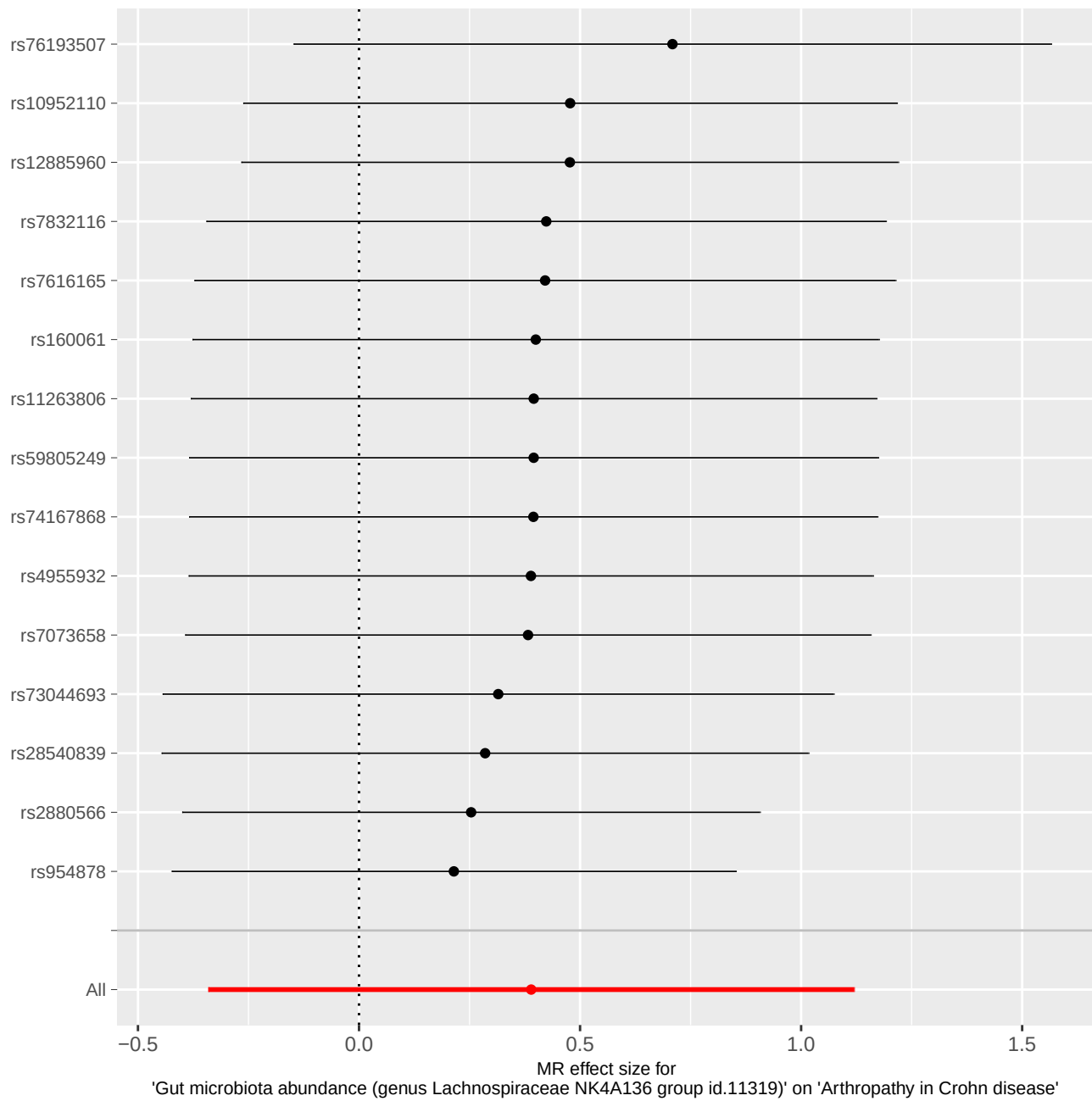


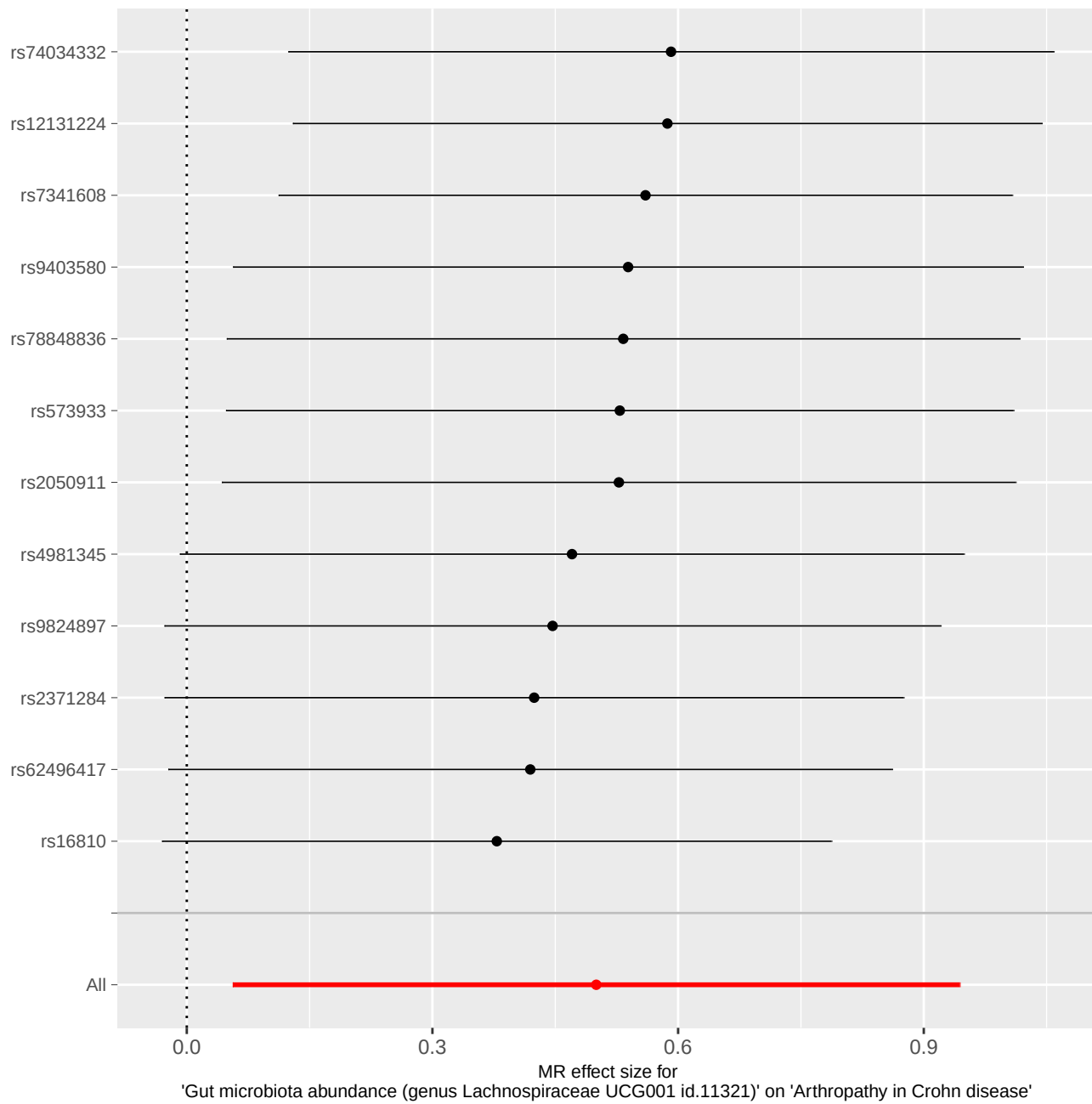


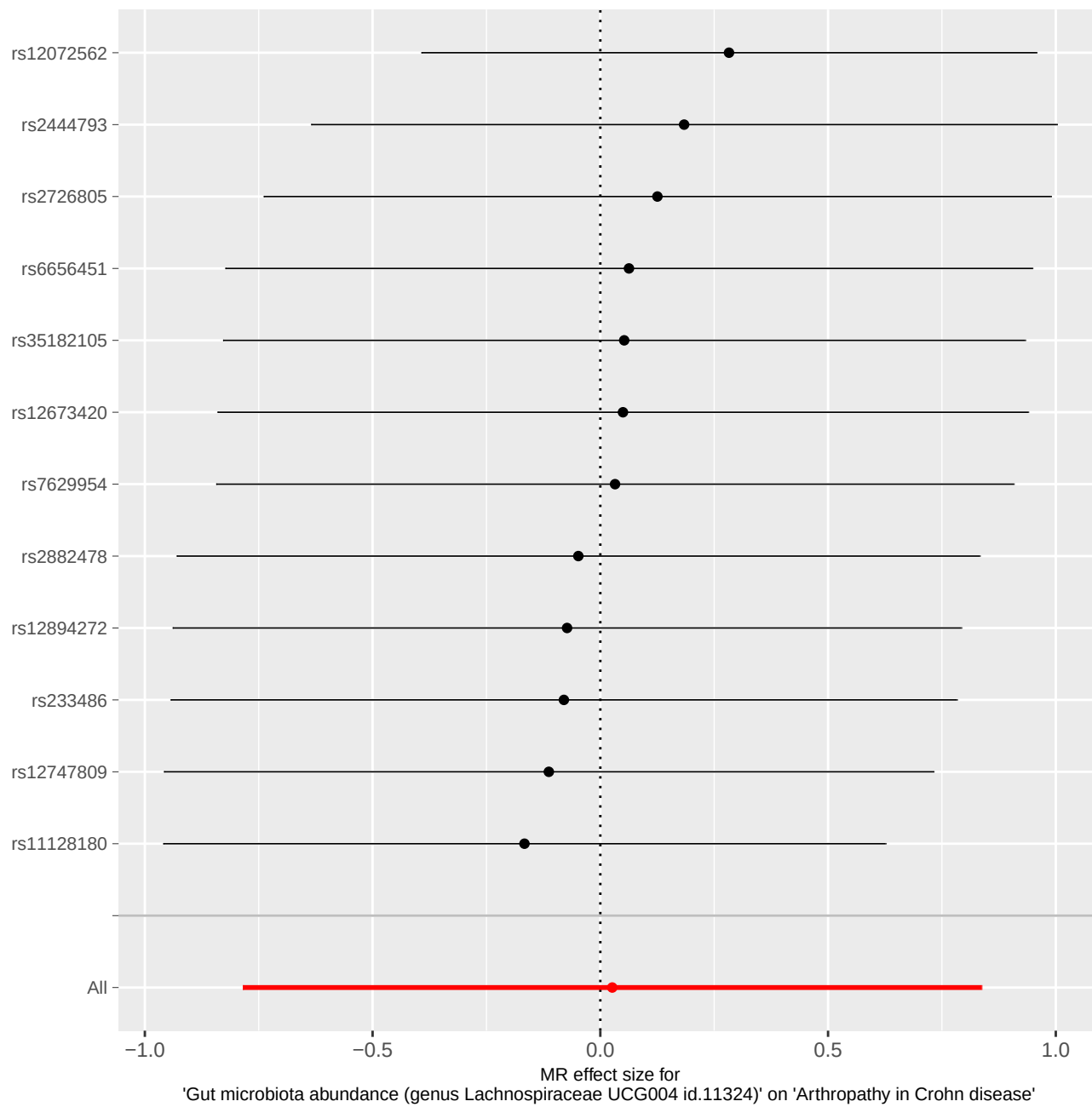


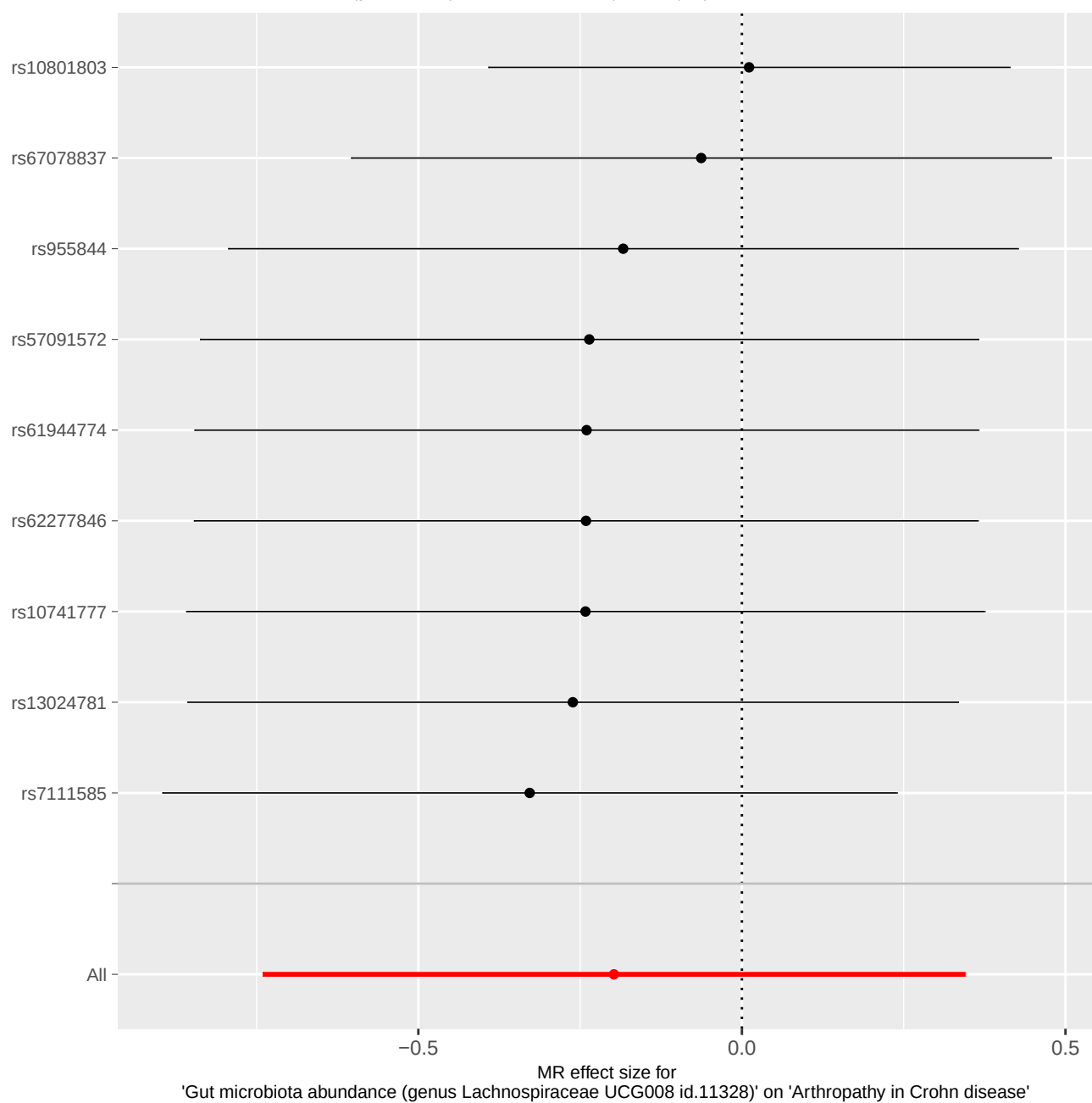
MR effect size for
'Gut microbiota abundance (genus Lachnospiraceae FCS020 group id.11314)' on 'Arthropathy in Crohn disease'

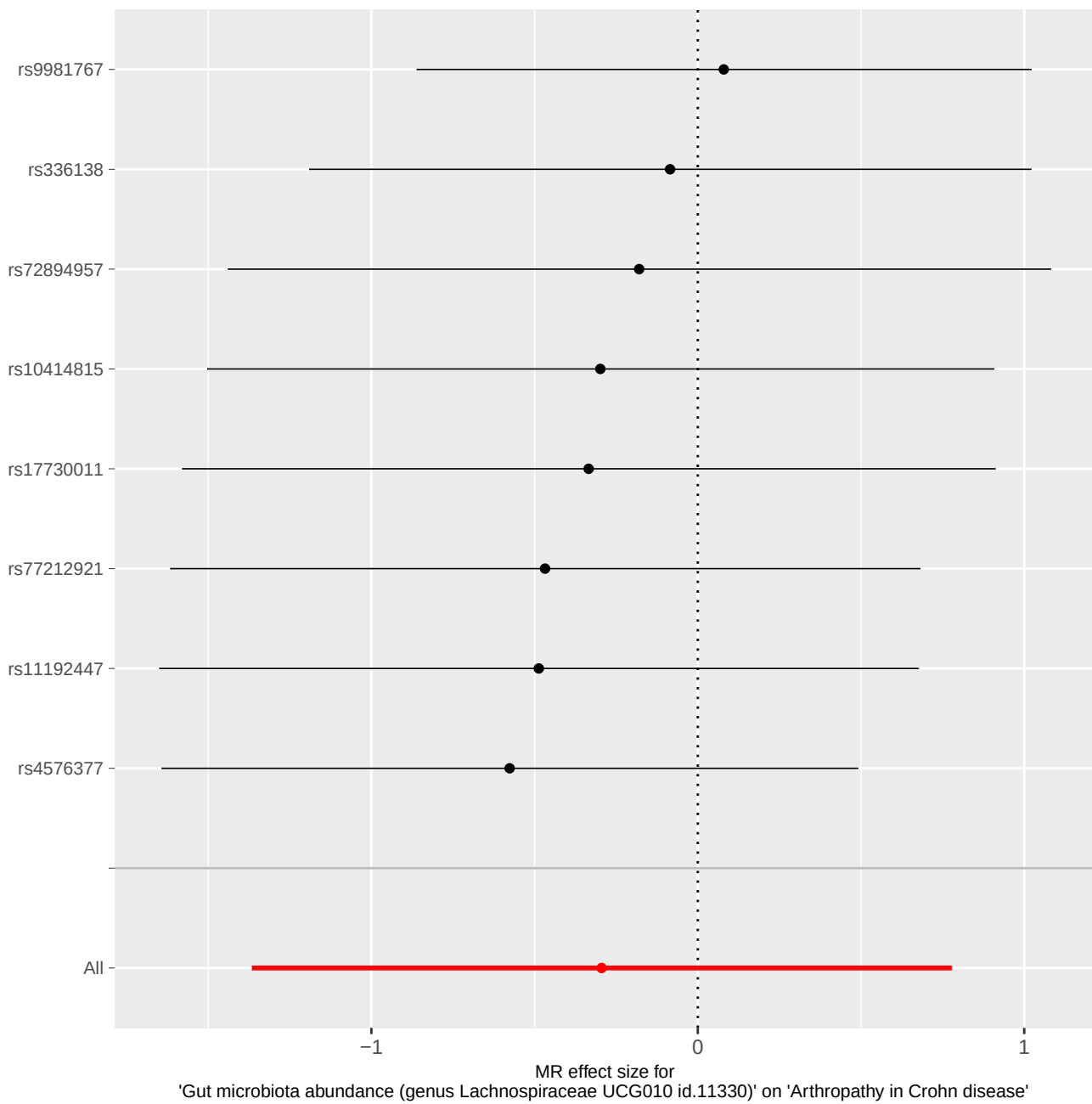


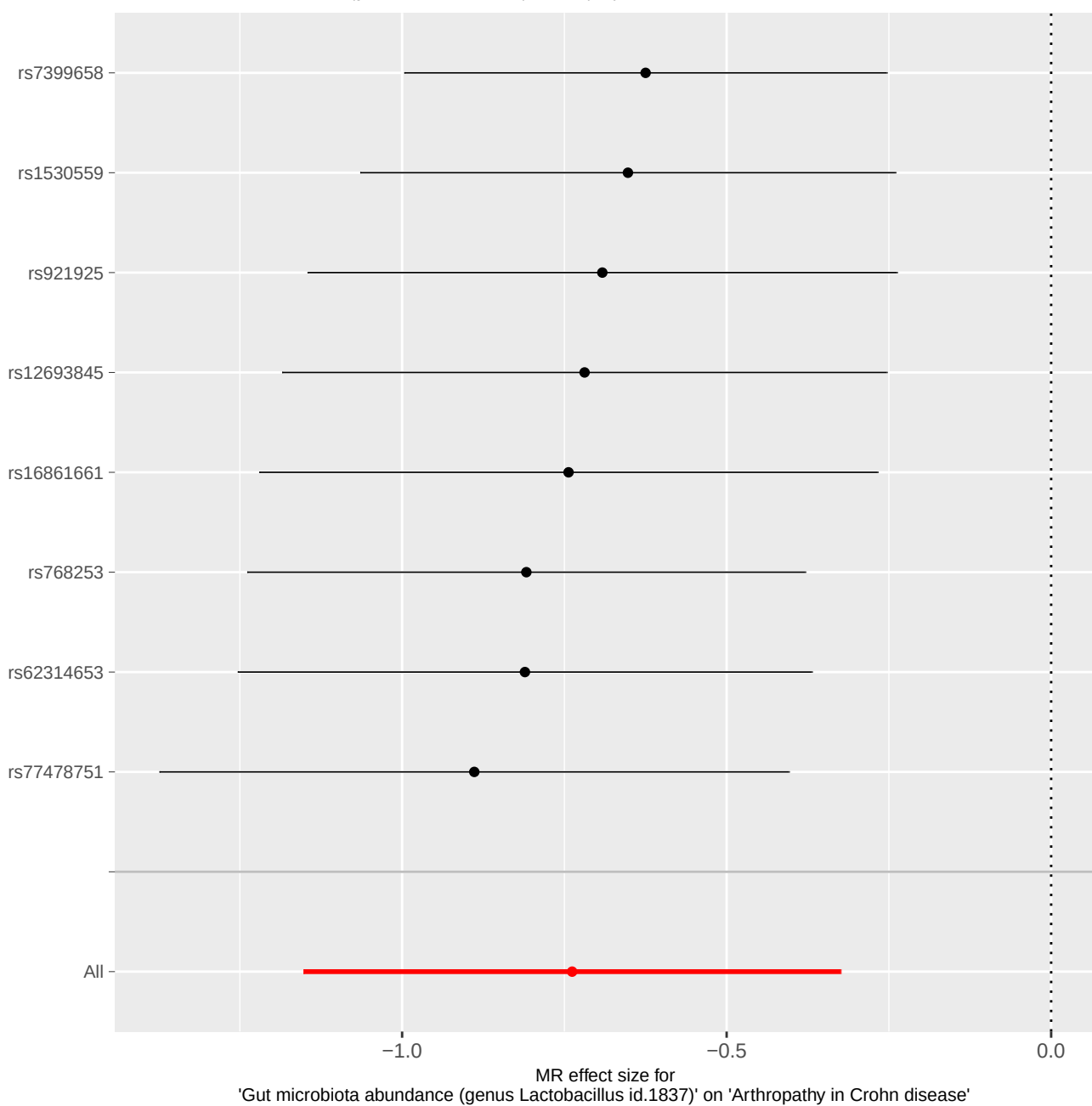


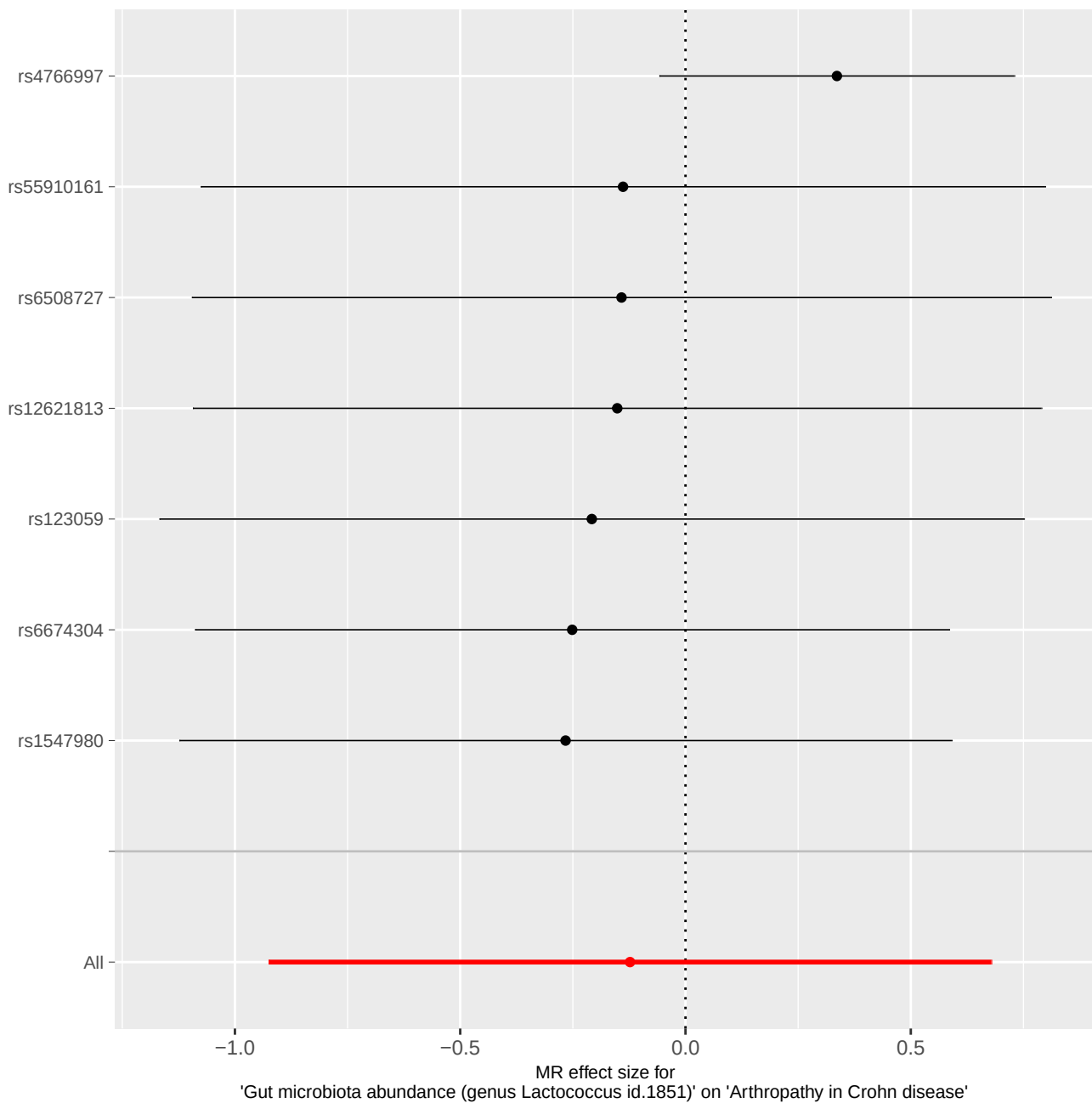


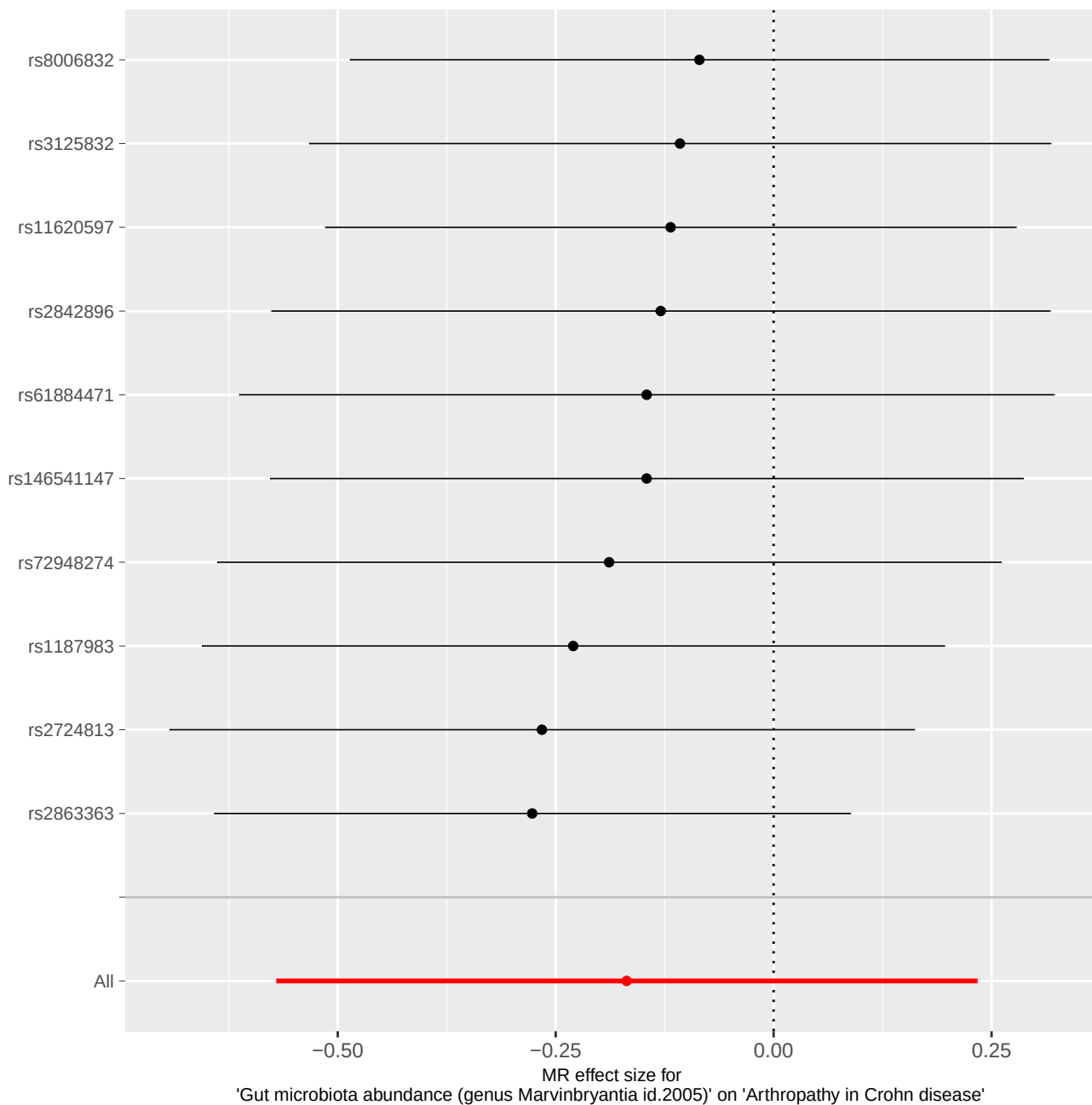


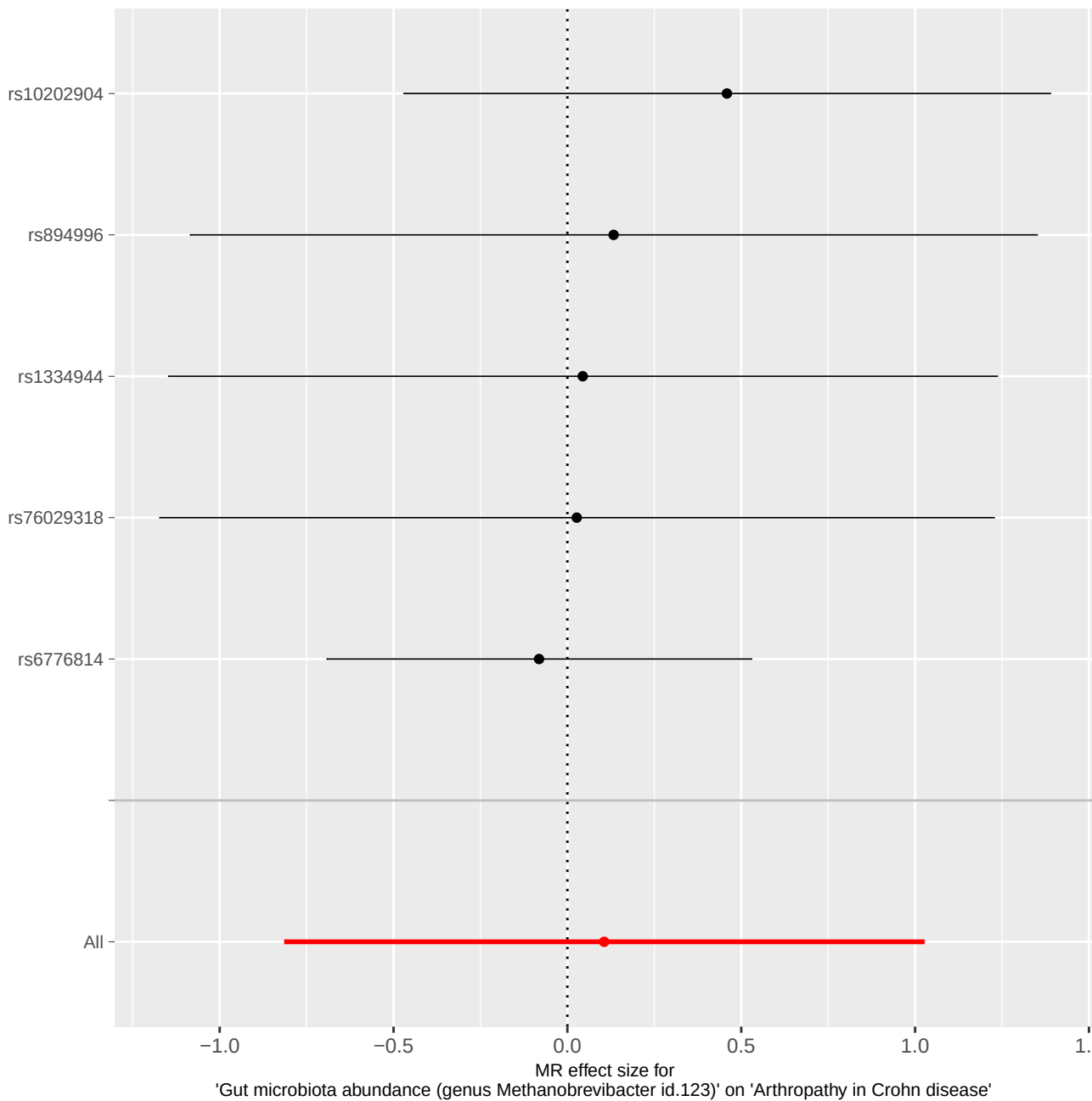


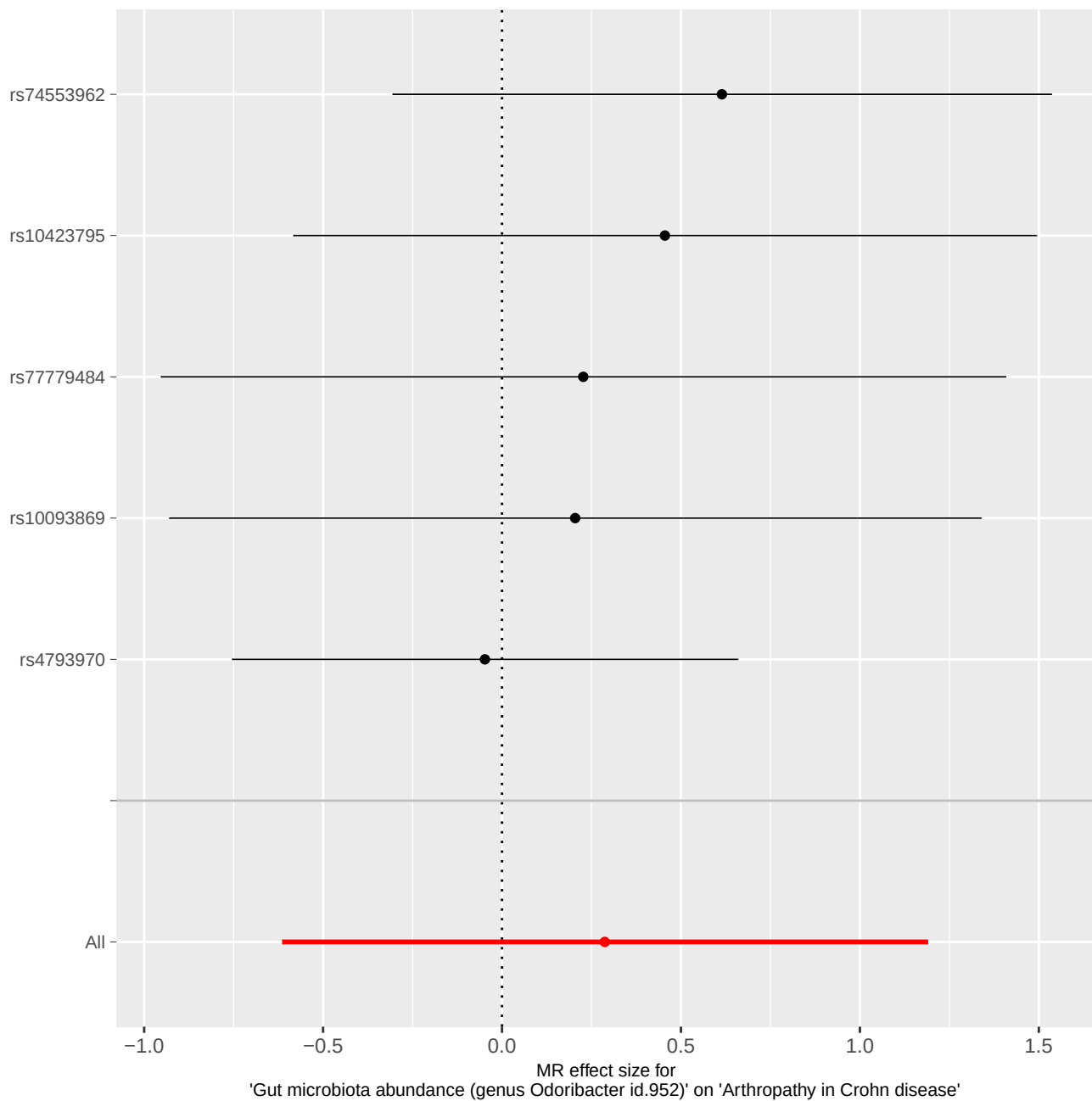




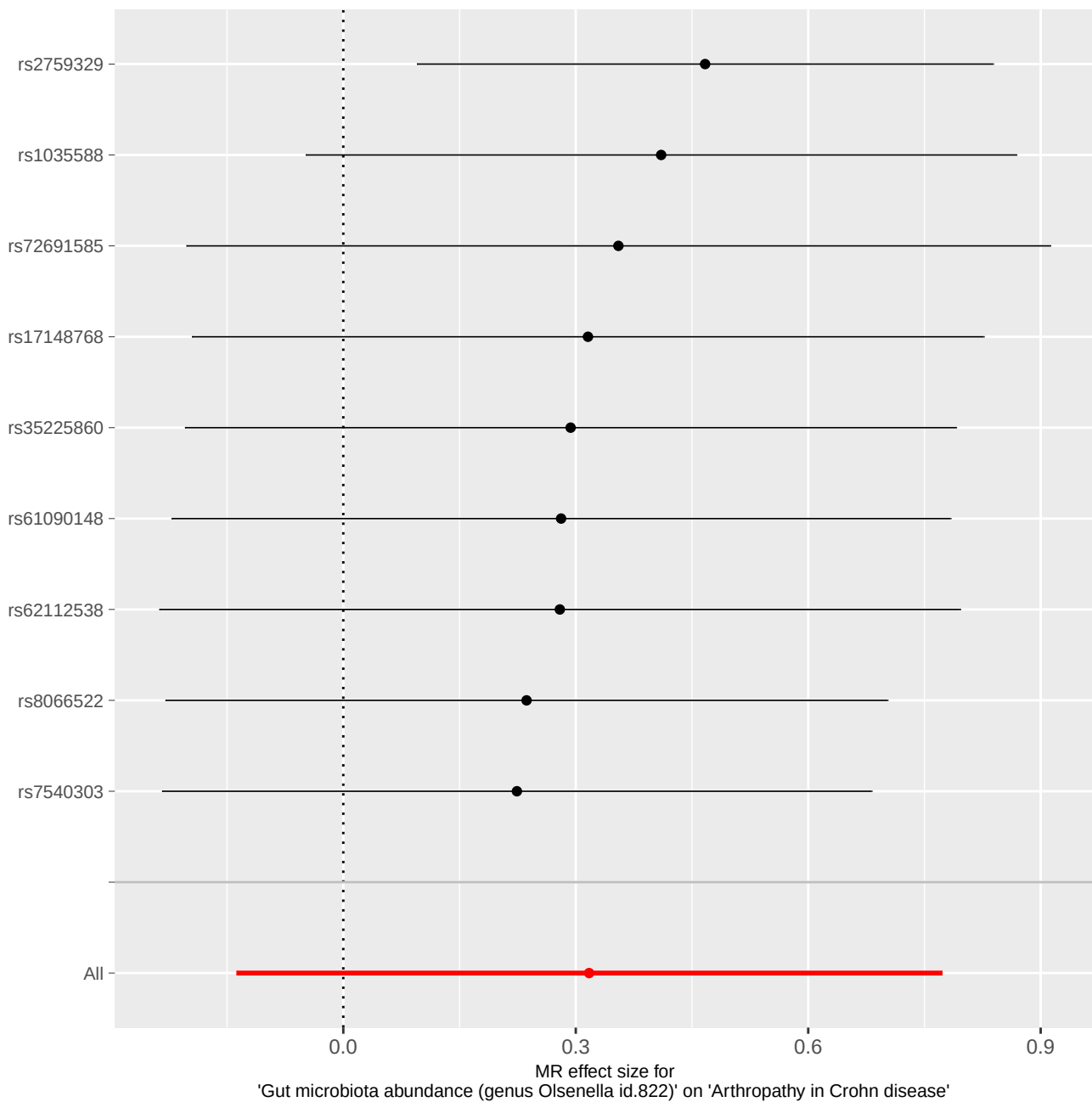


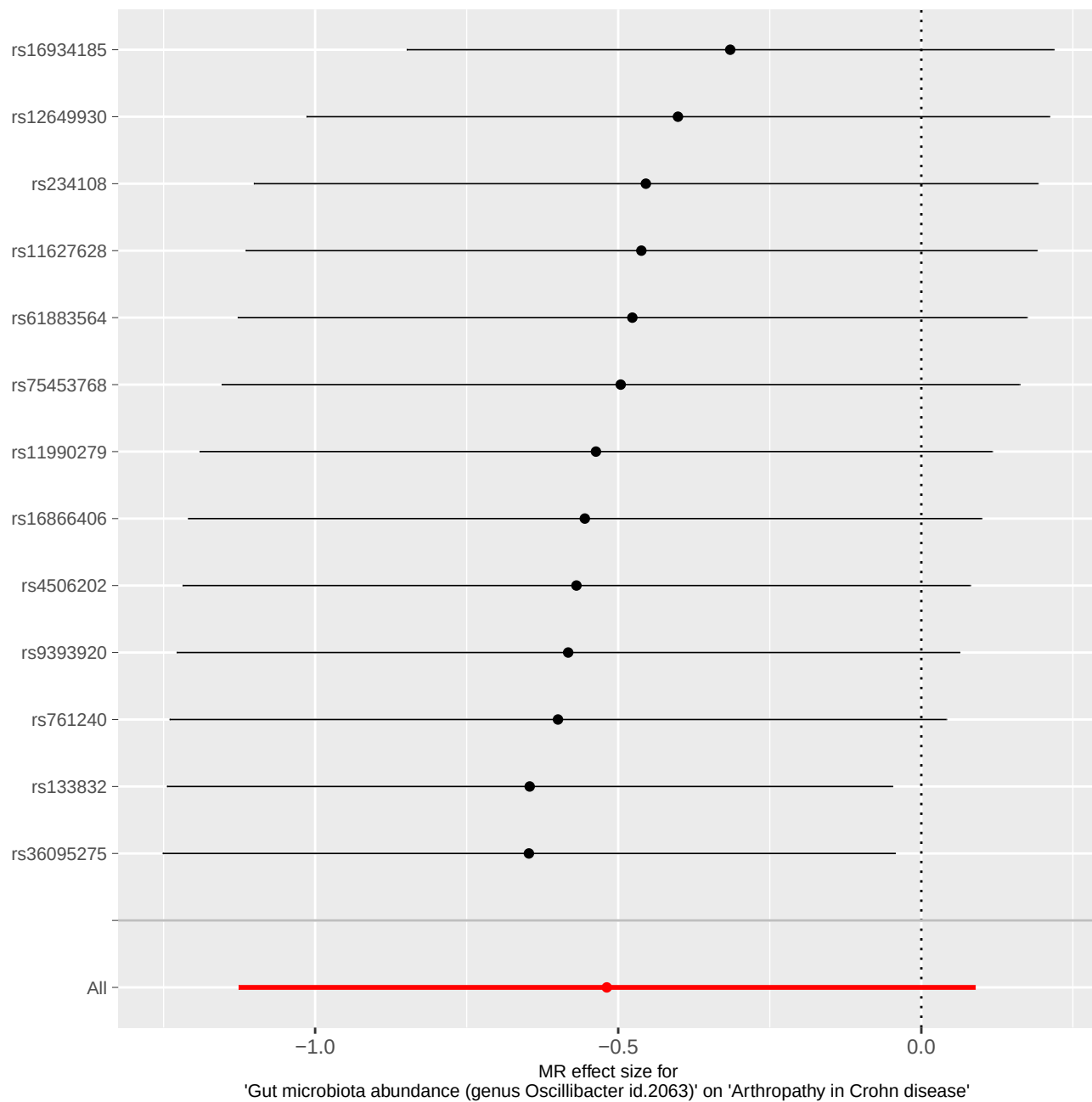




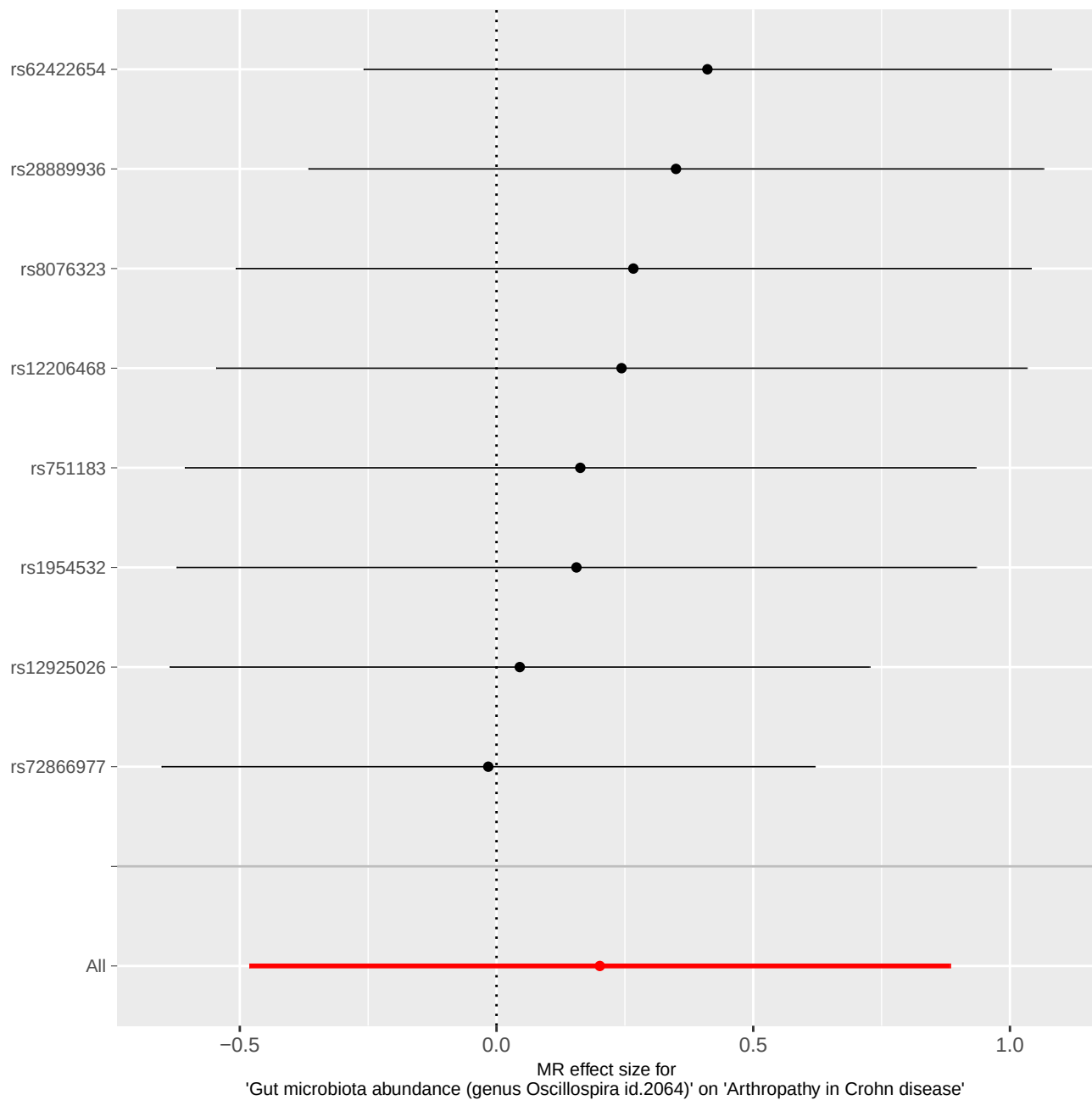


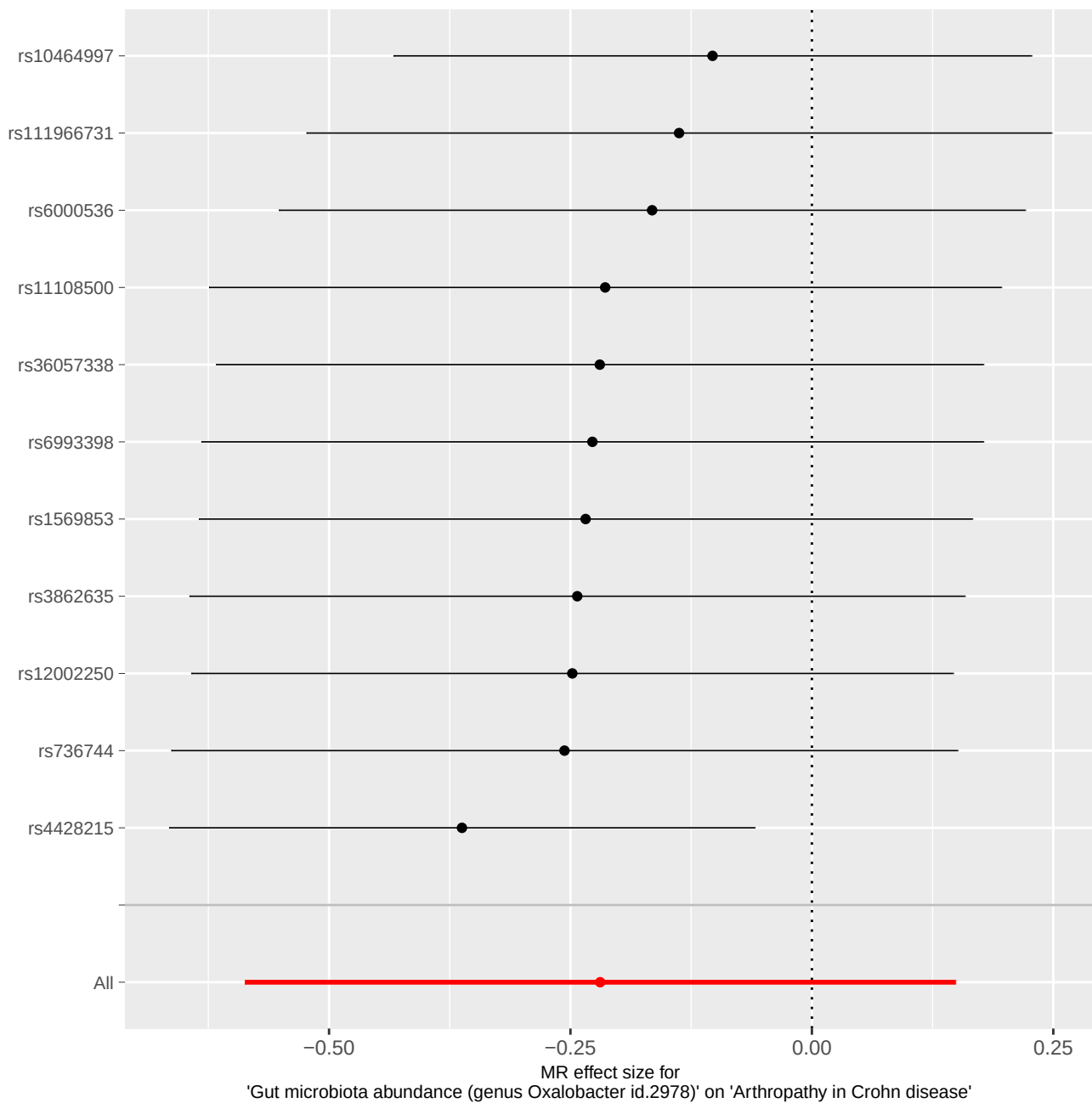
Batch 559 : Gut microbiota abundance (genus Olsenella id.822) on Arthropathy in Crohn disease

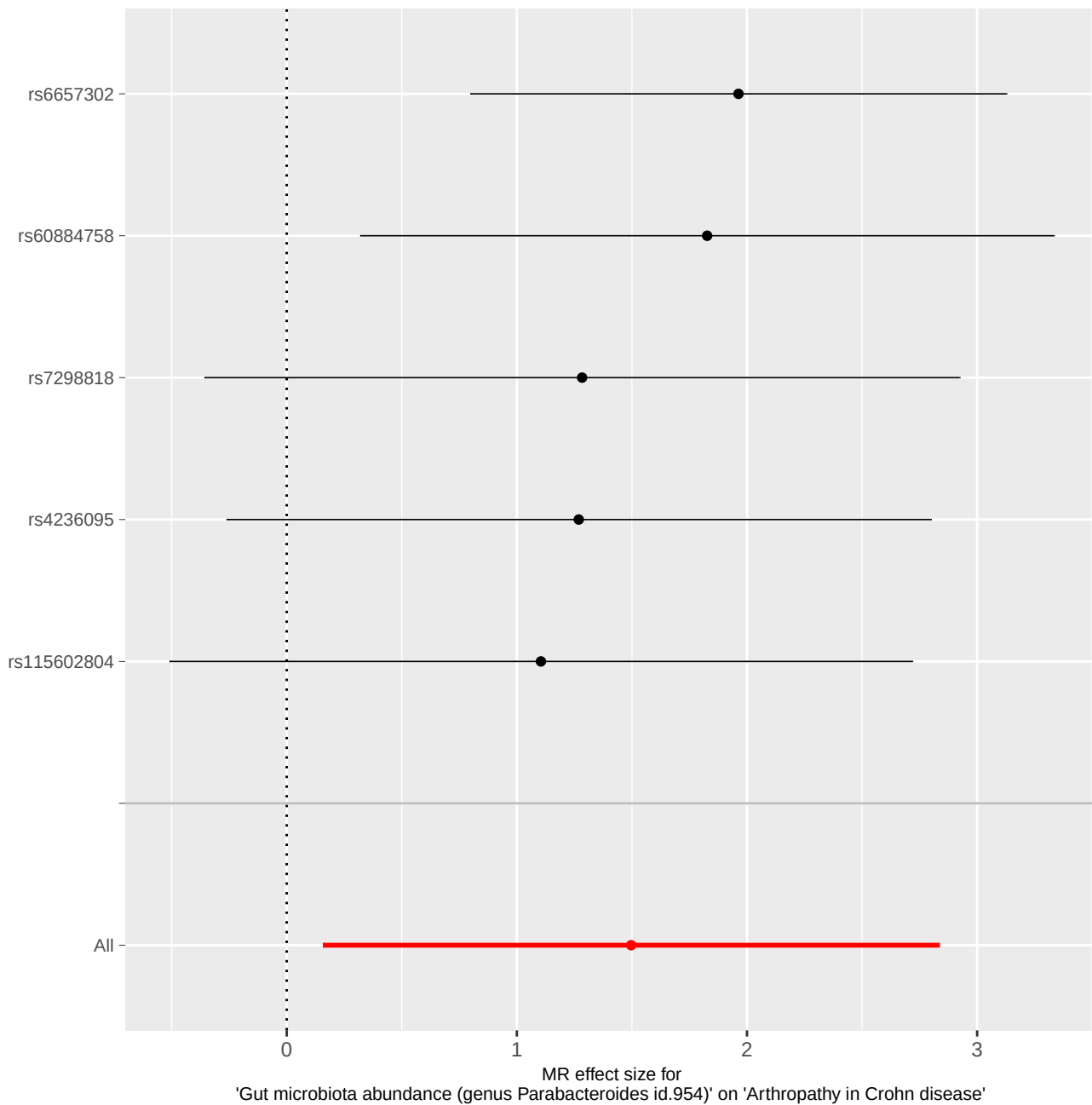


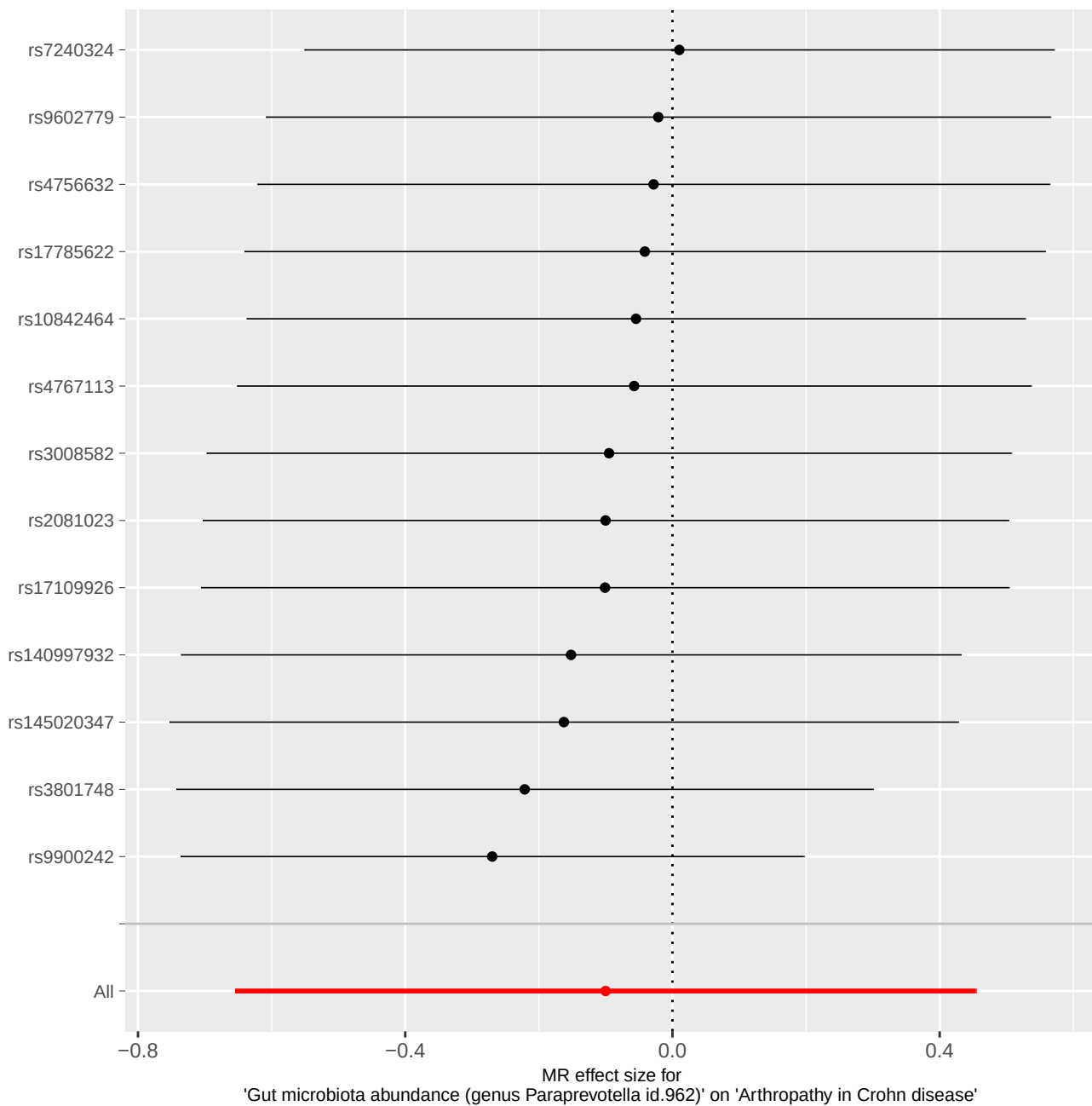


Batch 561 : Gut microbiota abundance (genus Oscillospira id.2064) on Arthropathy in Crohn disease

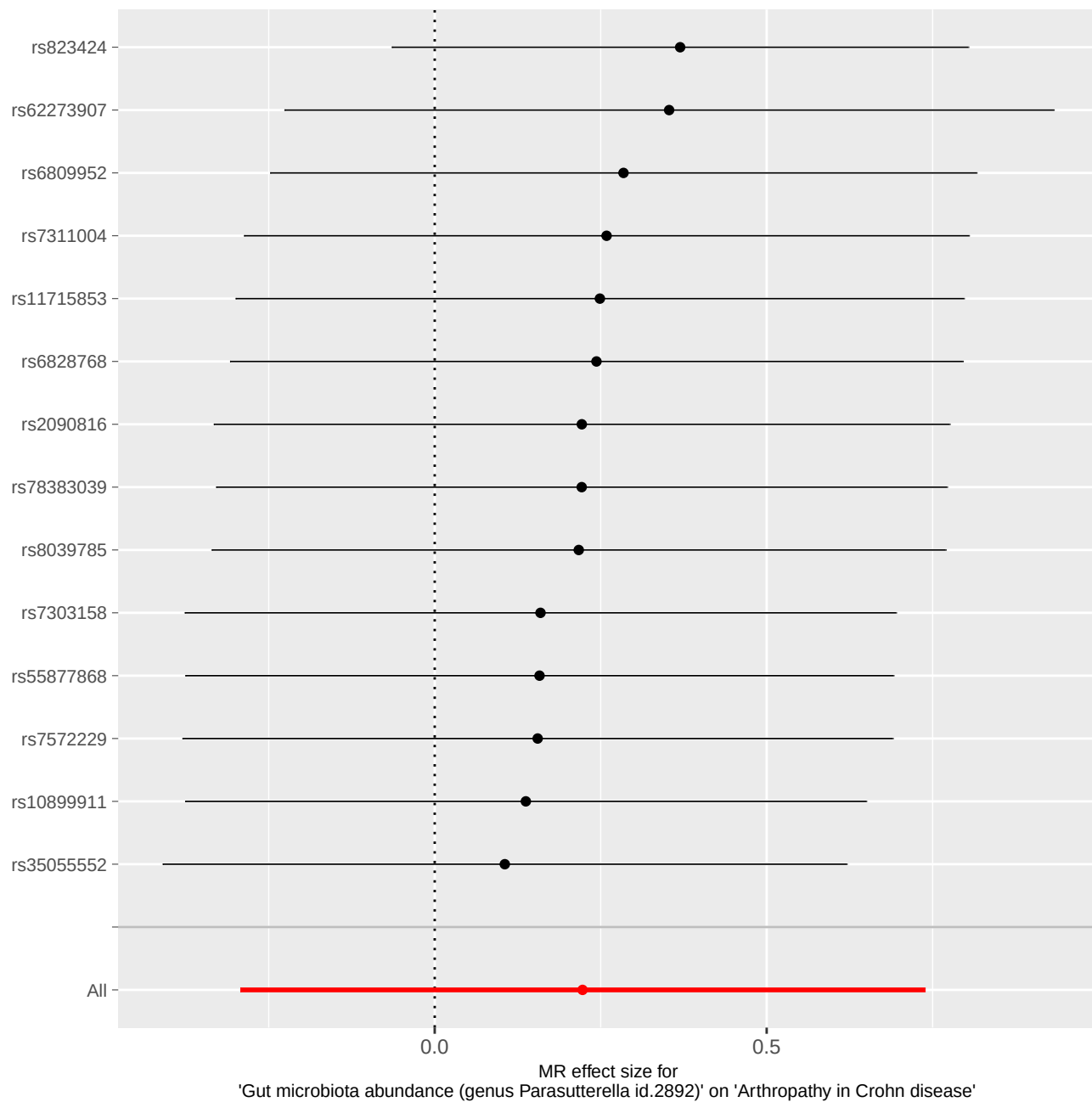


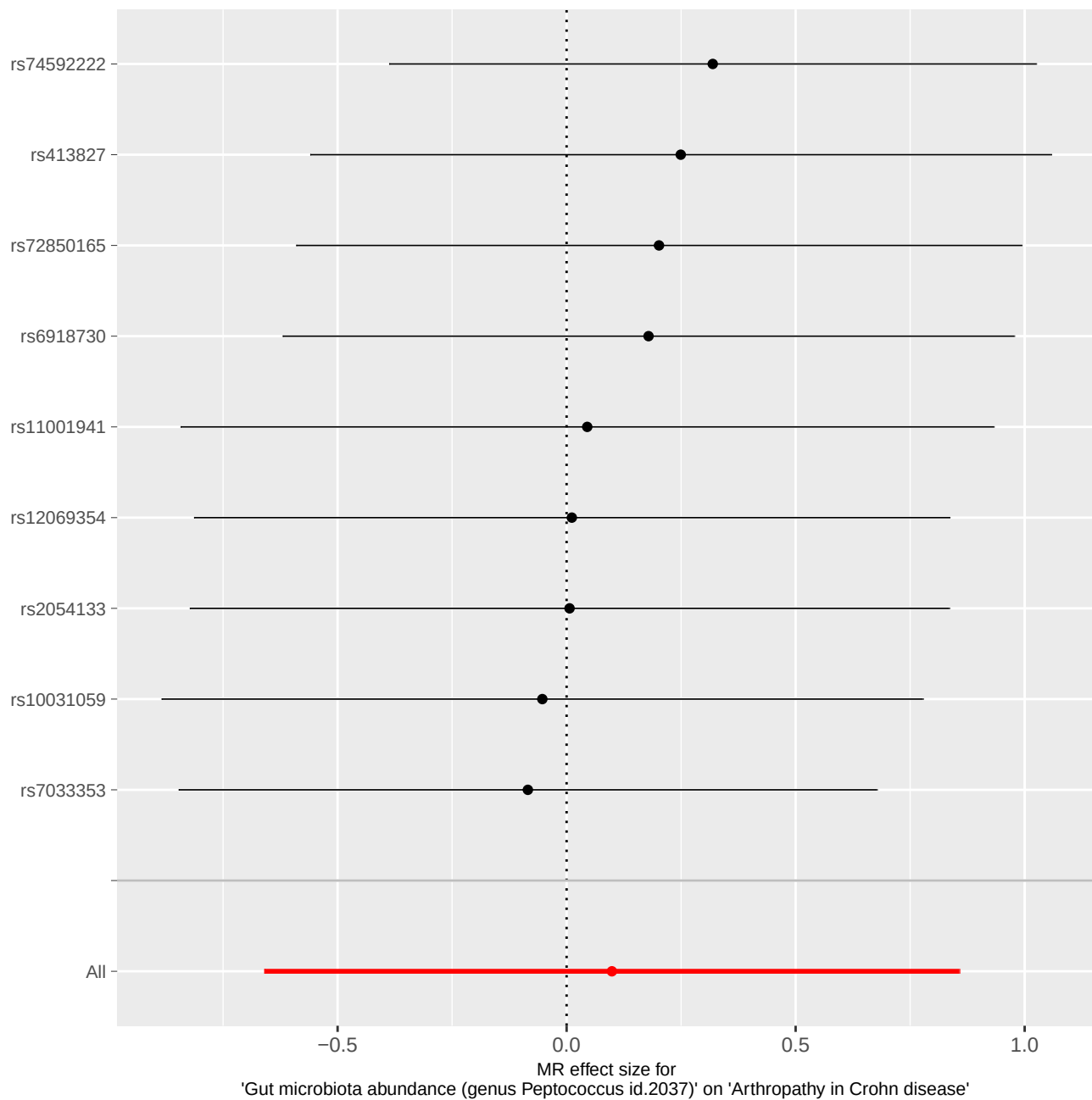




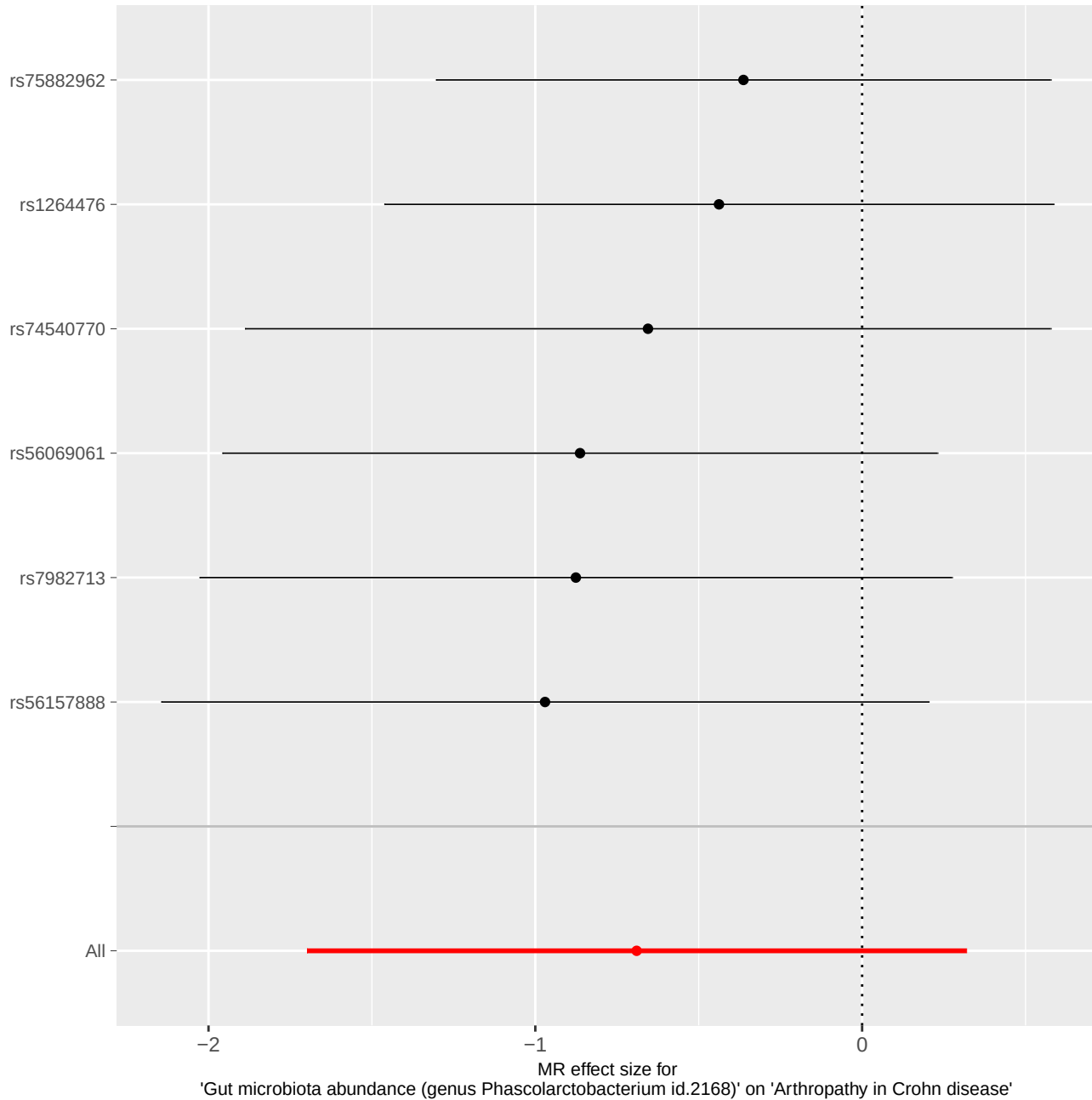


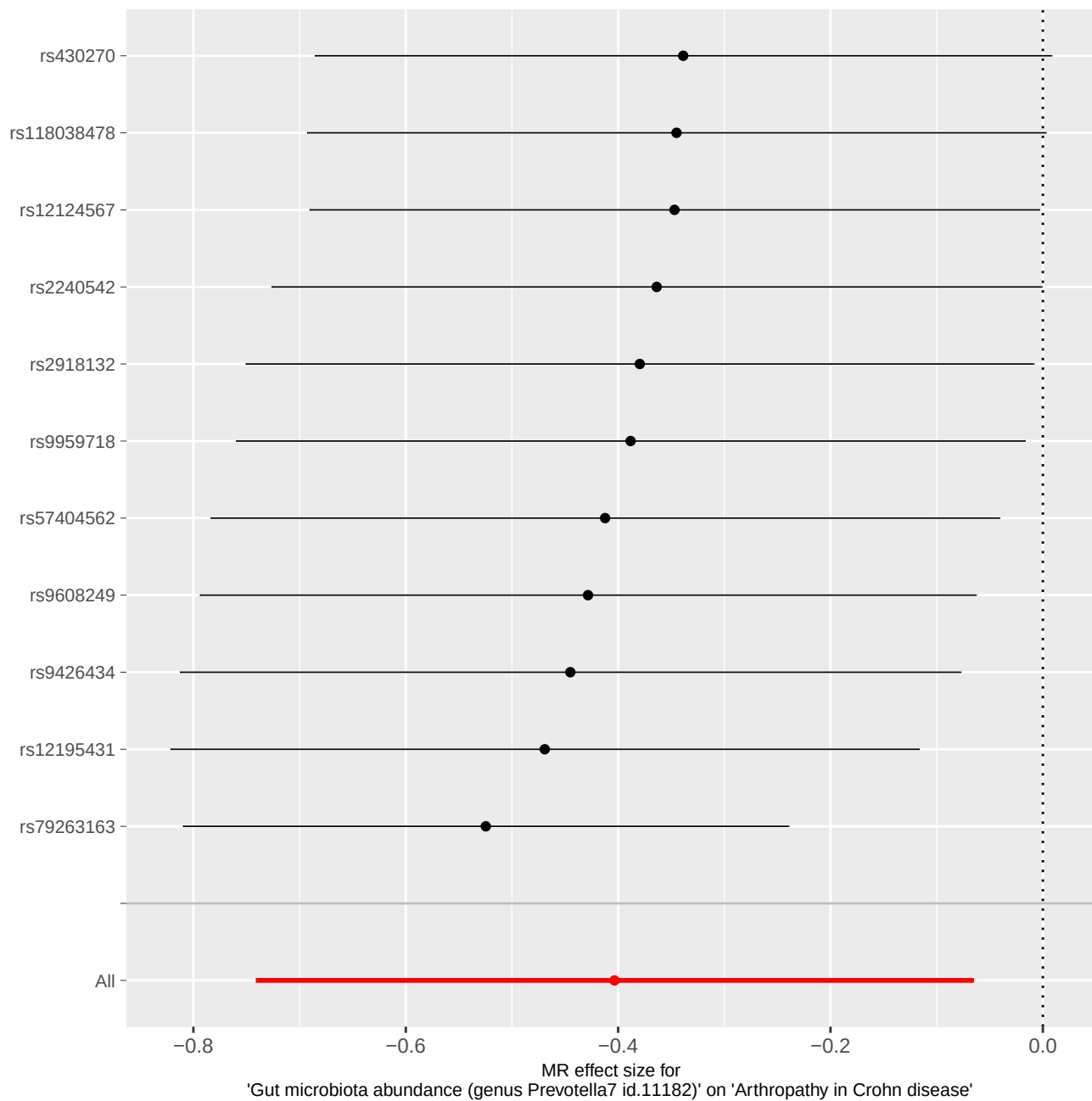
Batch 565 : Gut microbiota abundance (genus Parasutterella id.2892) on Arthropathy in Crohn disease

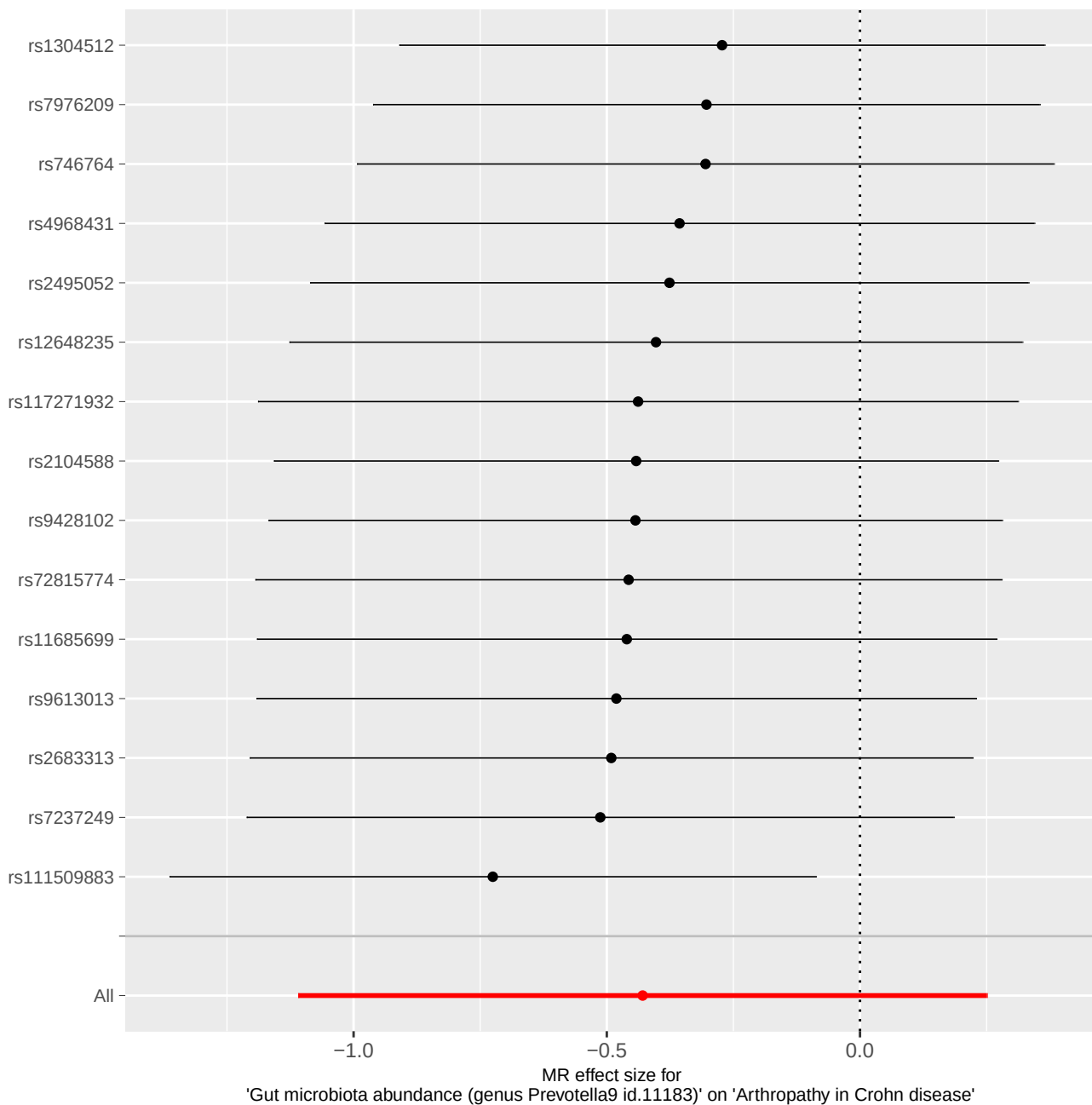


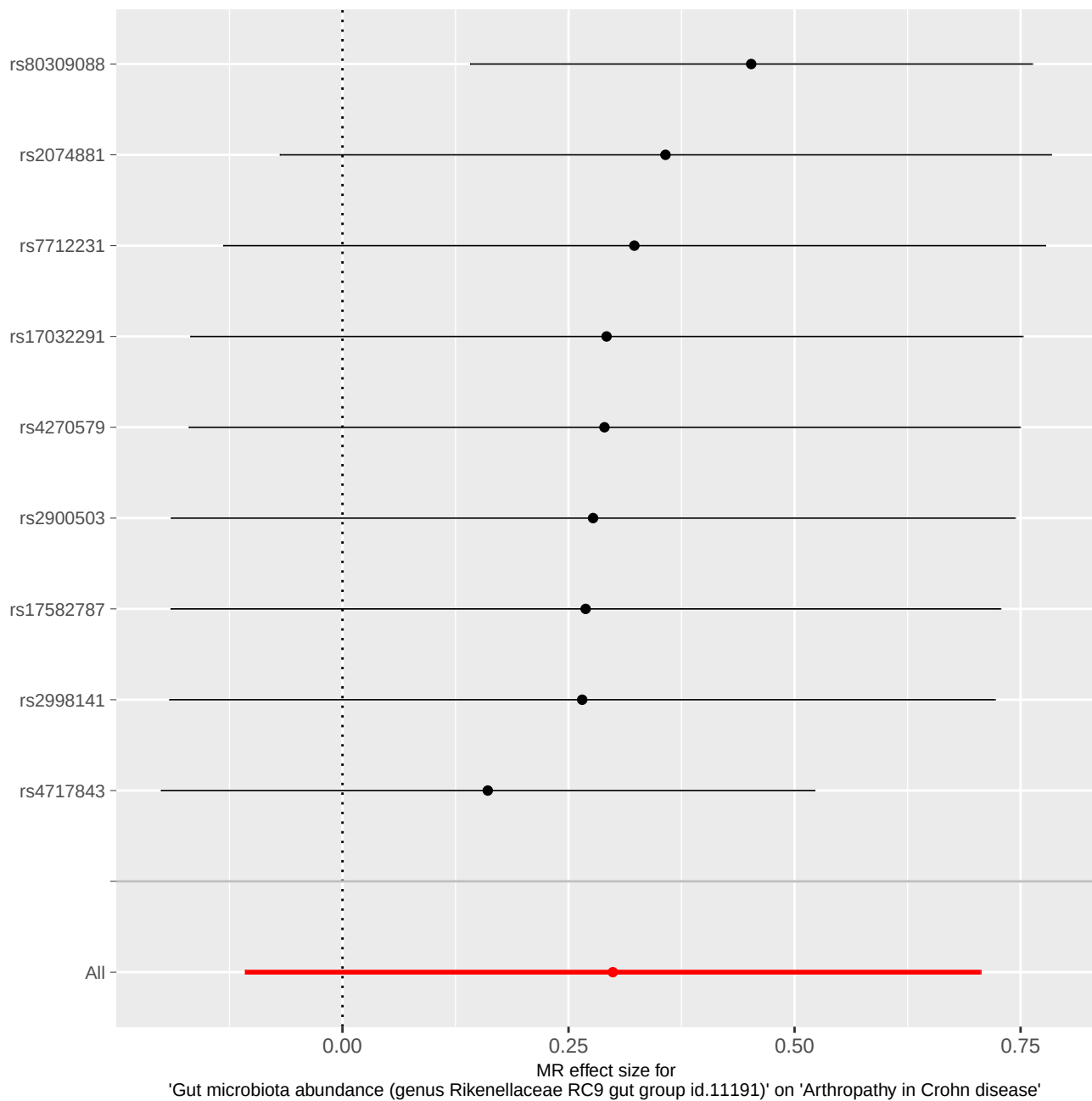


MR effect size for
'Gut microbiota abundance (genus Peptococcus id.2037)' on 'Arthropathy in Crohn disease'

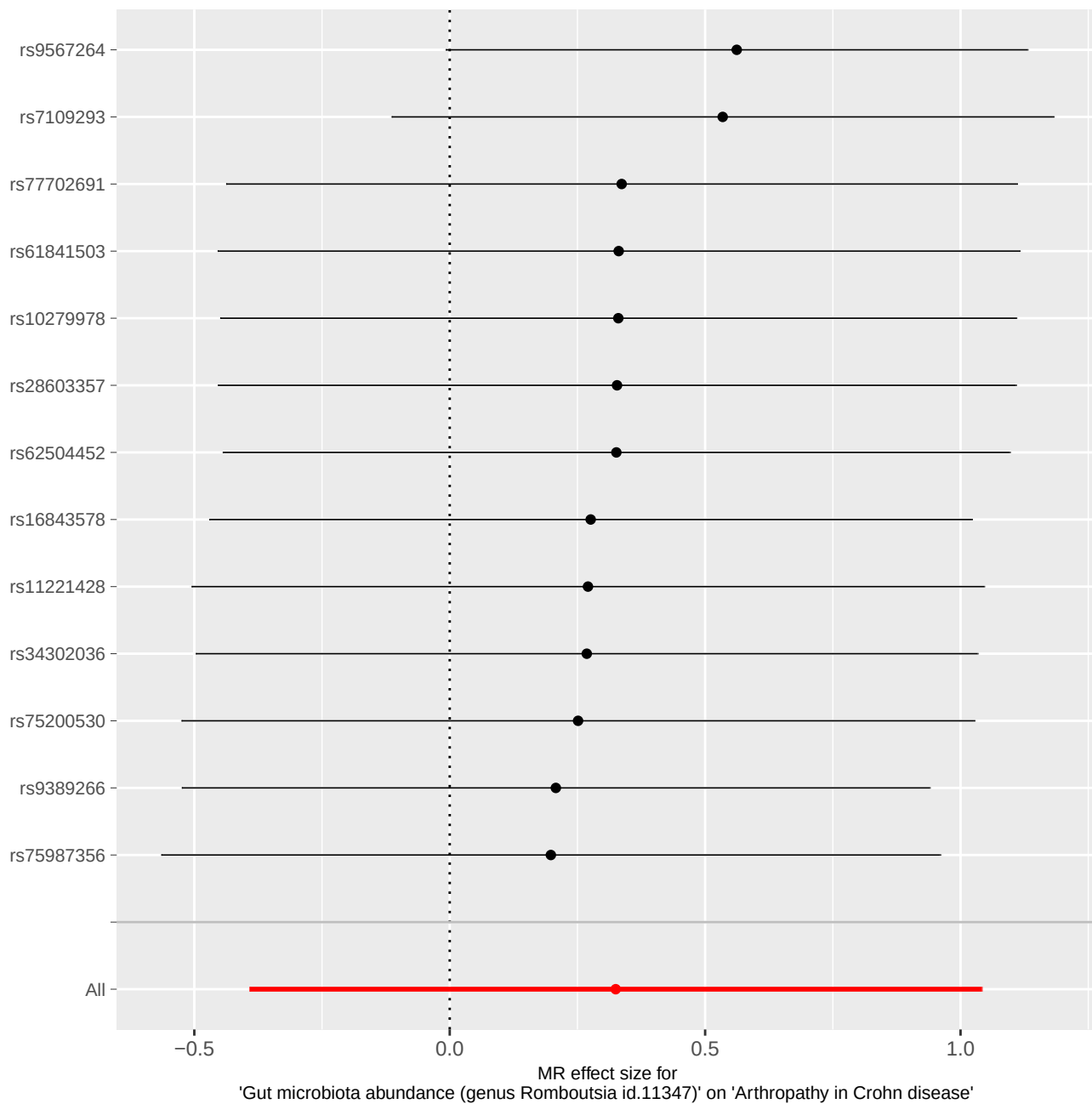


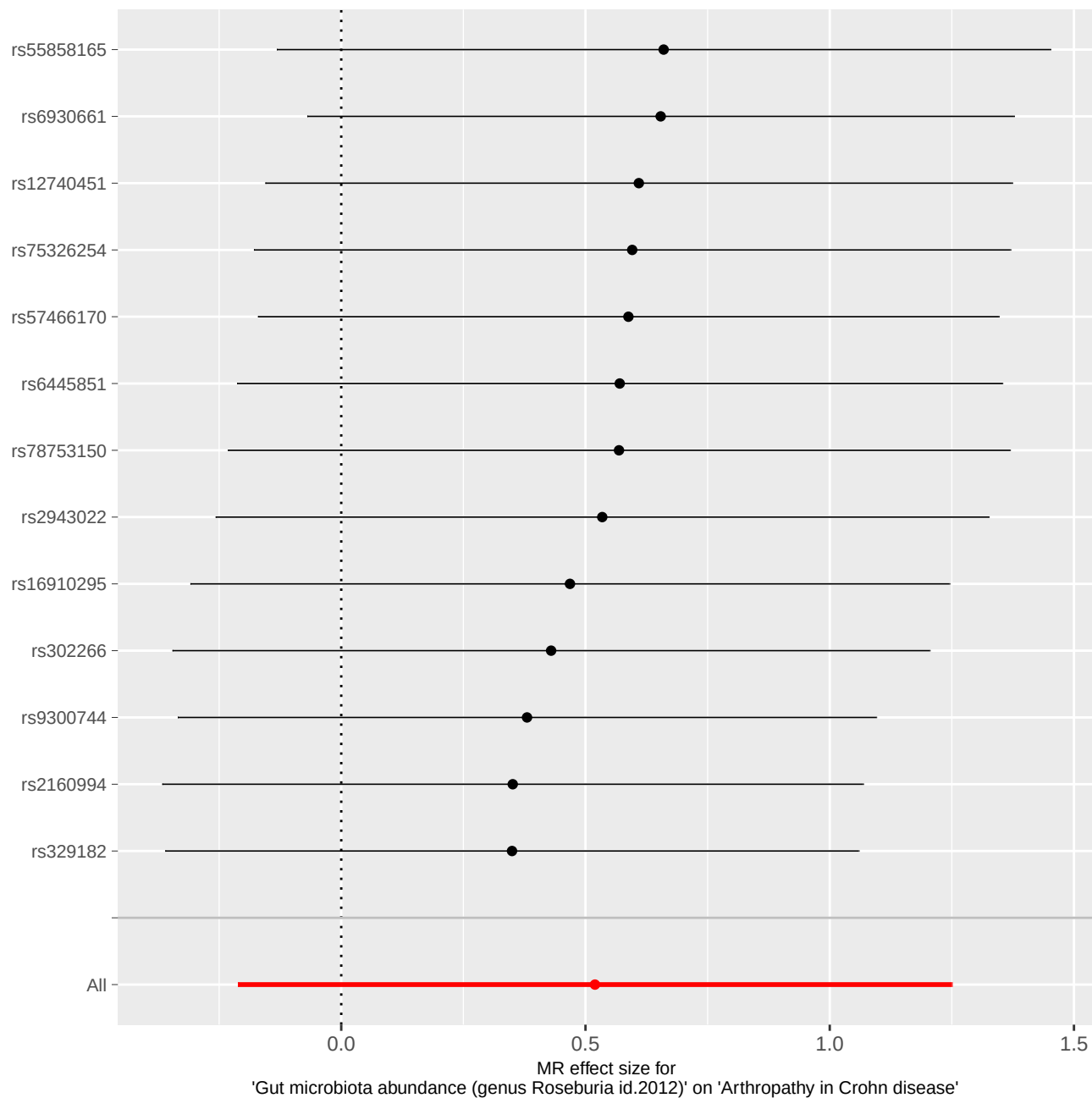


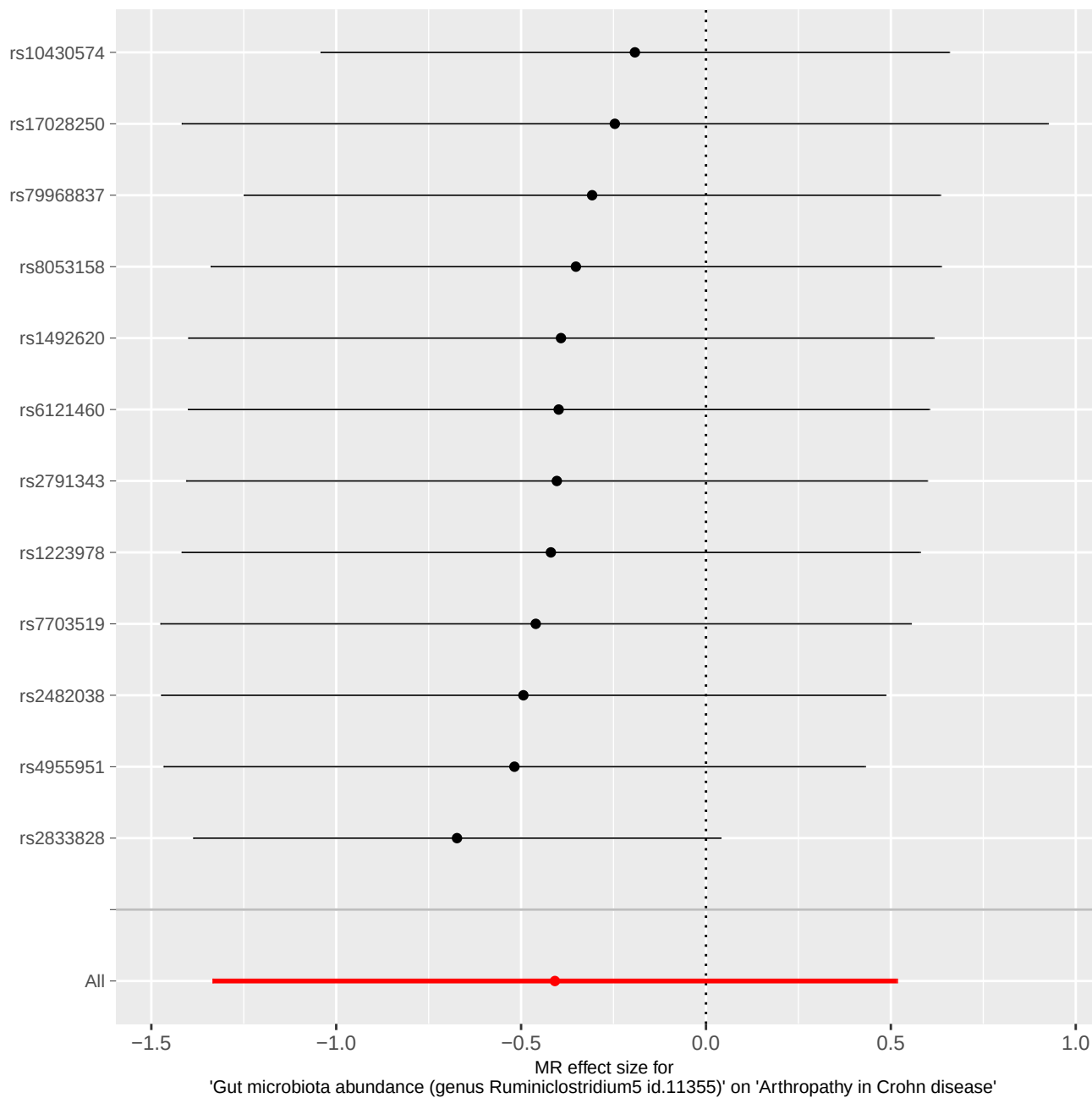


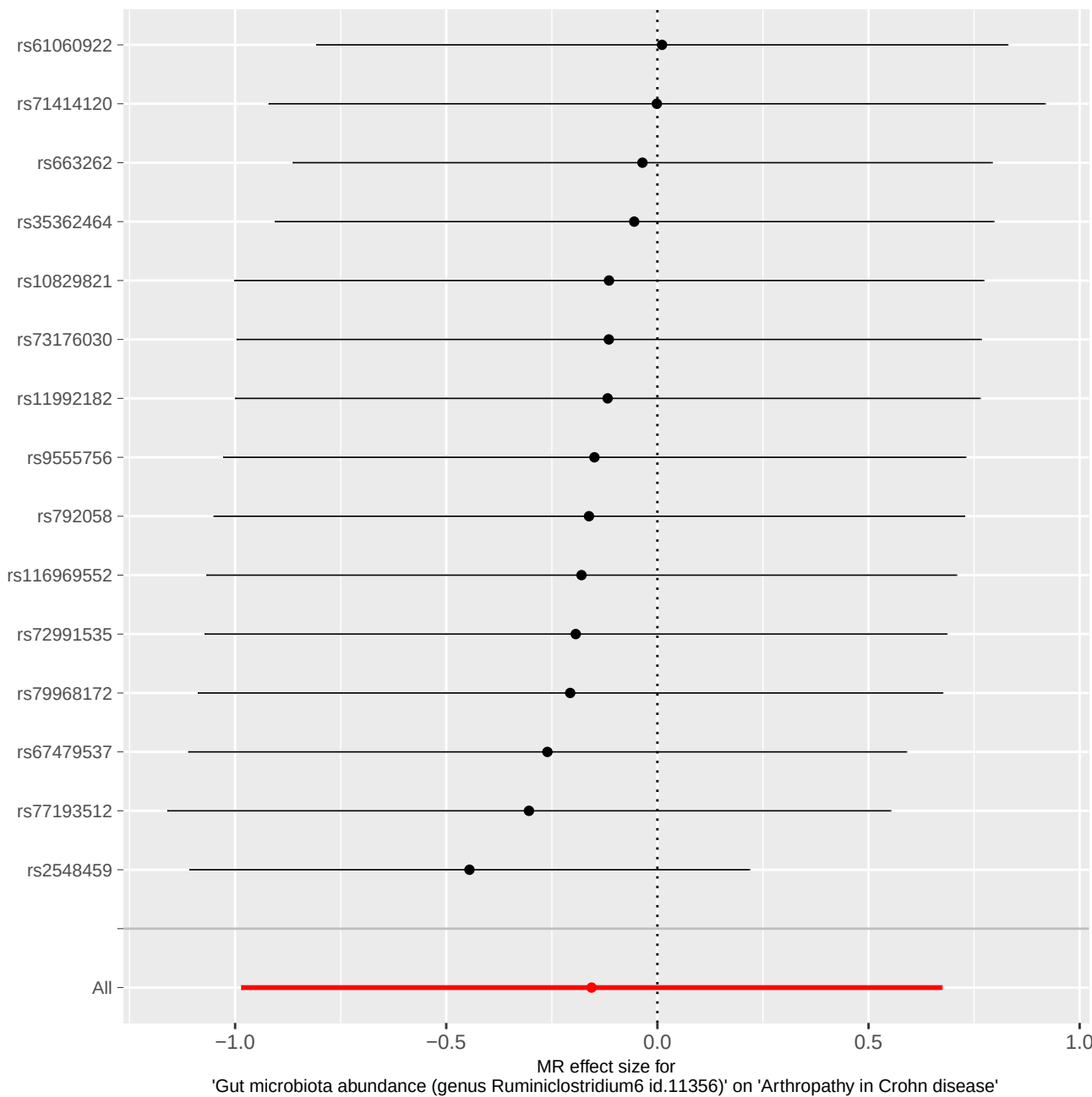


Batch 571 : Gut microbiota abundance (genus Romboutsia id.11347) on Arthropathy in Crohn disease

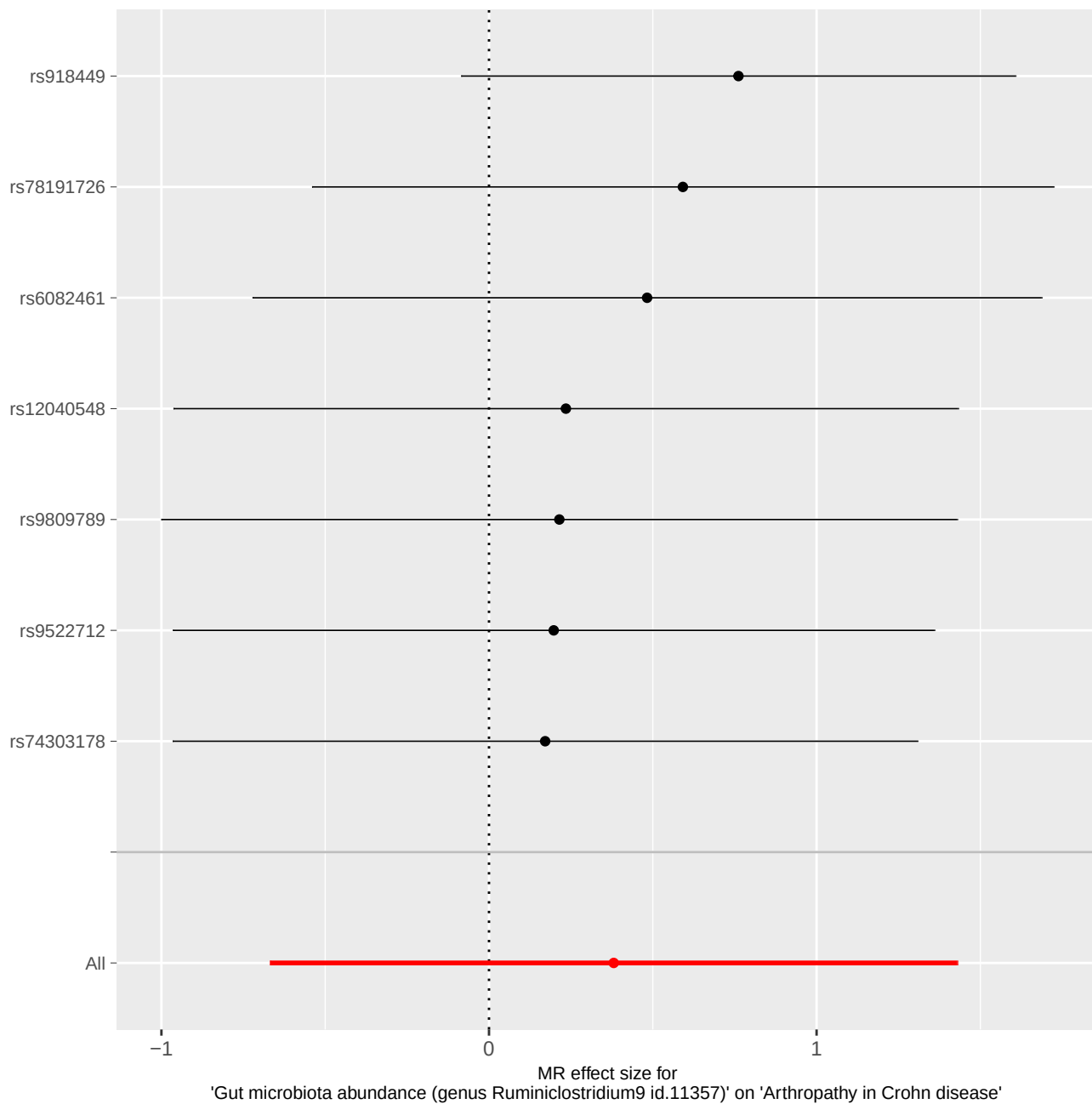


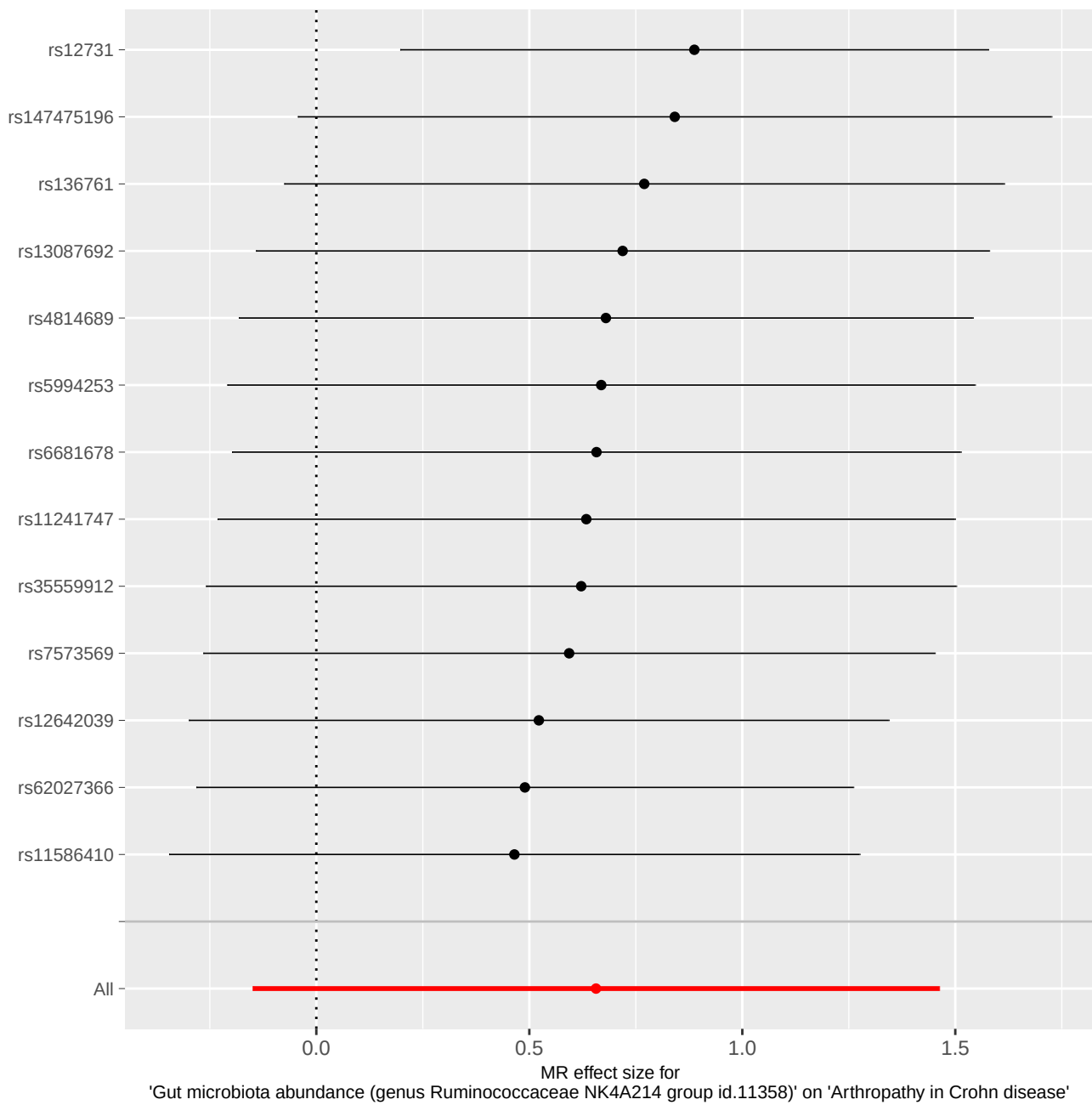


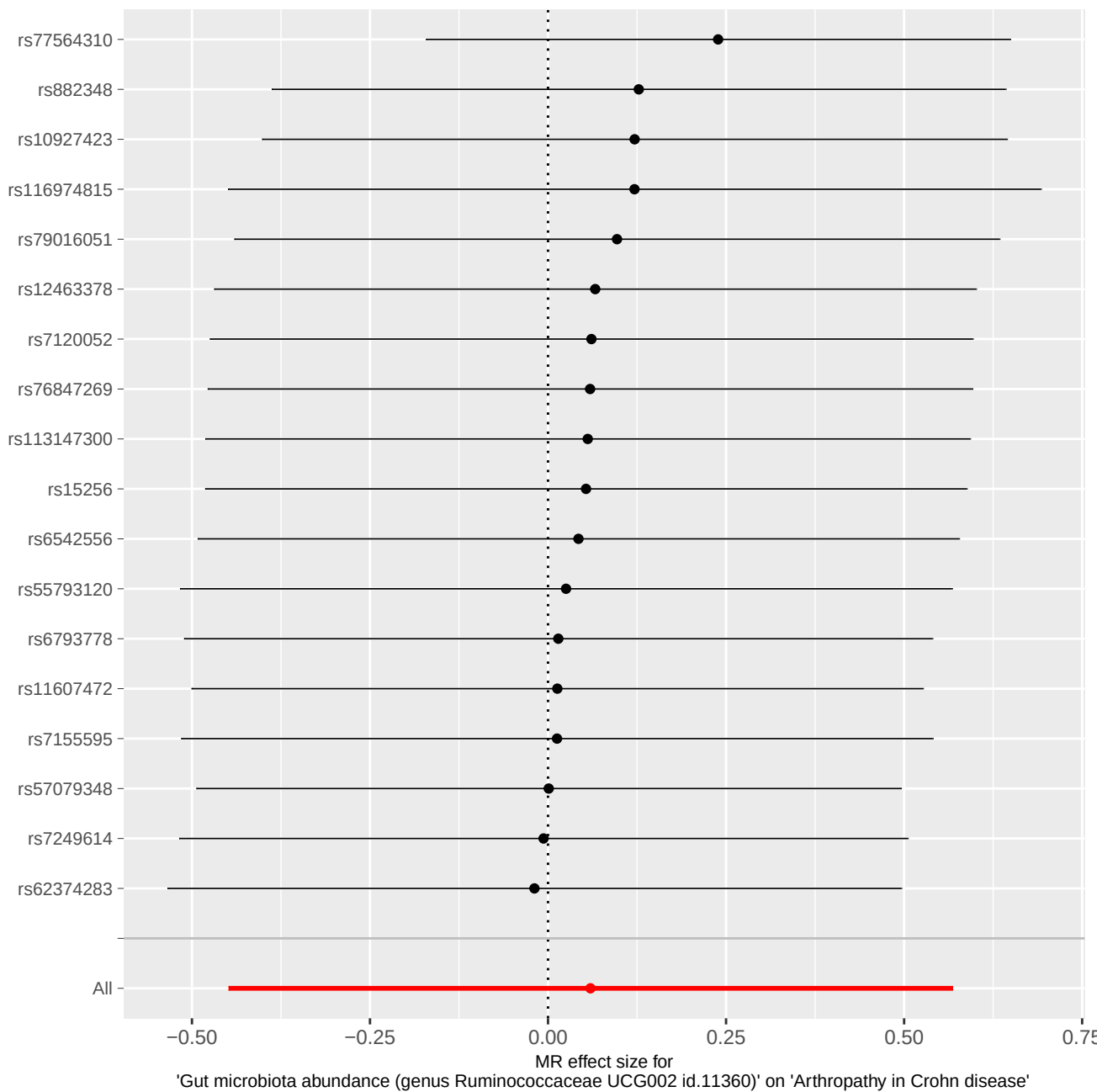




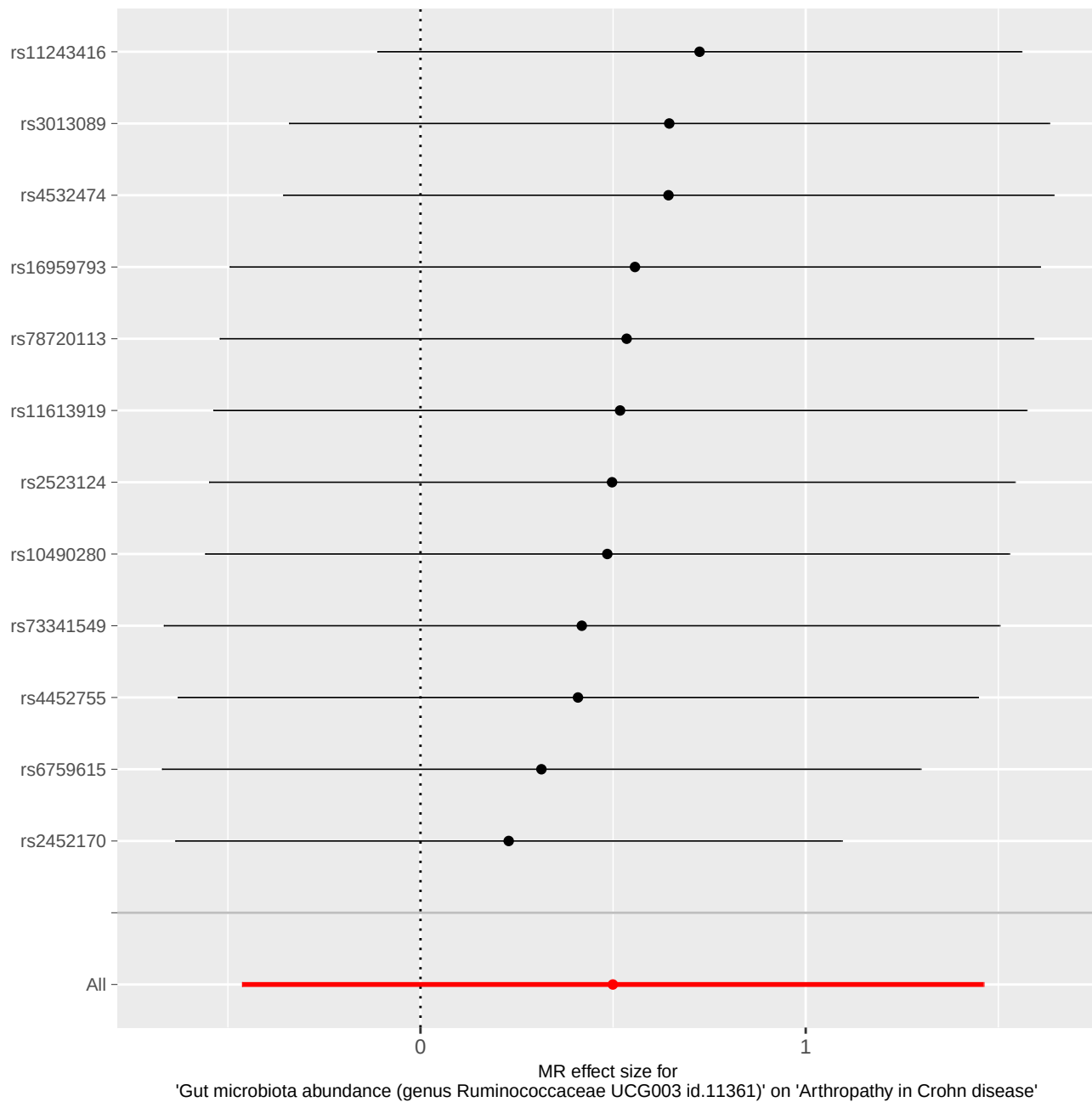
Batch 575 : Gut microbiota abundance (genus Ruminiclostridium9 id.11357) on Arthropathy in Crohn disease

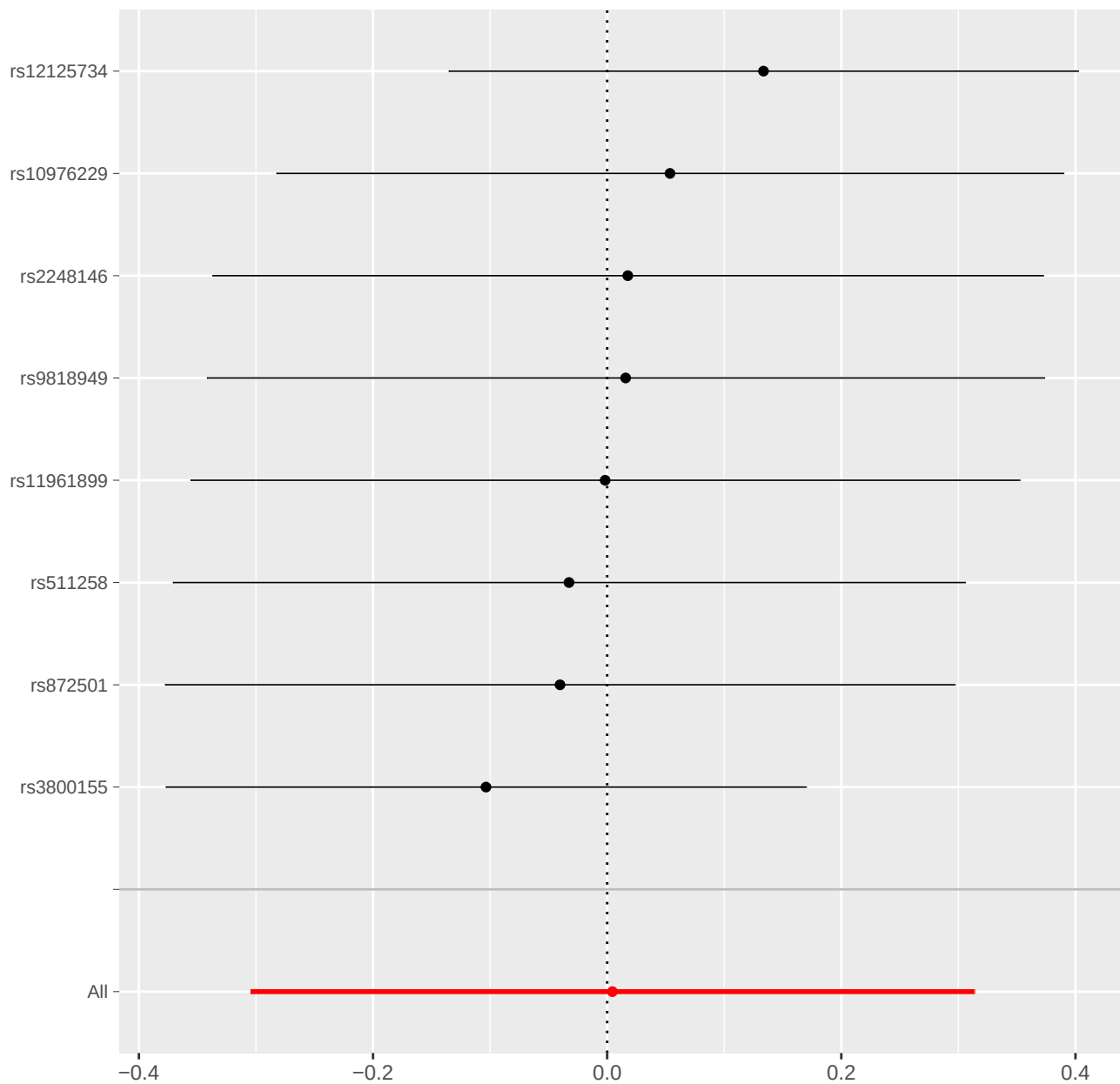




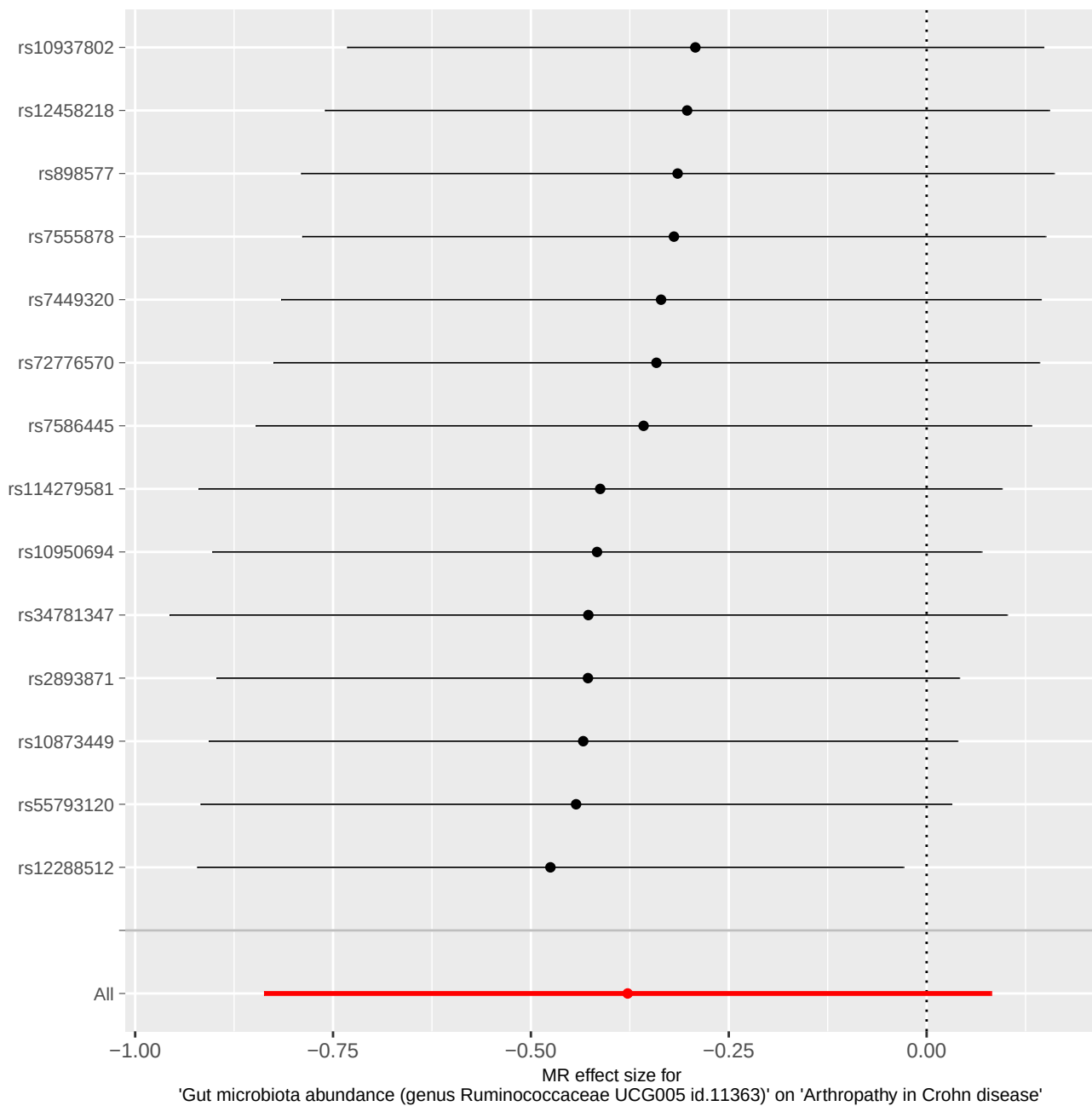


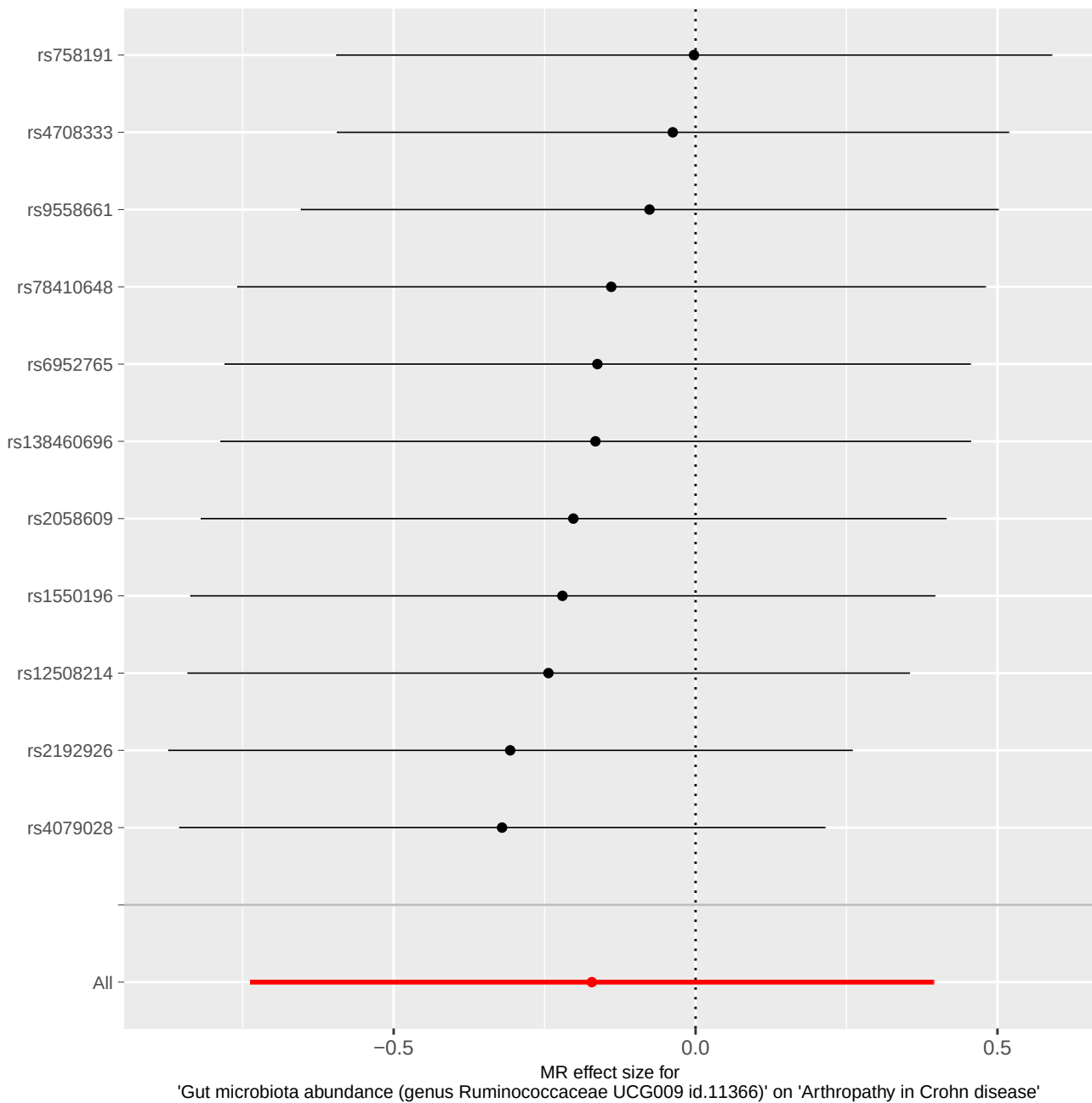
MR effect size for
'Gut microbiota abundance (genus Ruminococcaceae UCG002 id.11360)' on 'Arthropathy in Crohn disease'

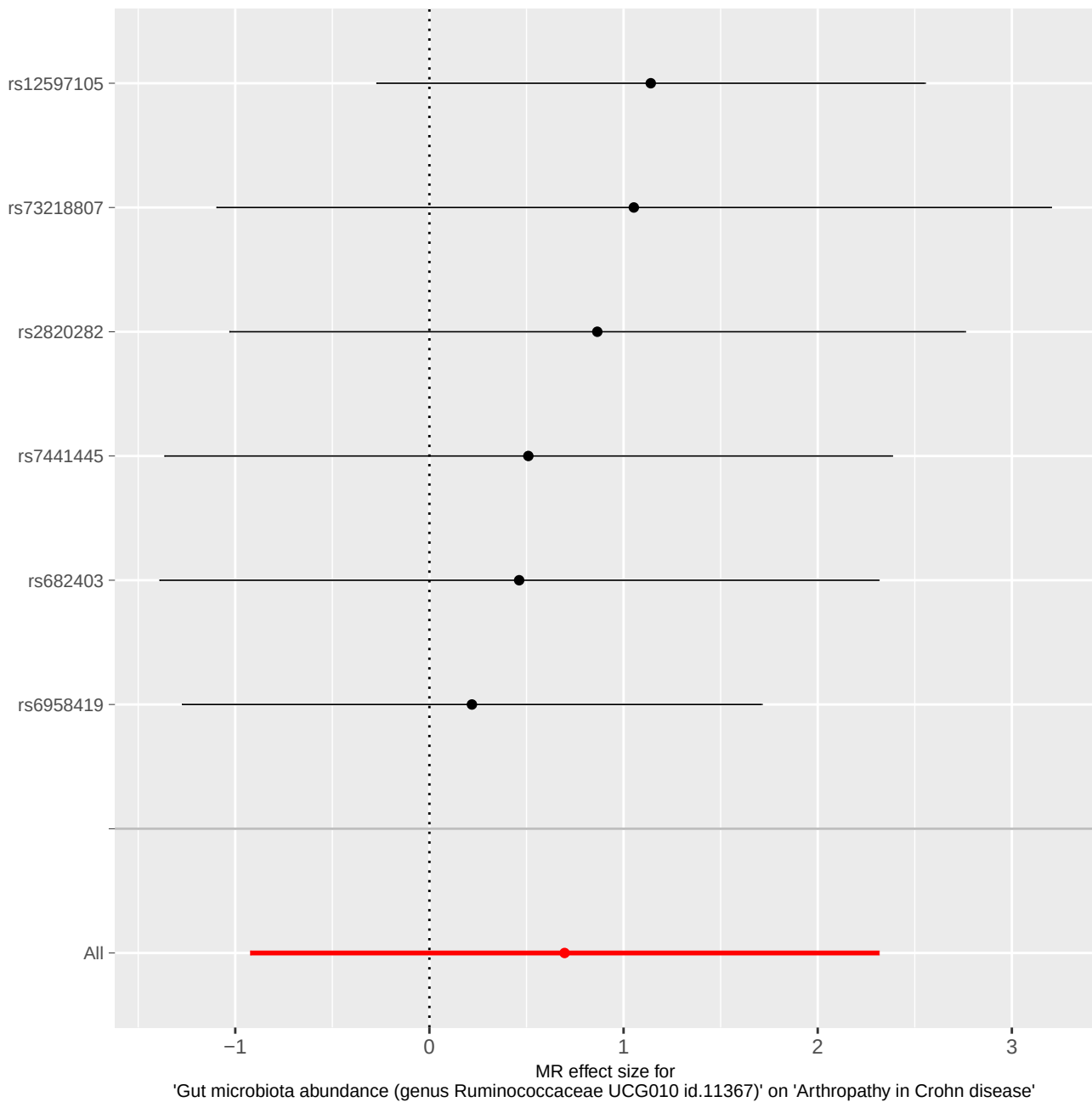


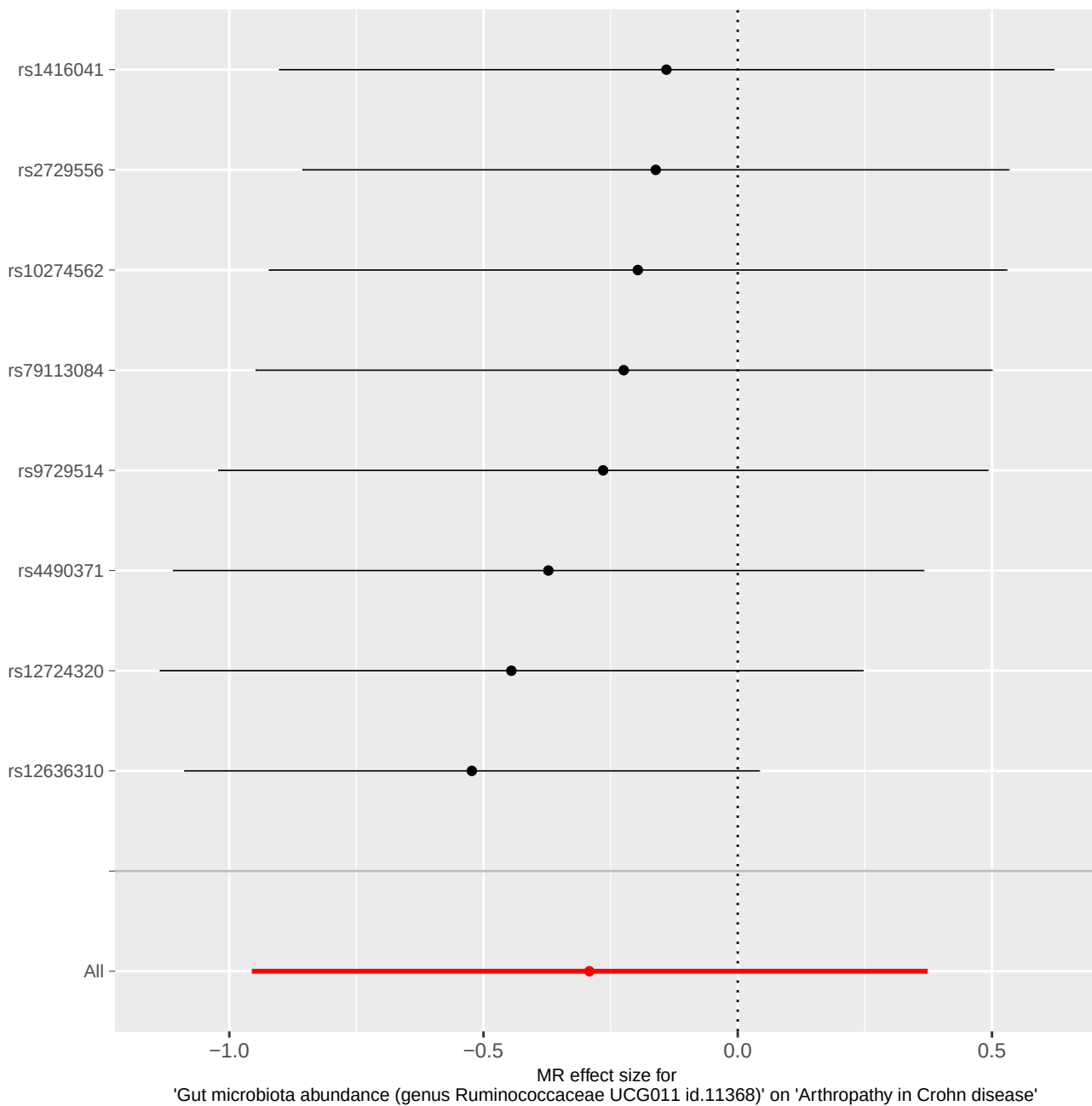


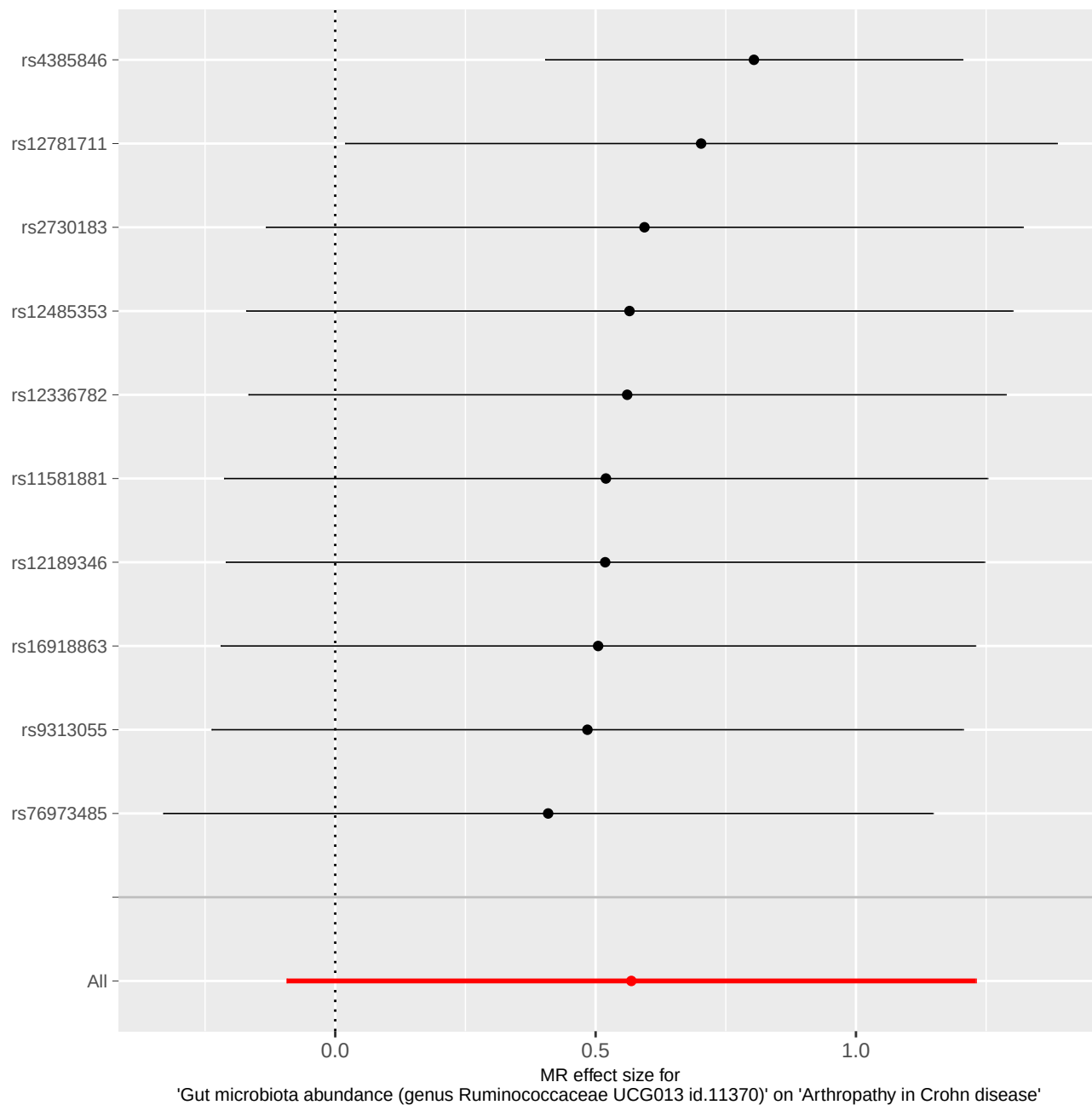
MR effect size for
'Gut microbiota abundance (genus Ruminococcaceae UCG004 id.11362)' on 'Arthropathy in Crohn disease'

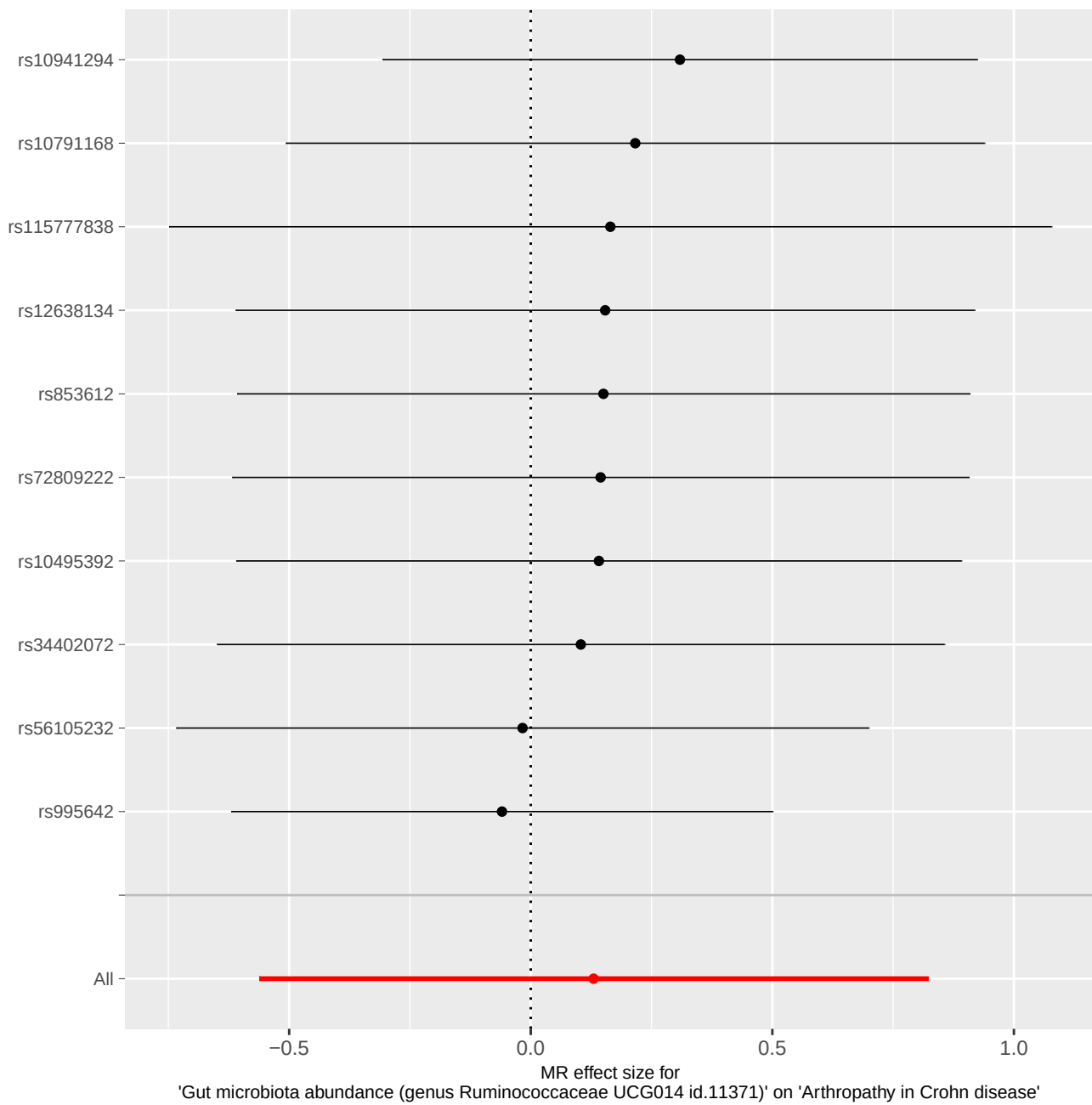


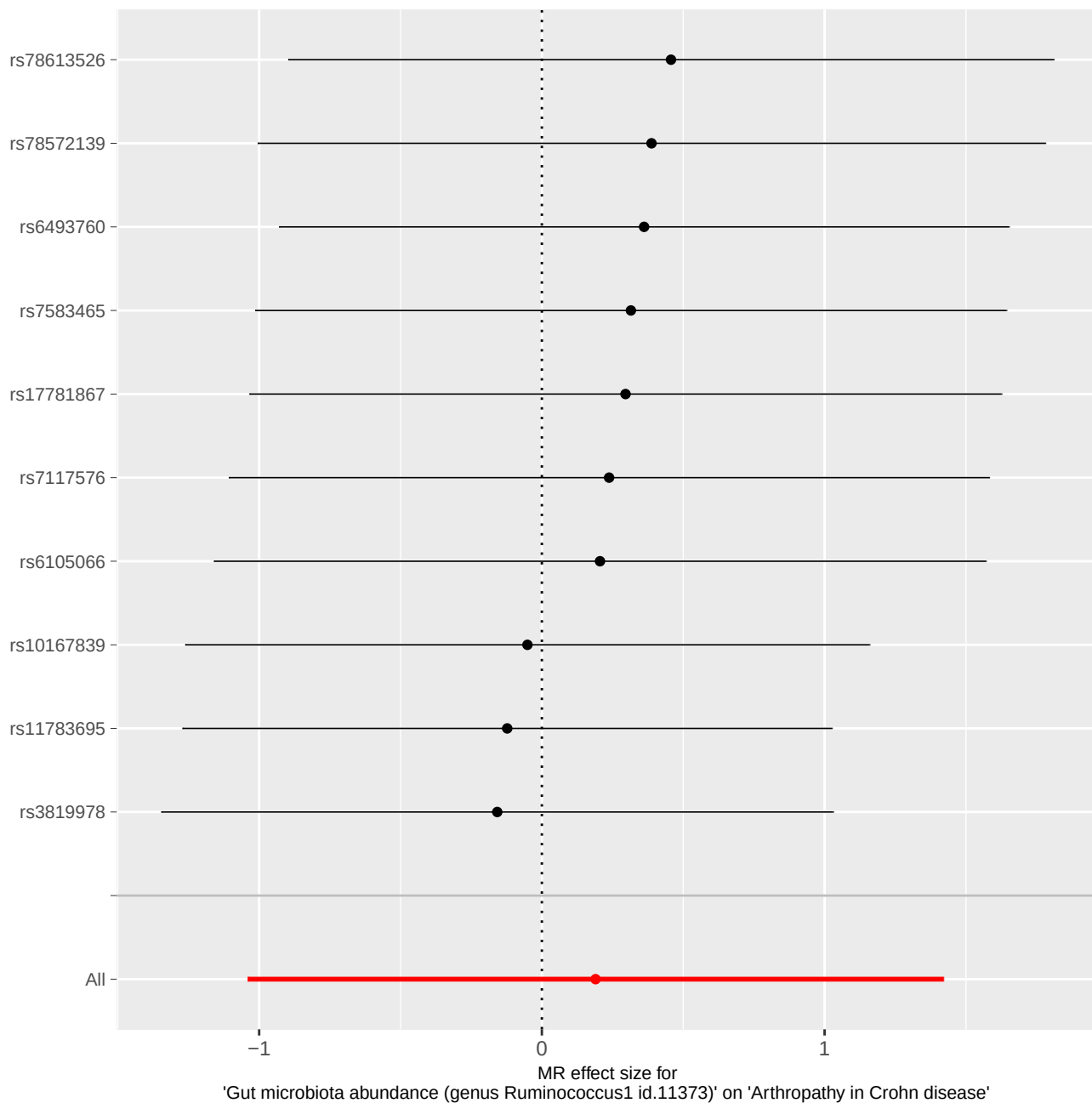


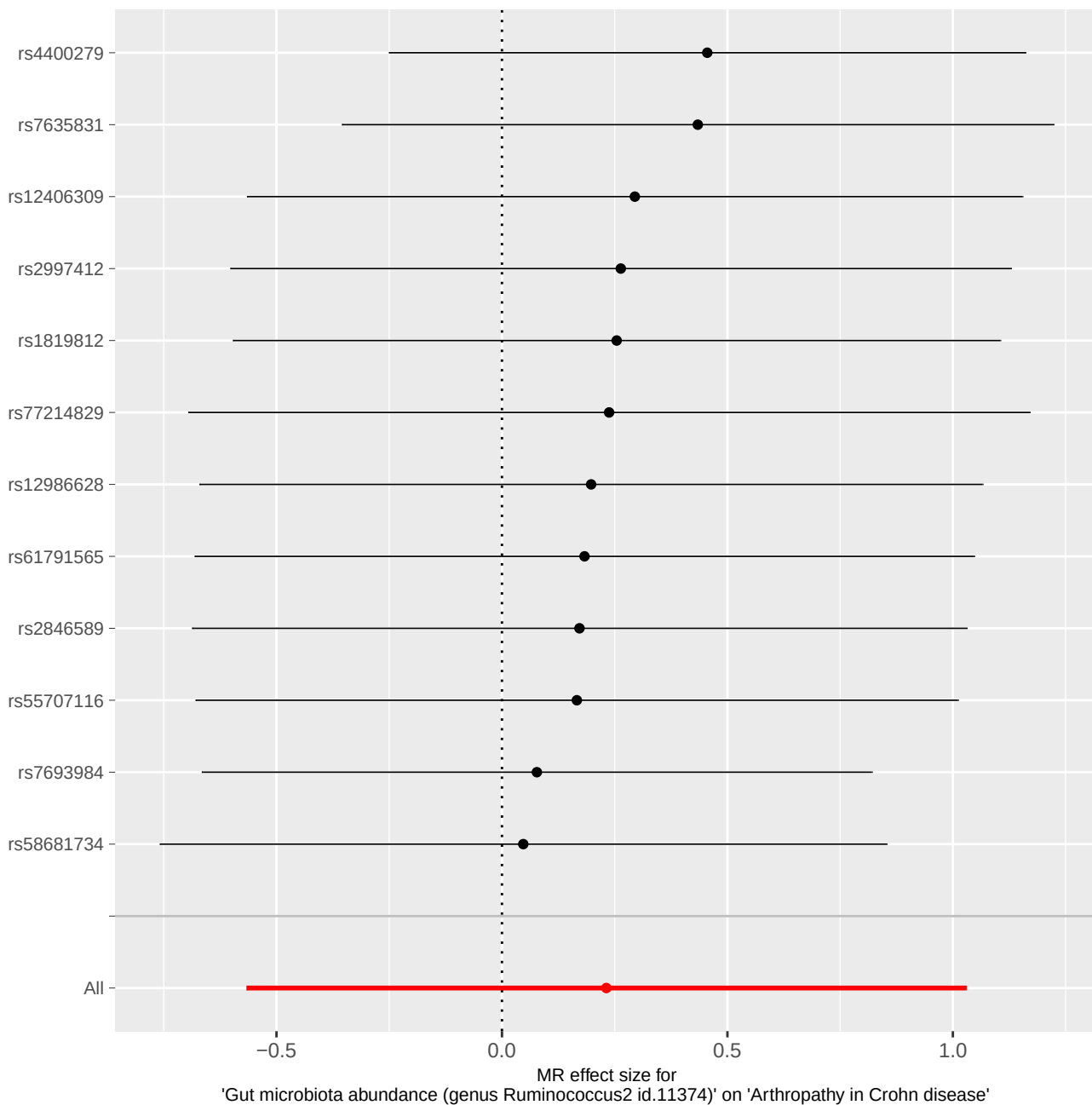


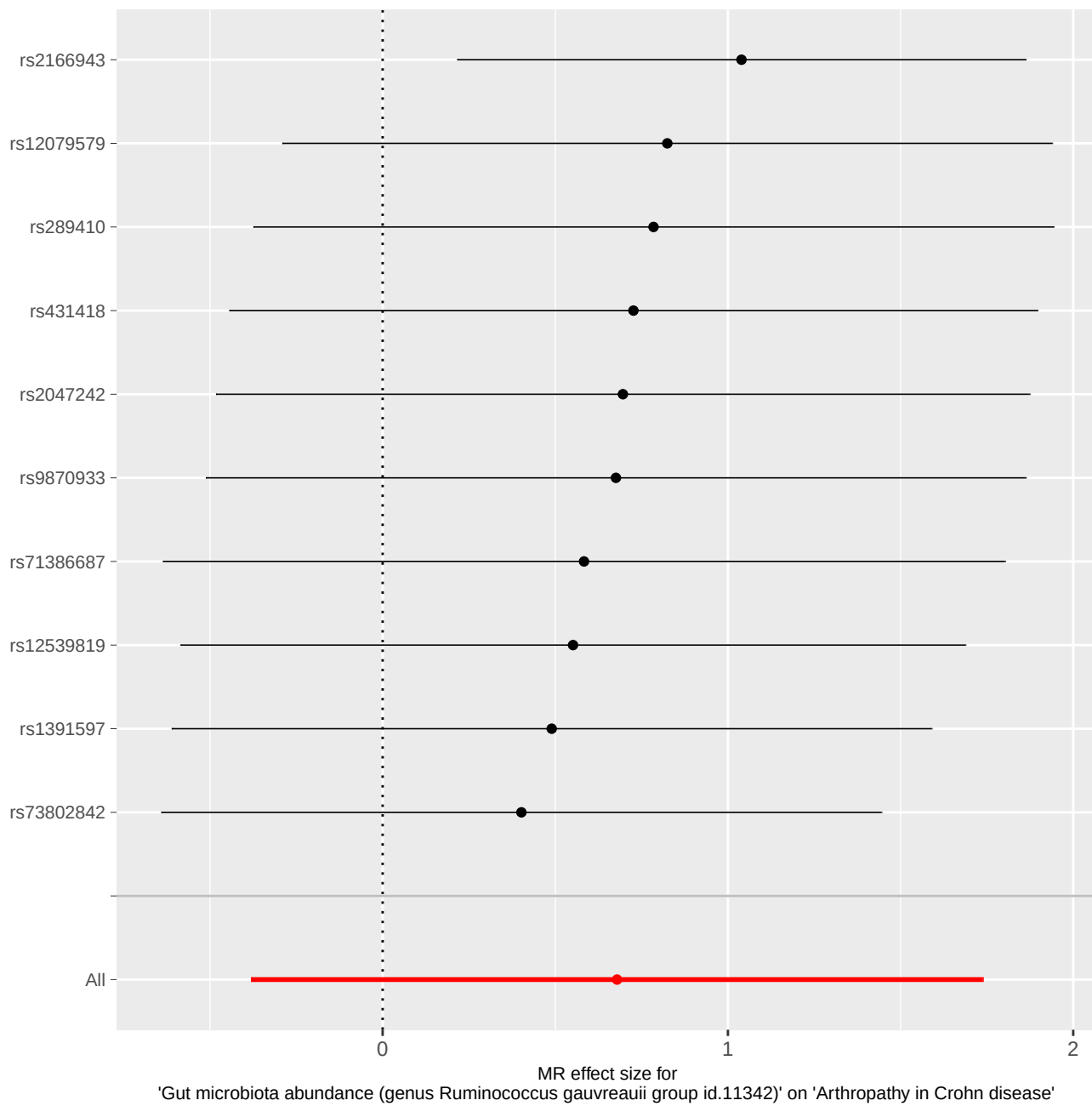


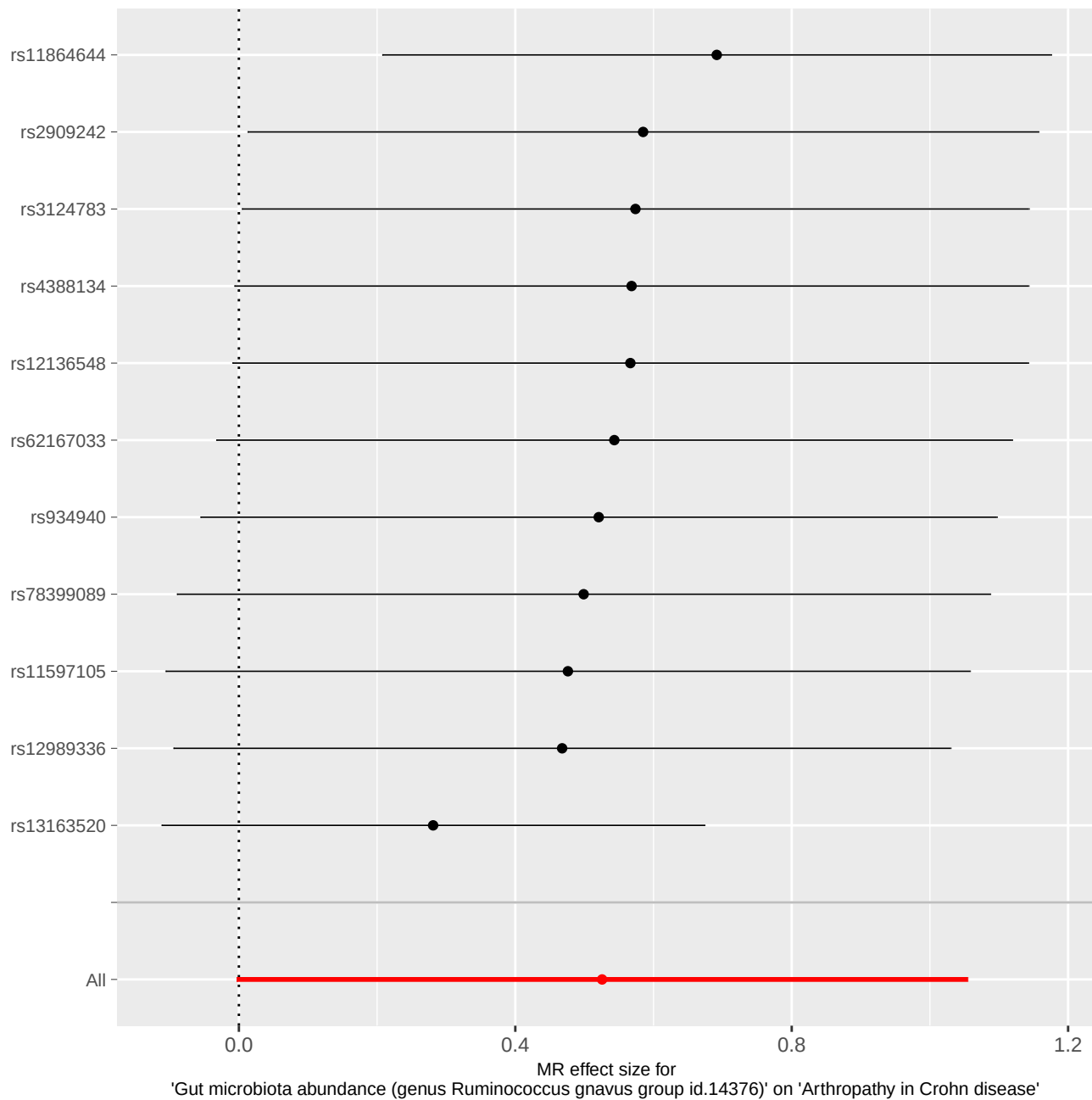


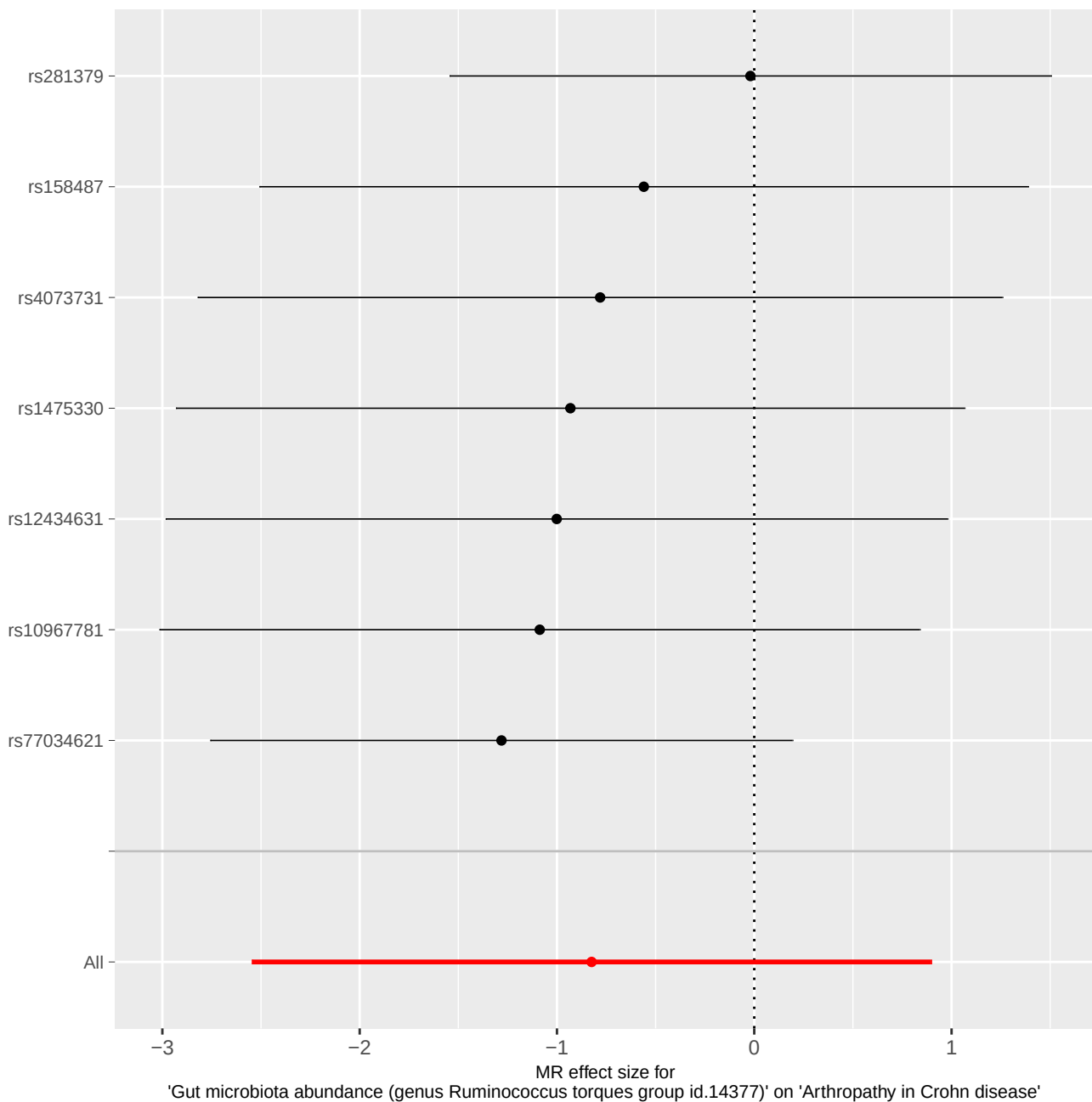


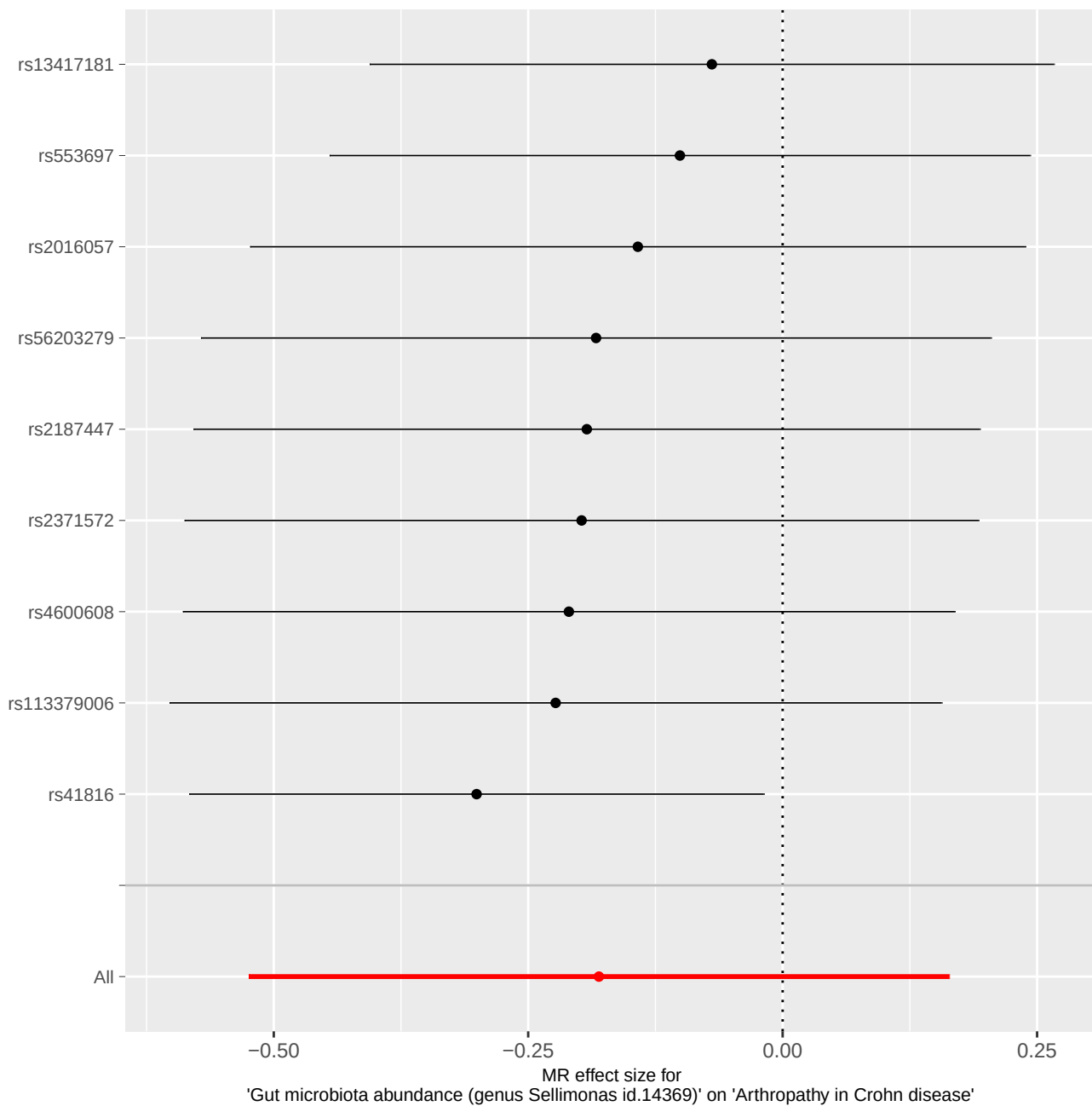


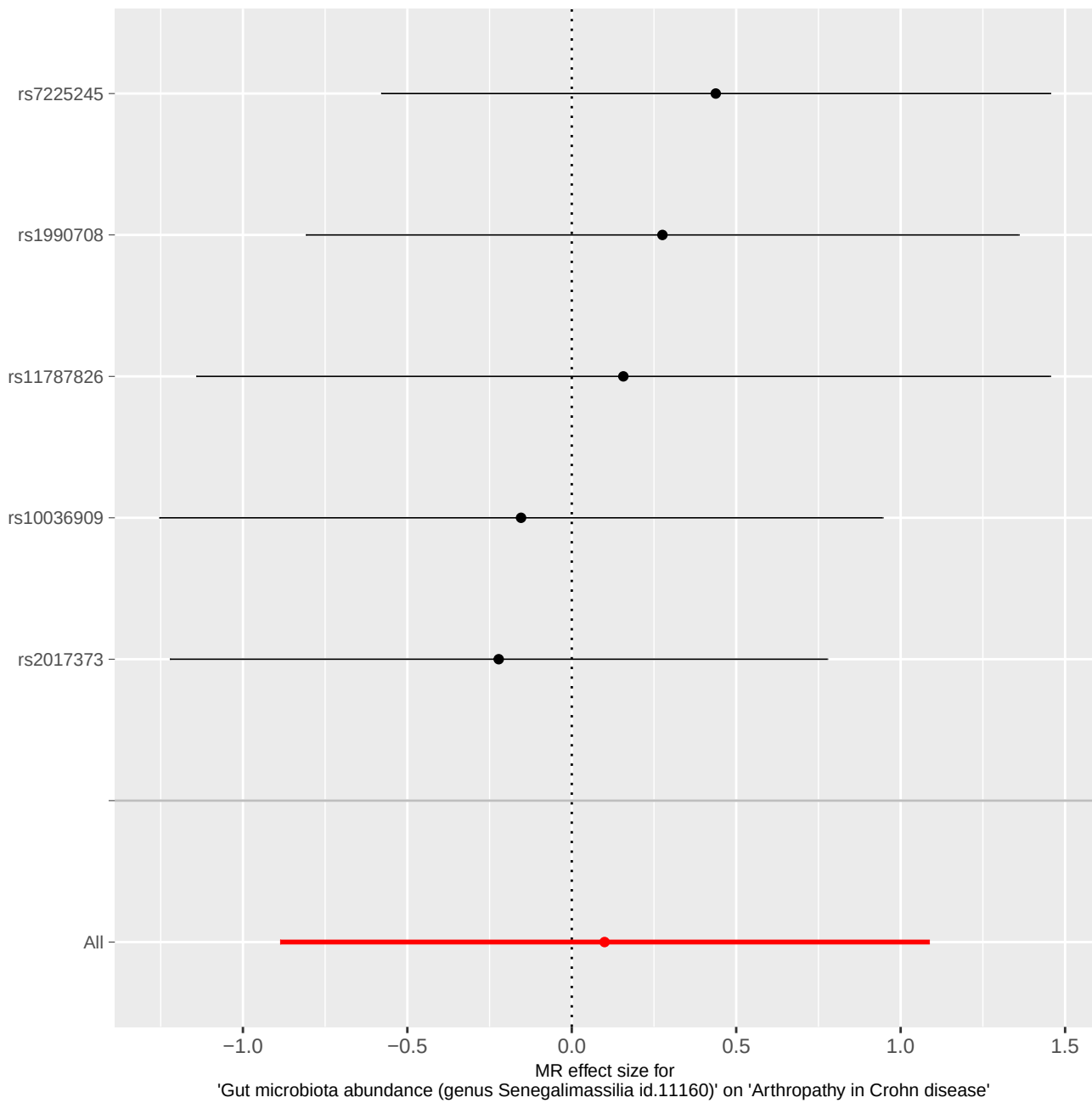


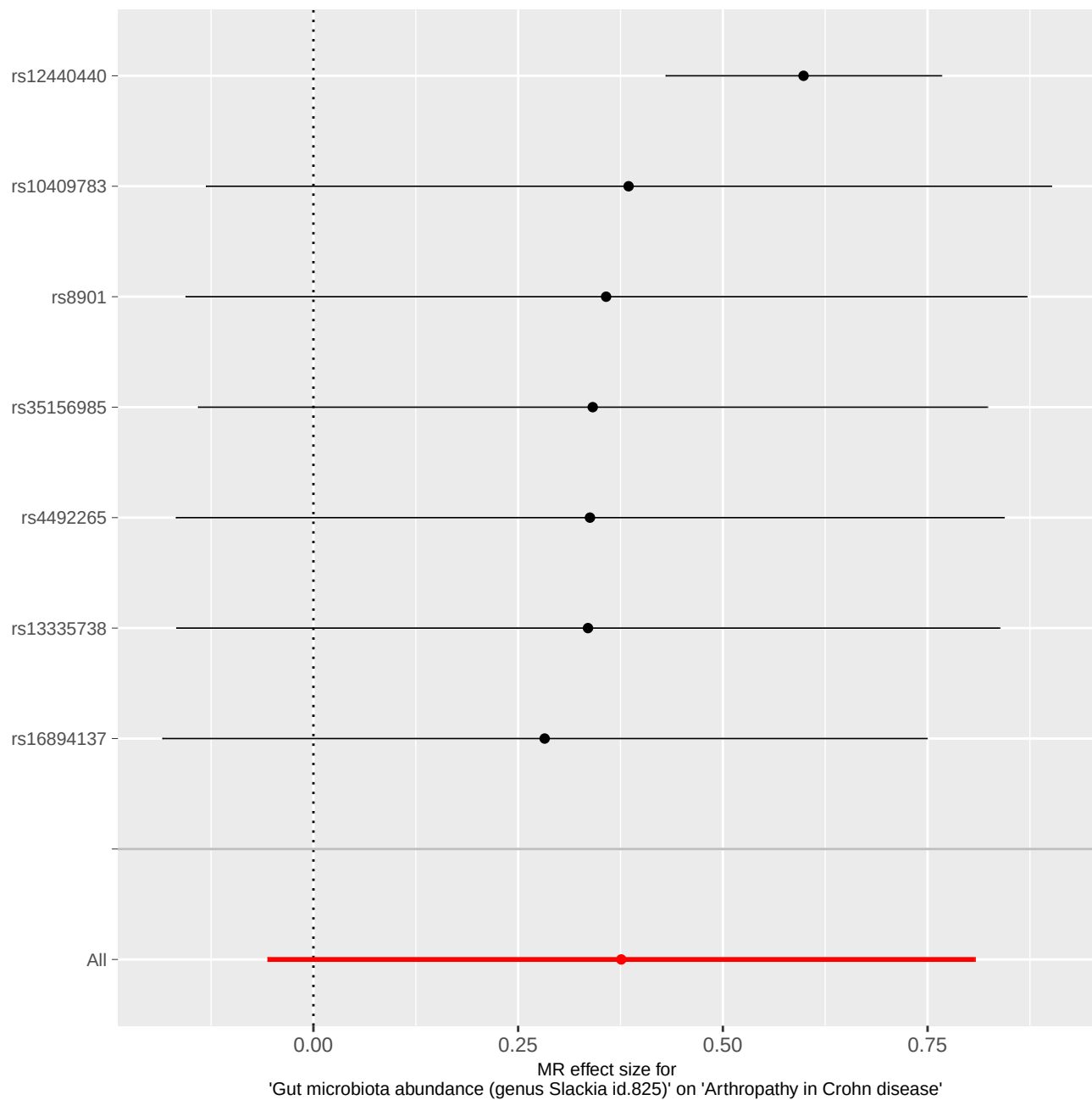


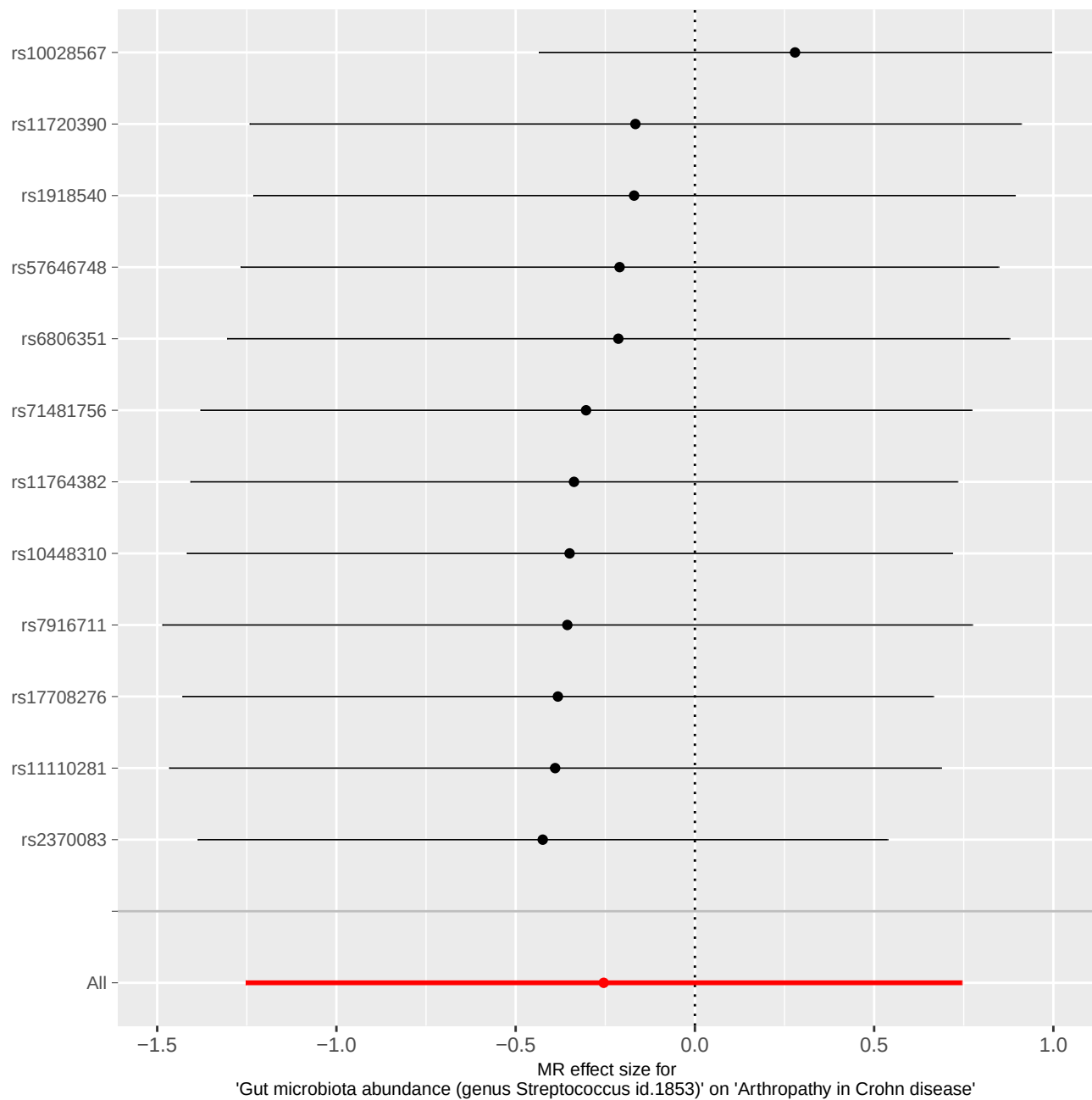


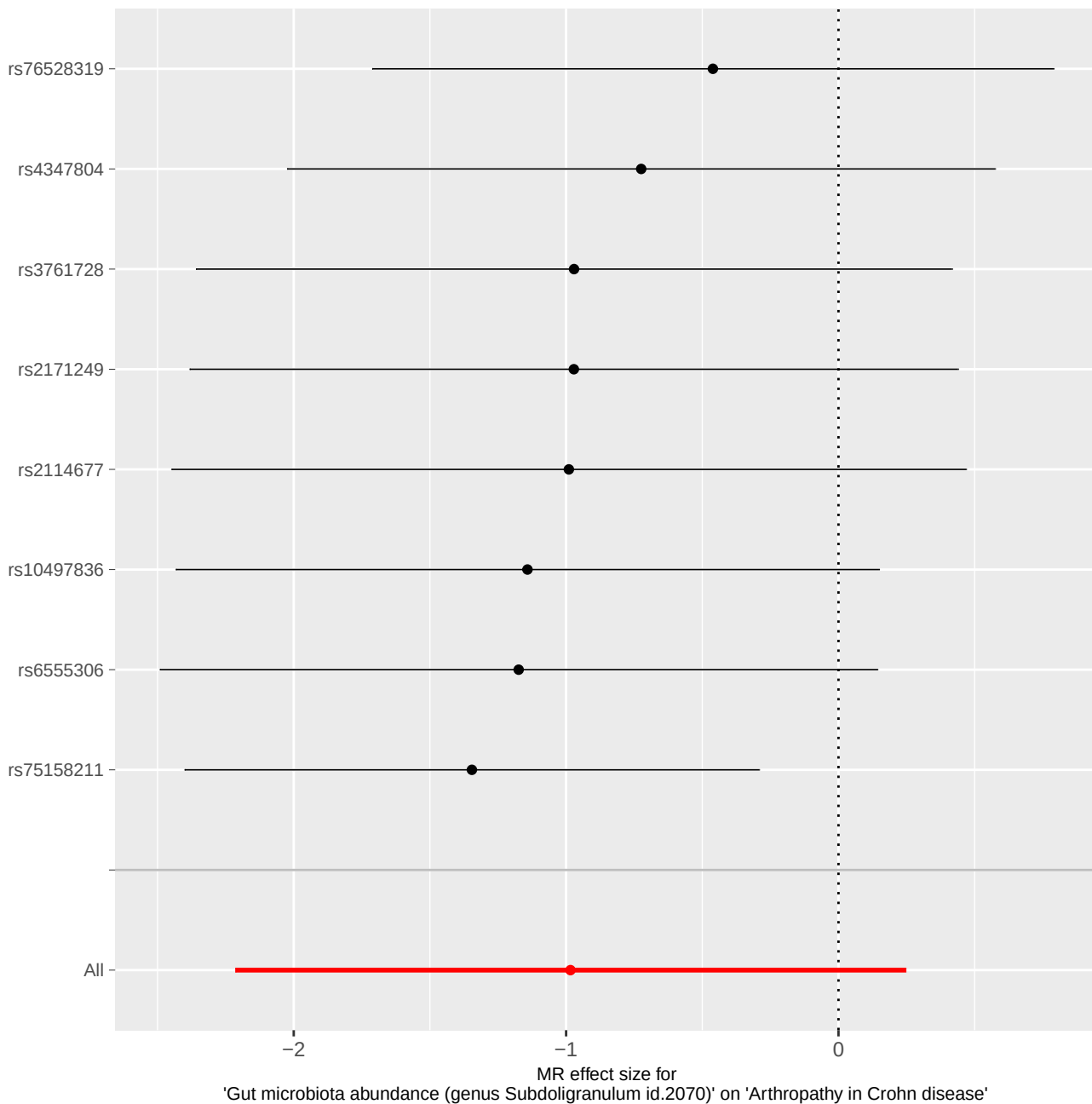


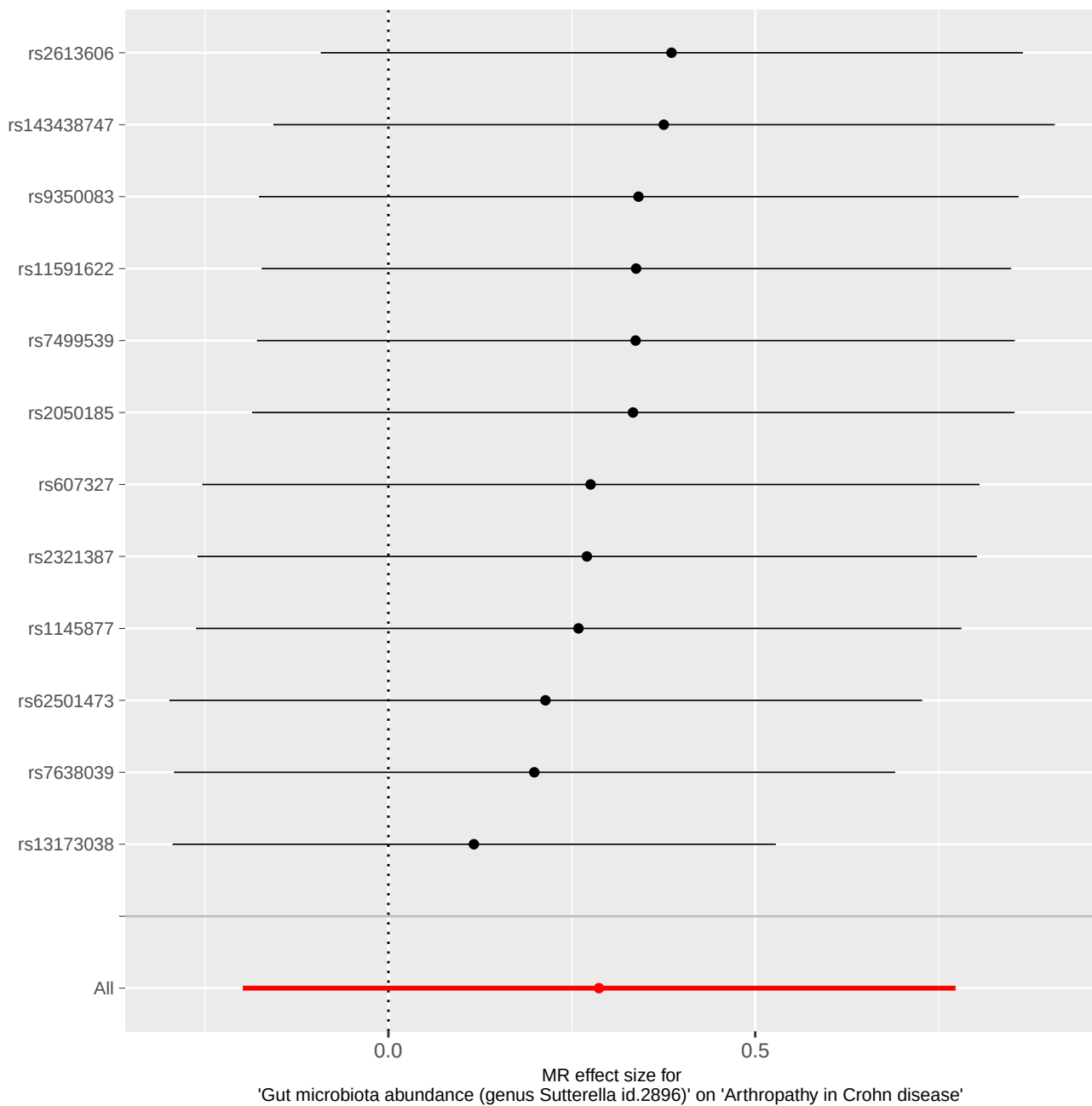


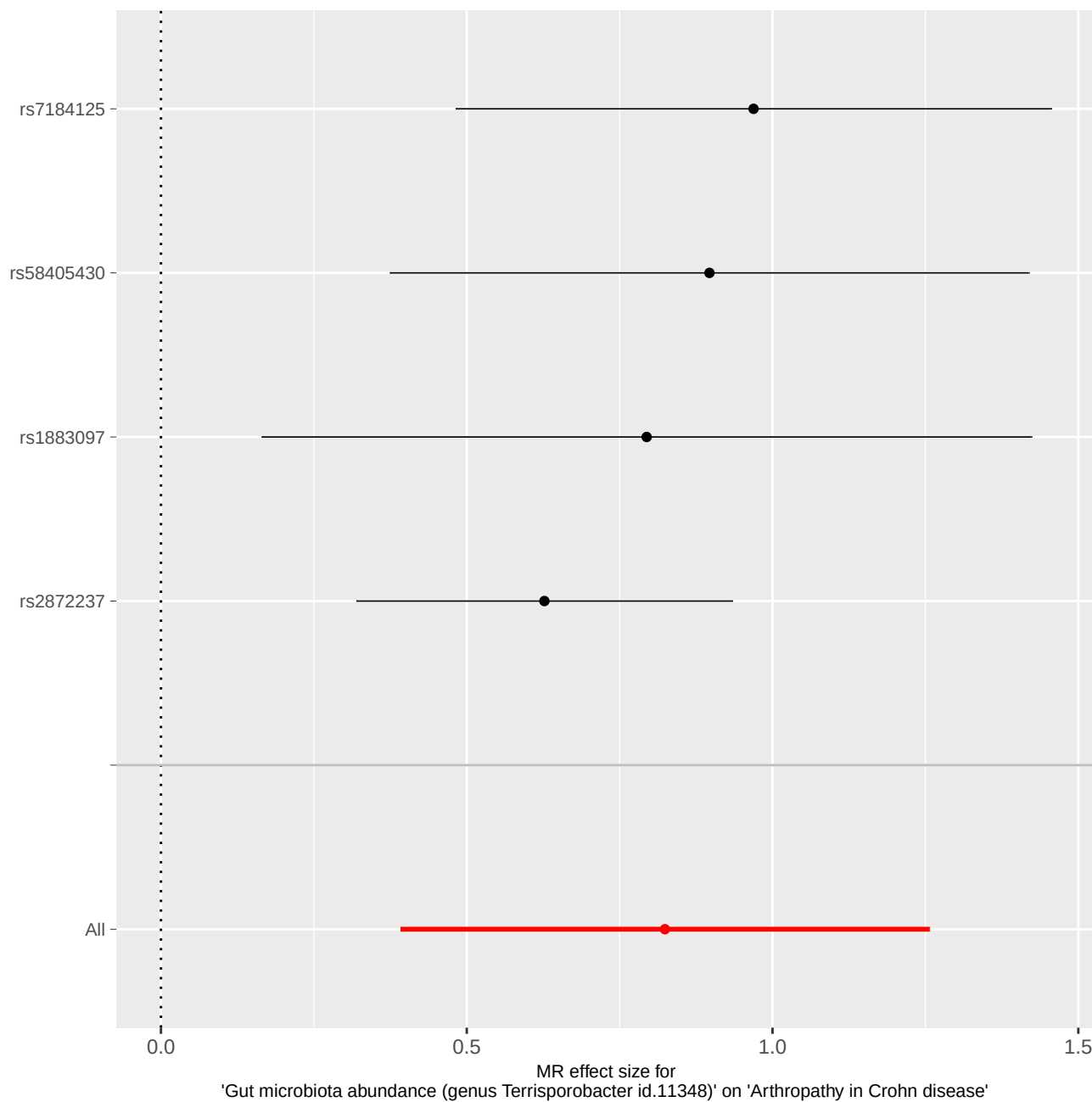


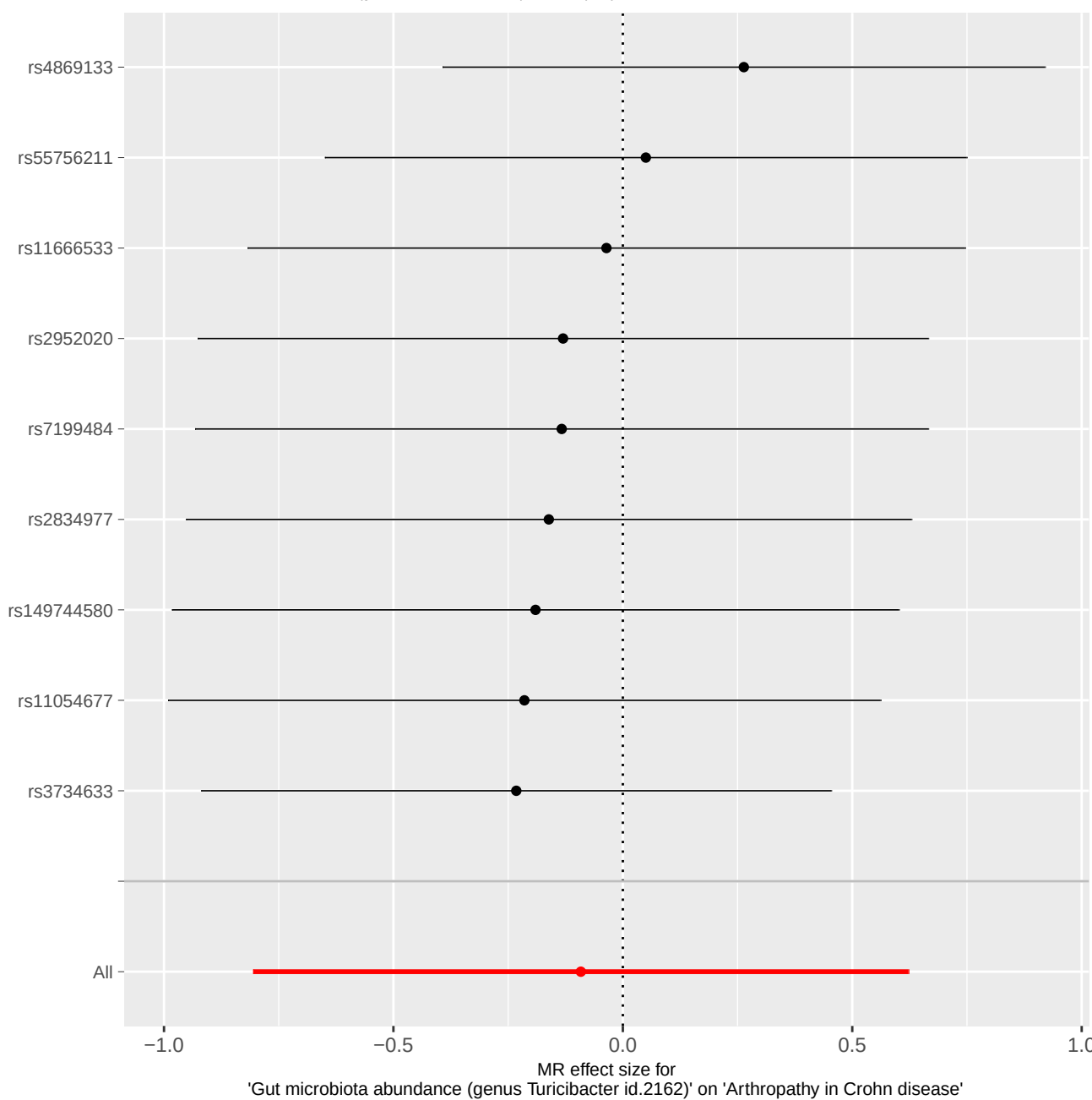




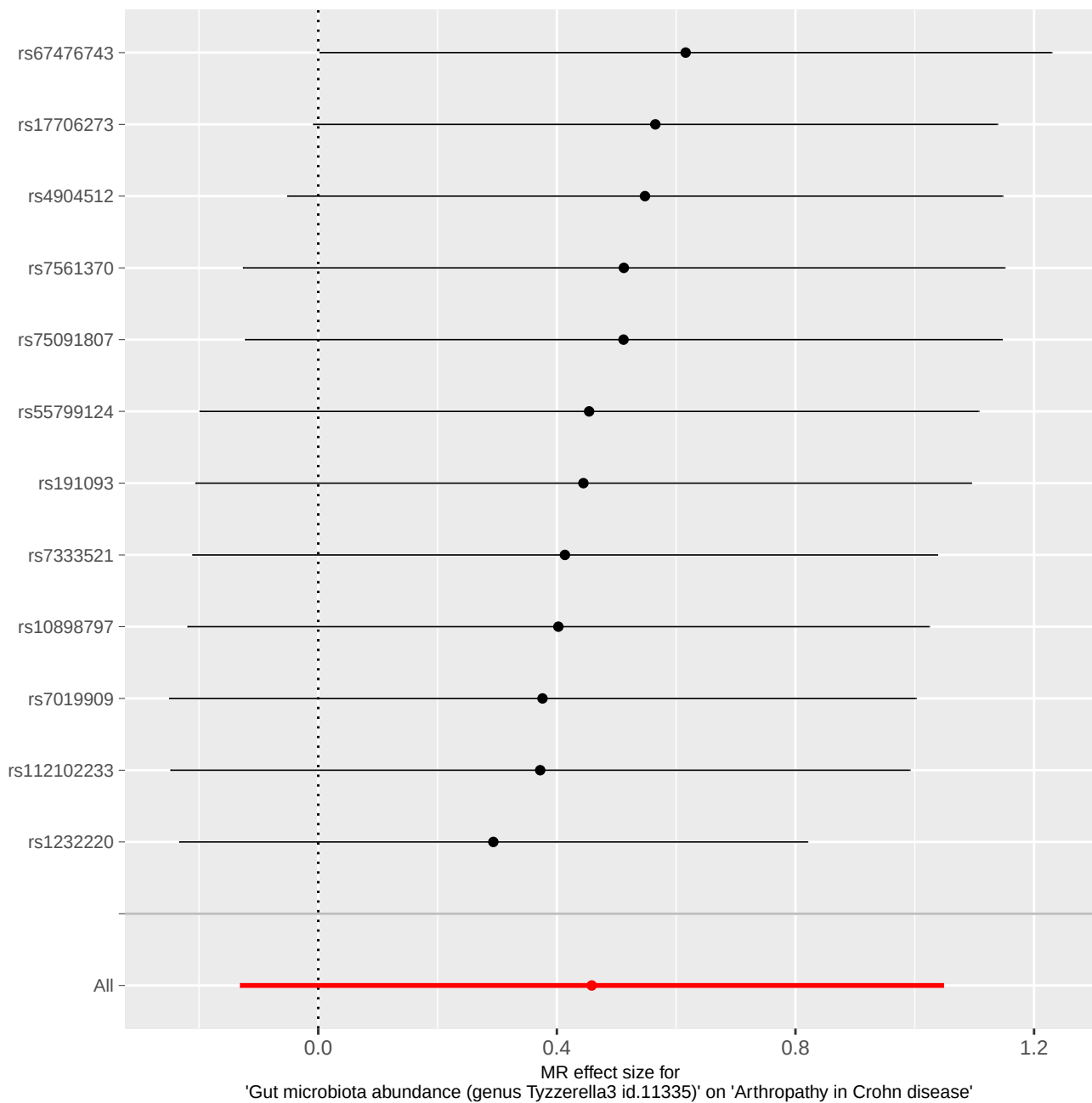


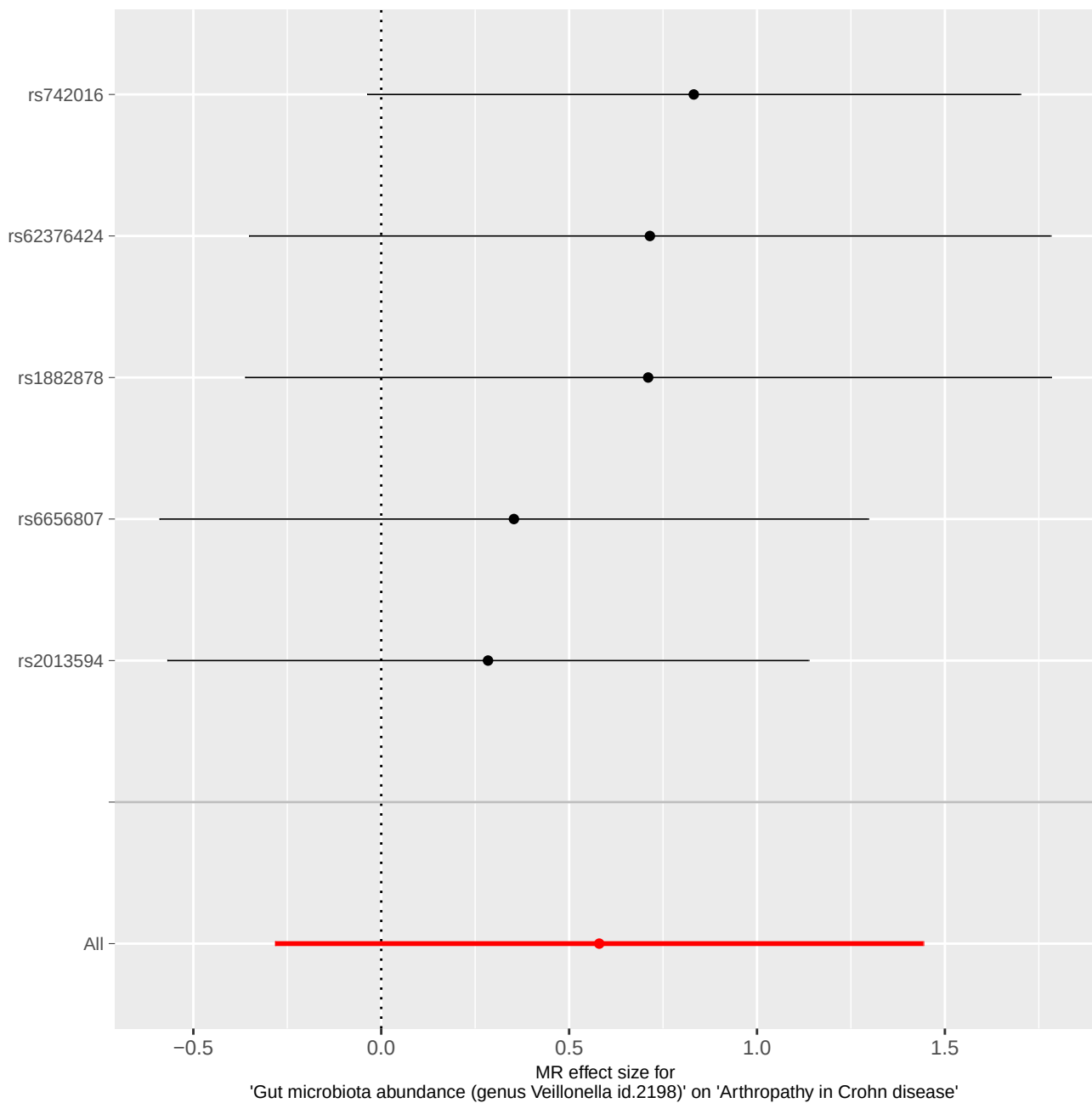


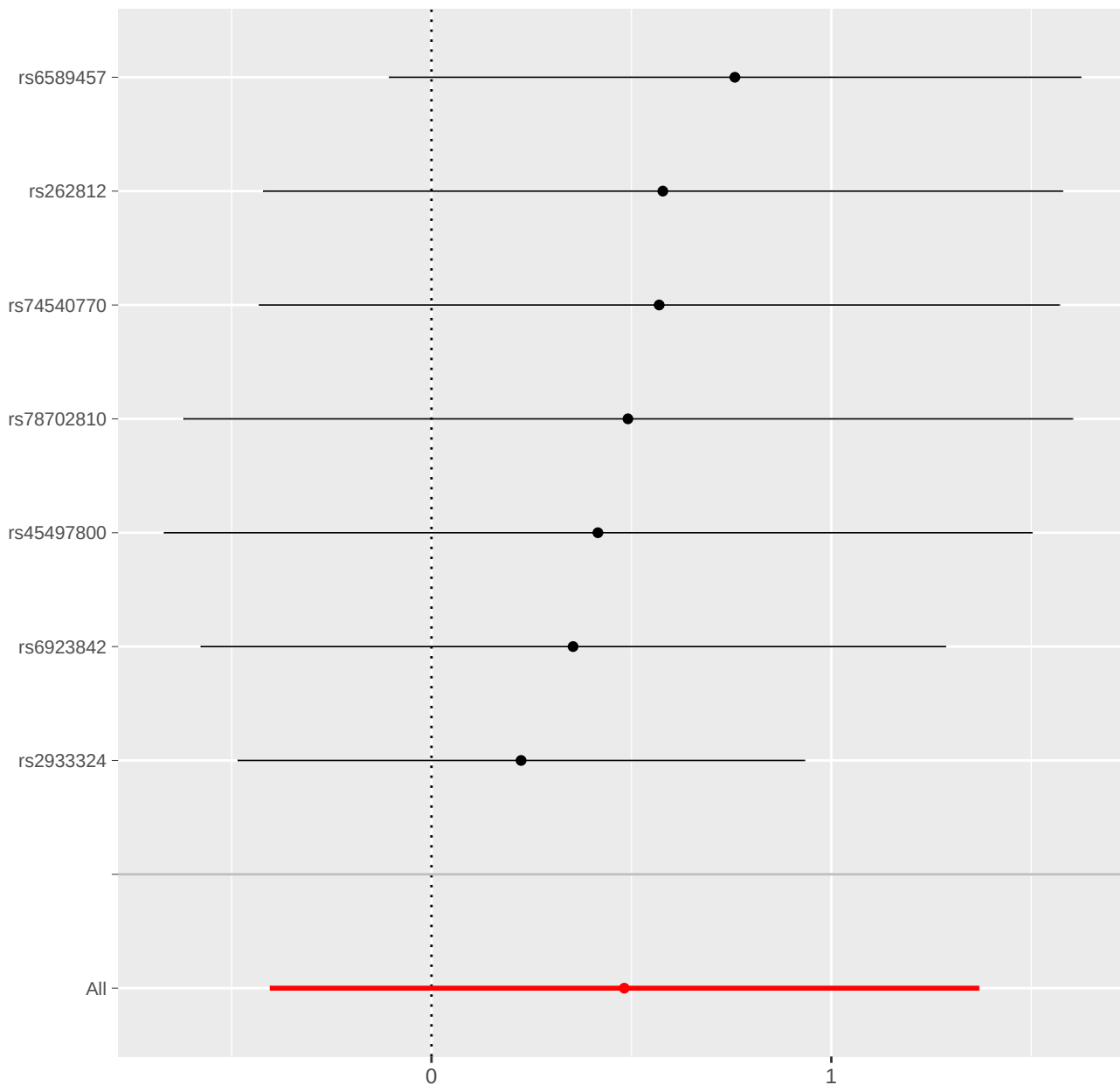




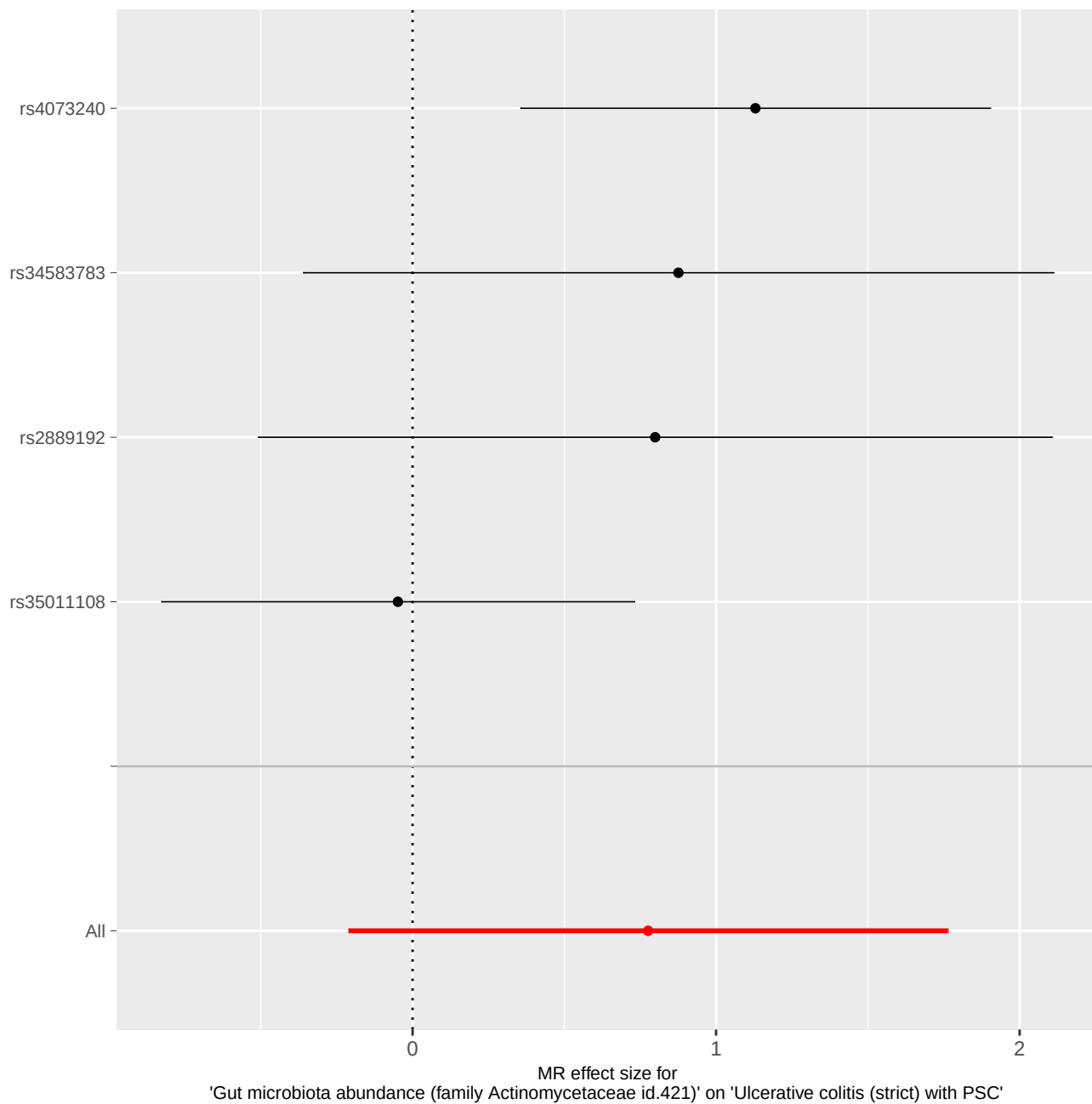
Batch 599 : Gut microbiota abundance (genus Tyzzerella3 id.11335) on Arthropathy in Crohn disease

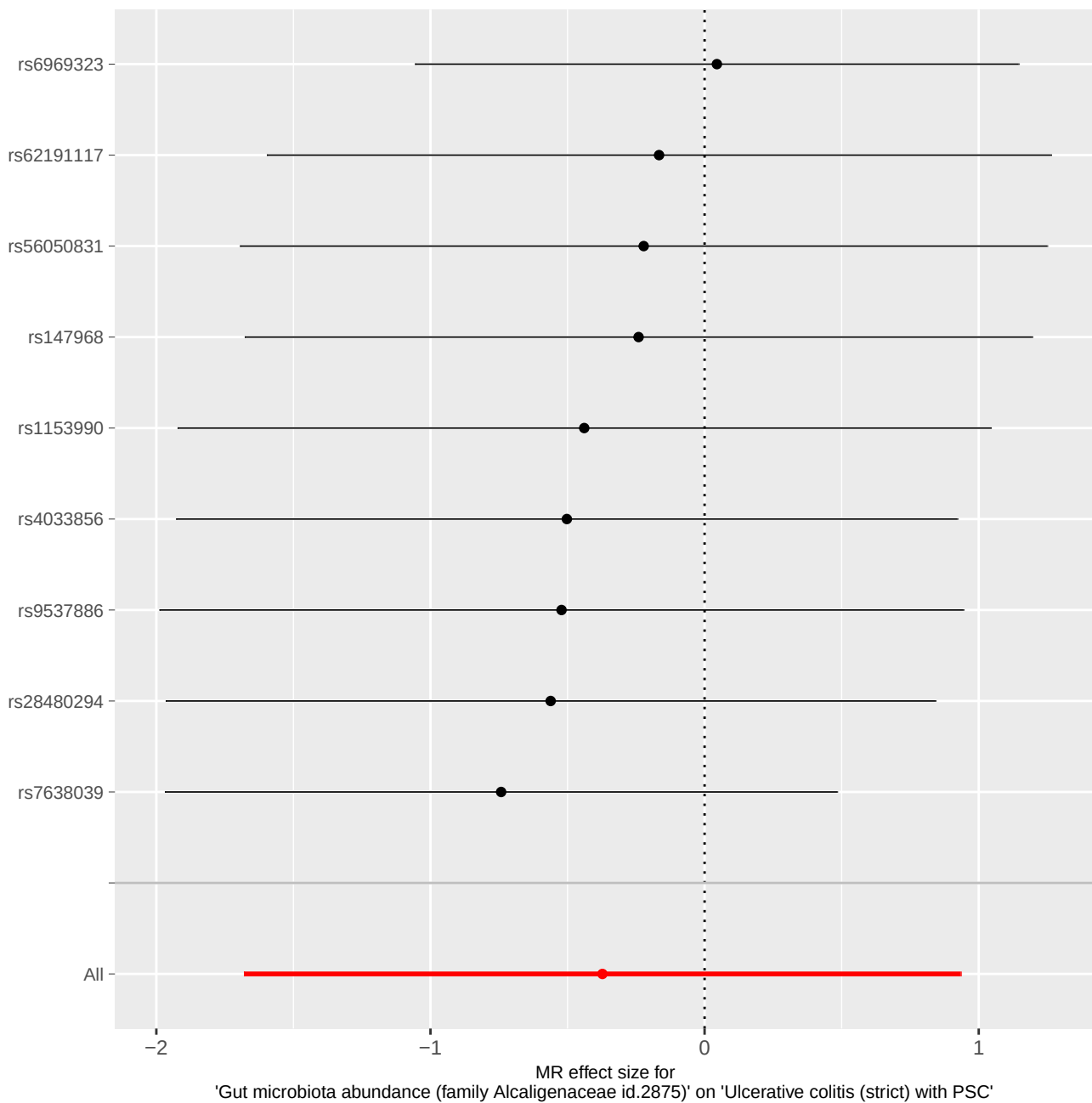


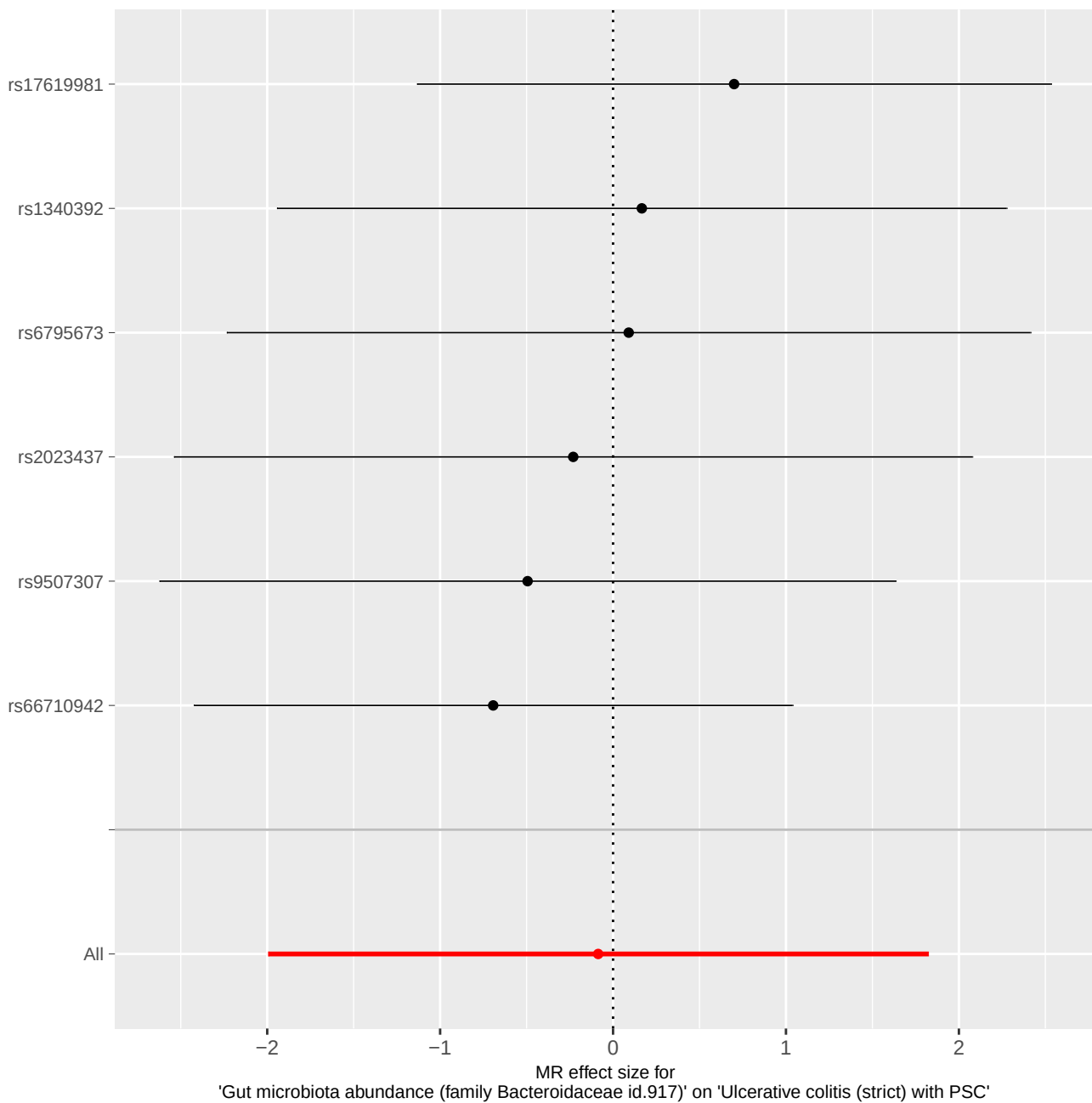


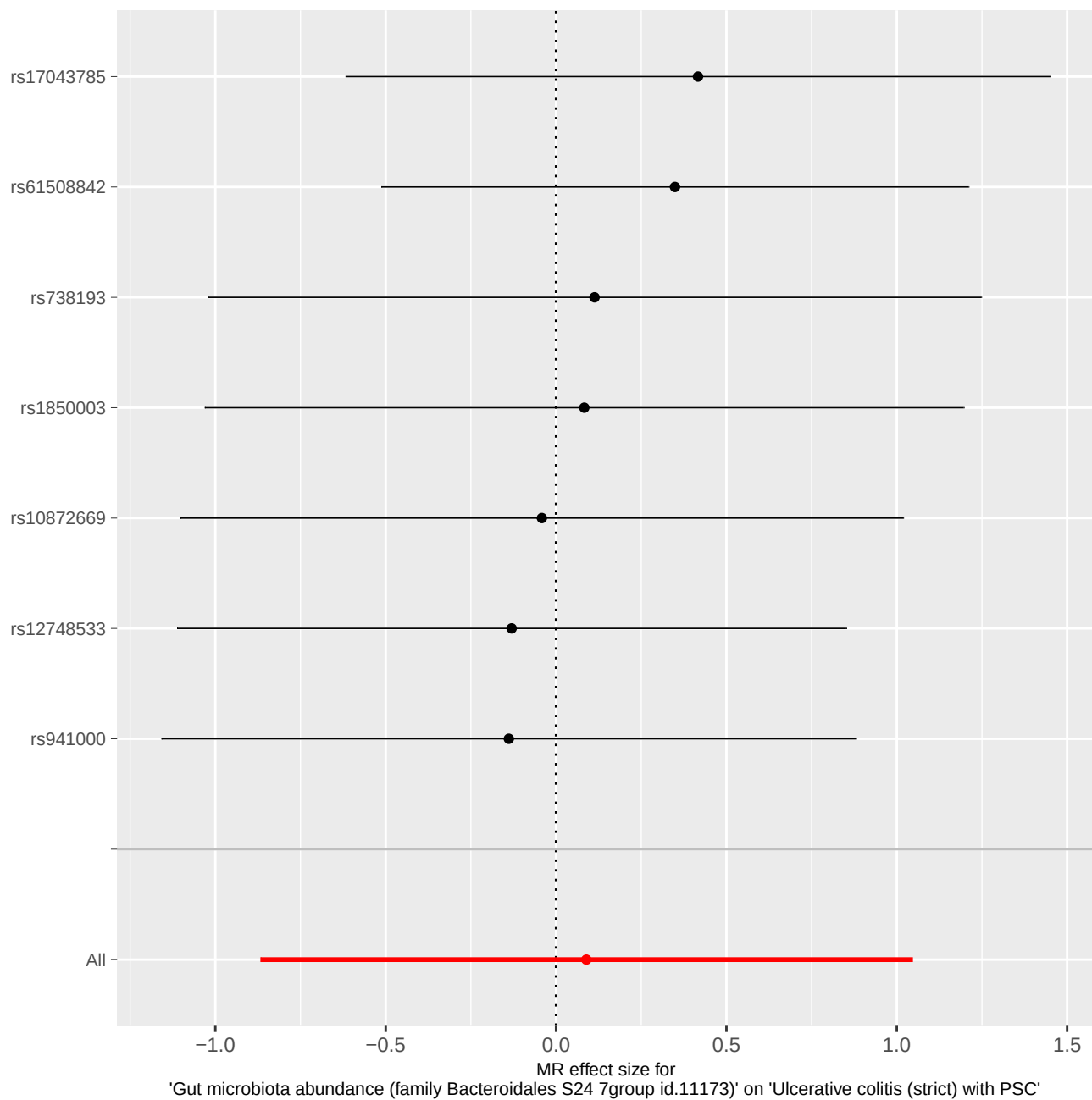


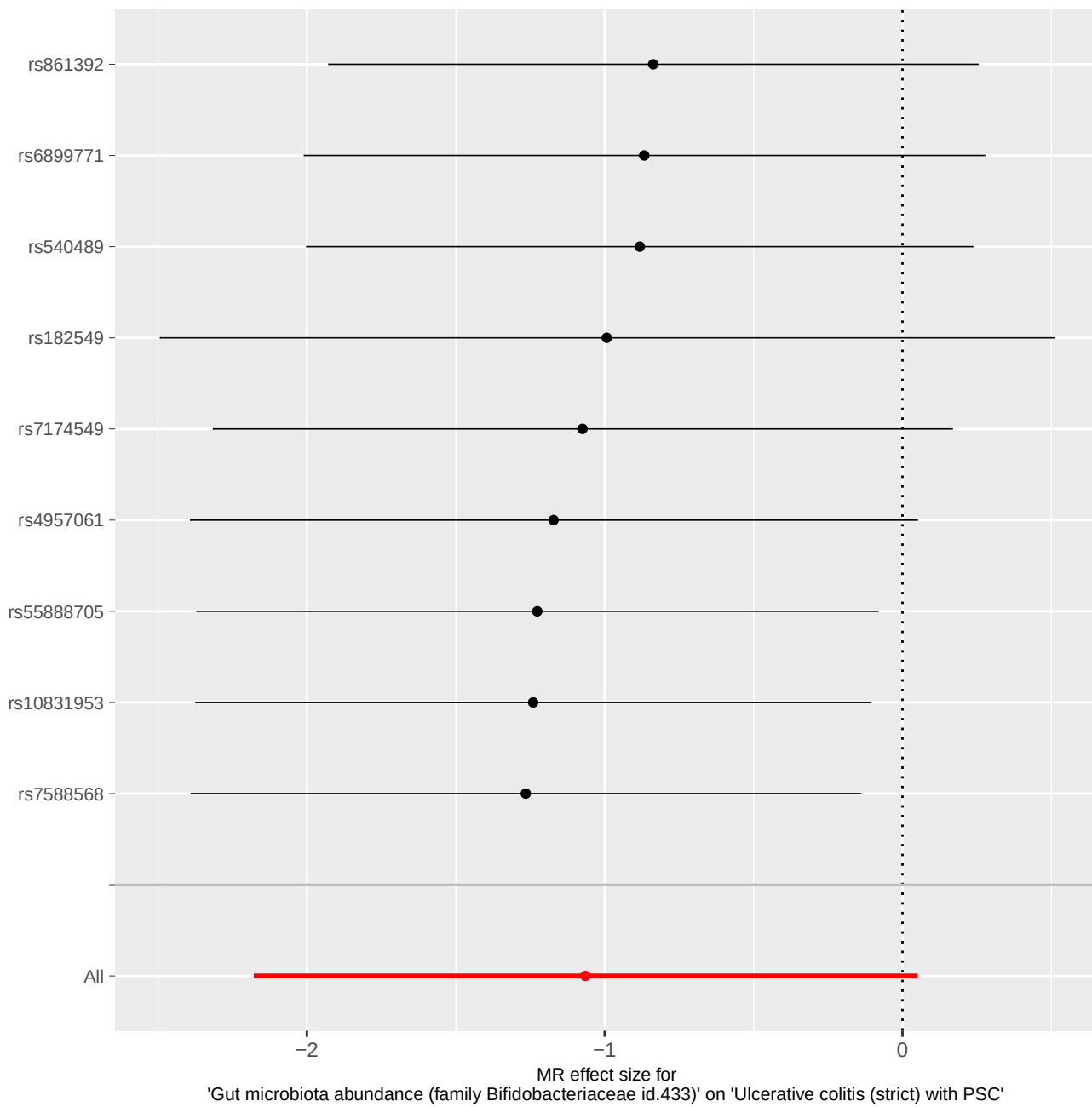
MR effect size for
'Gut microbiota abundance (family Acidaminococcaceae id.2166)' on 'Ulcerative colitis (strict) with PSC'

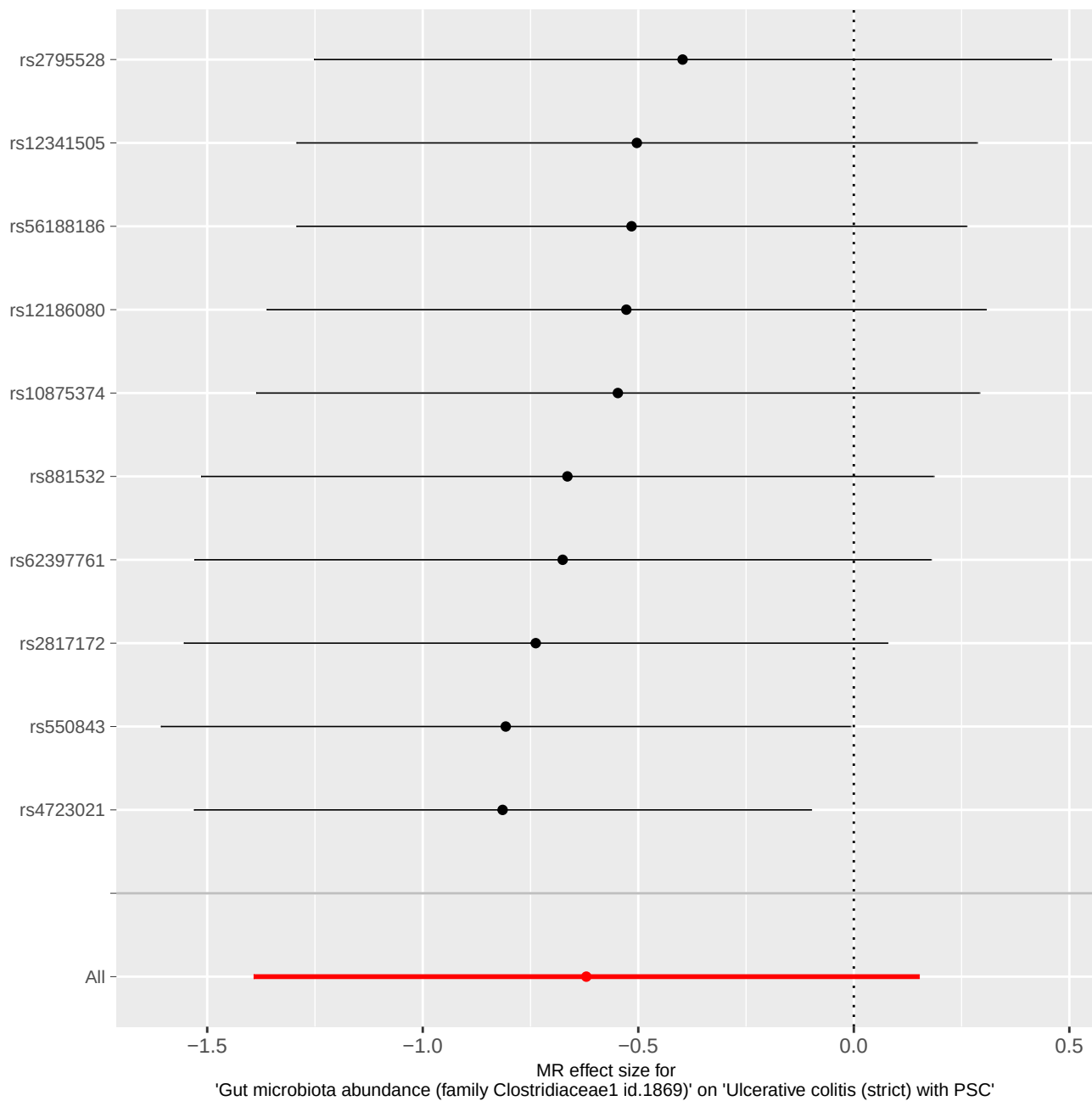


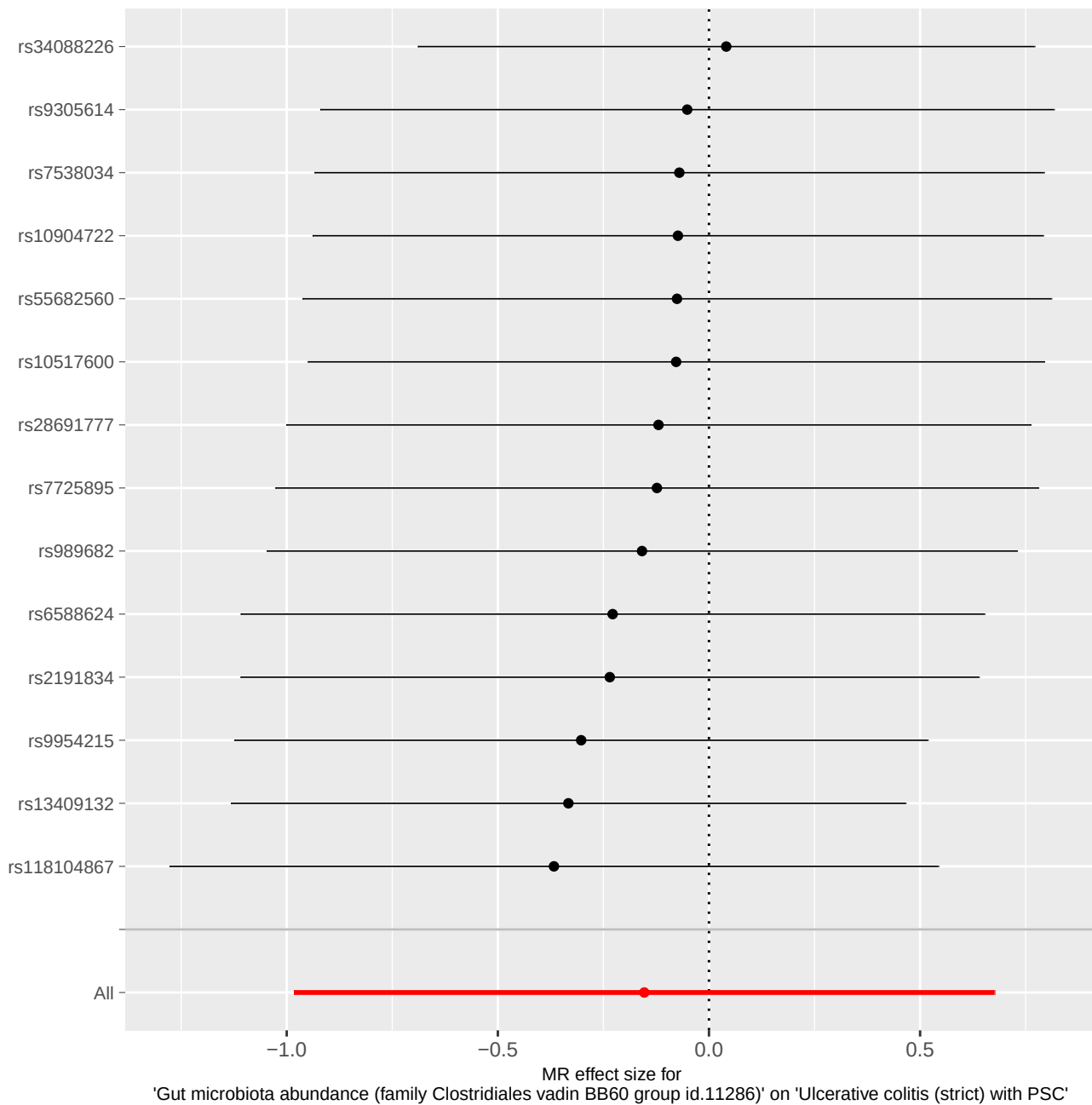


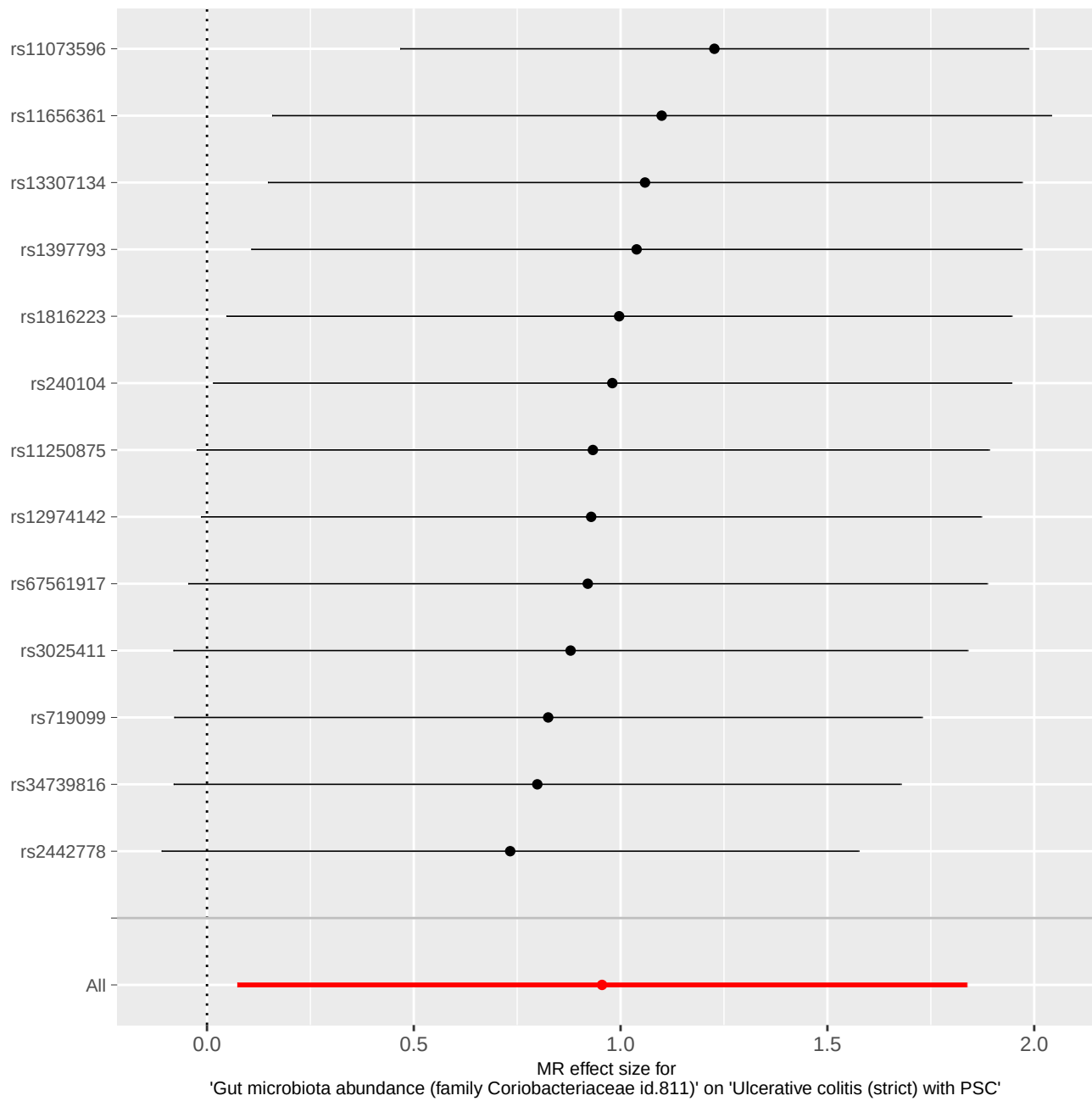


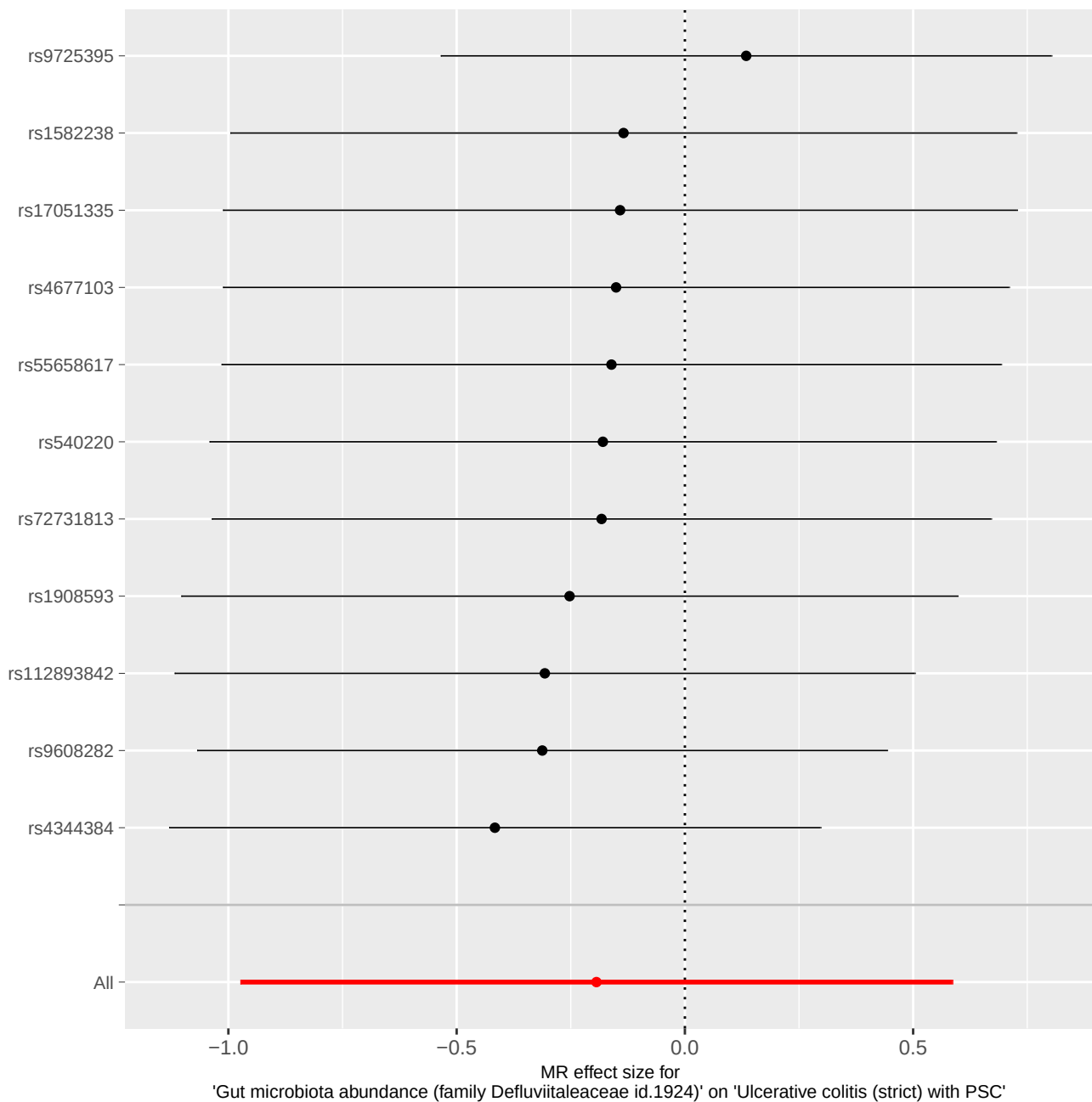


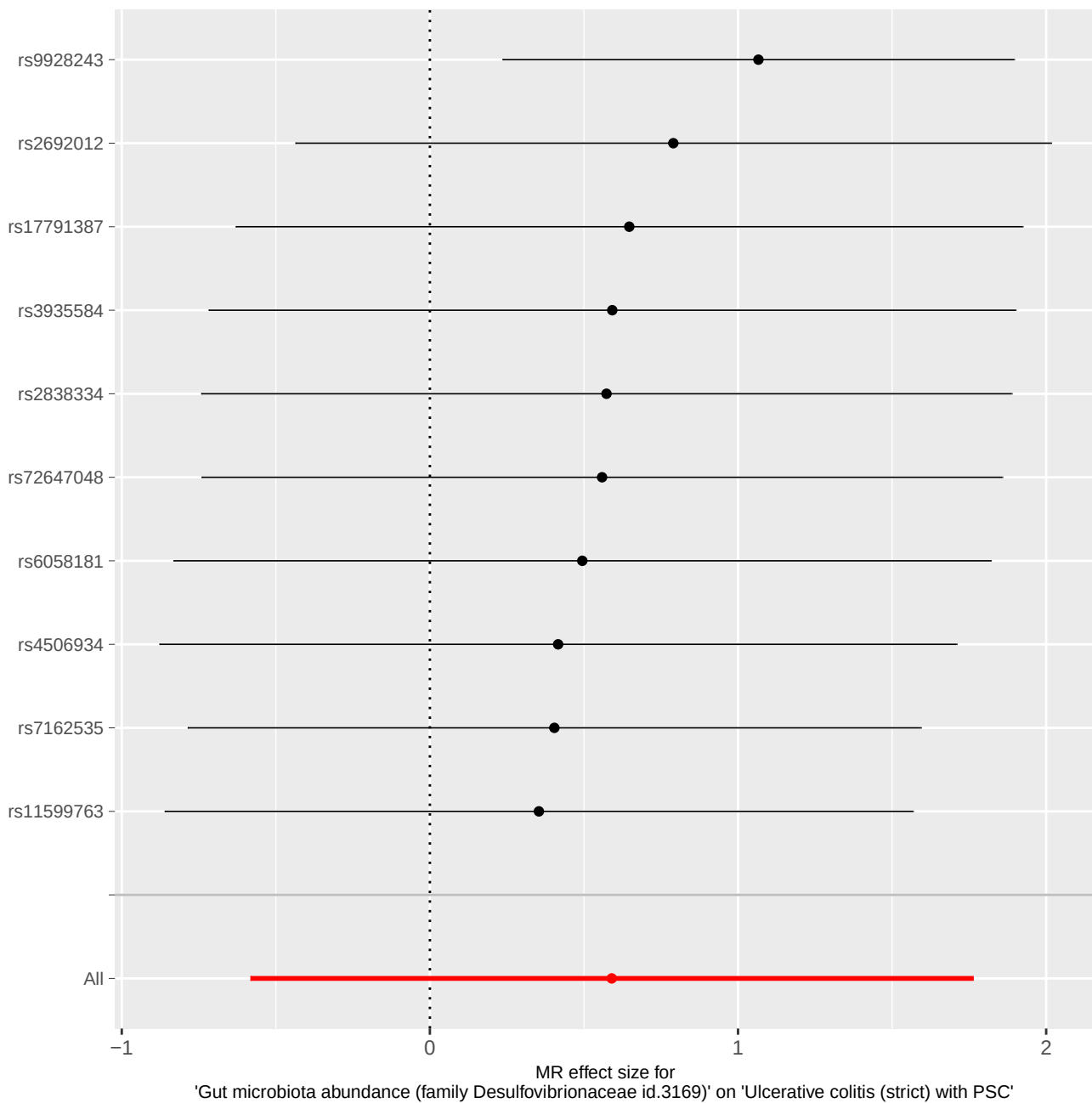


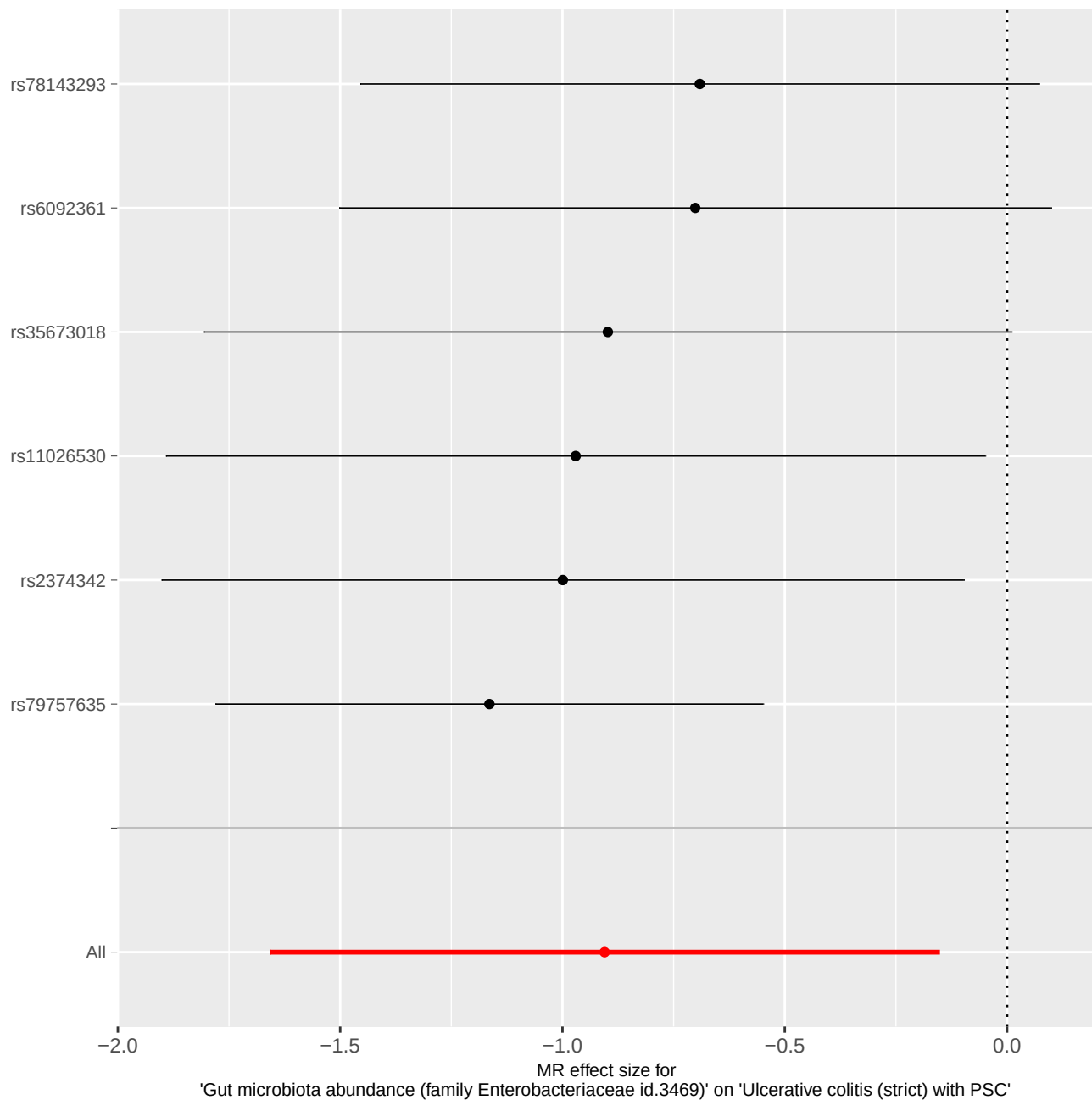


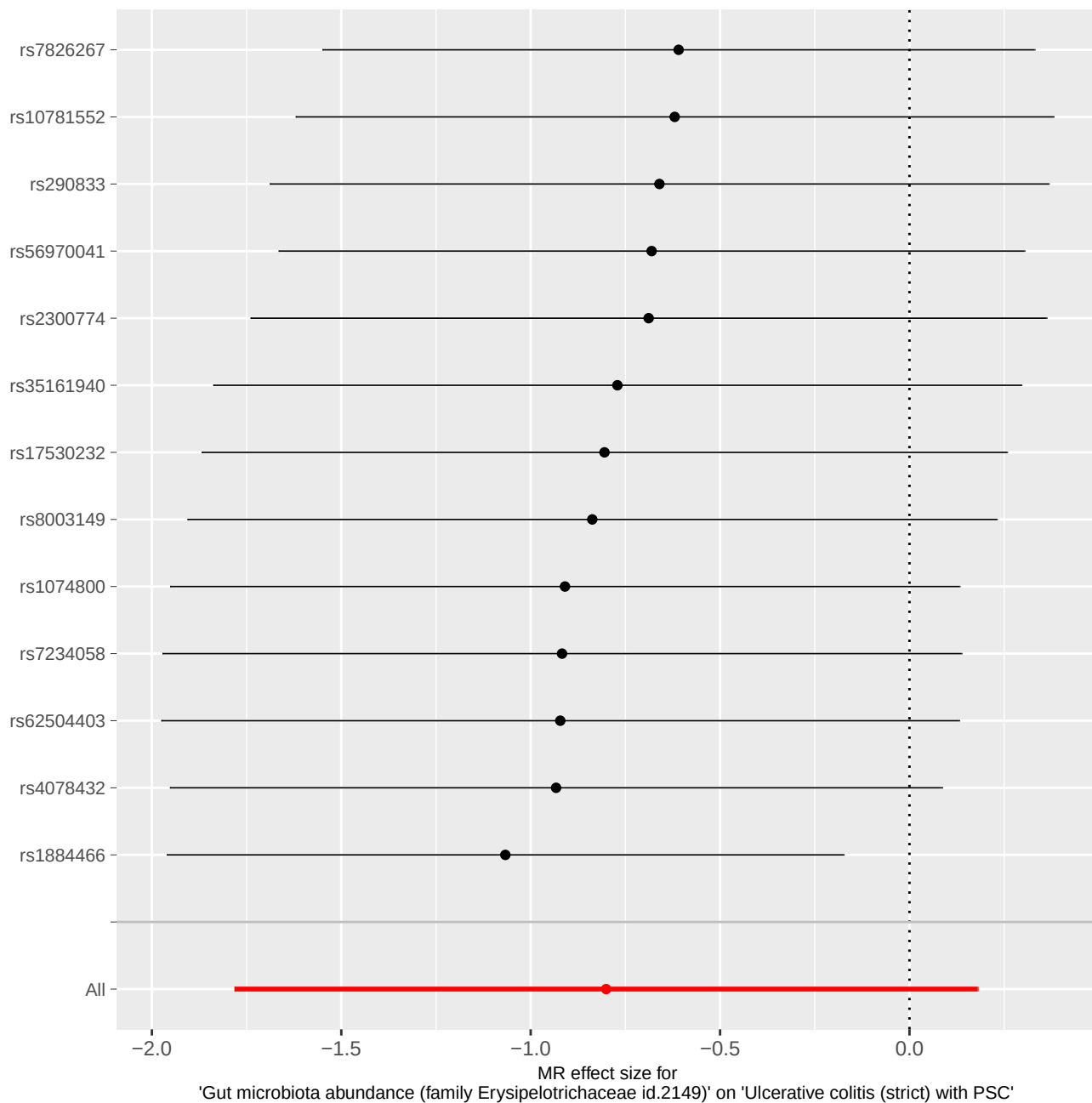


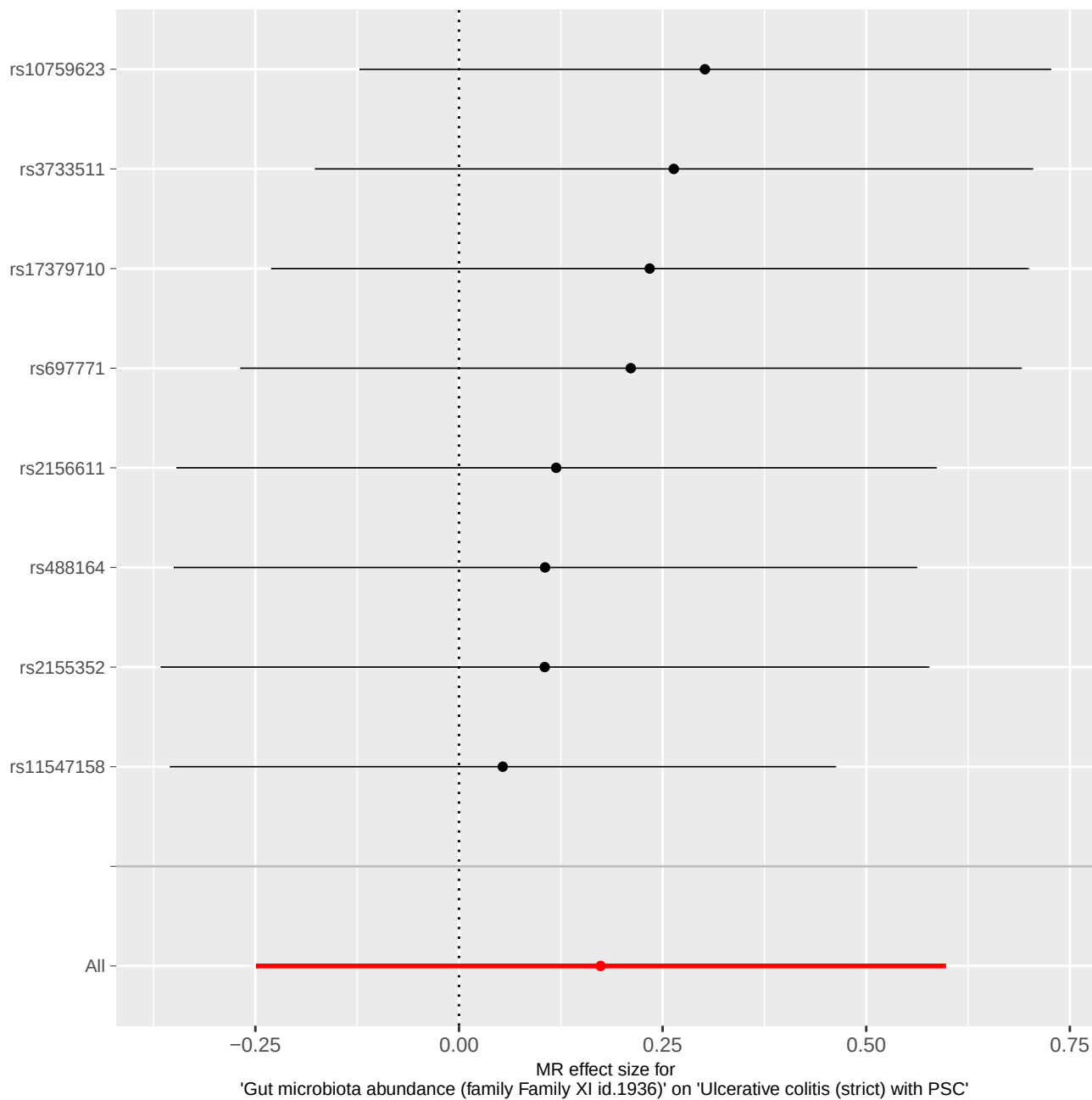


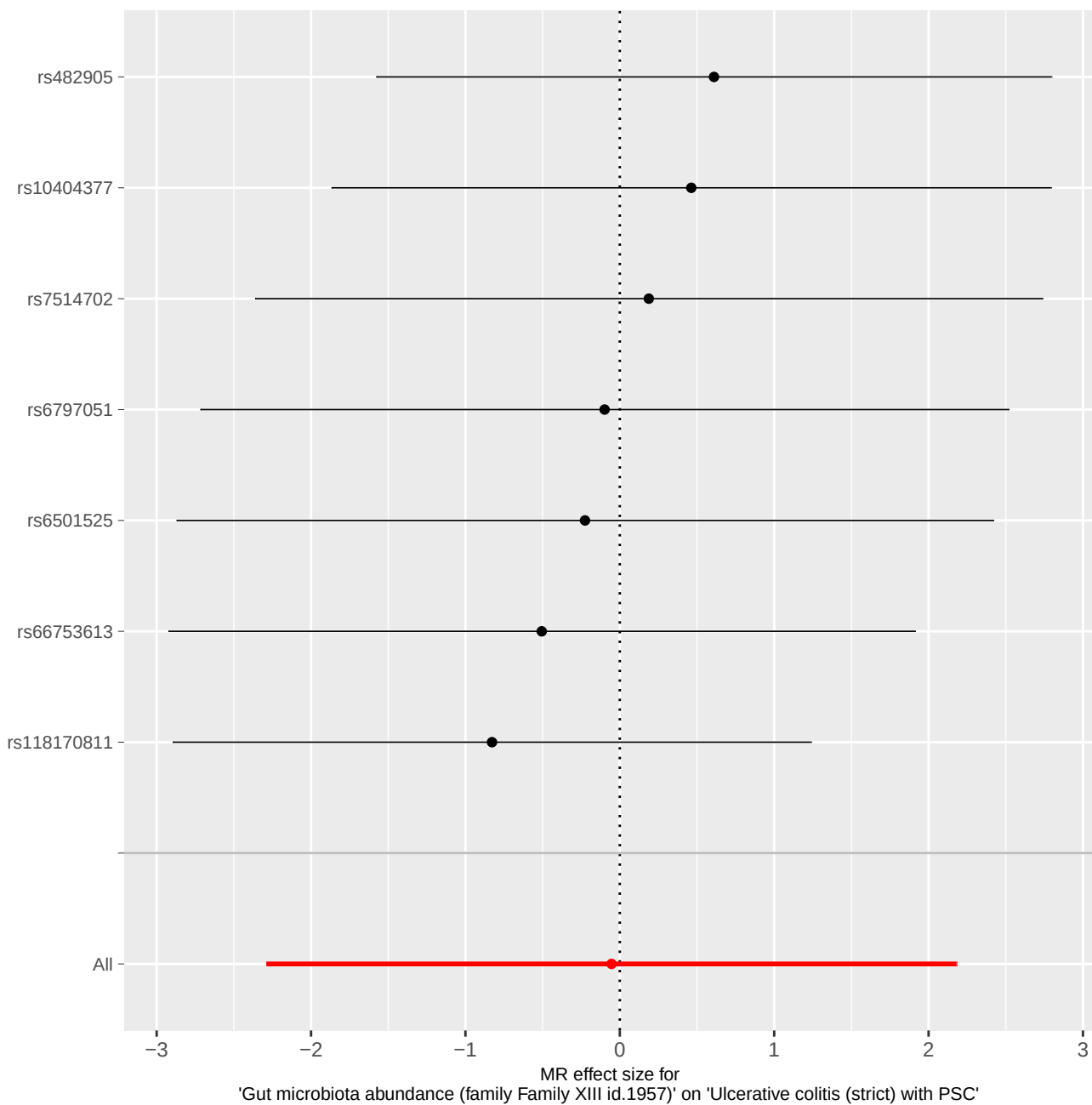


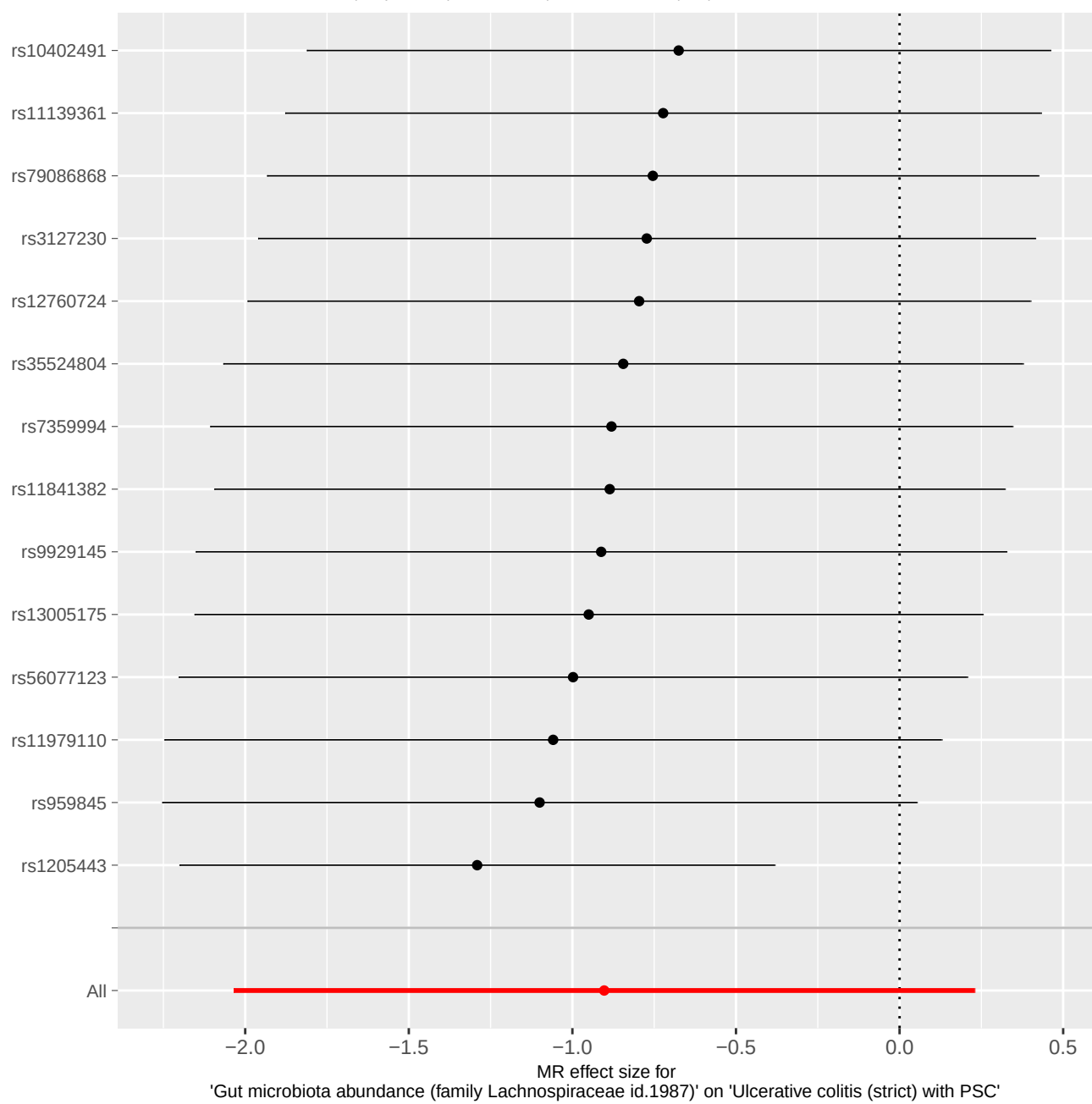


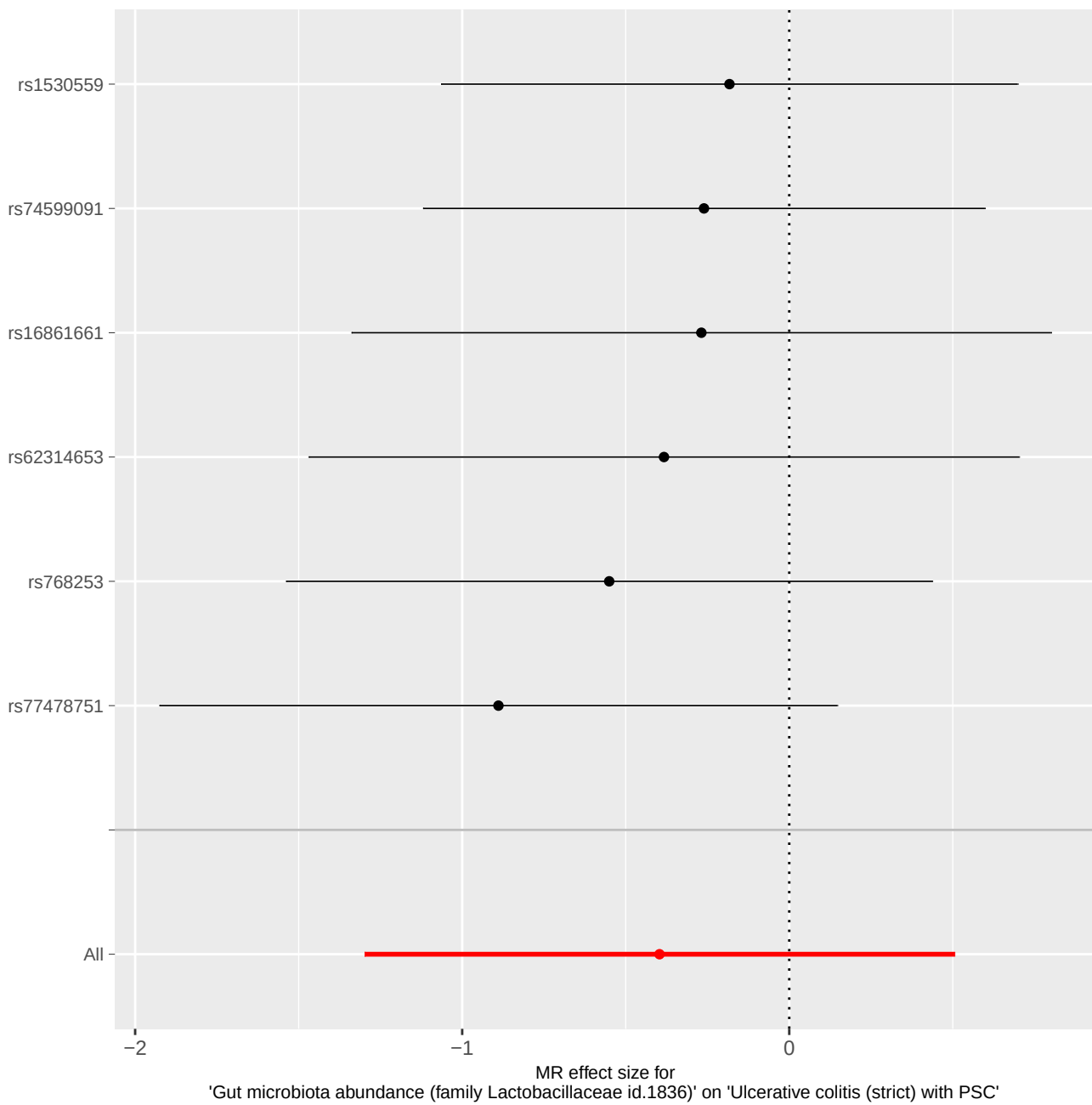


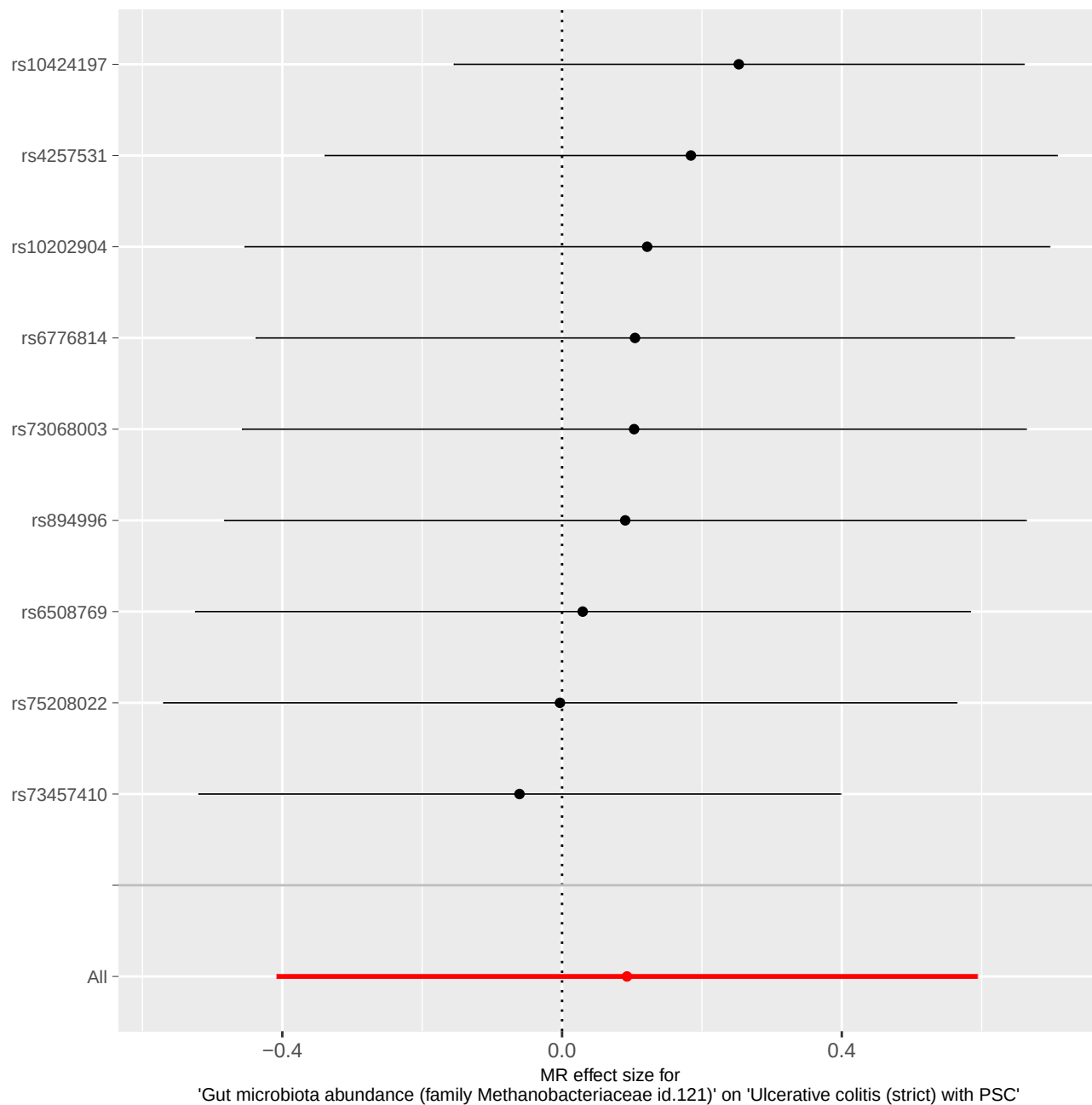


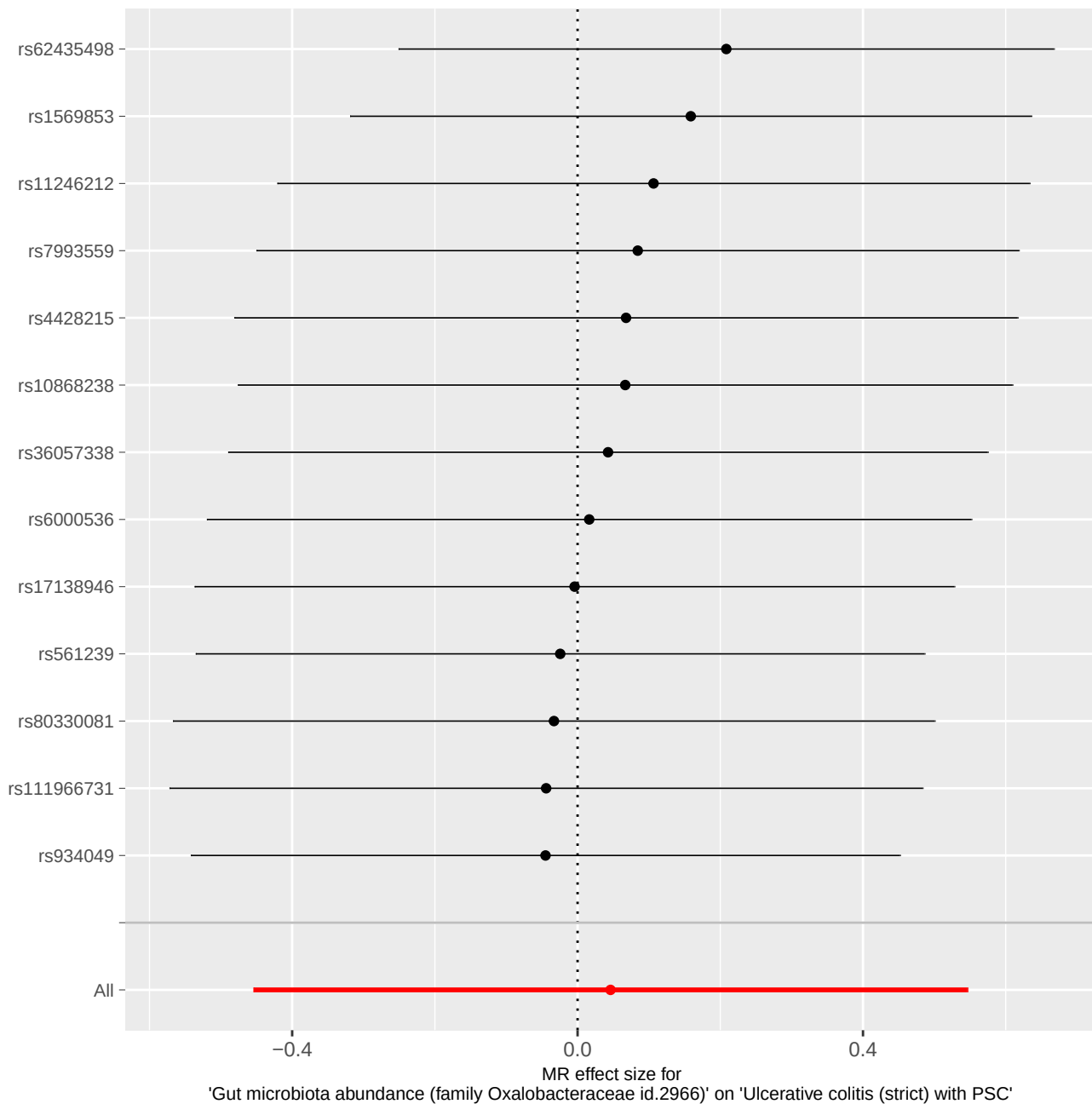


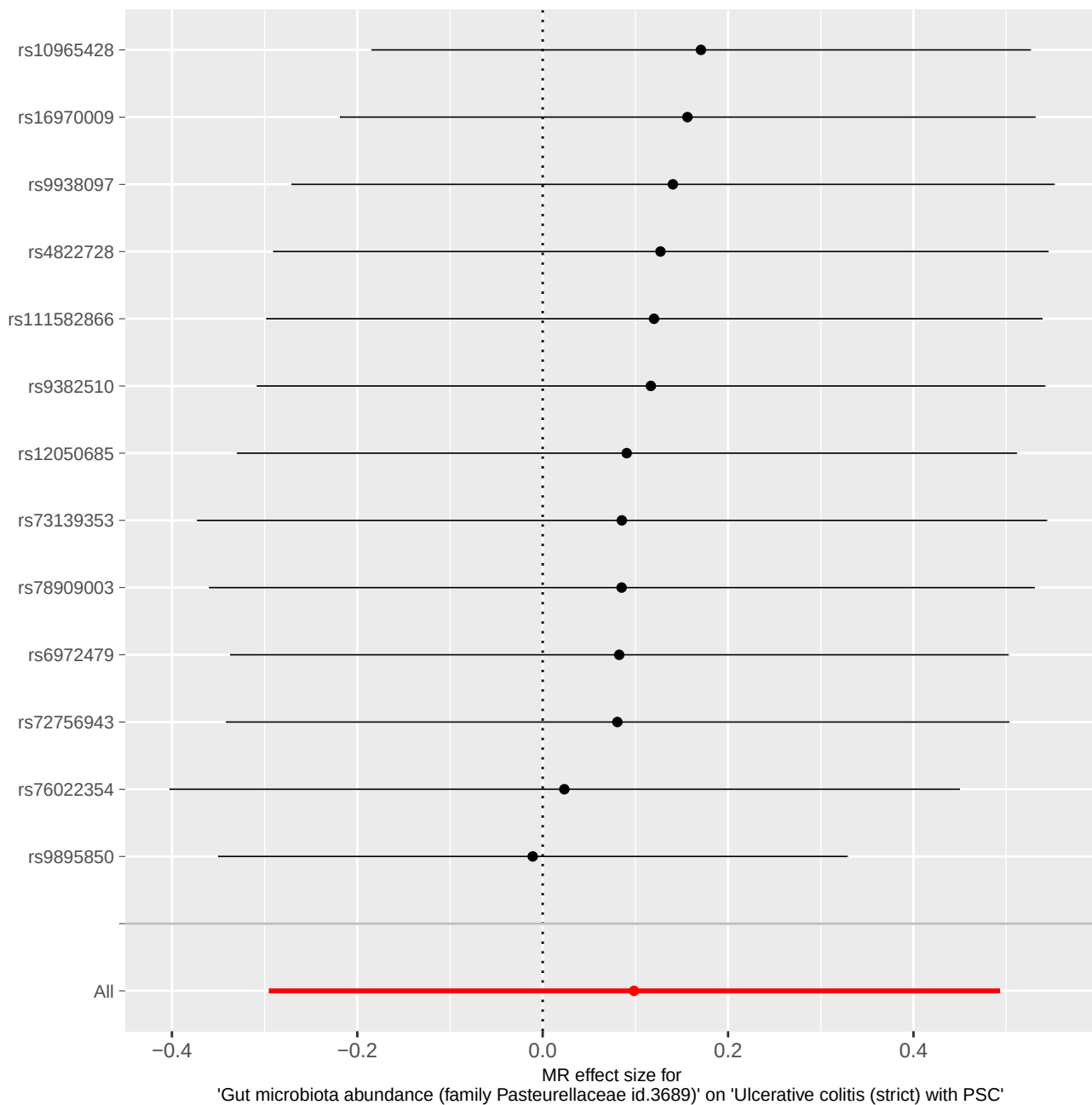


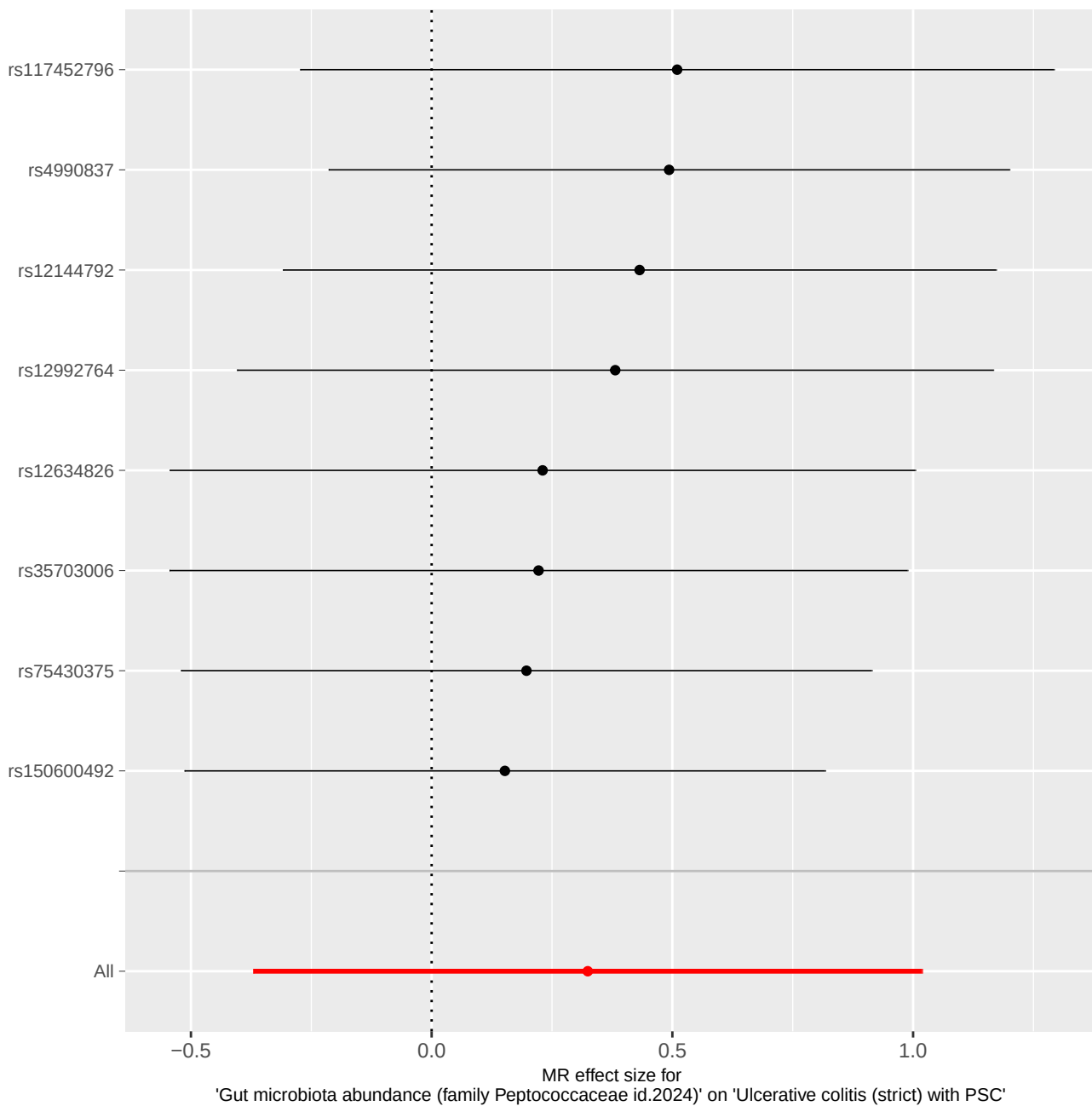


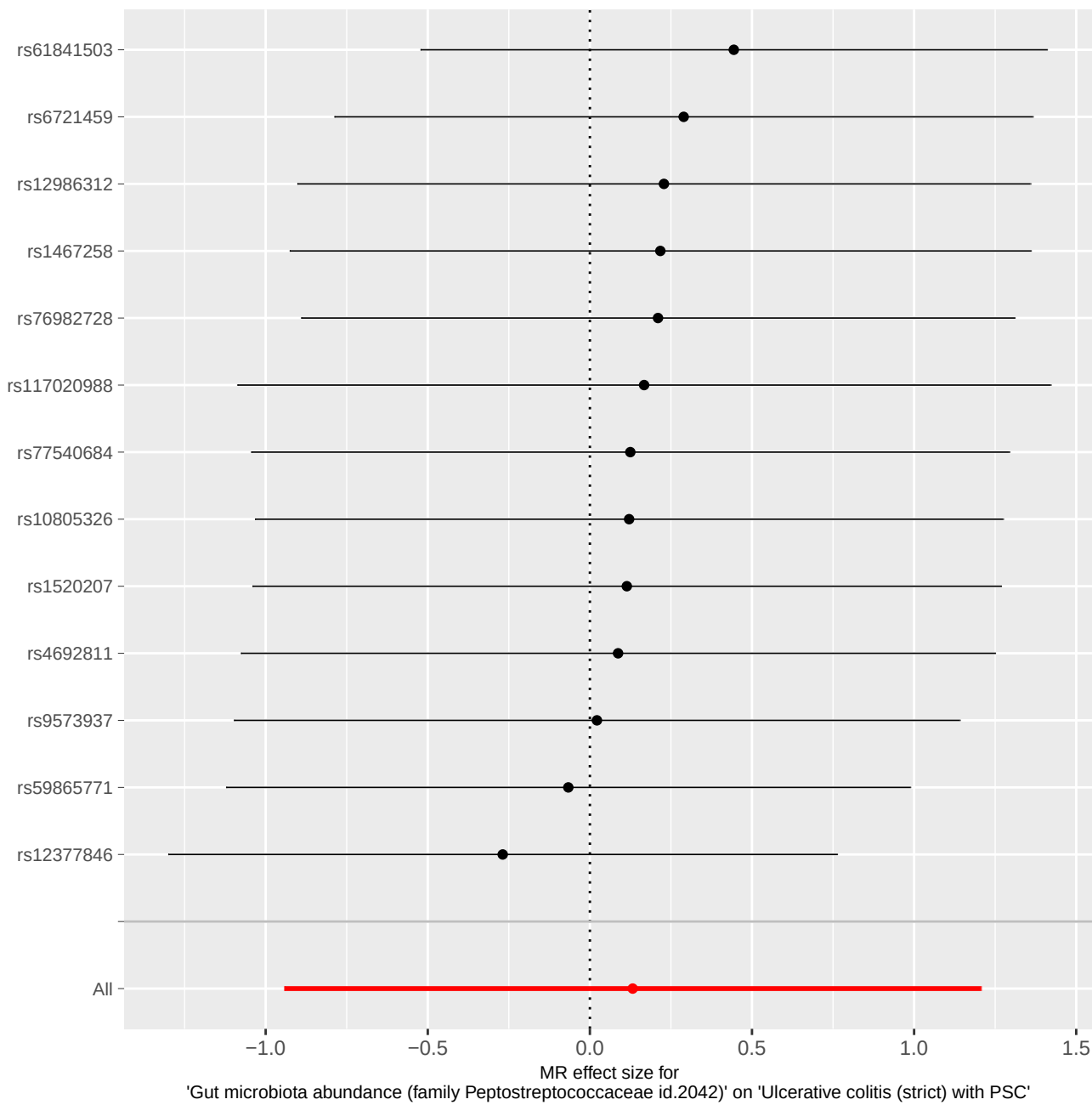


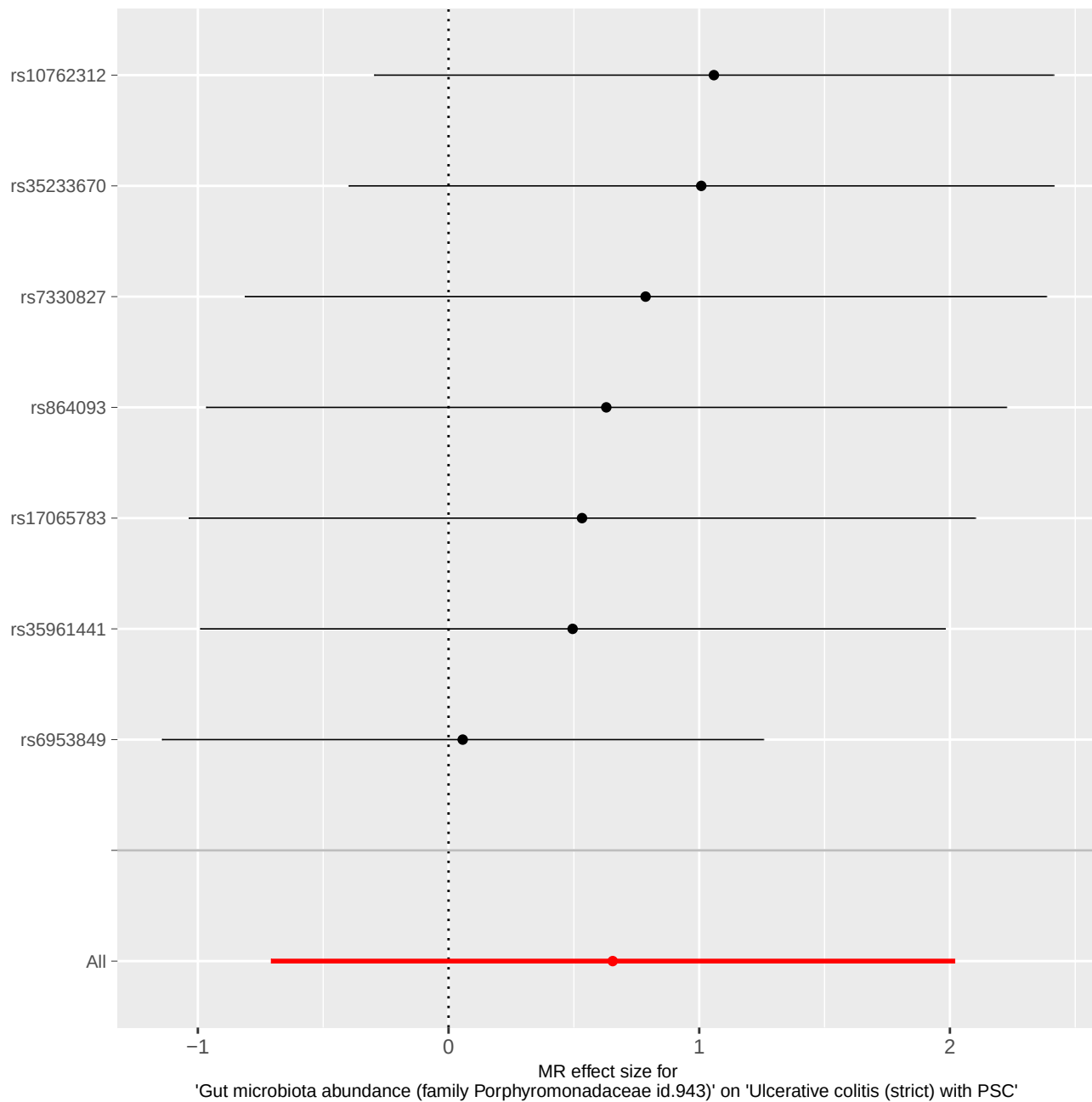


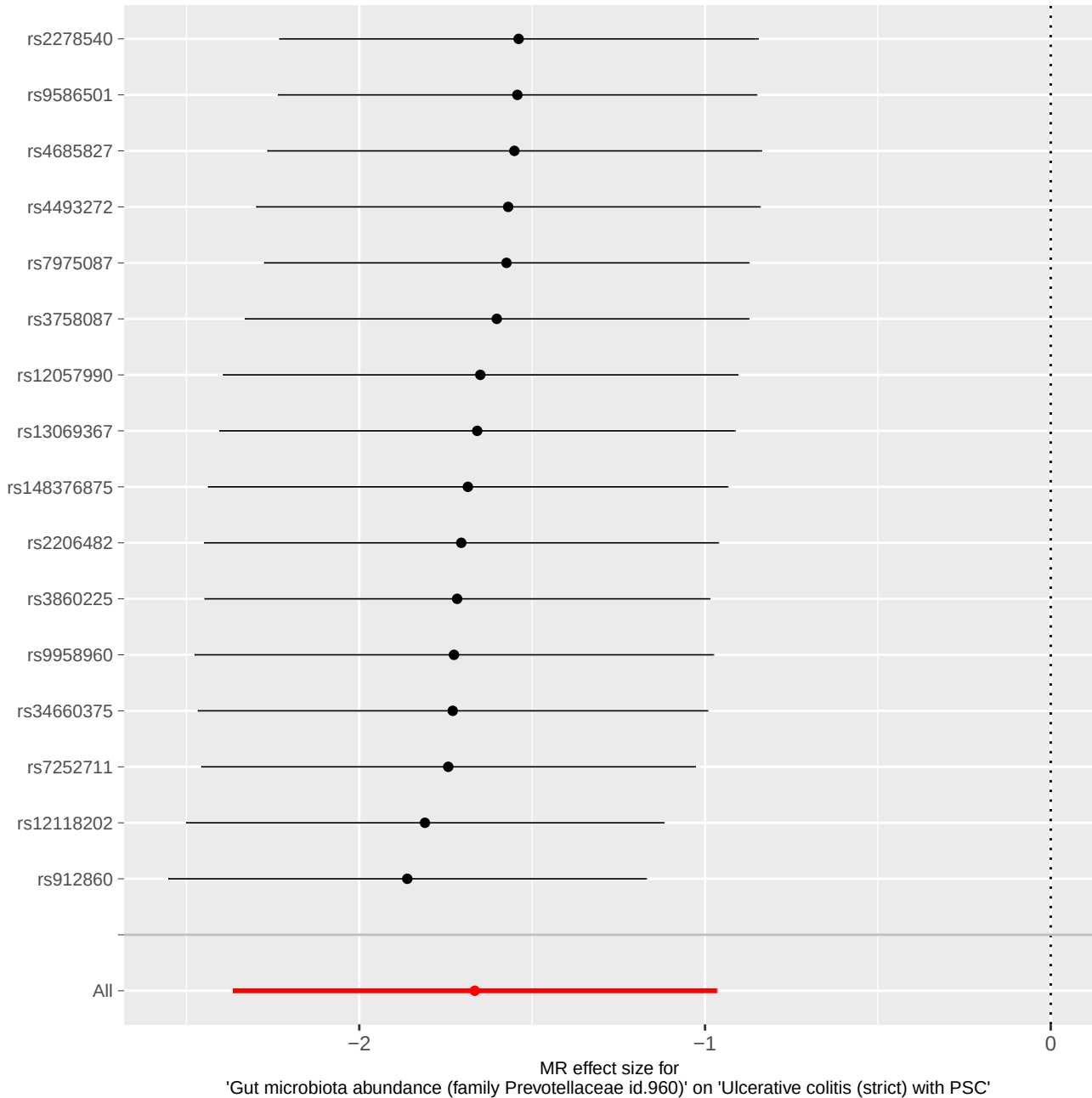


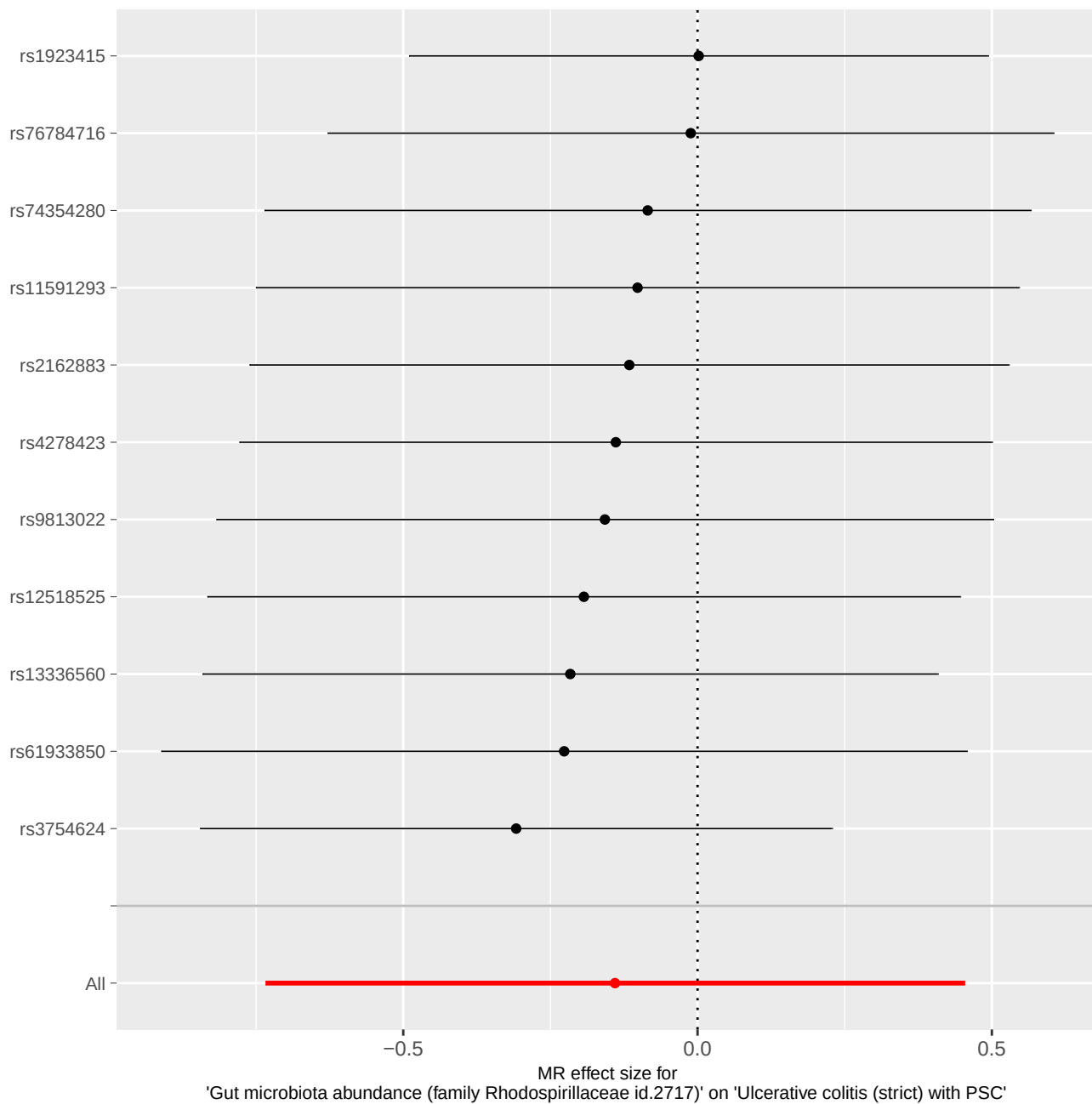


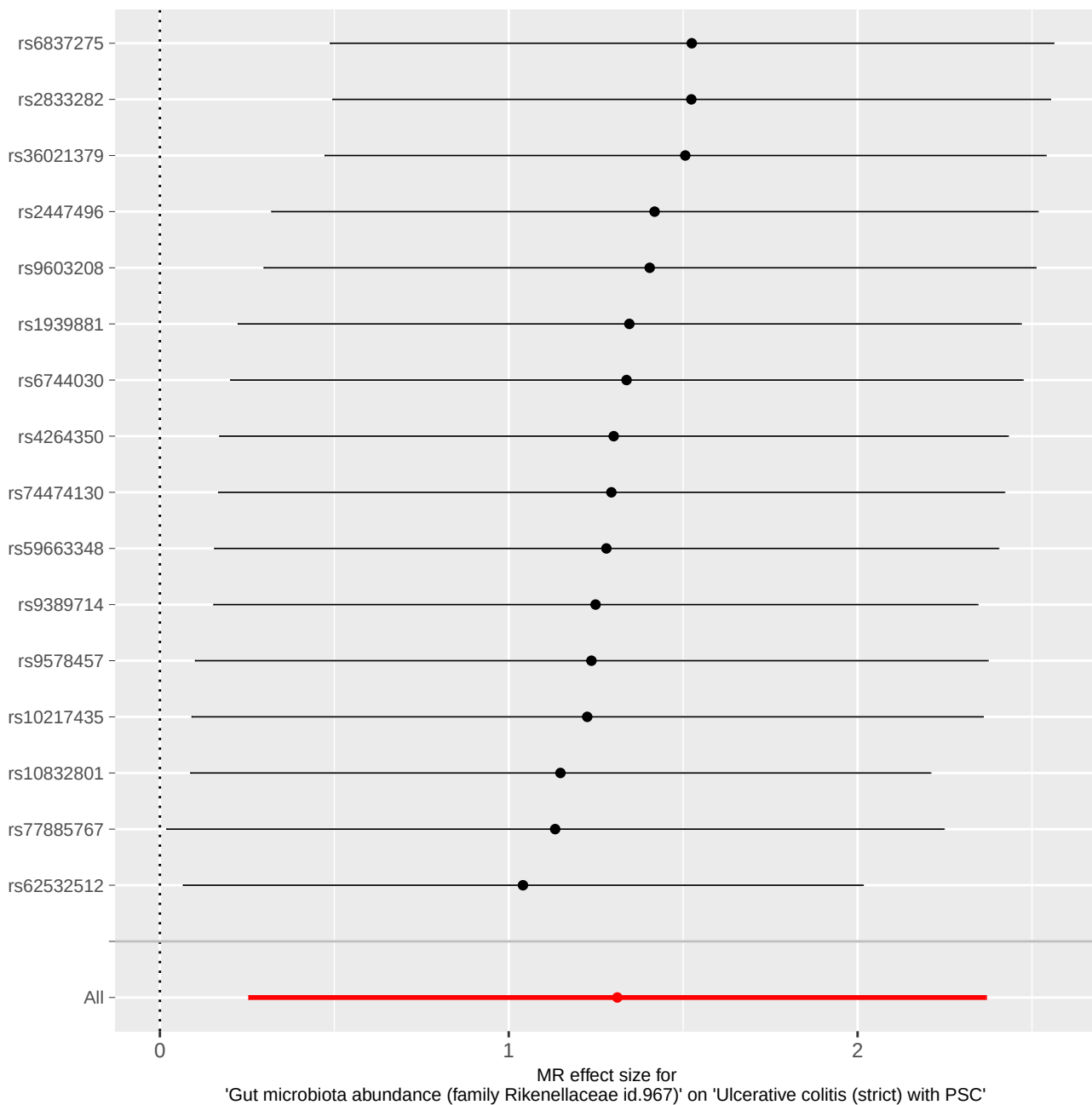


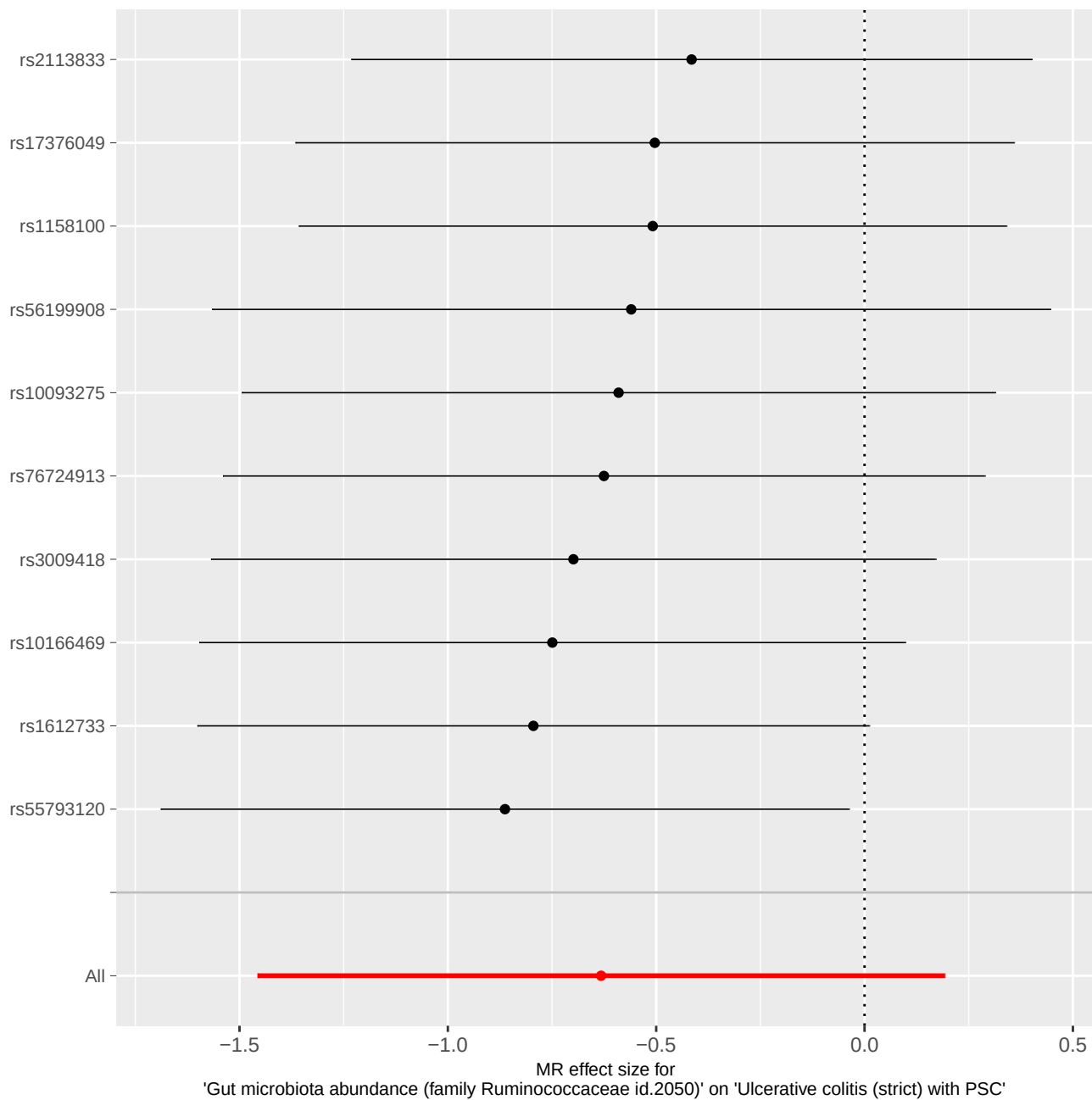






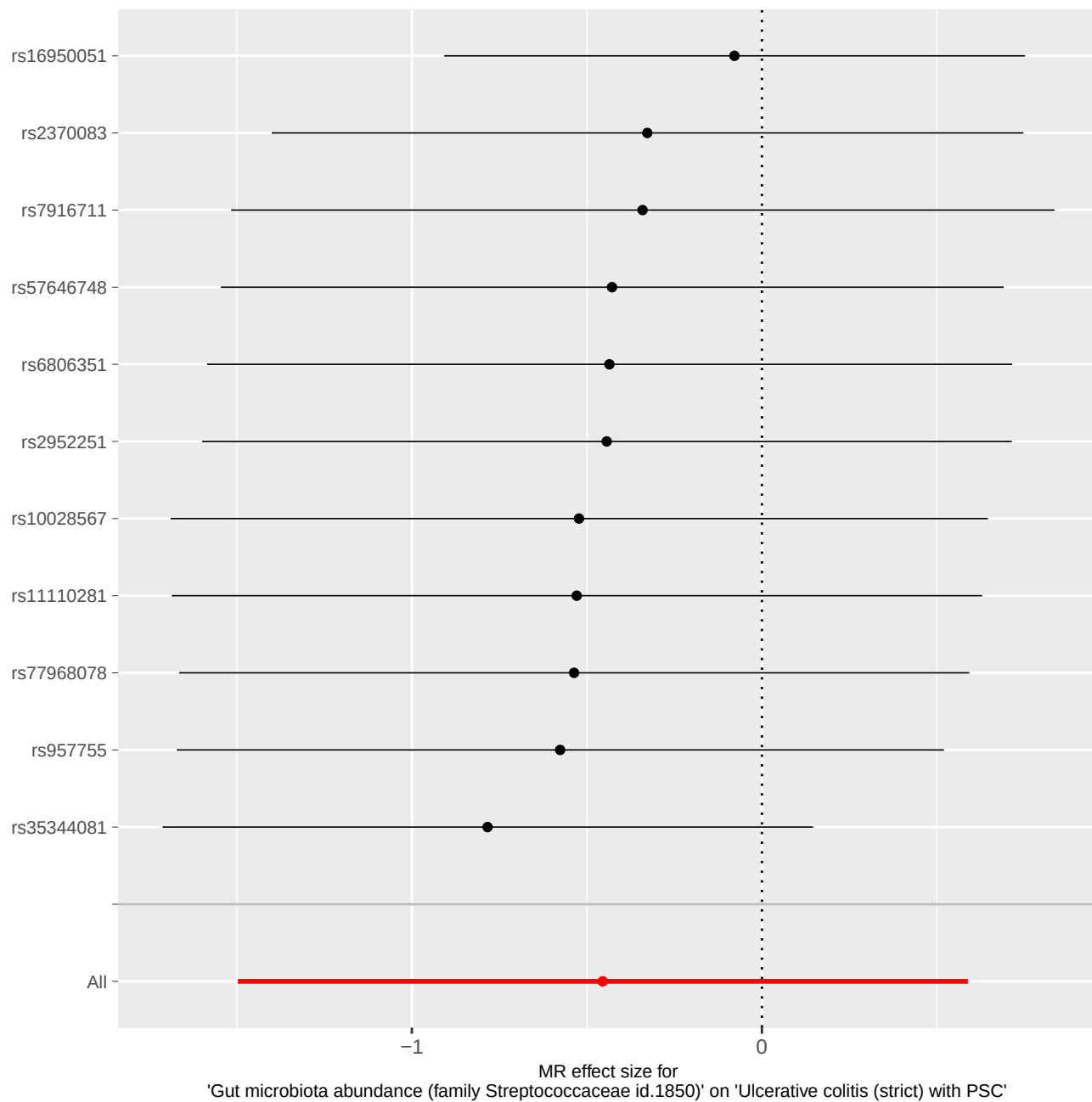


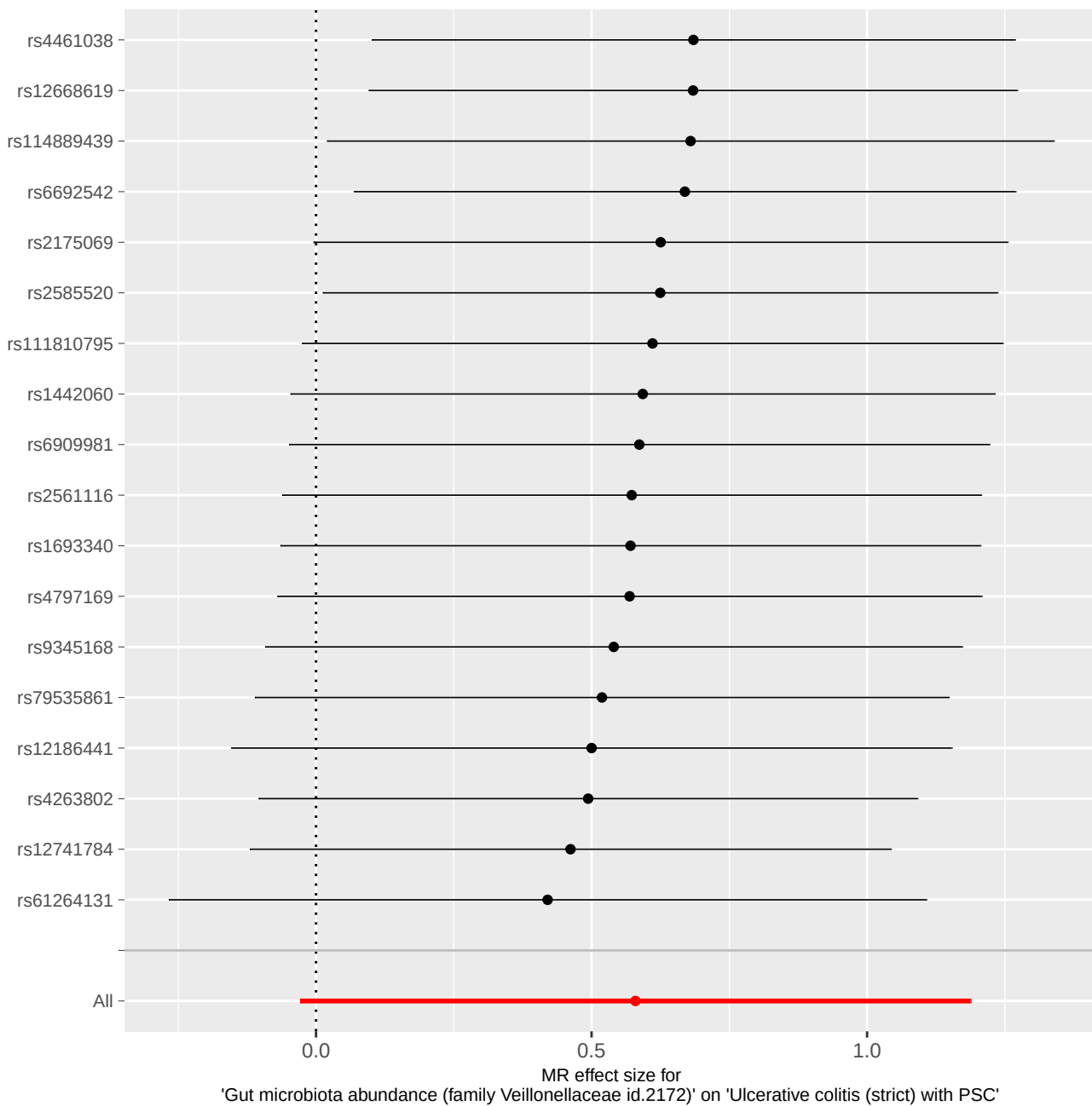




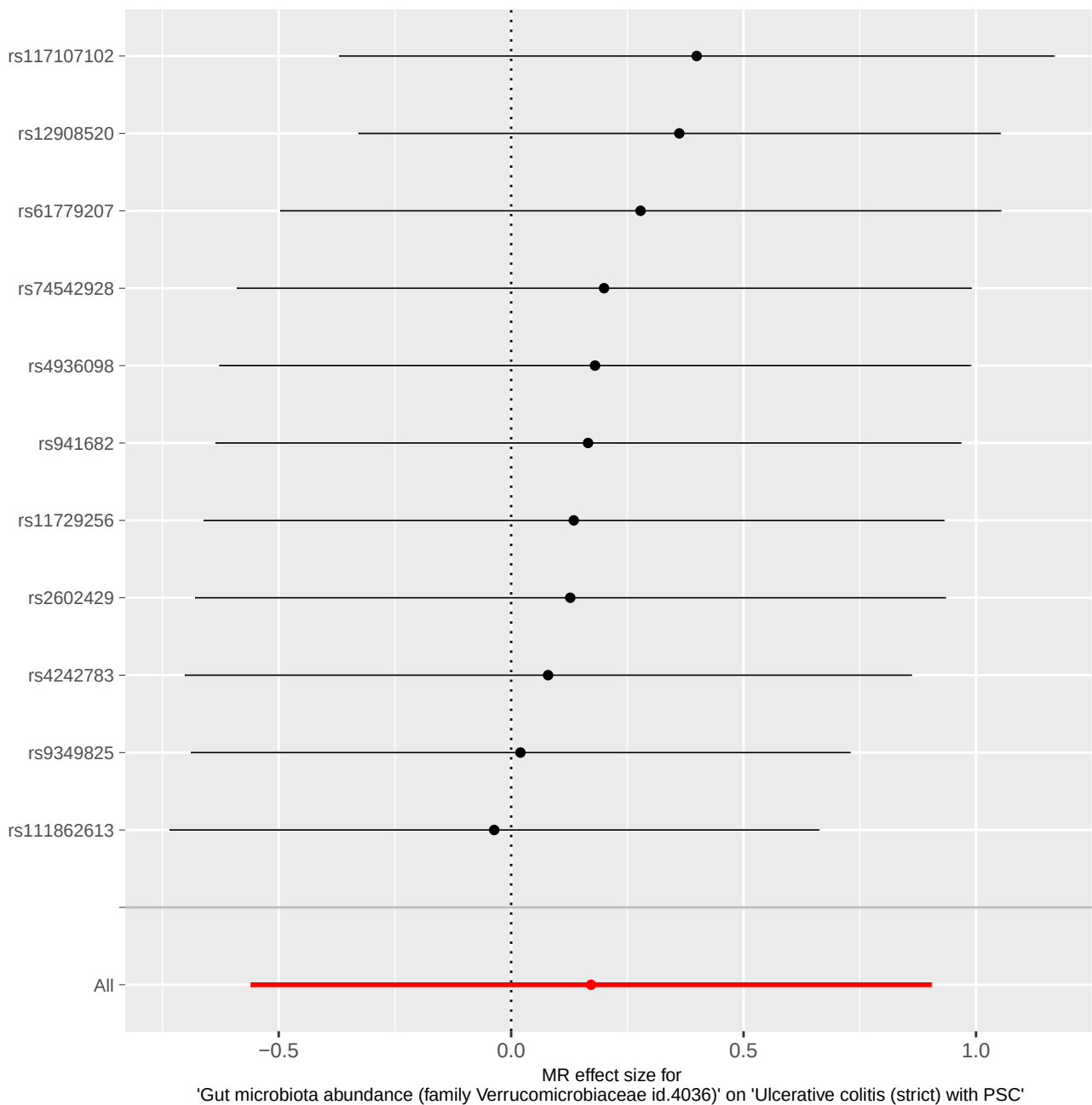
MR effect size for

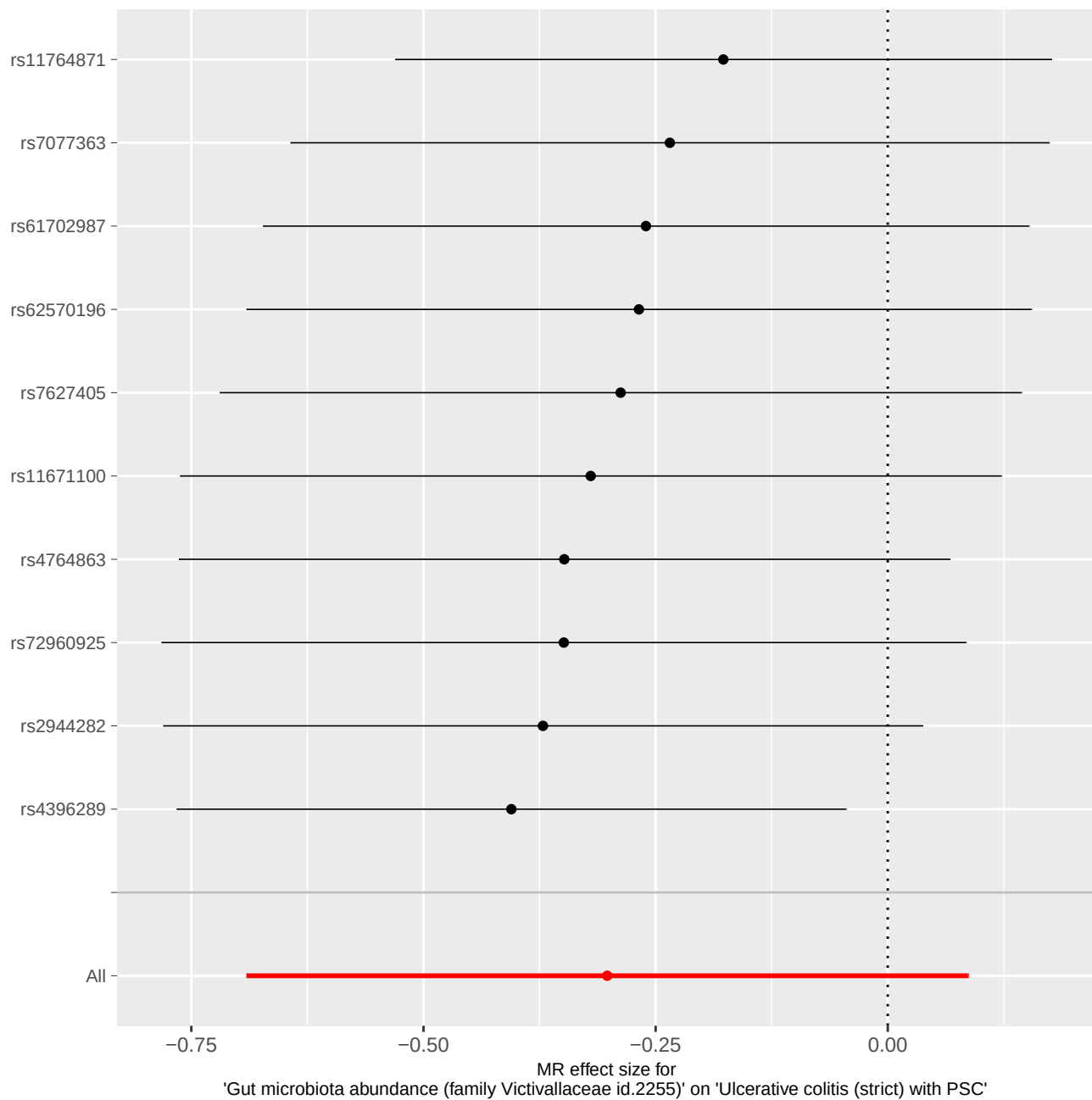
'Gut microbiota abundance (family Ruminococcaceae id.2050)' on 'Ulcerative colitis (strict) with PSC'

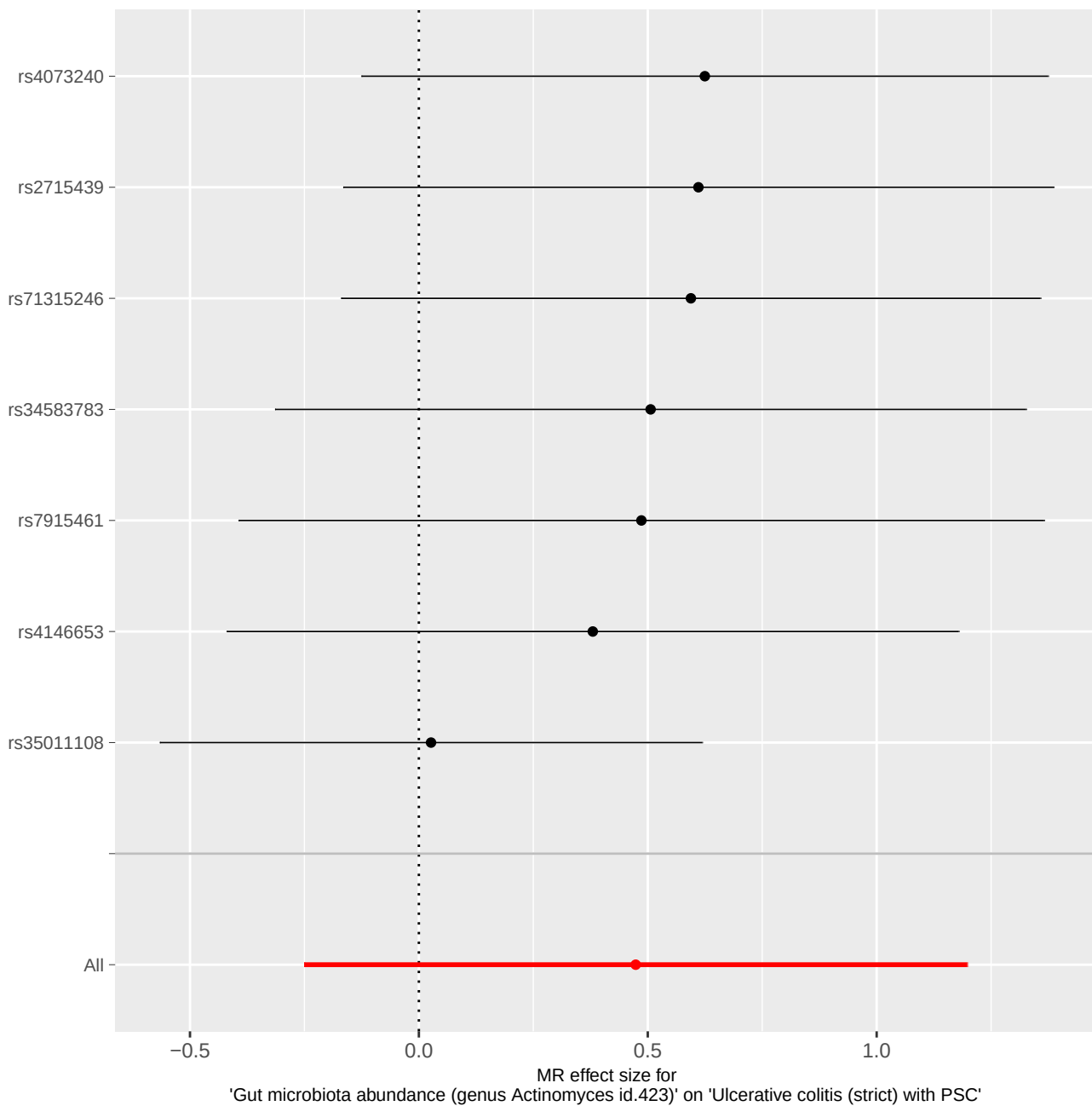


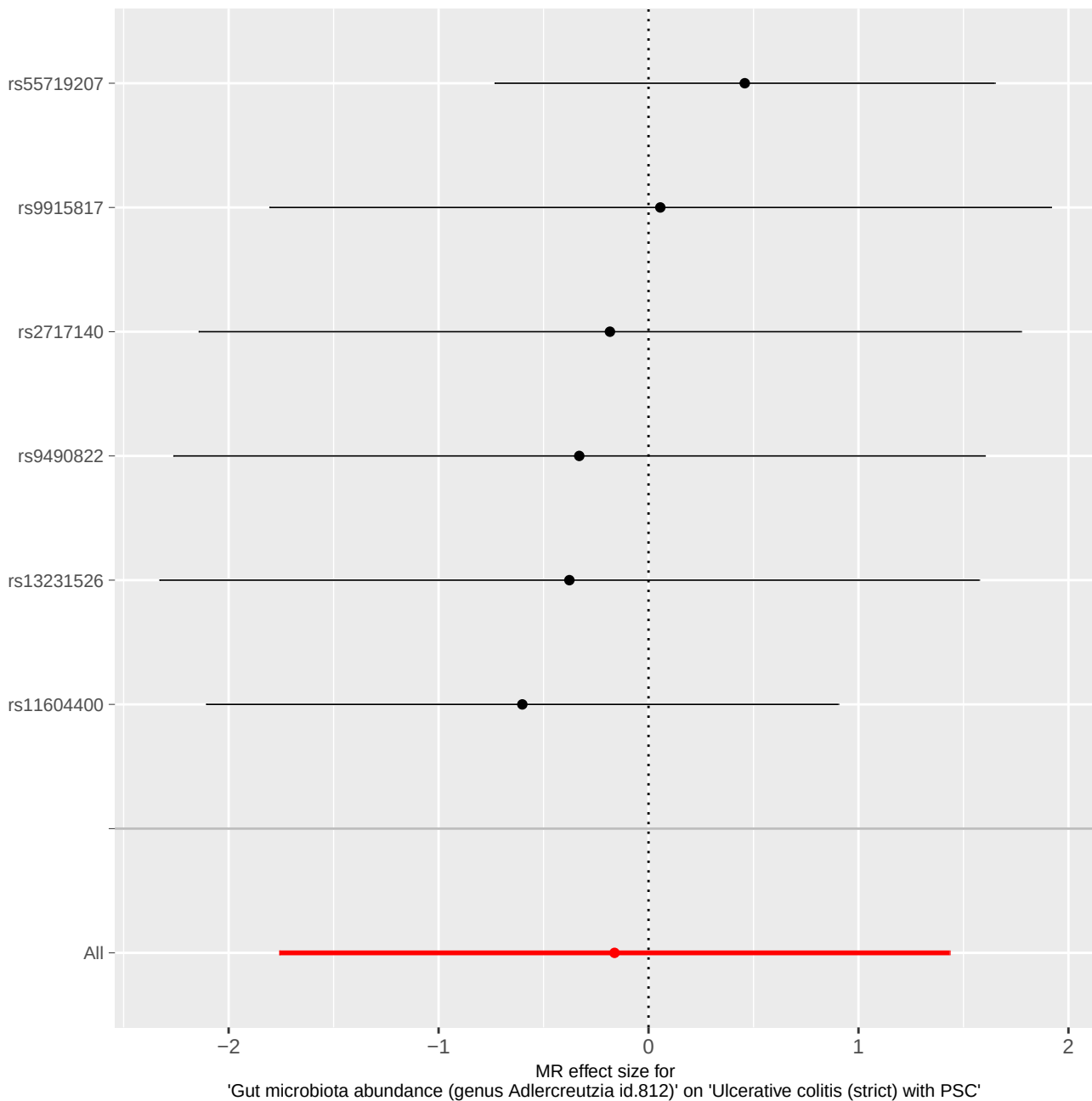


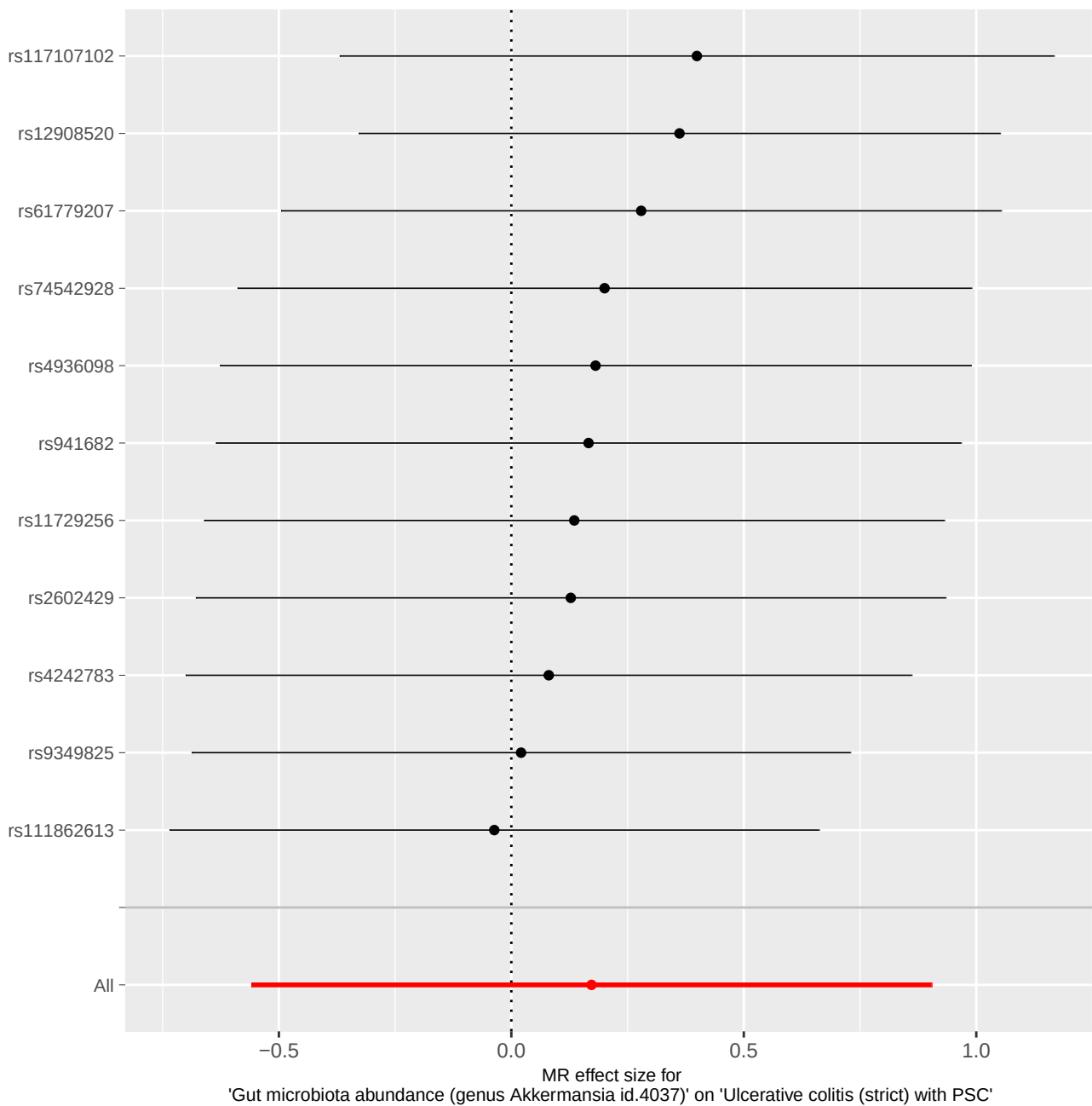
MR effect size for
'Gut microbiota abundance (family Veillonellaceae id.2172)' on 'Ulcerative colitis (strict) with PSC'

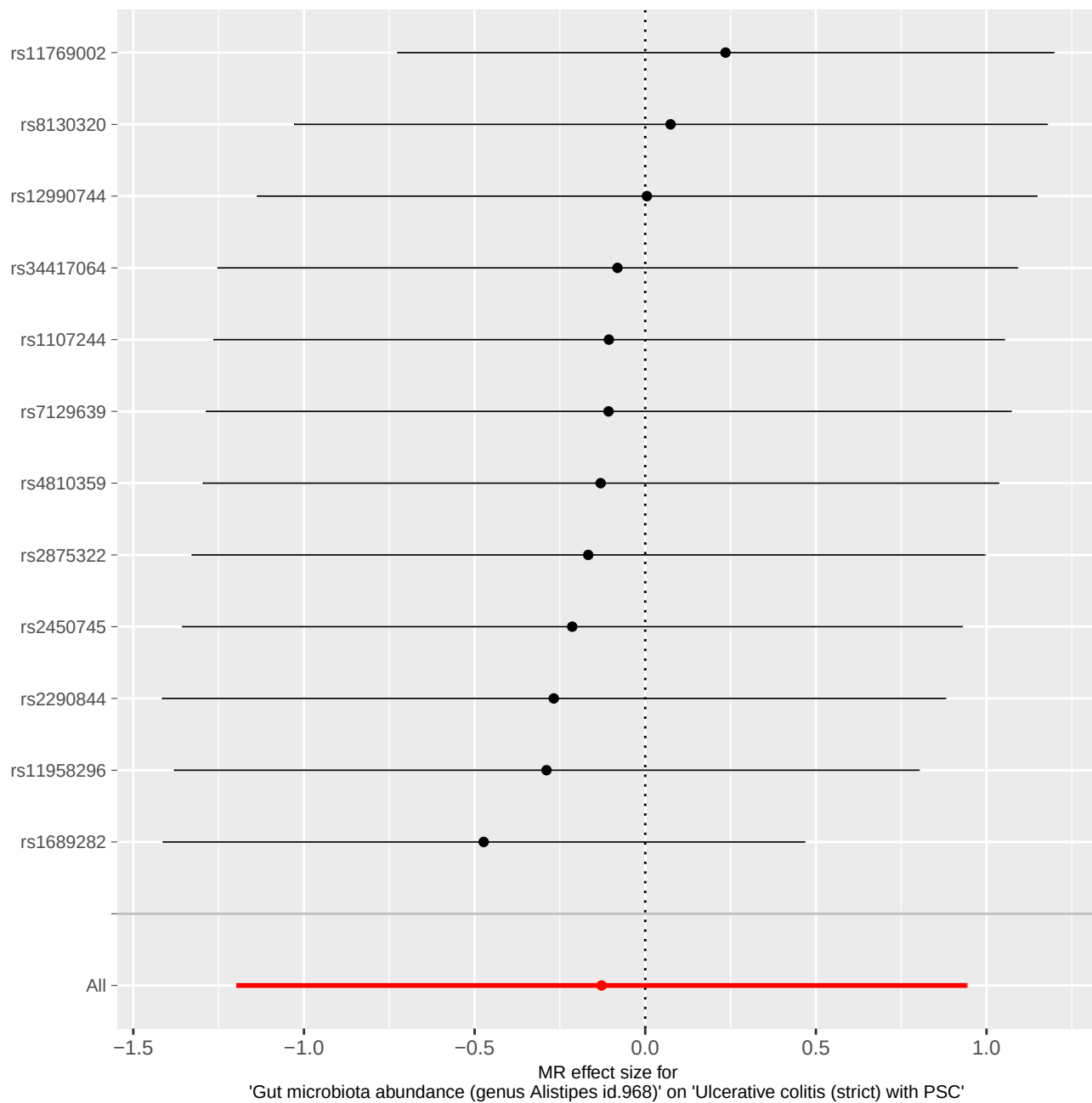


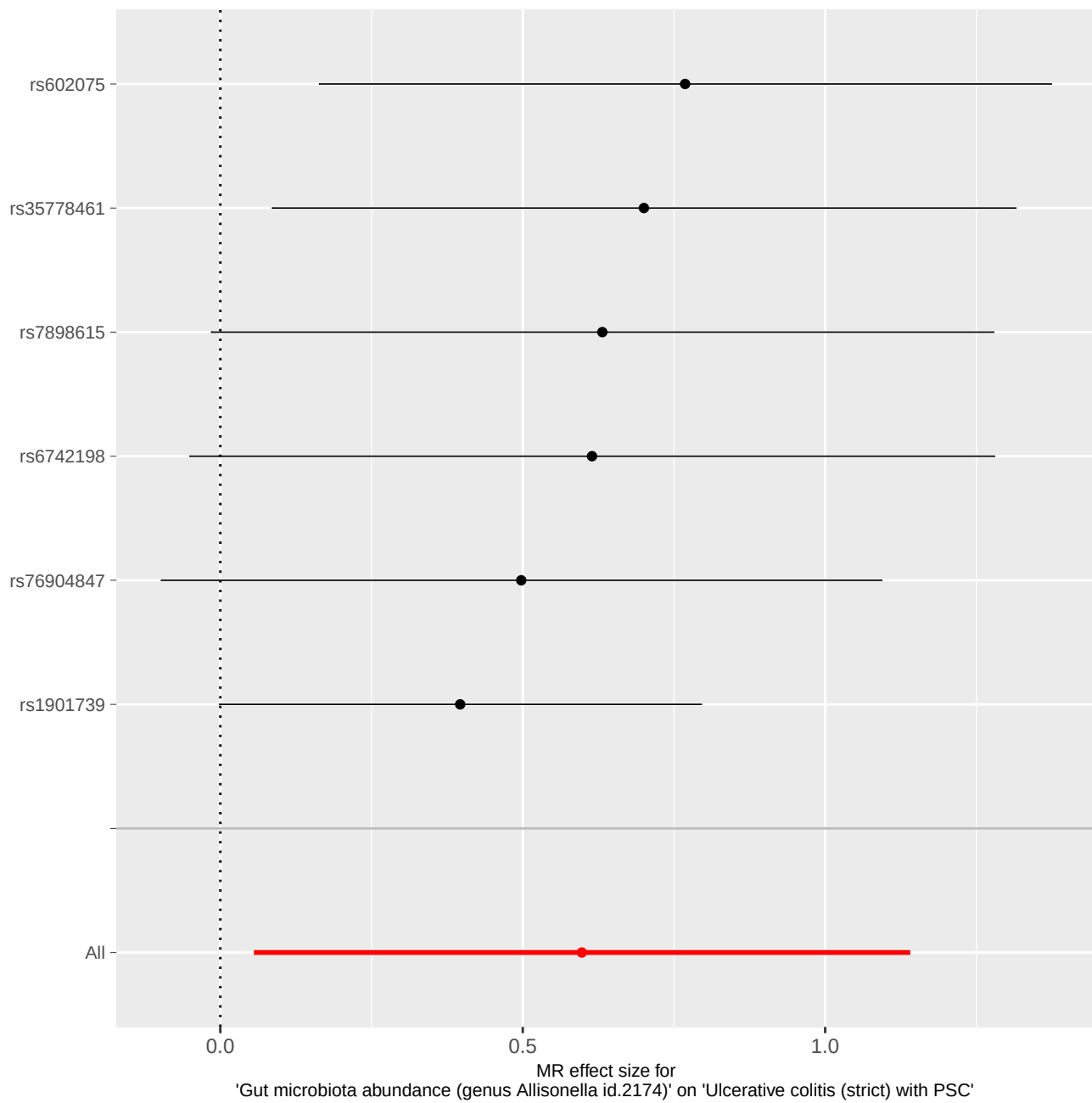


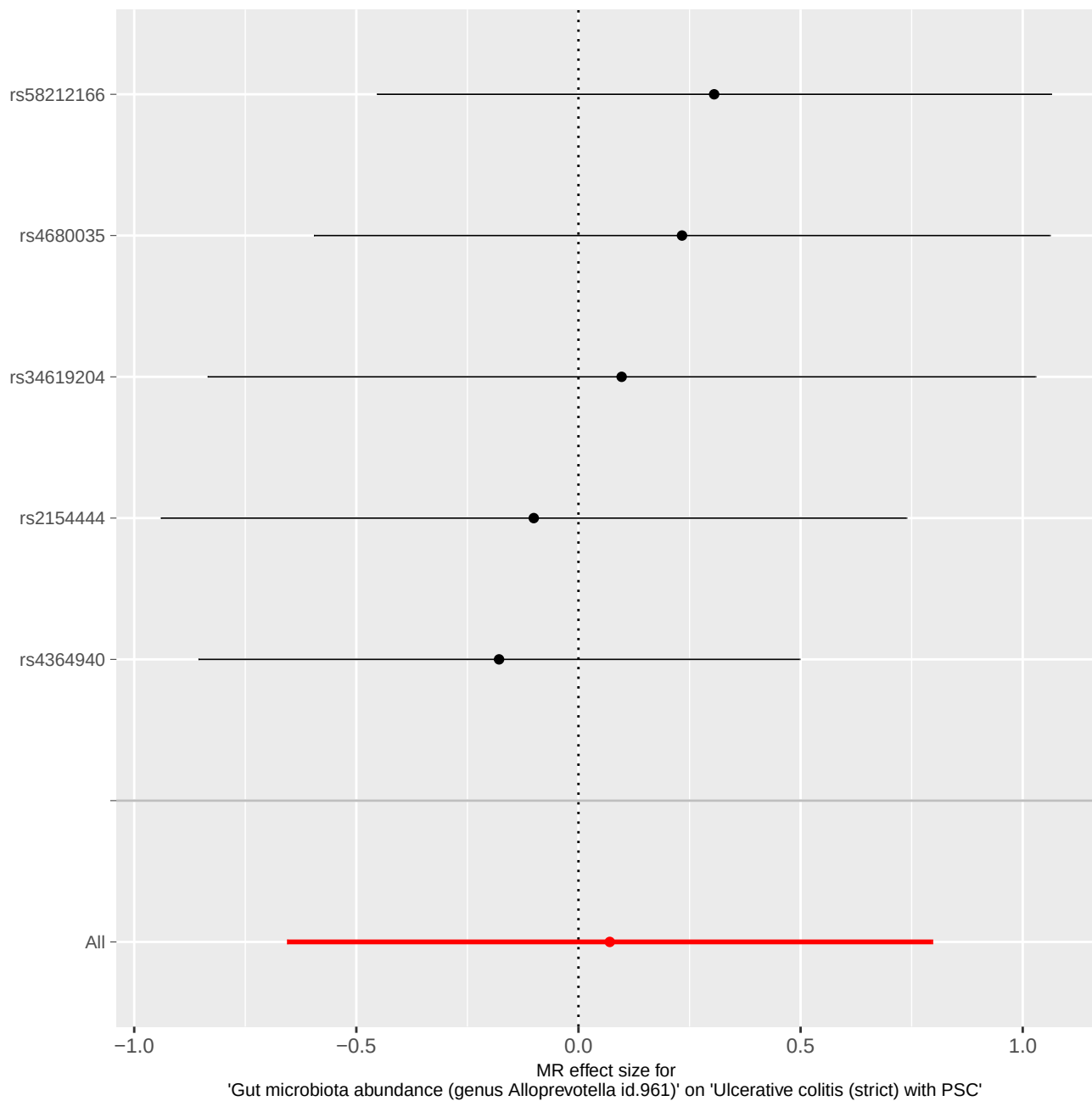


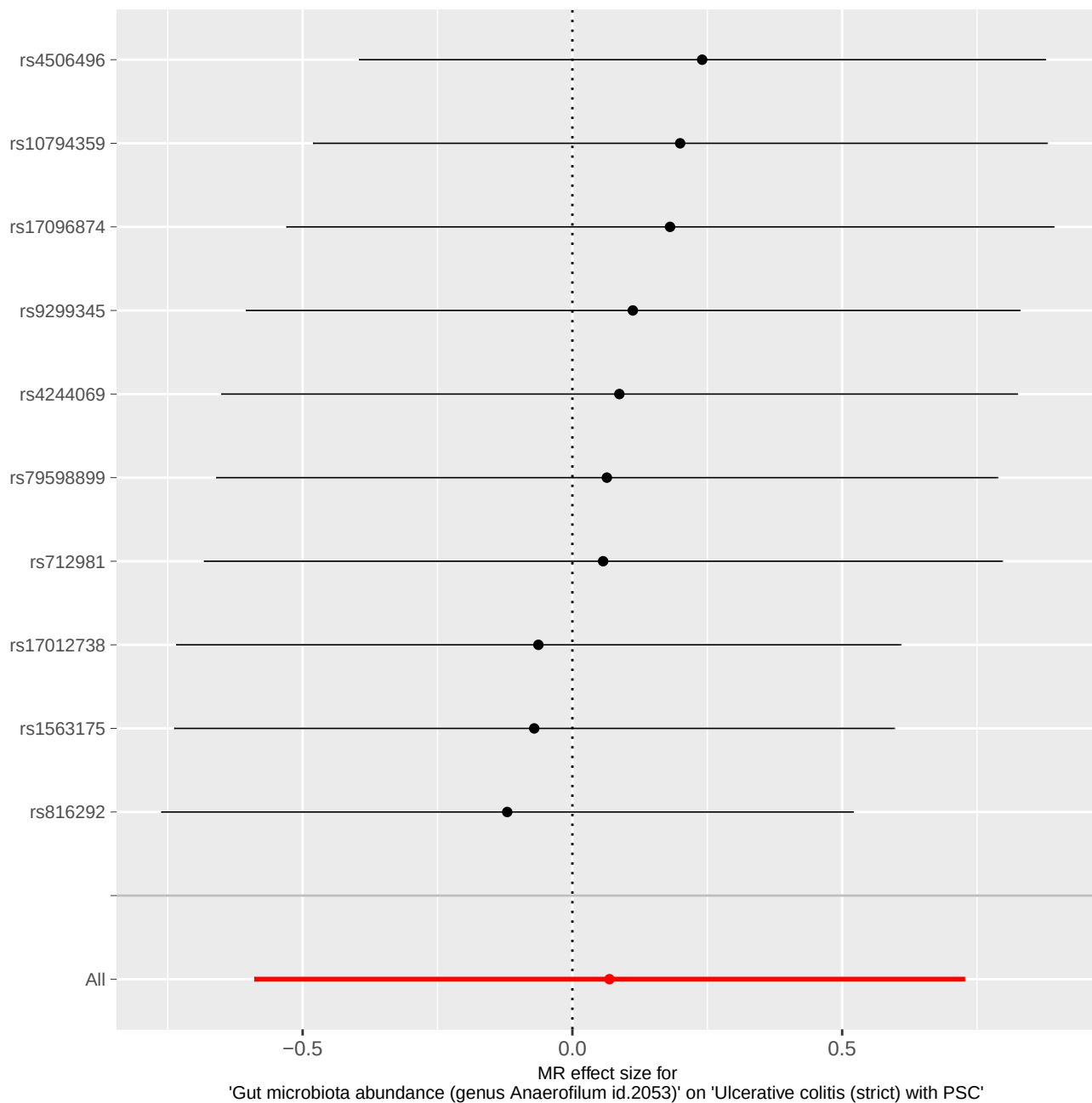


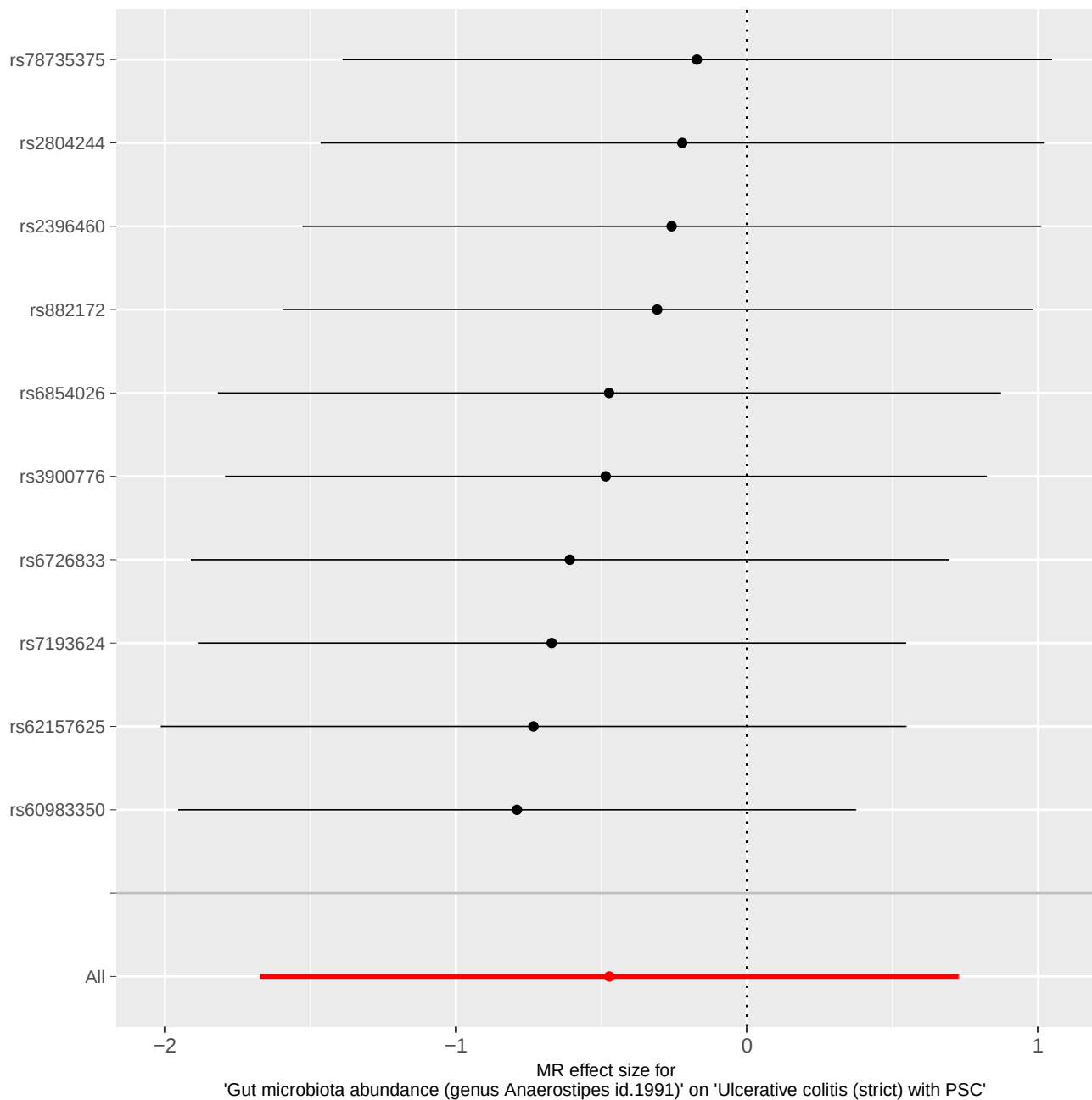


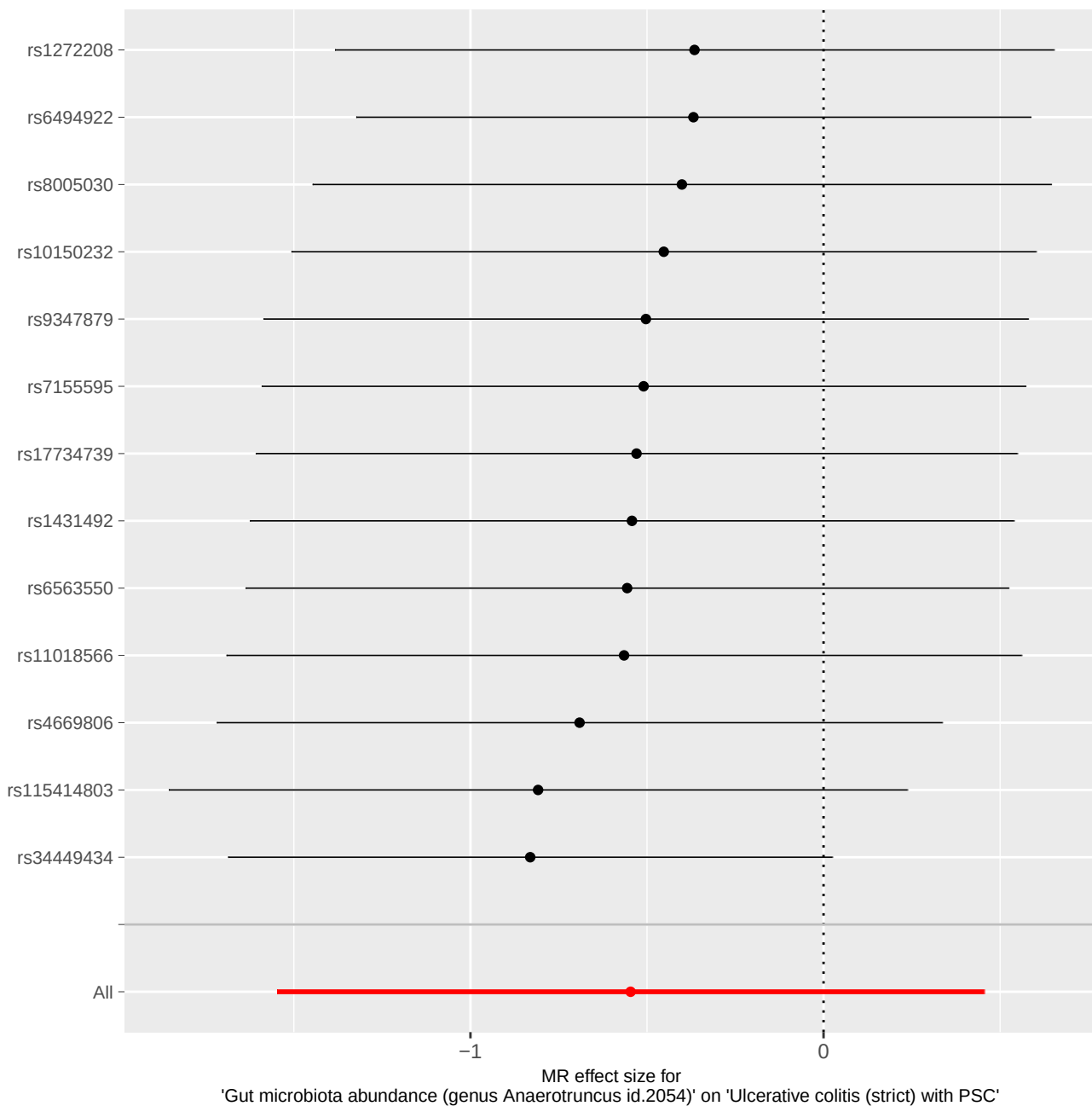


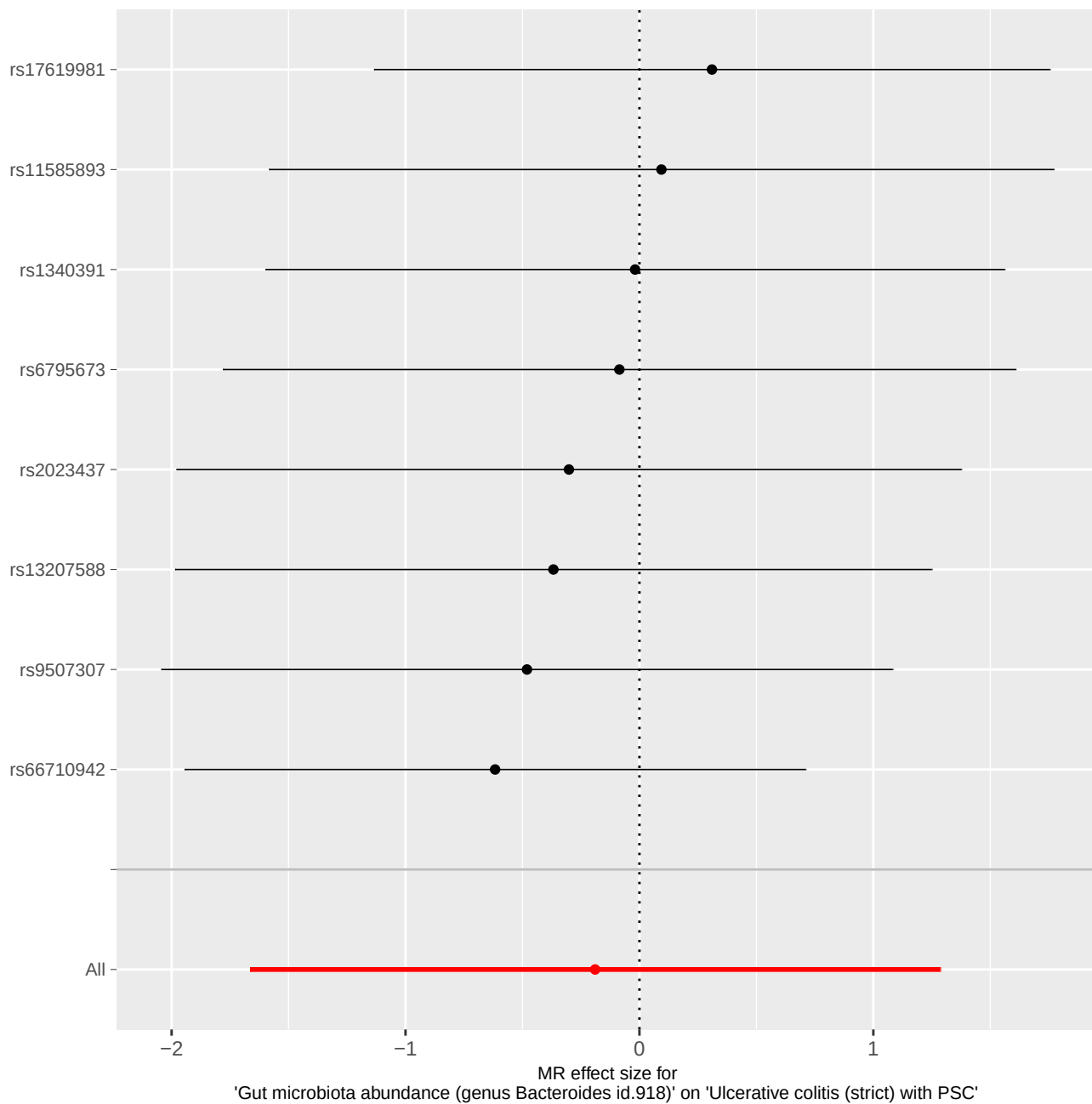




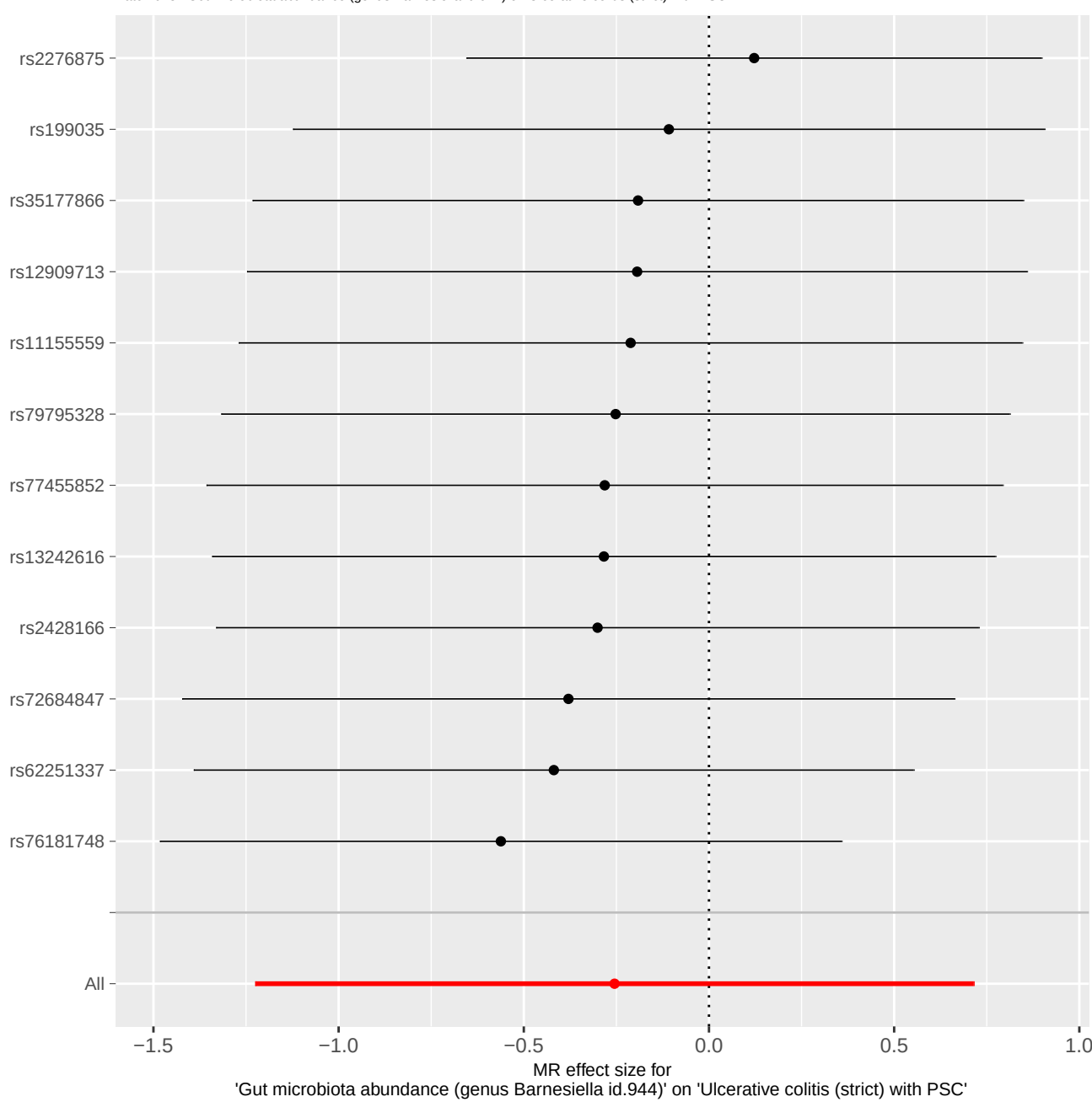


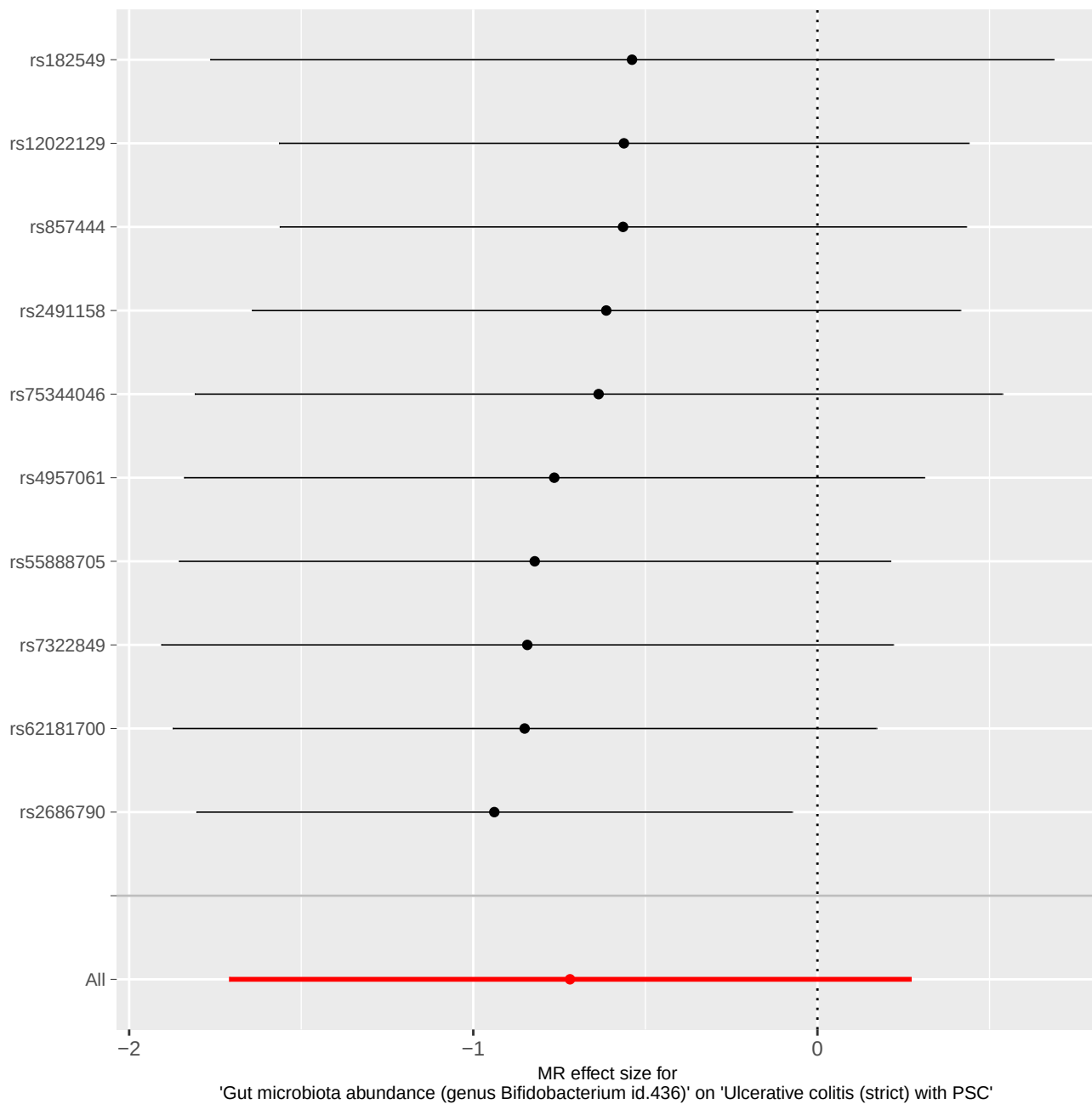


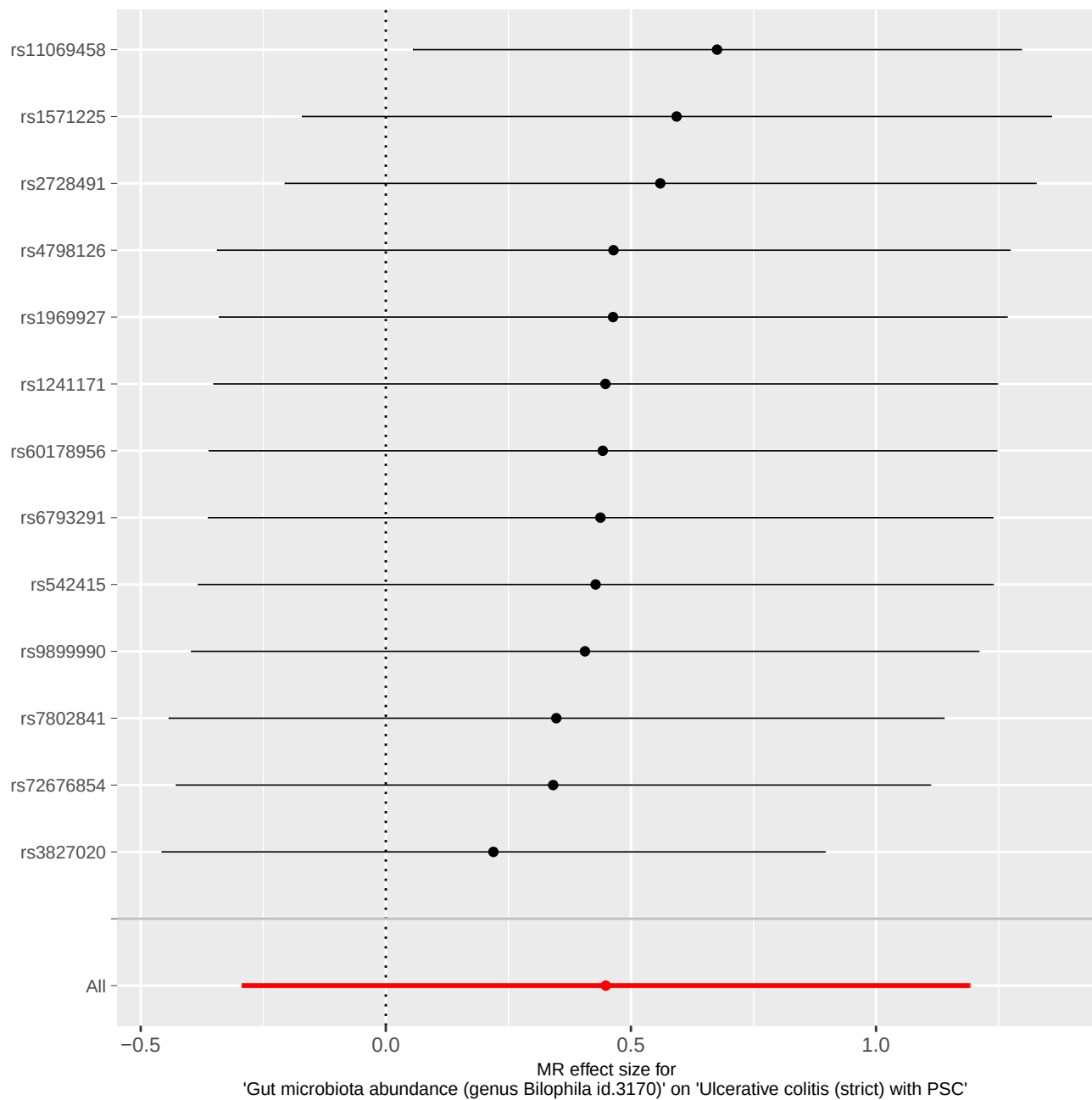


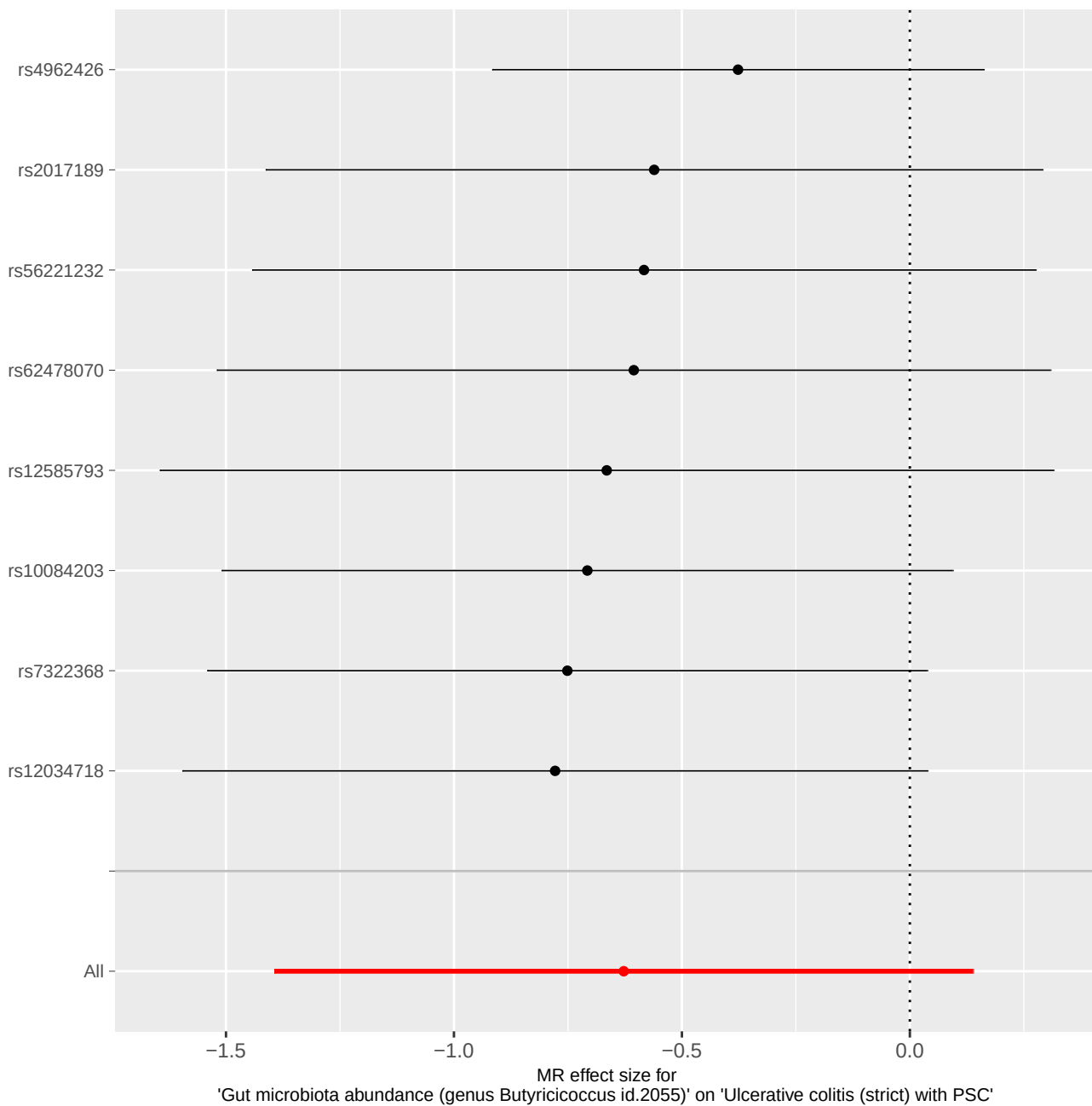


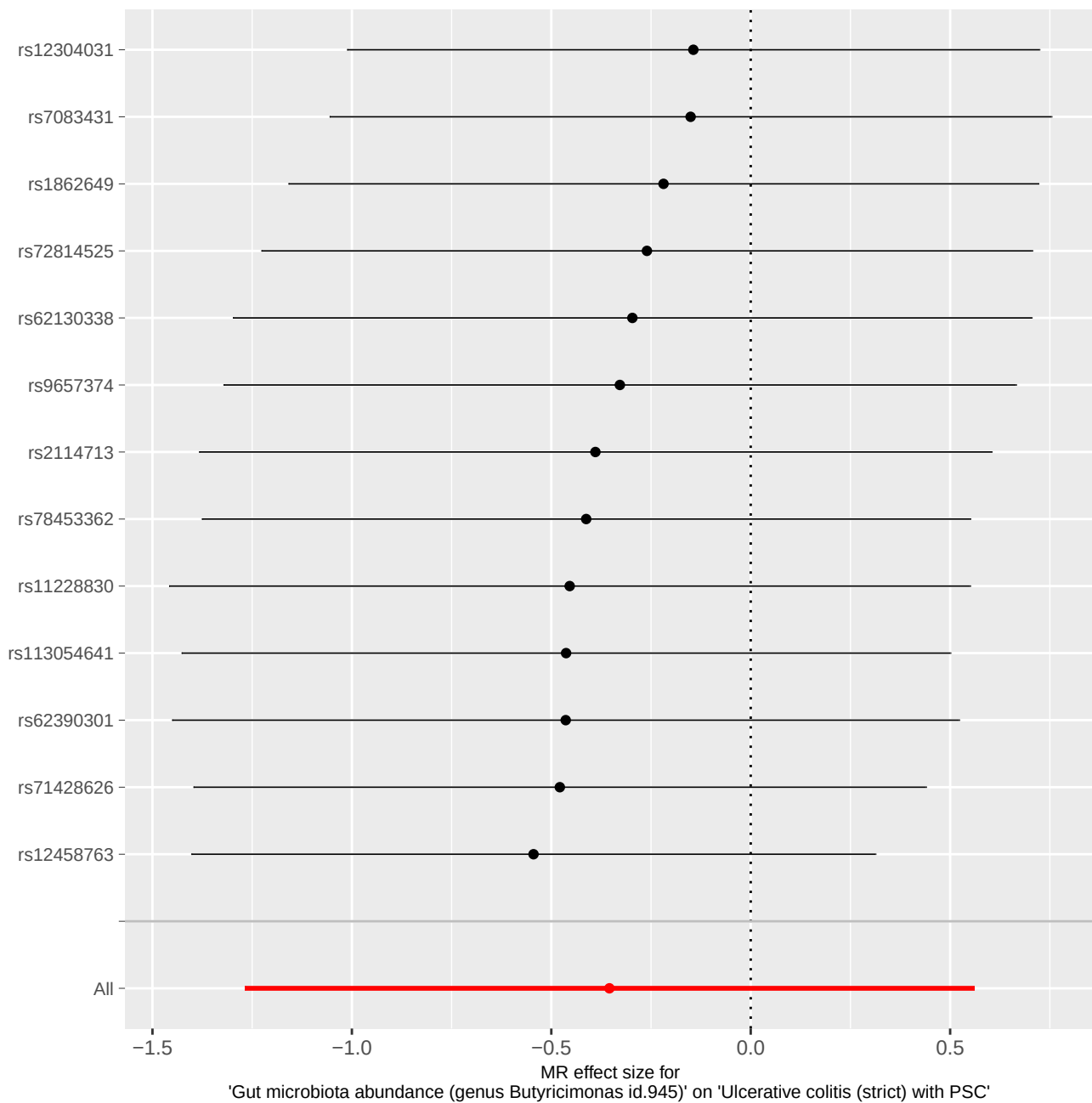
MR effect size for
'Gut microbiota abundance (genus Bacteroides id.918)' on 'Ulcerative colitis (strict) with PSC'

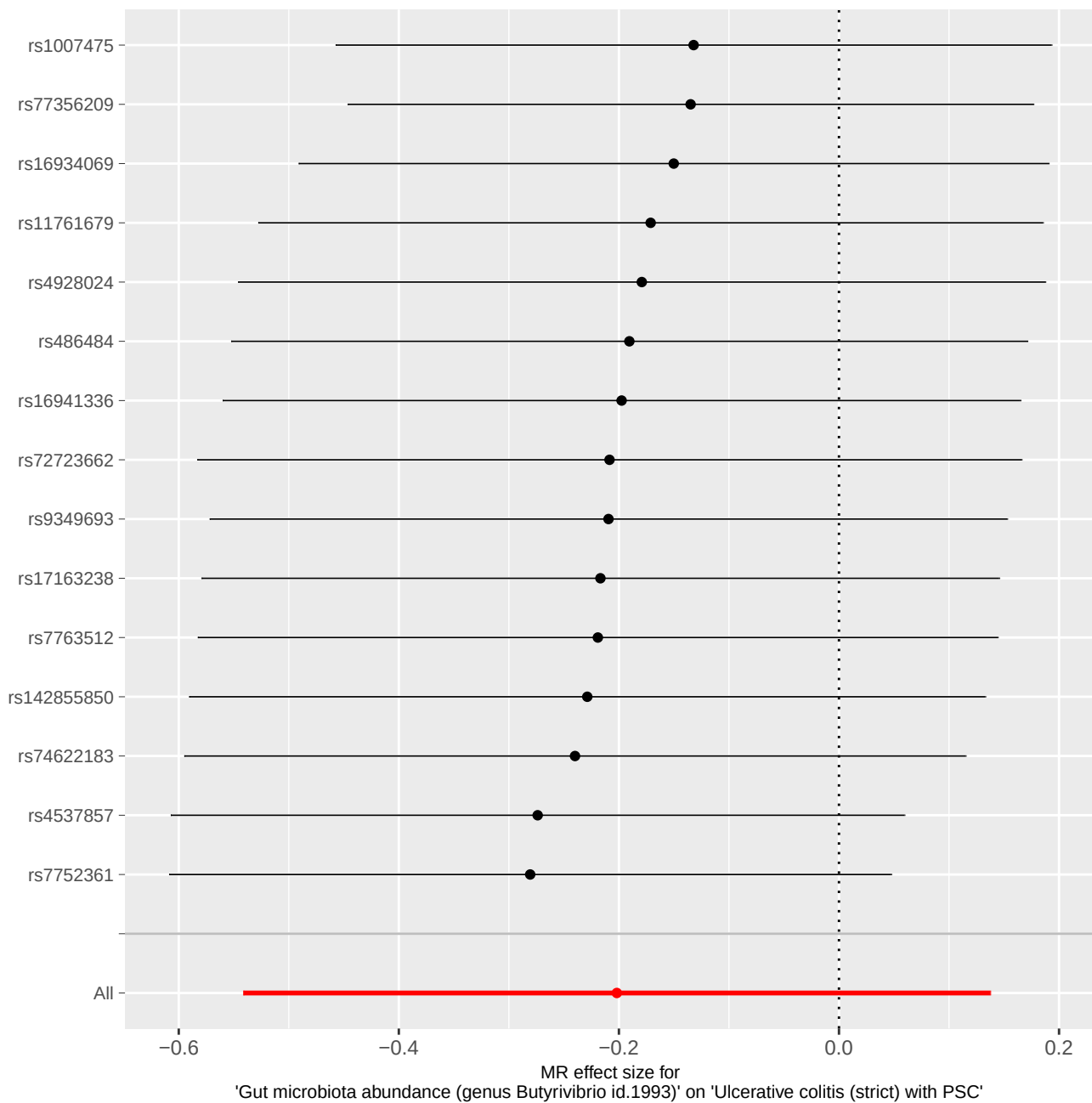




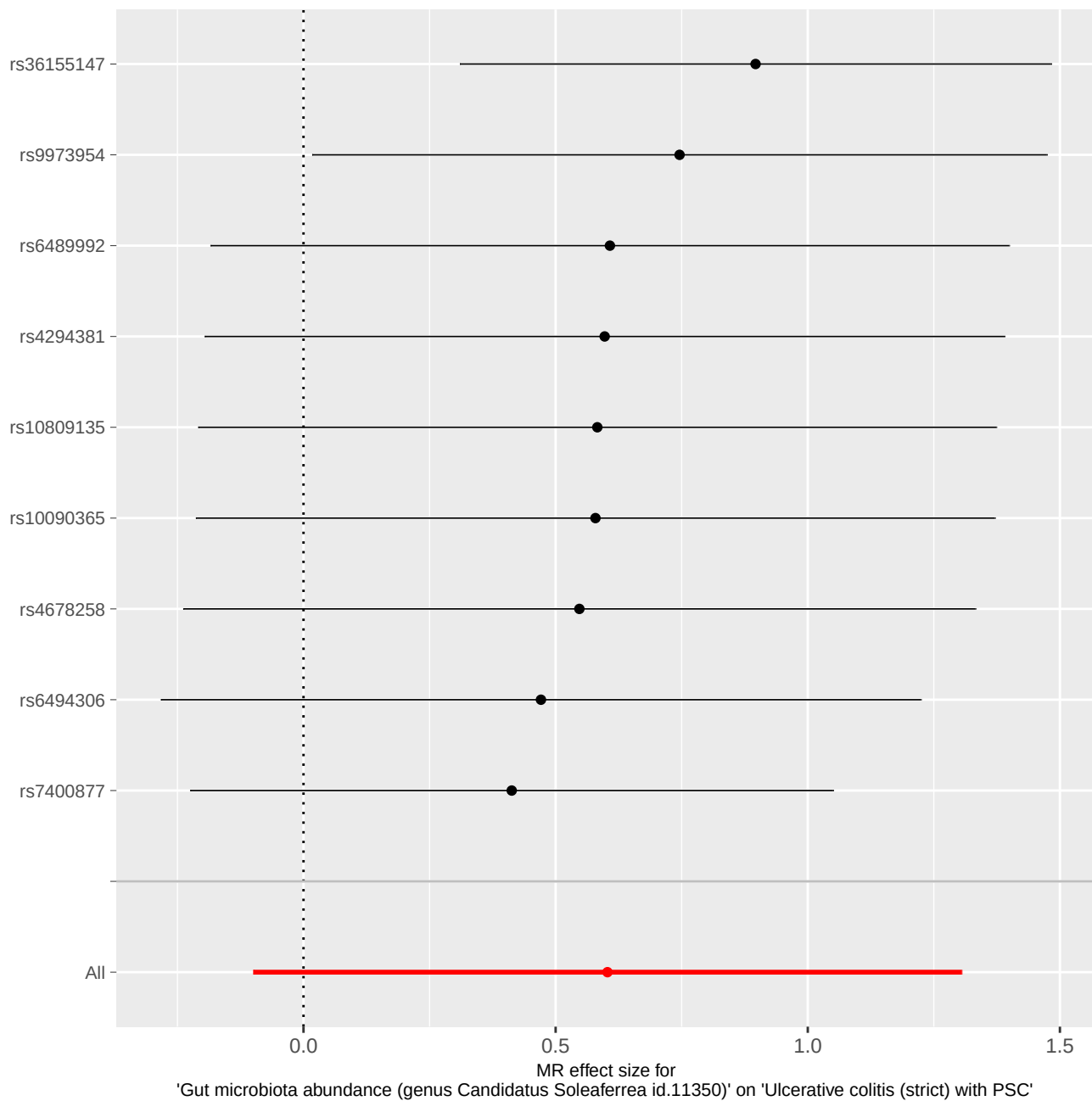


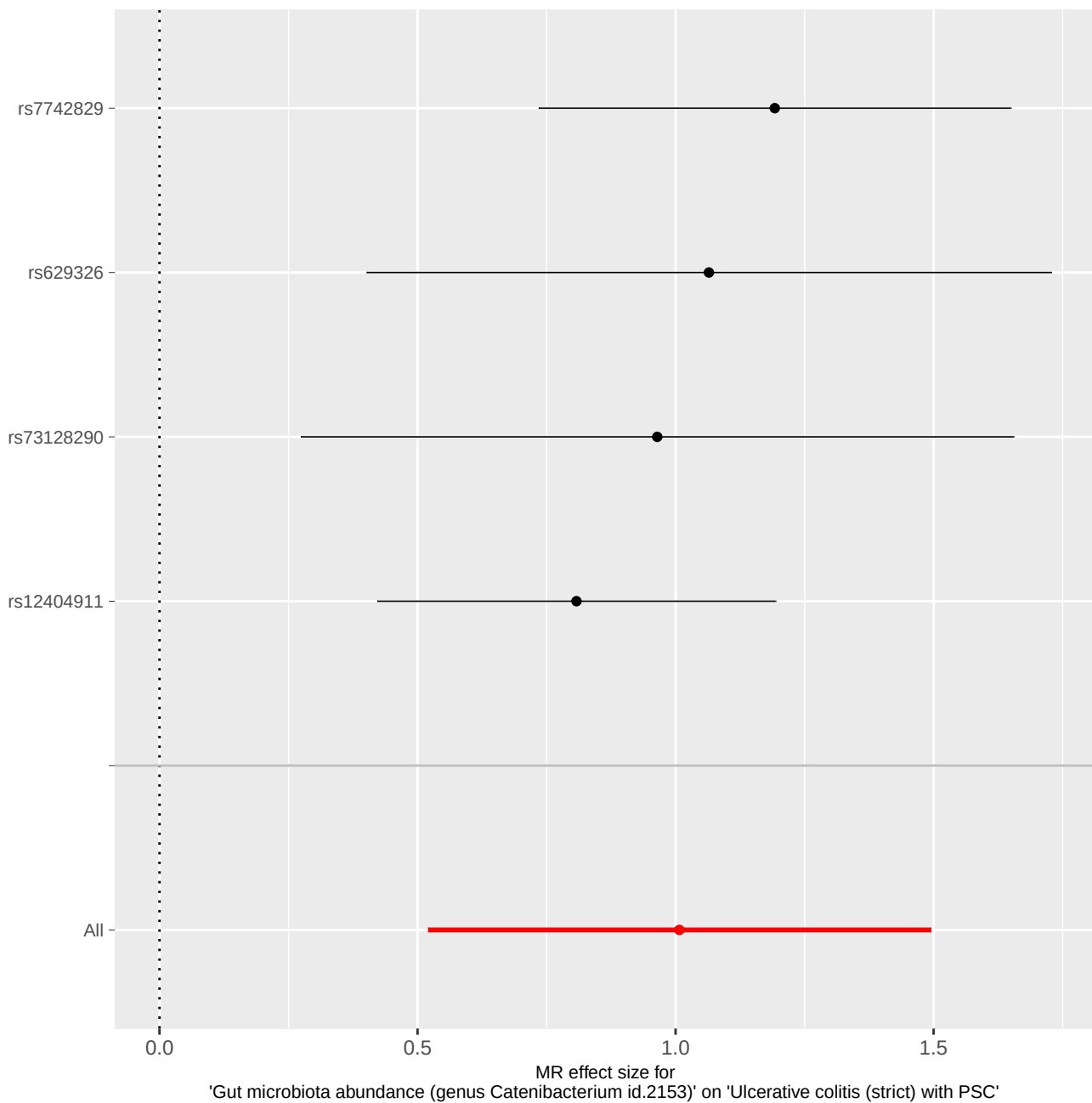


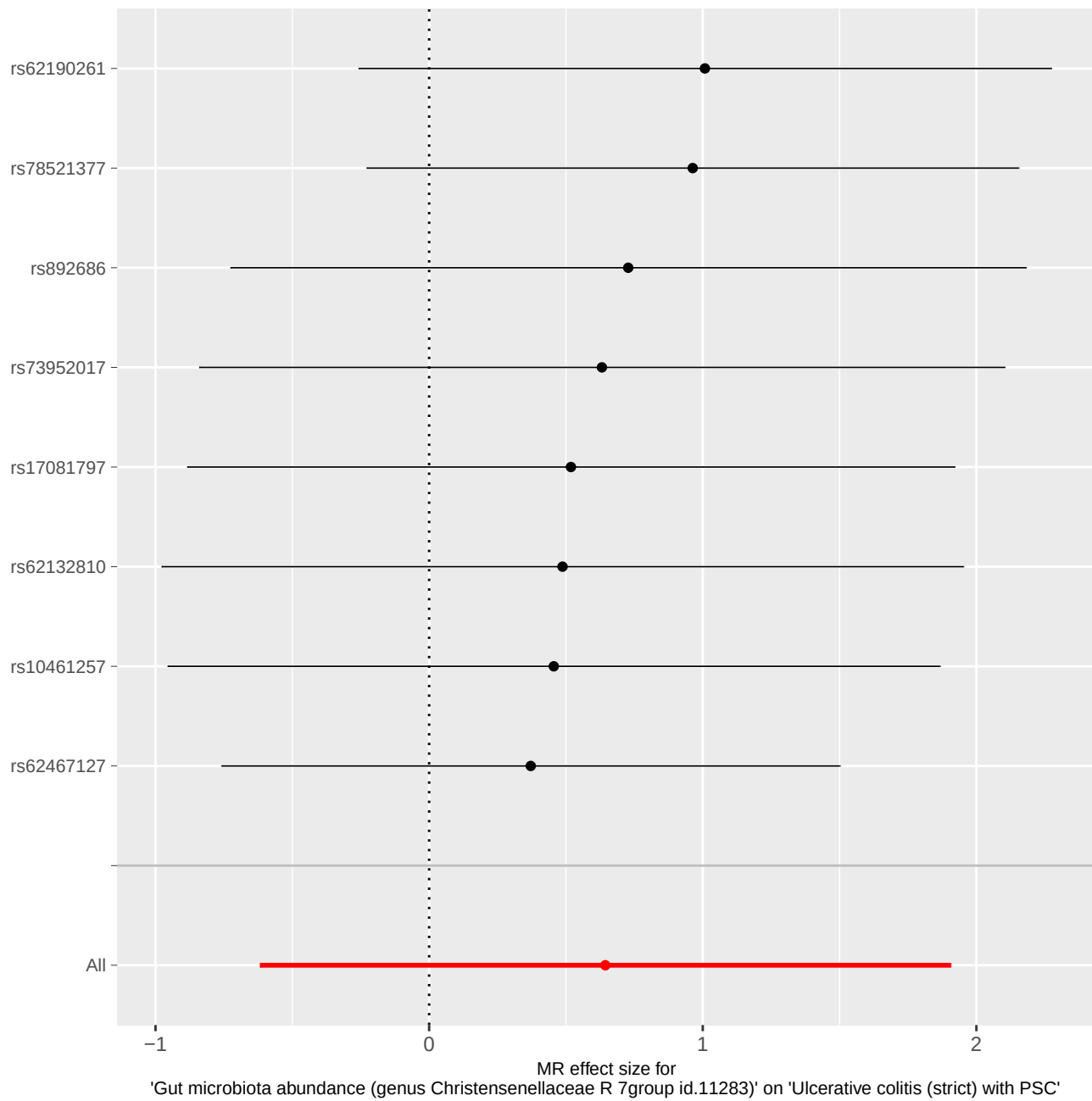


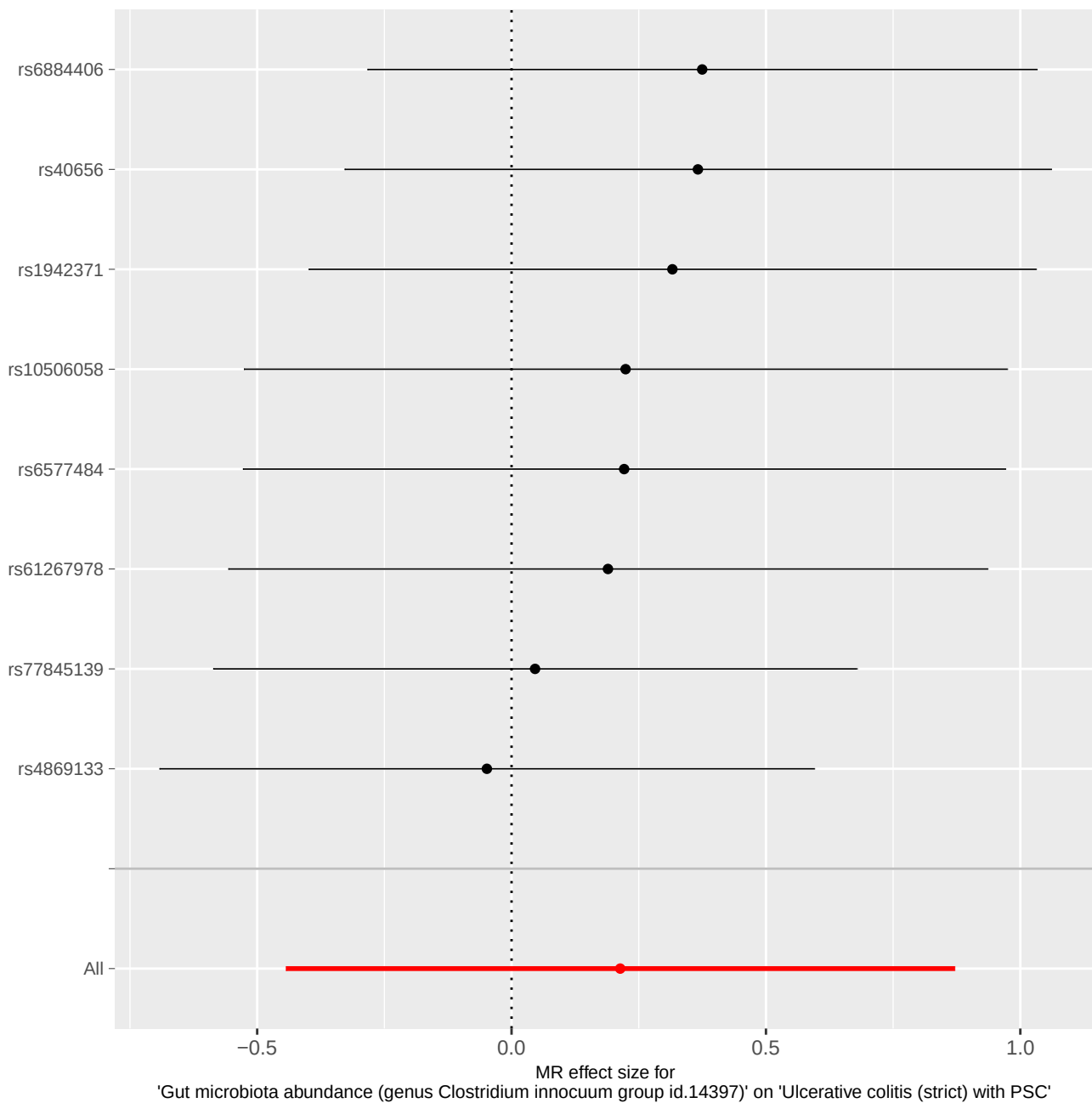


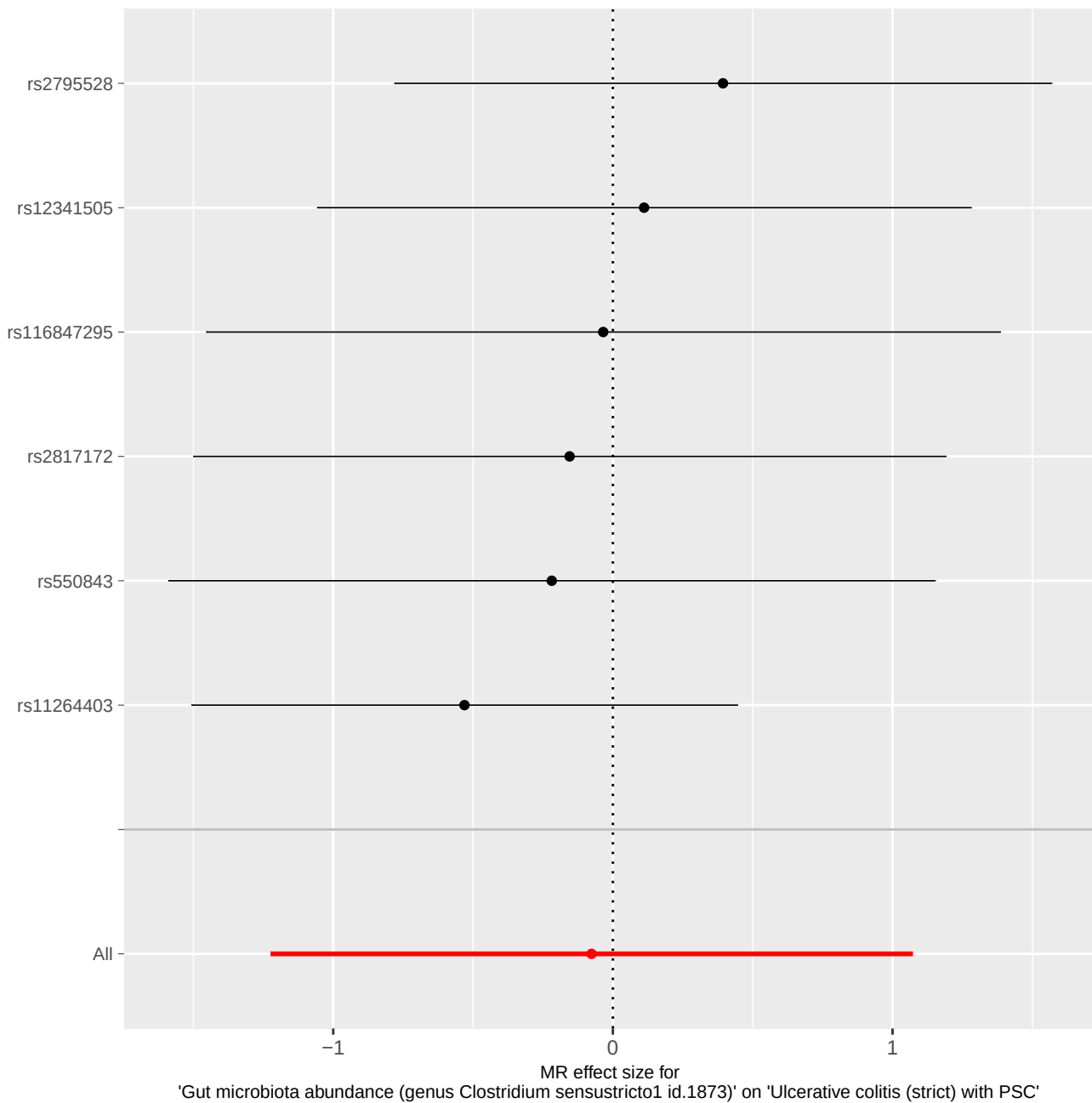
MR effect size for
'Gut microbiota abundance (genus Butyrivibrio id.1993) on 'Ulcerative colitis (strict) with PSC'

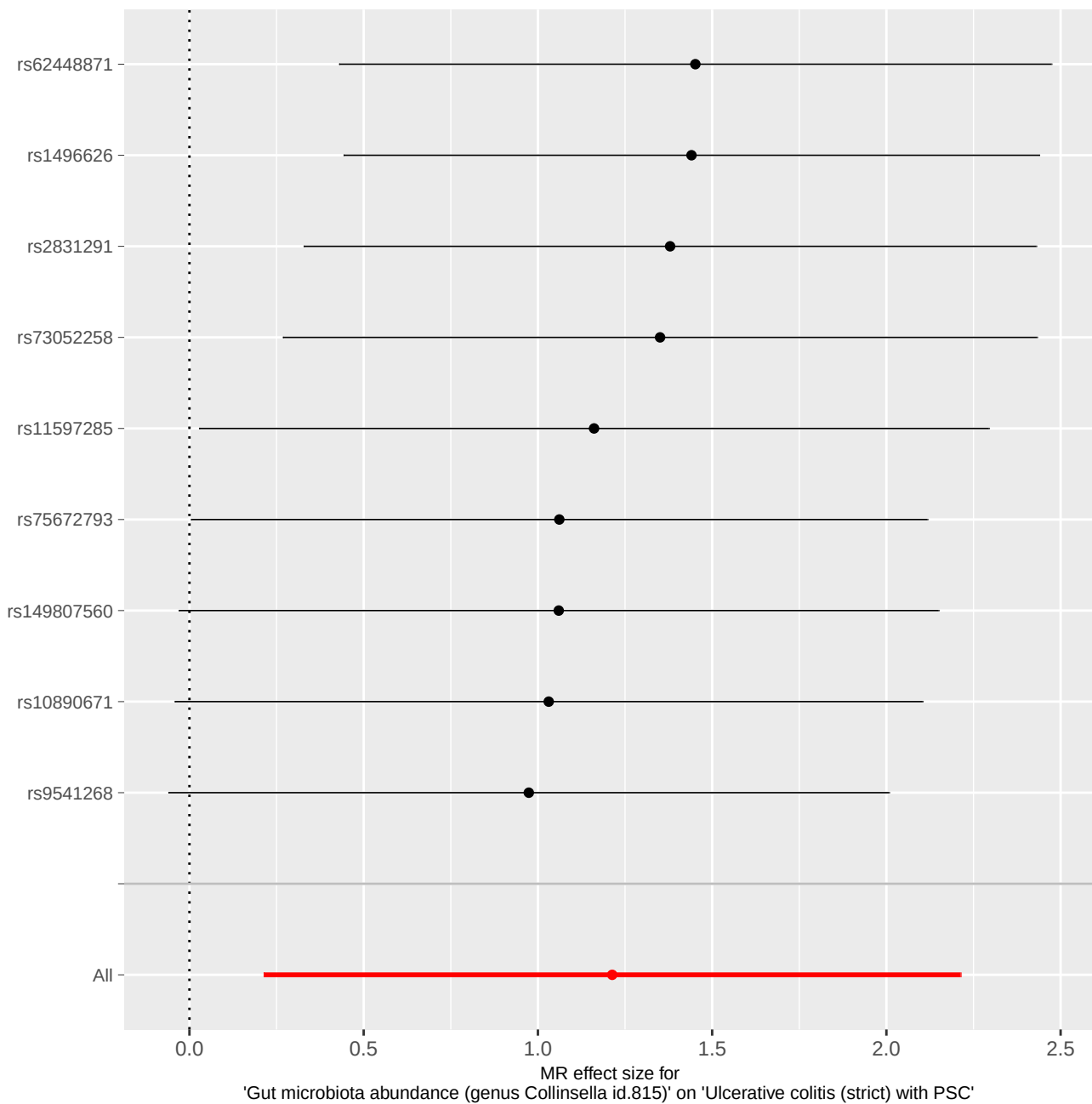


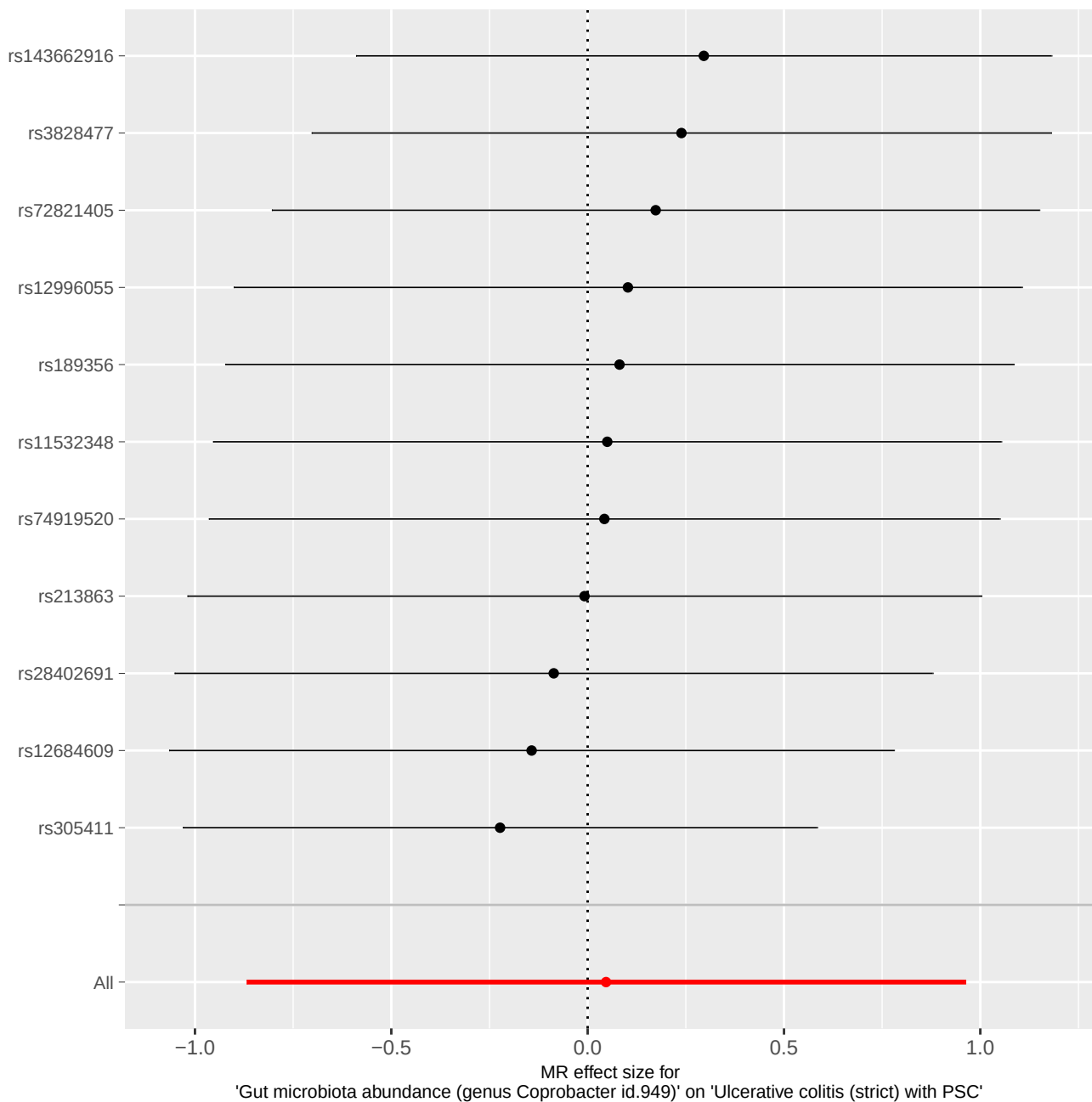


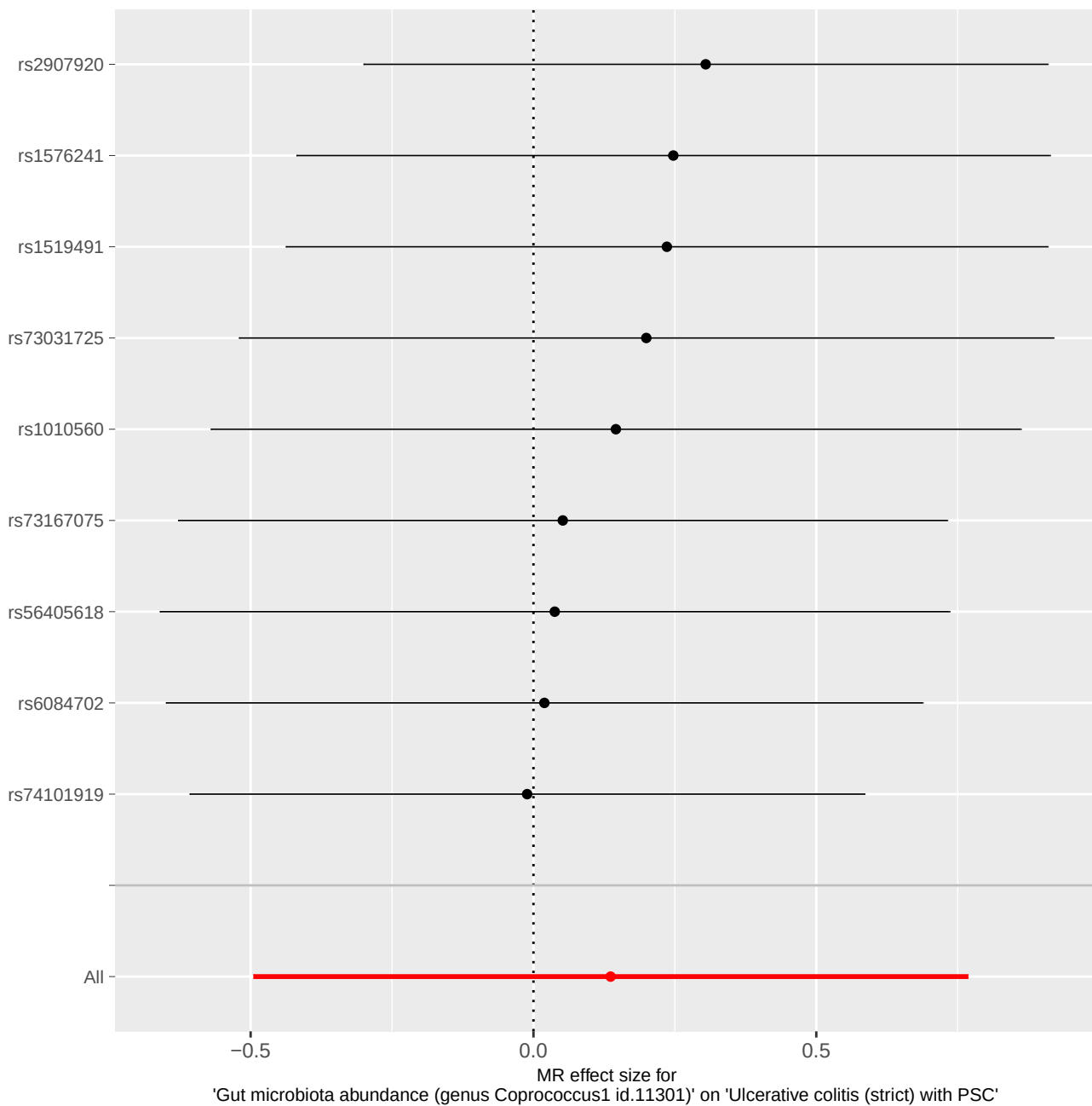


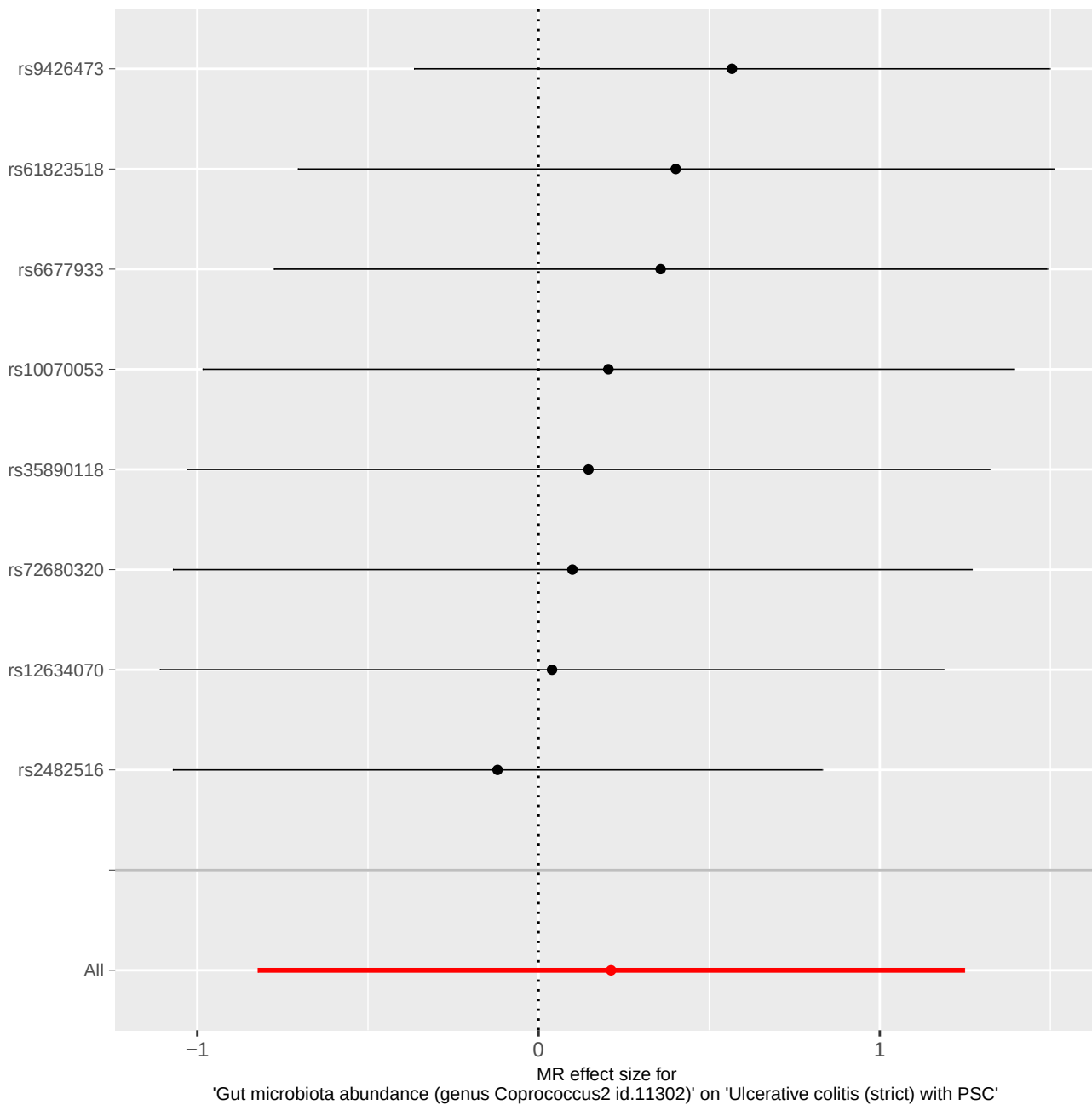


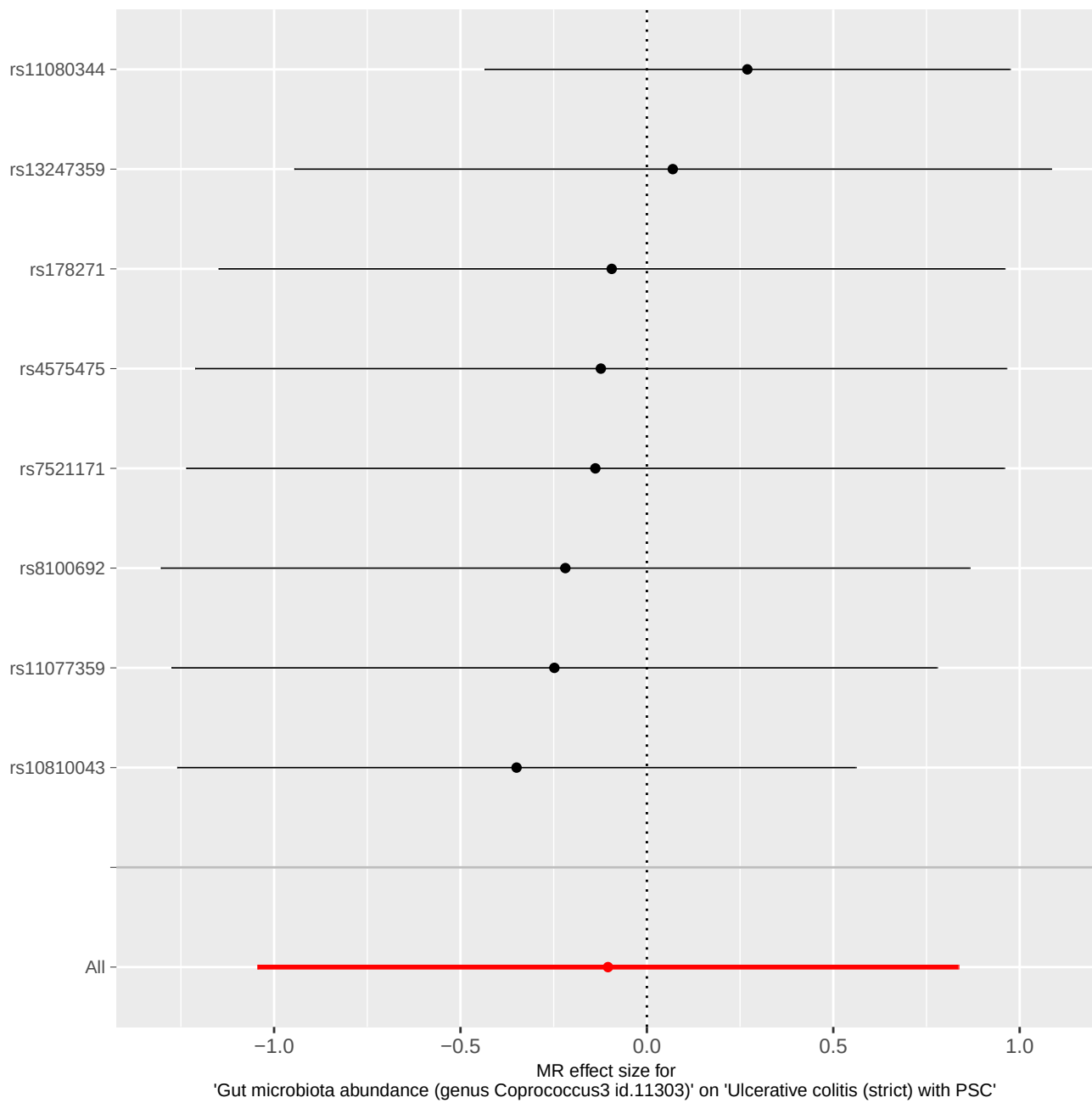


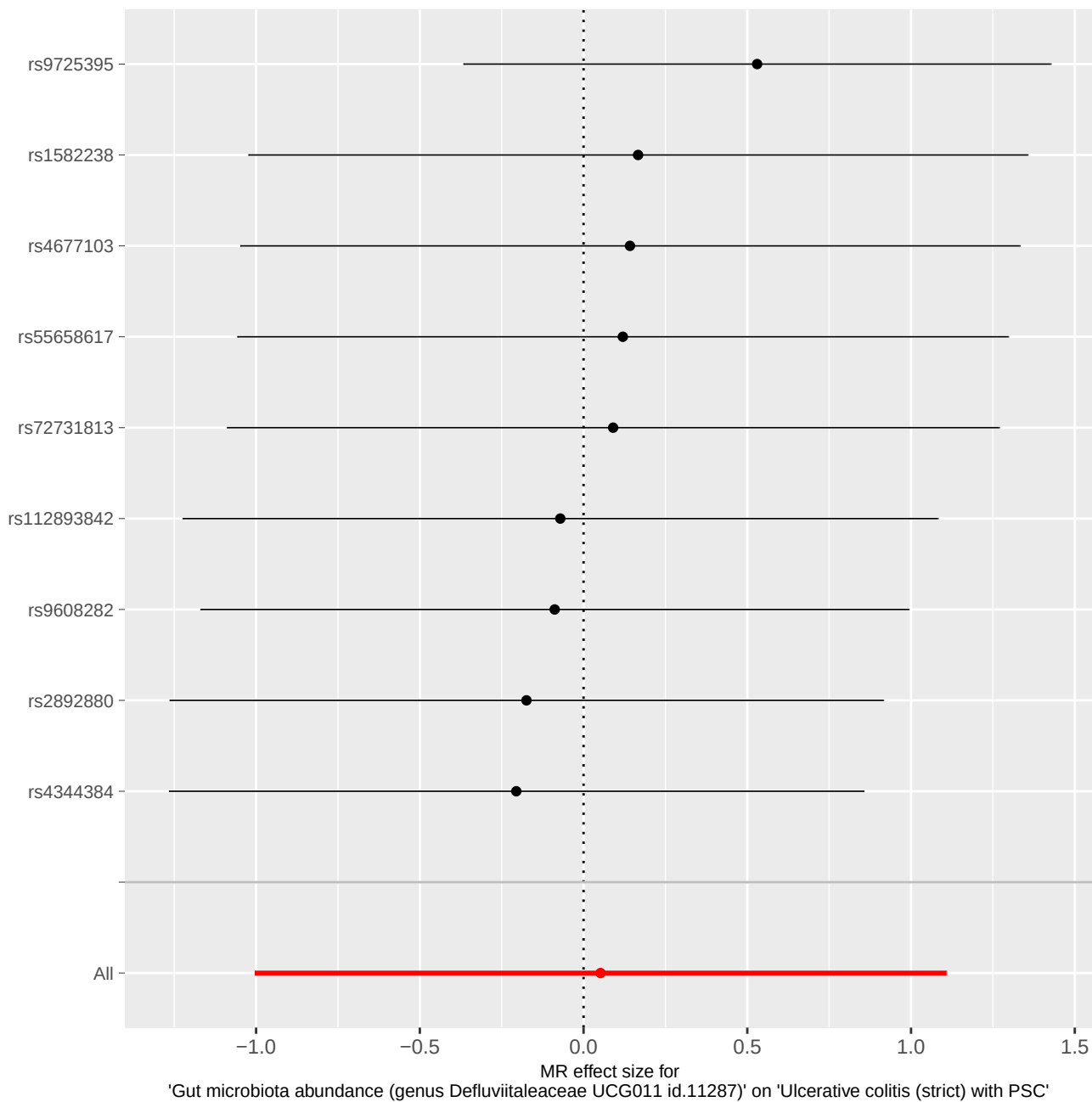


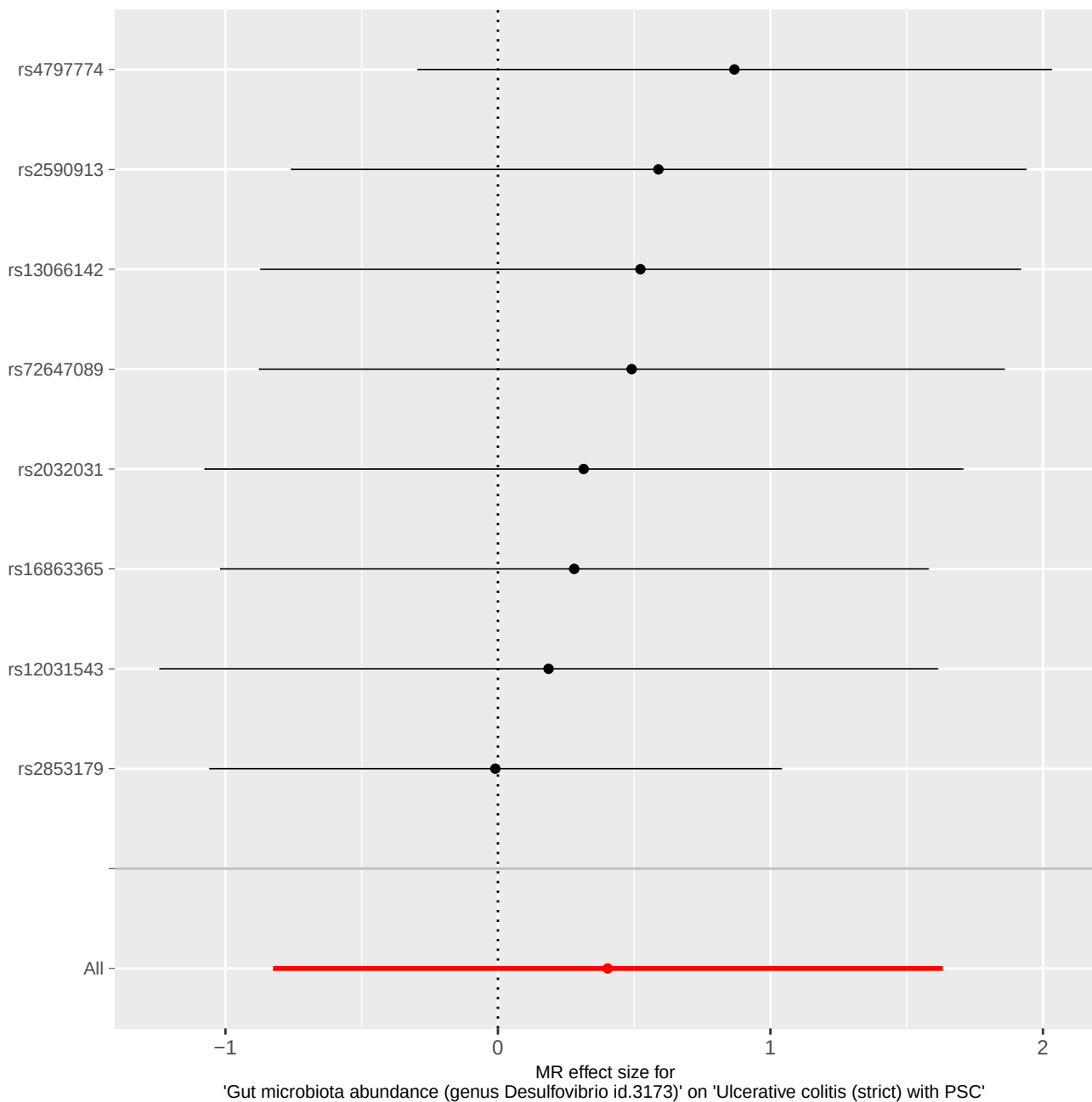


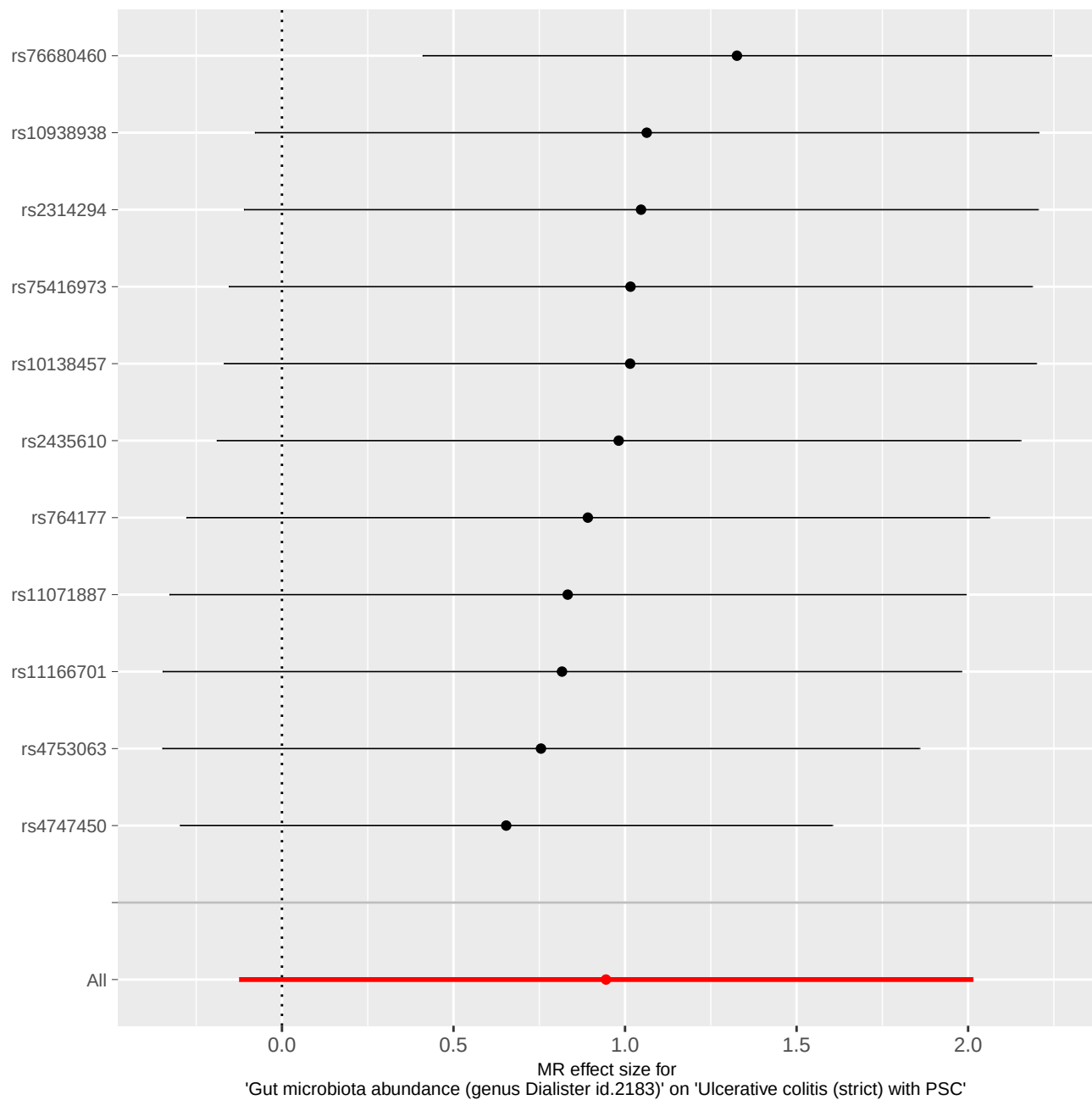


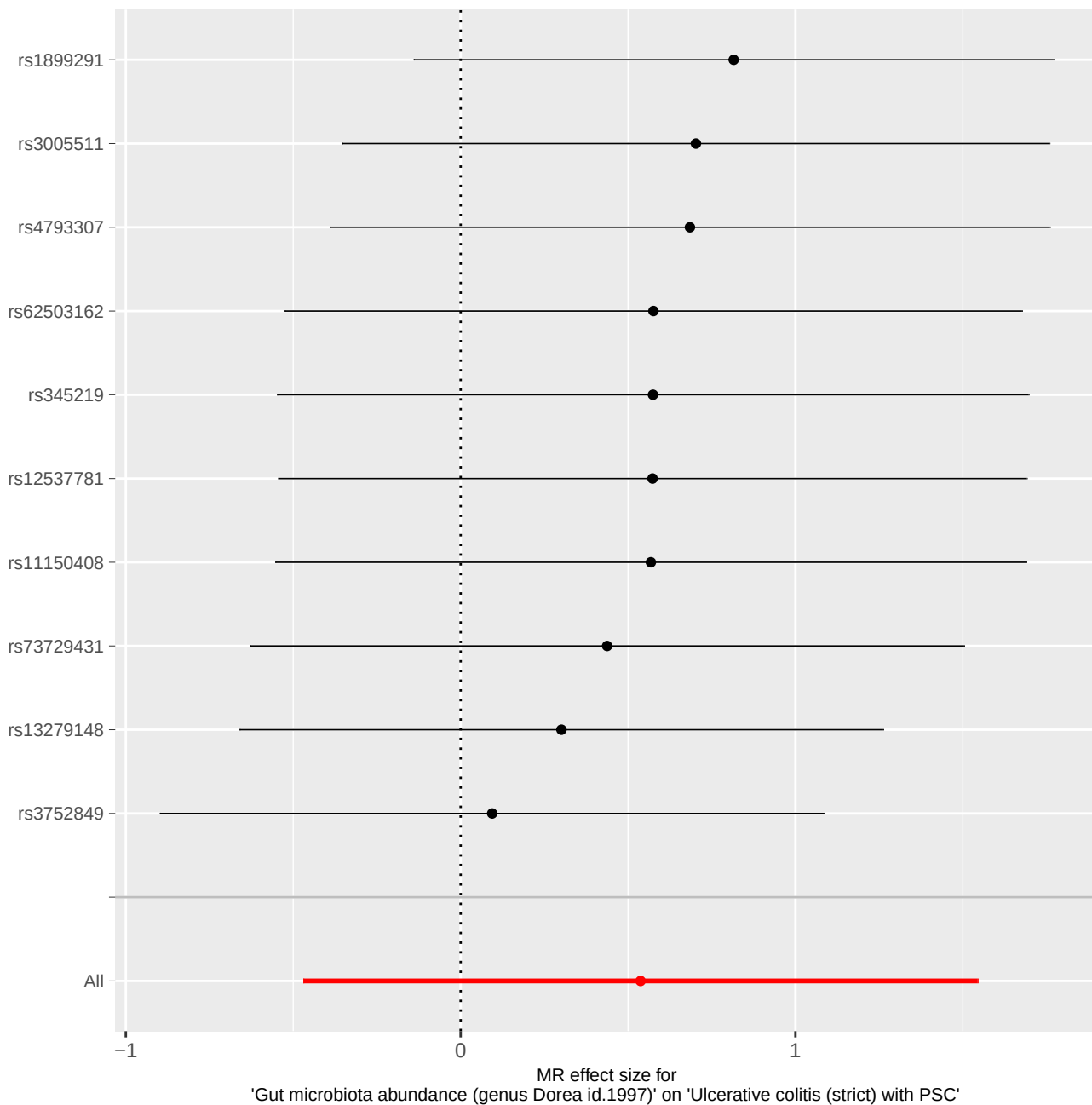


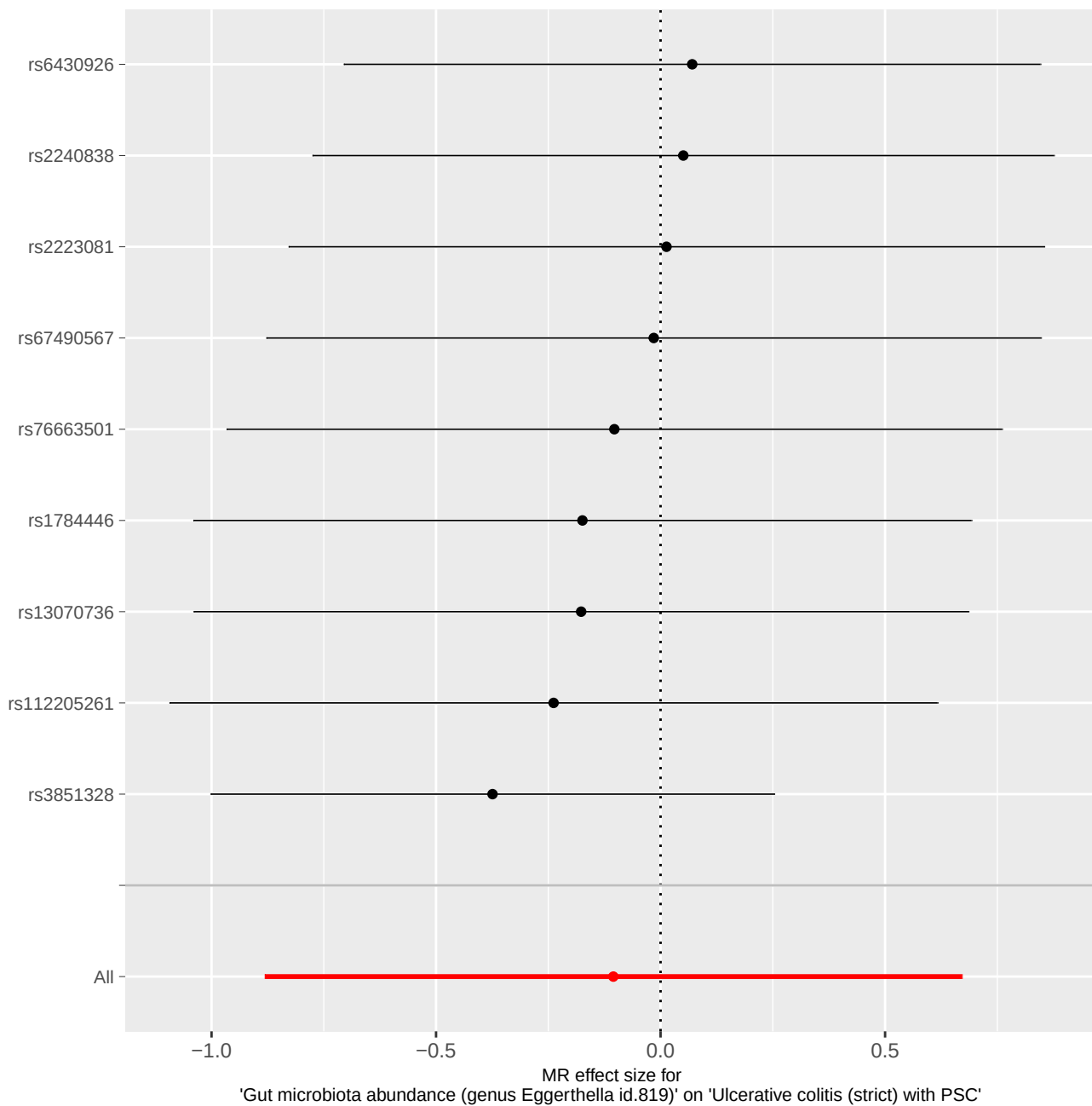




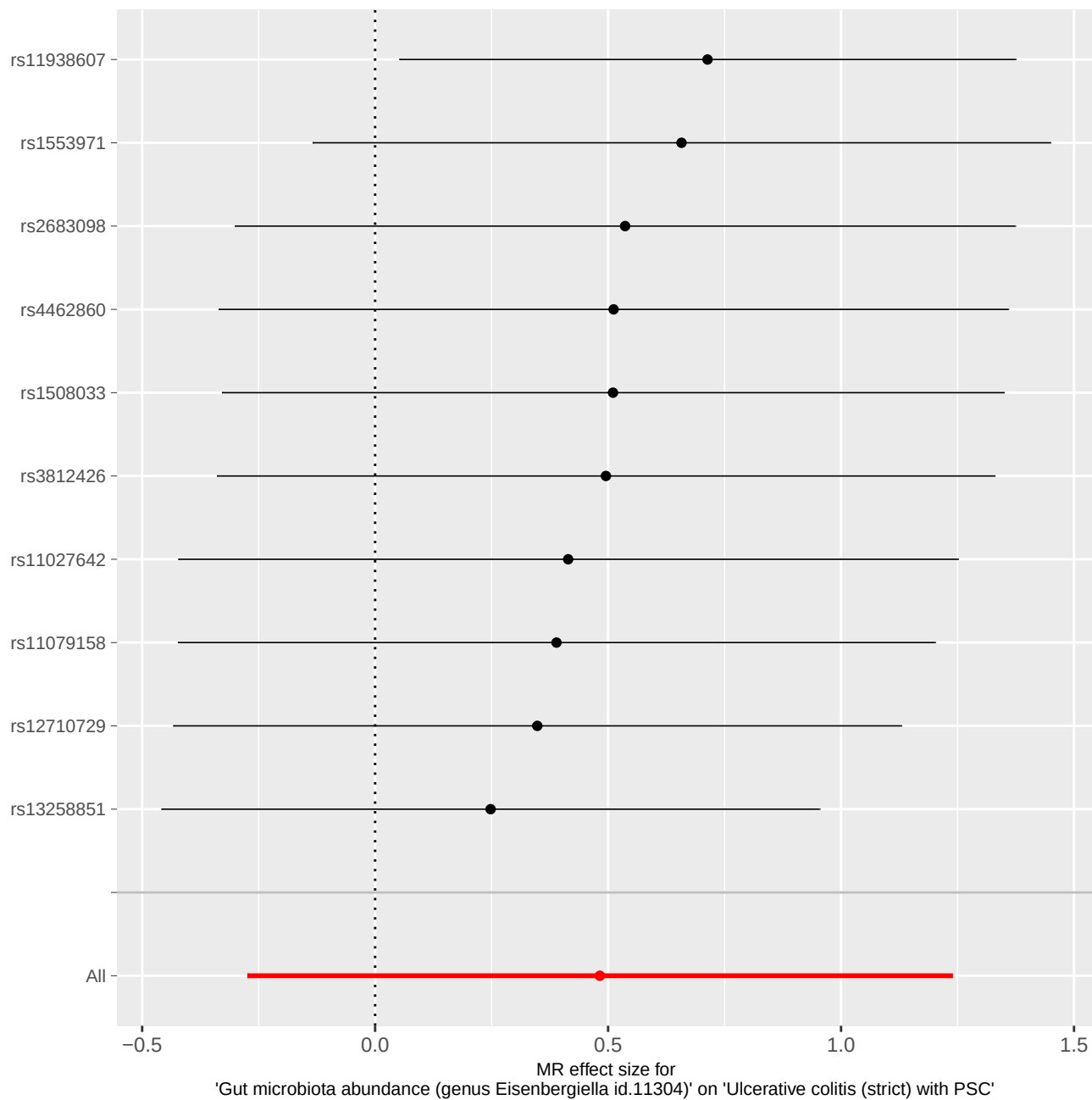


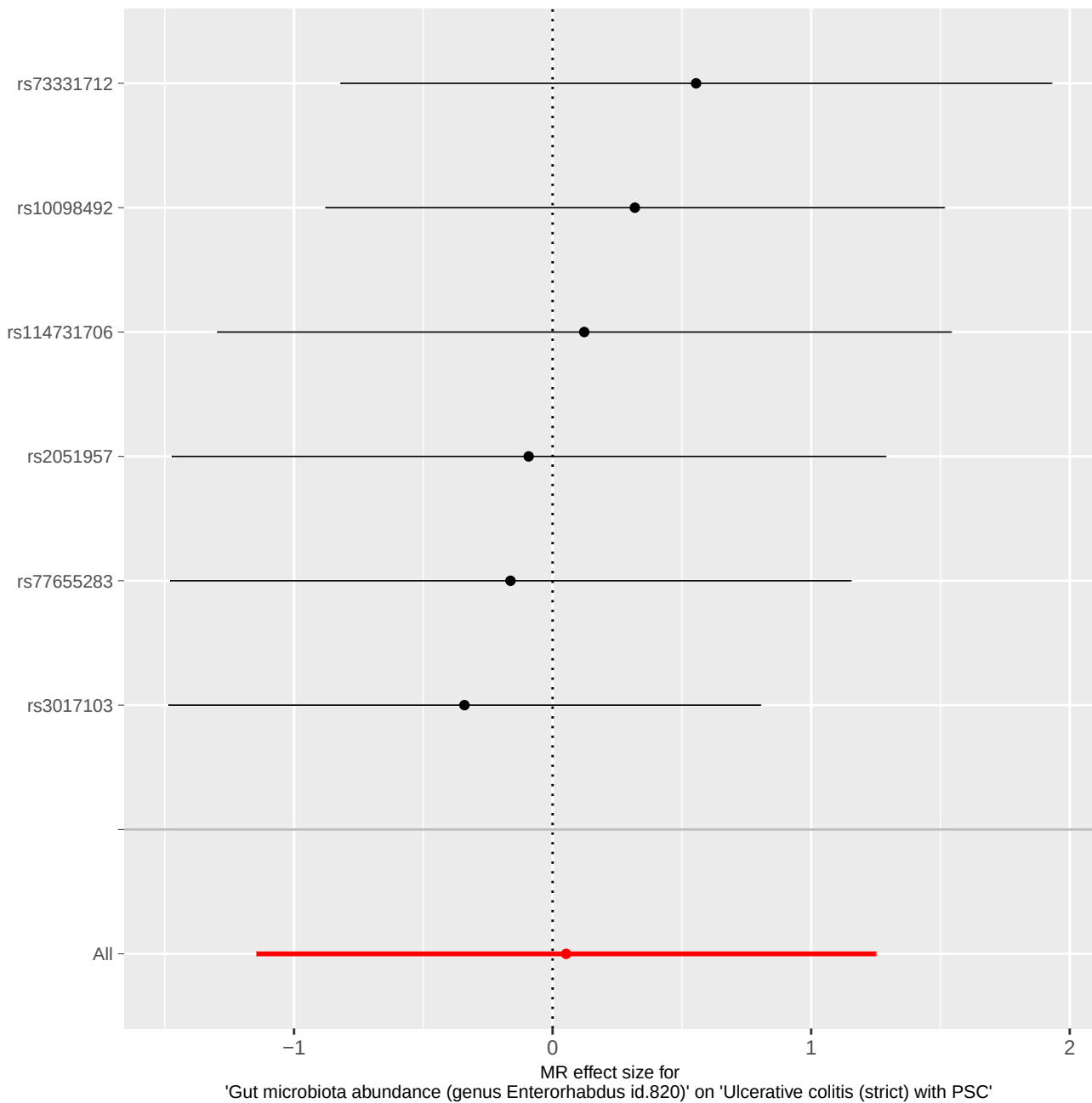


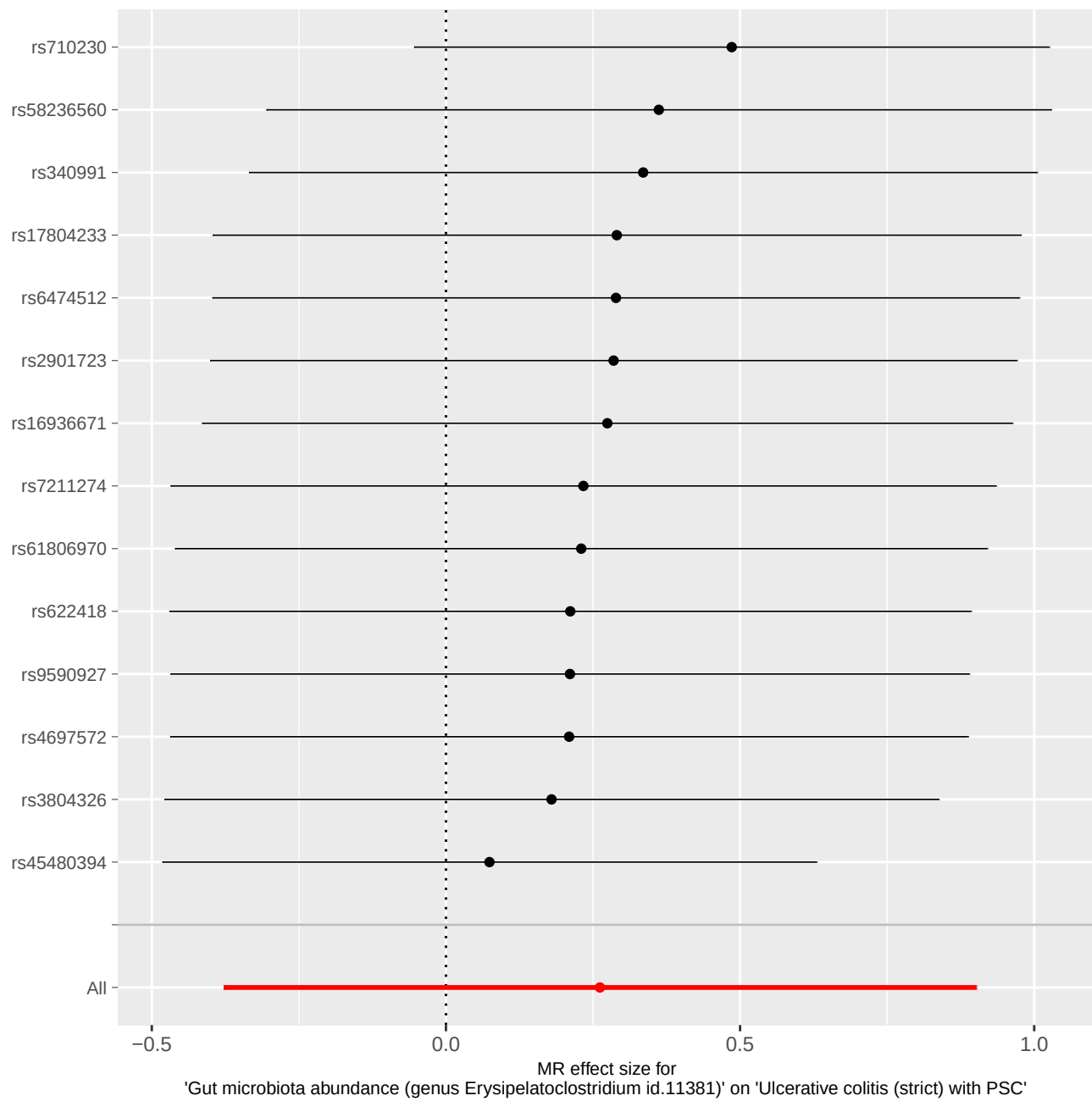


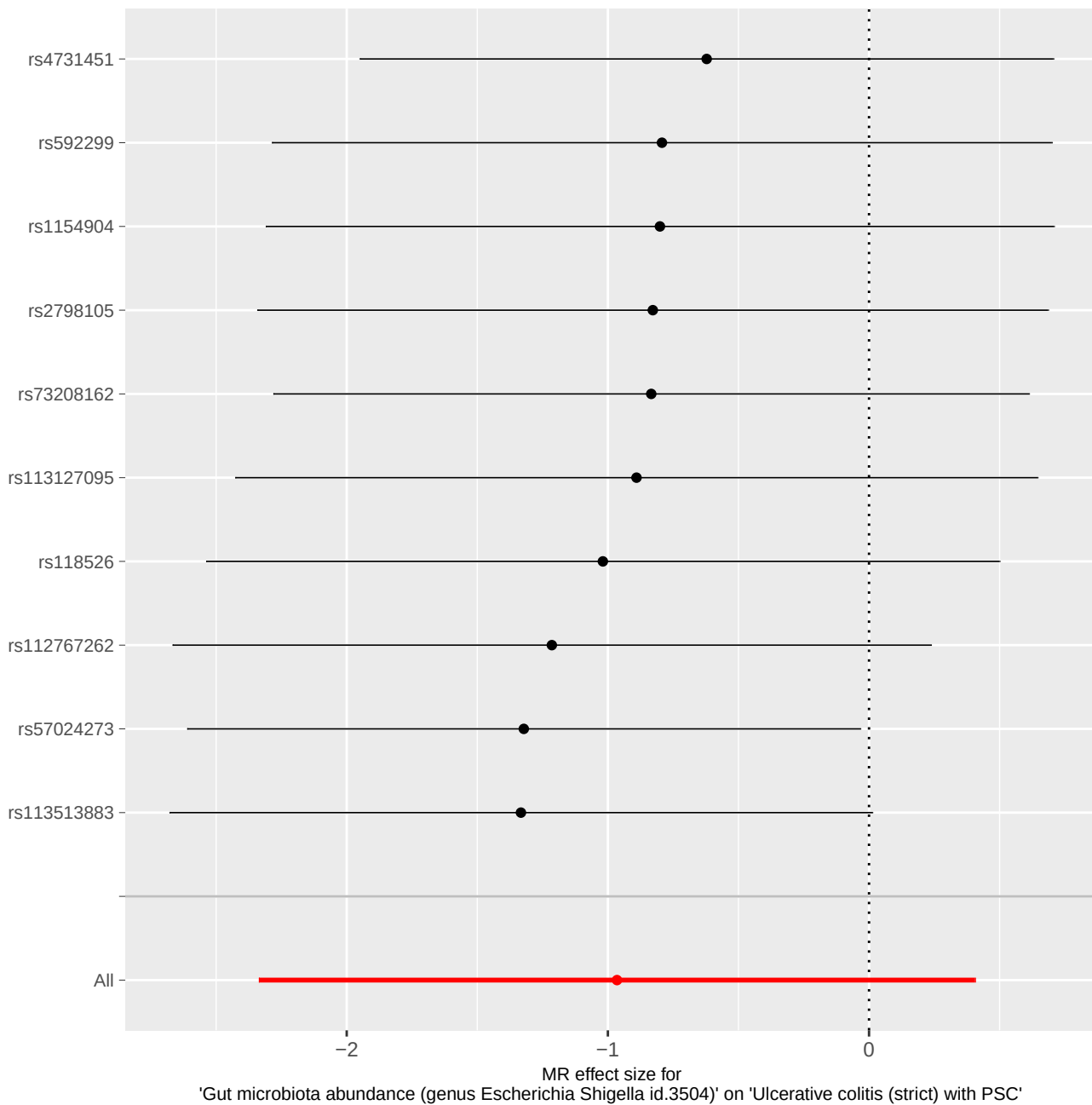


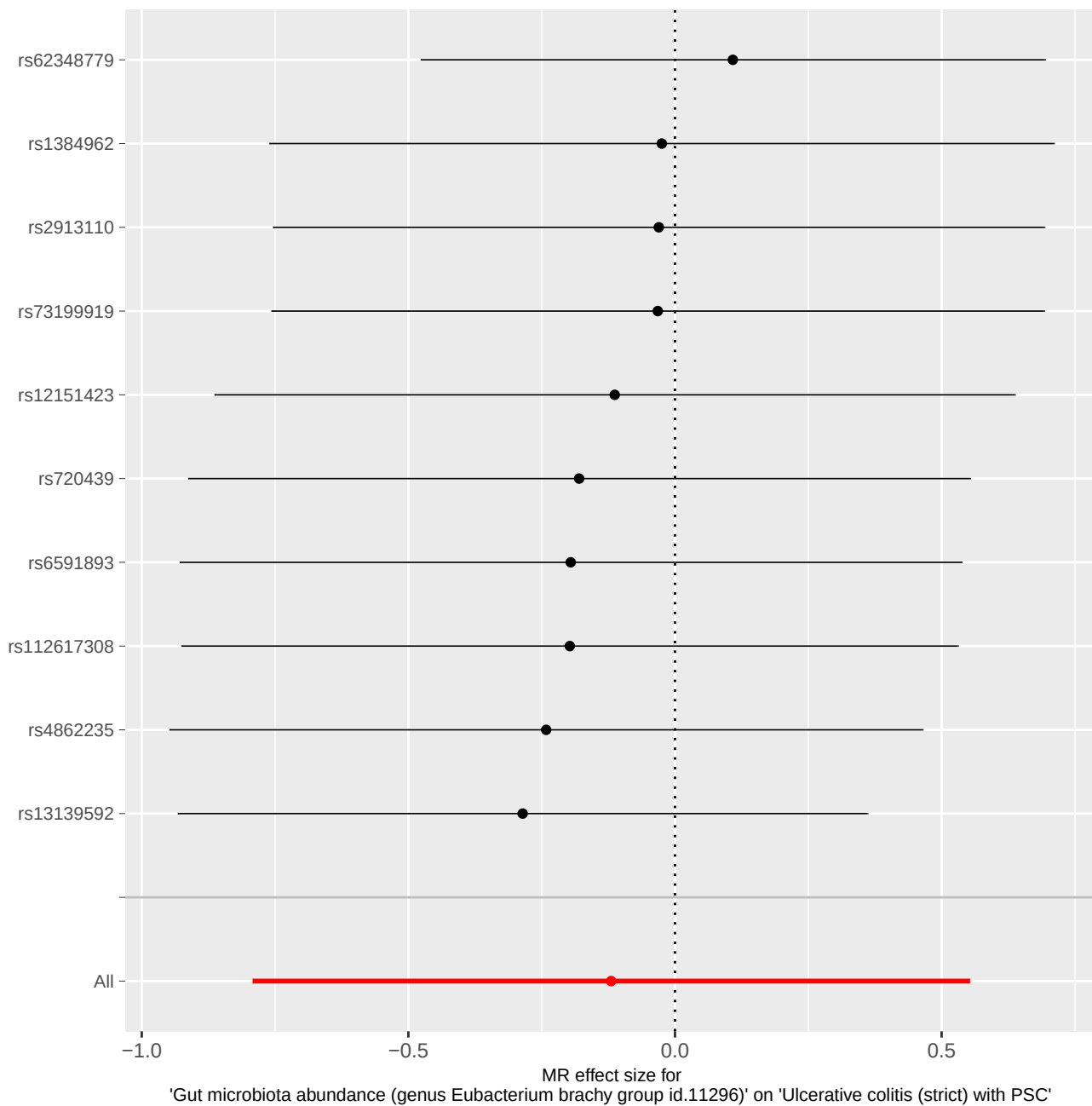
MR effect size for
'Gut microbiota abundance (genus Eggerthella id.819)' on 'Ulcerative colitis (strict) with PSC'

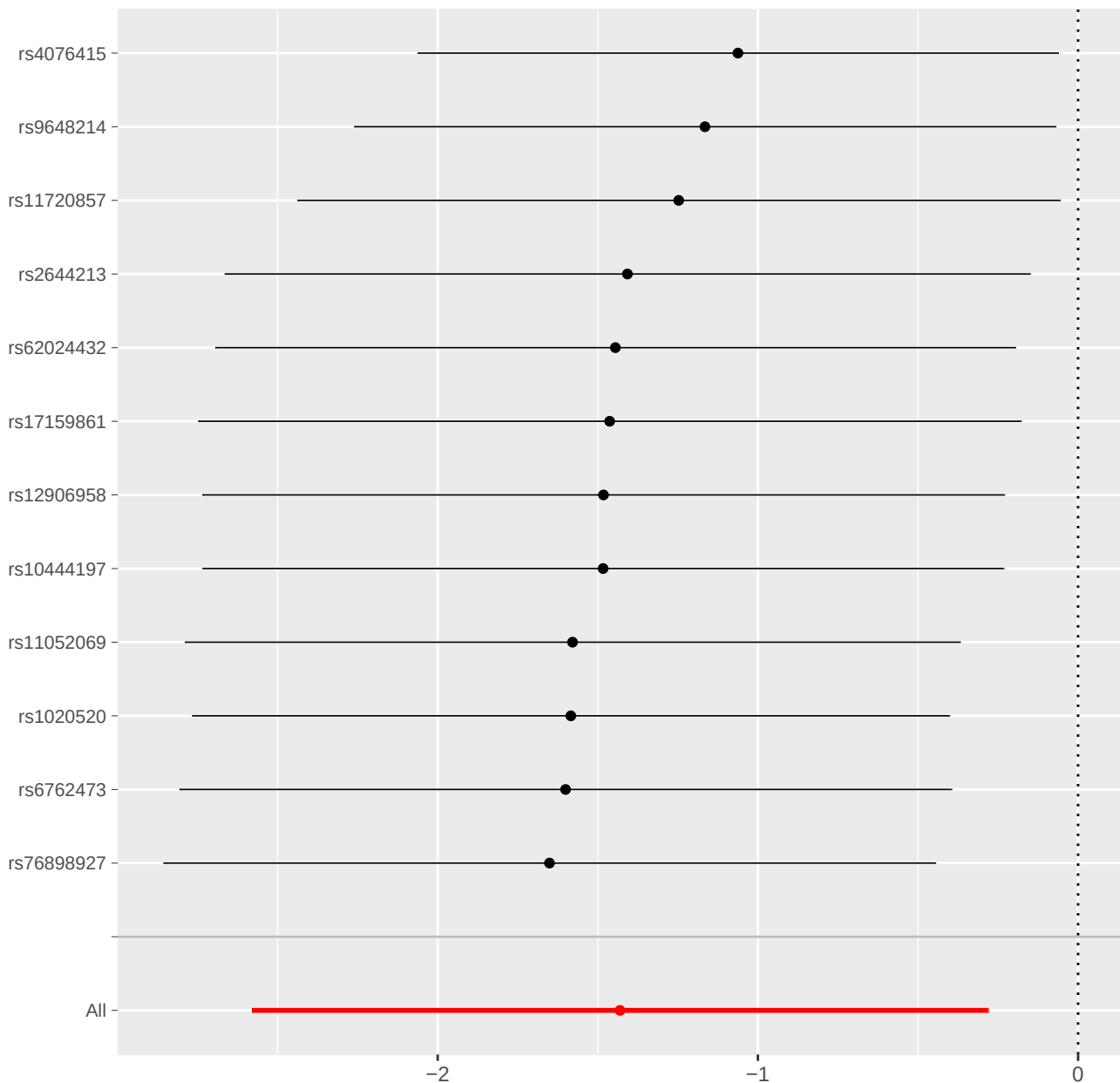


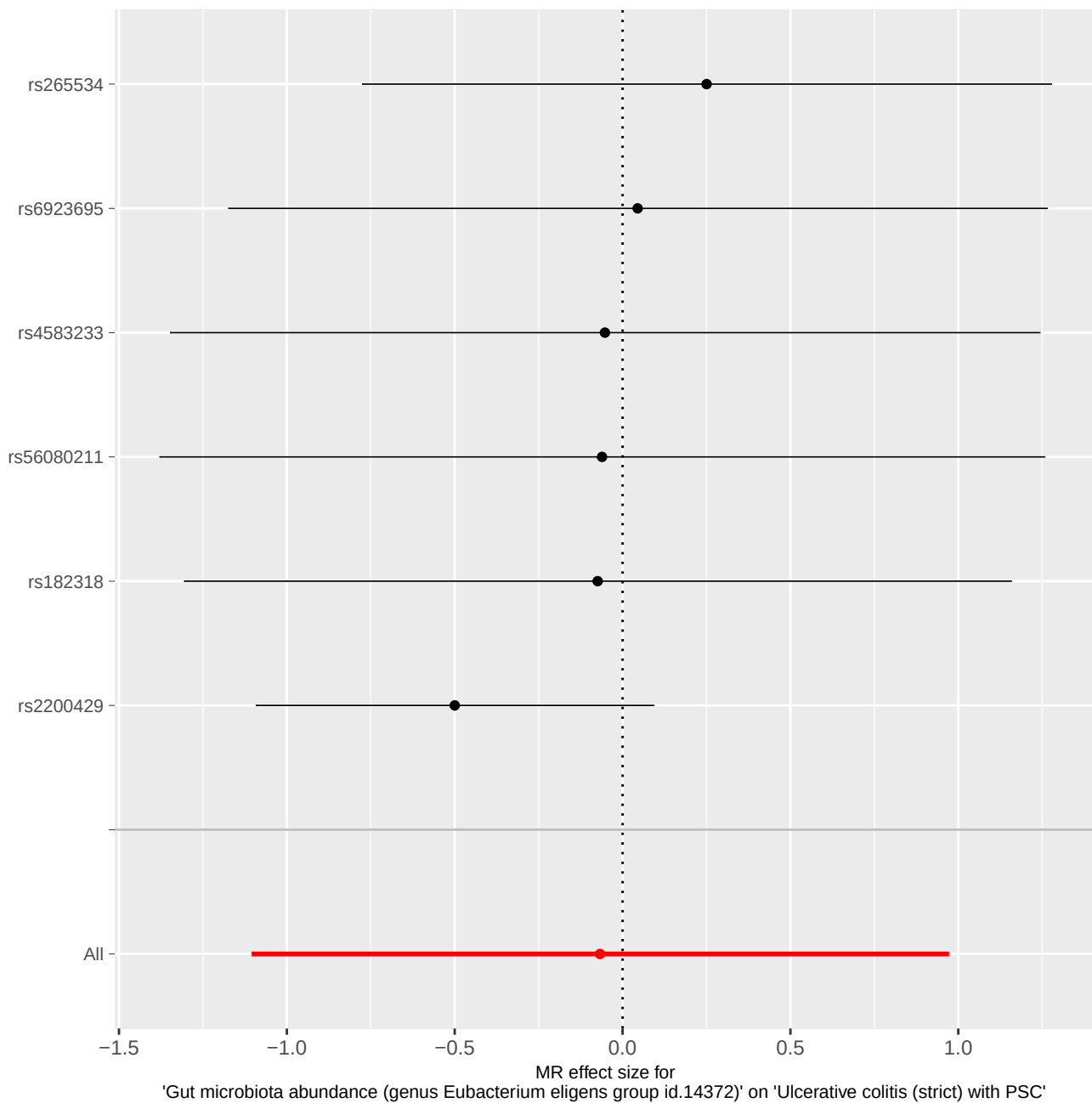


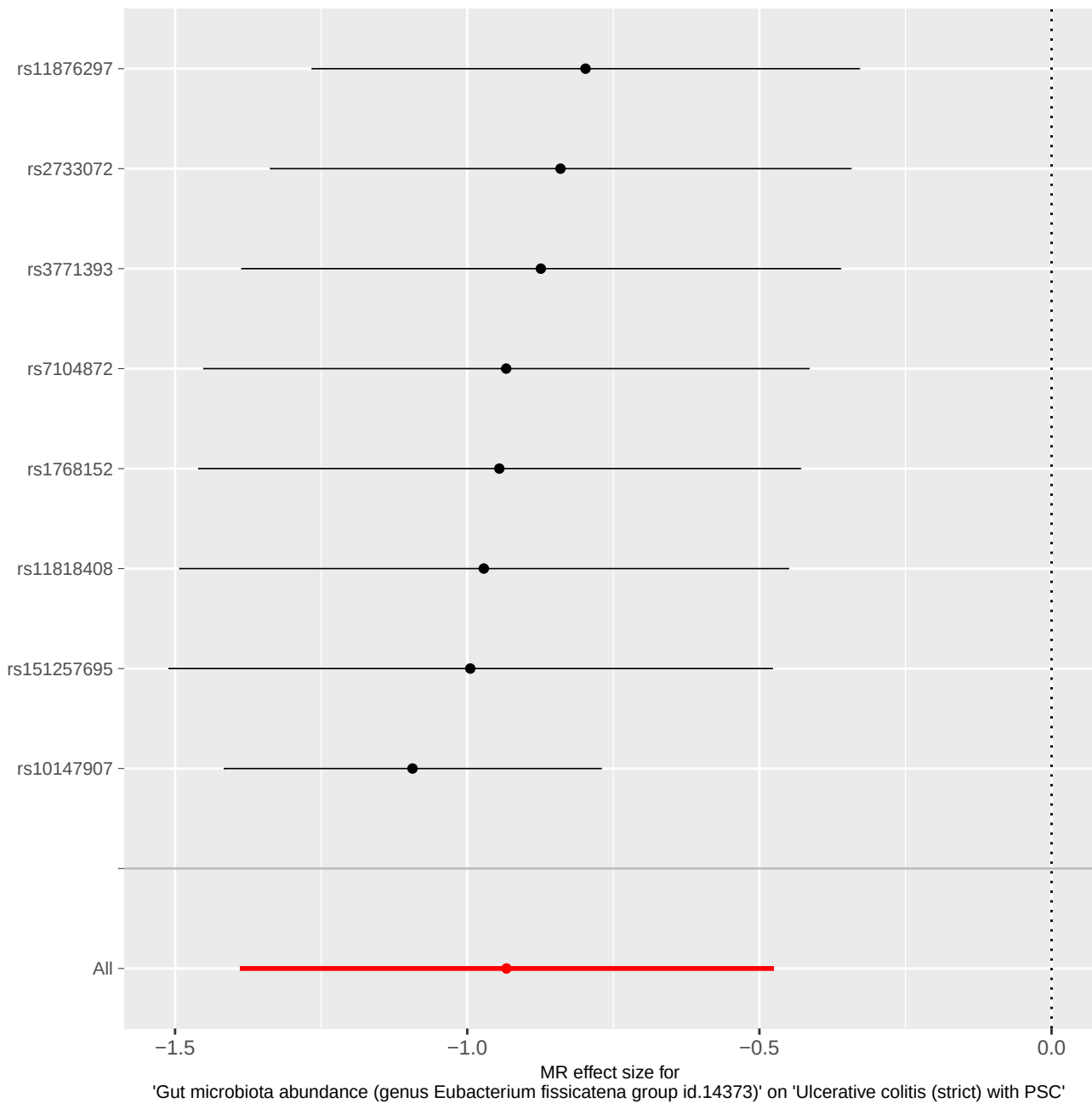


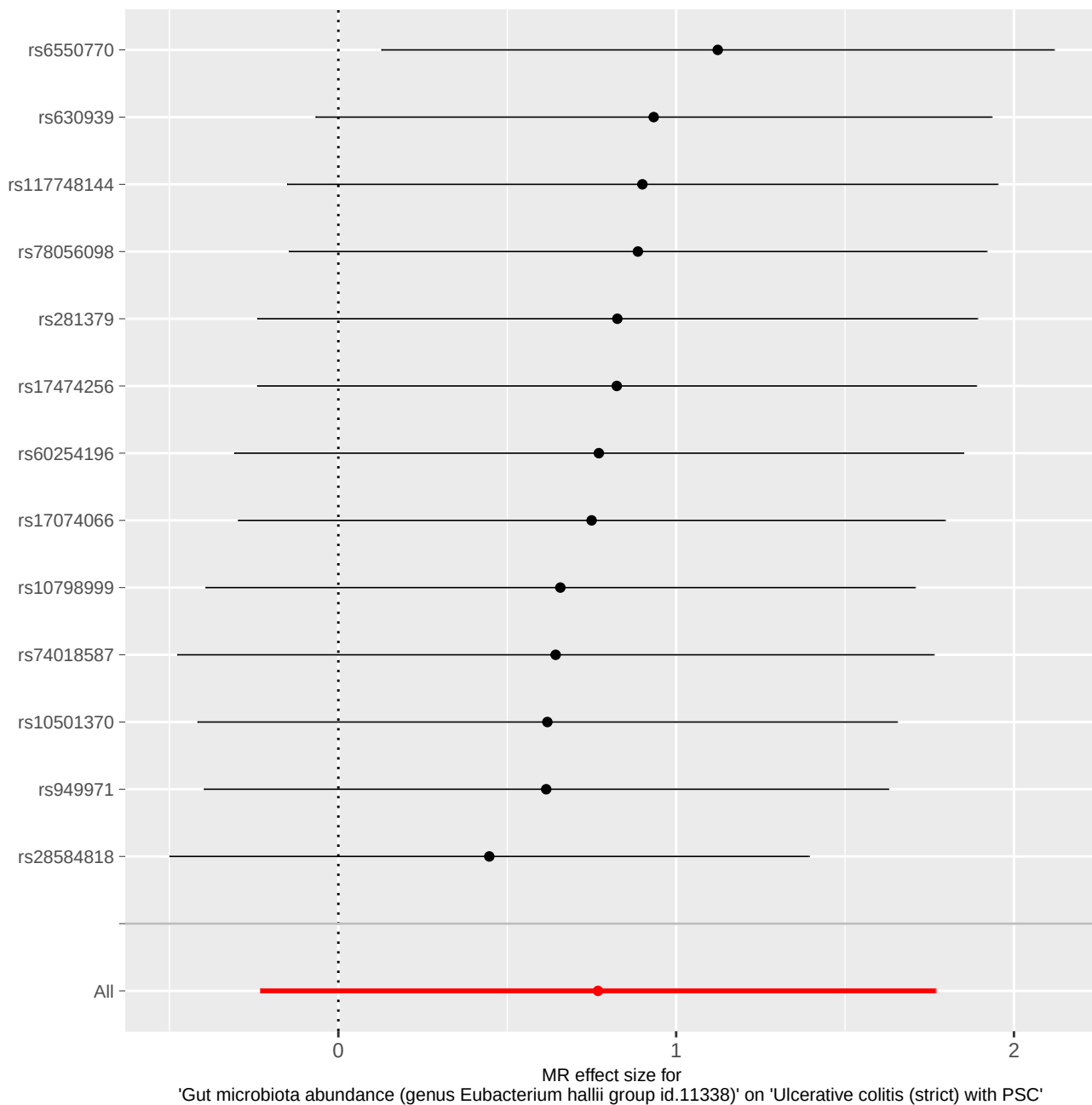




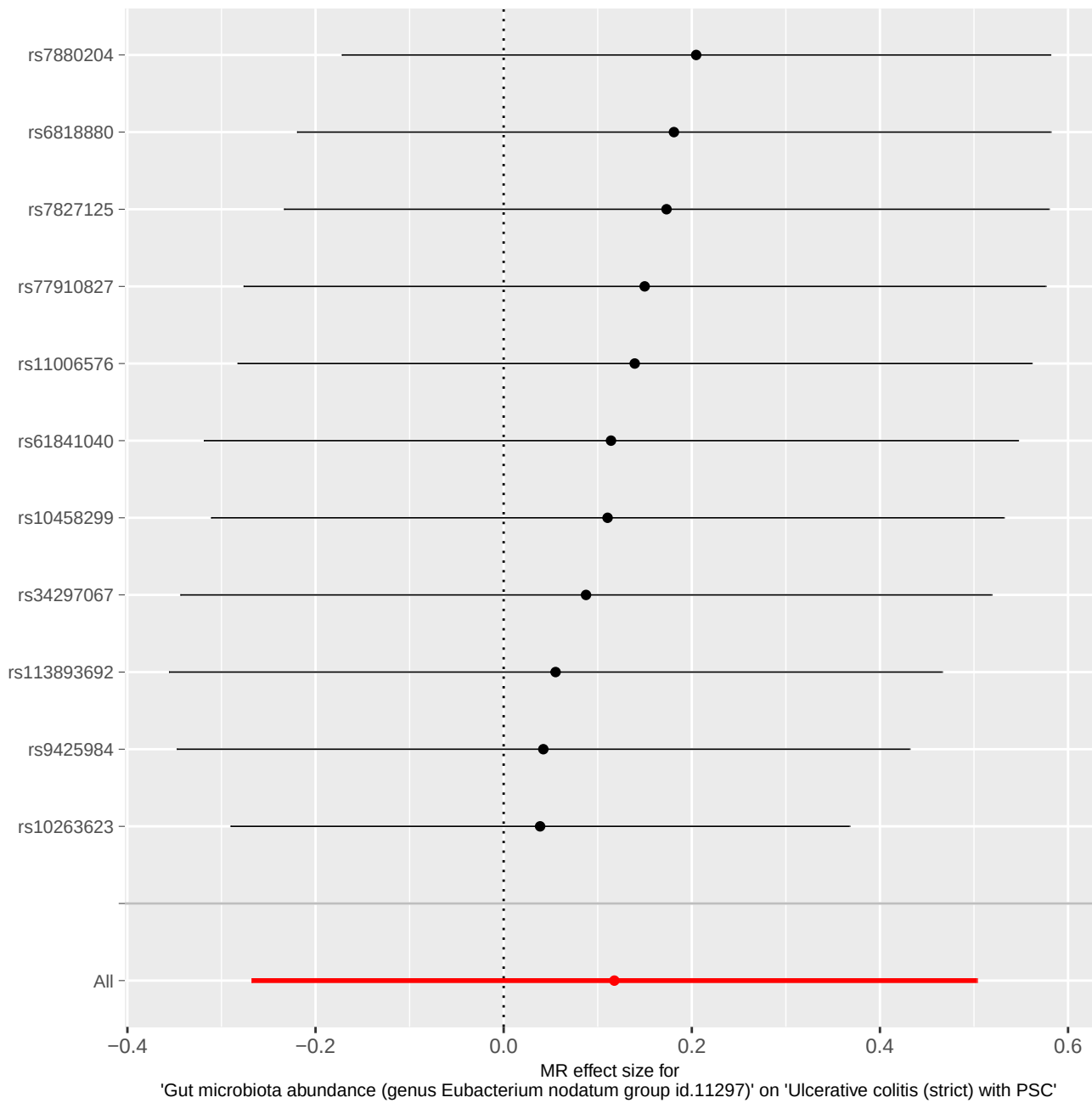


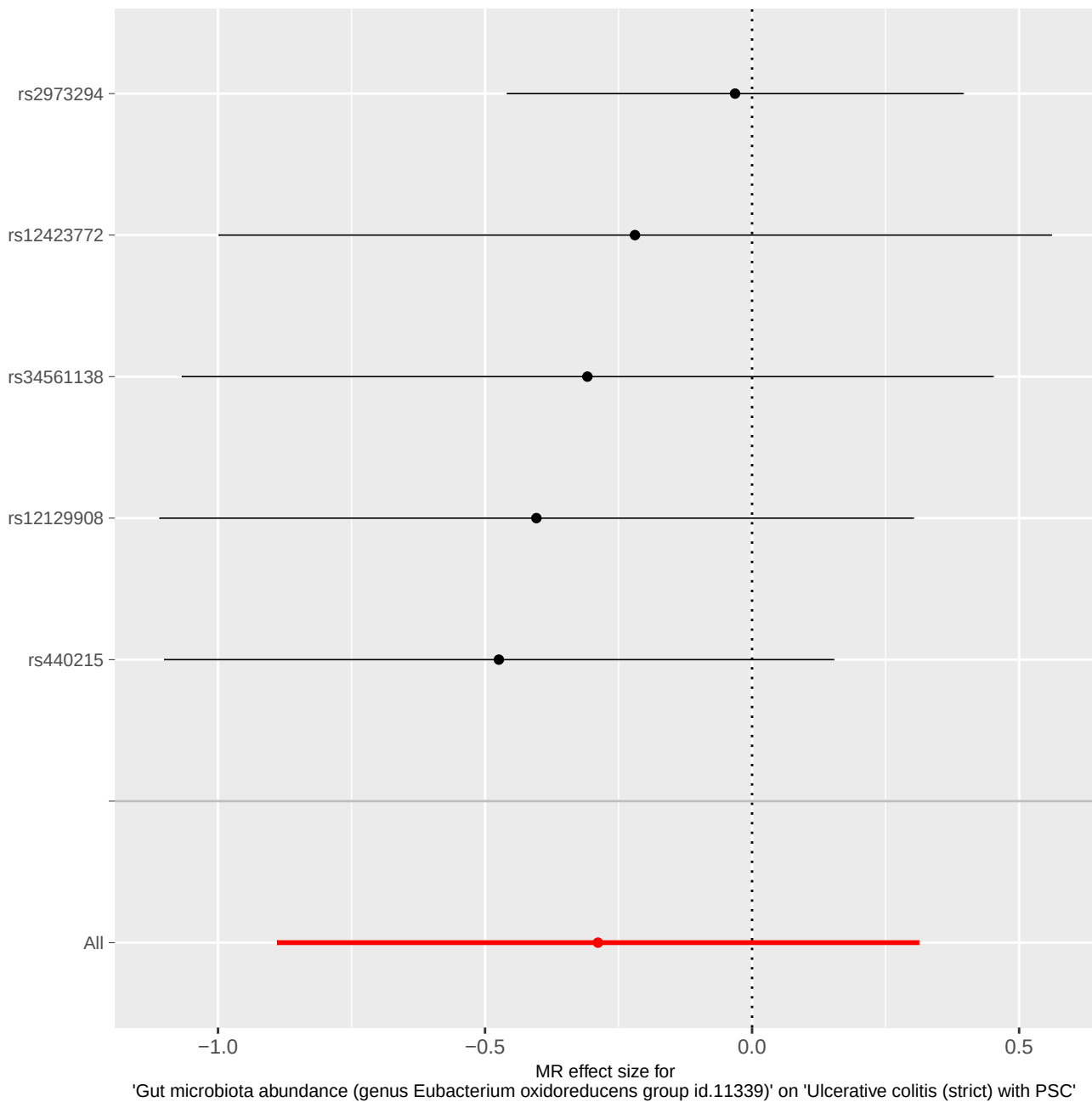


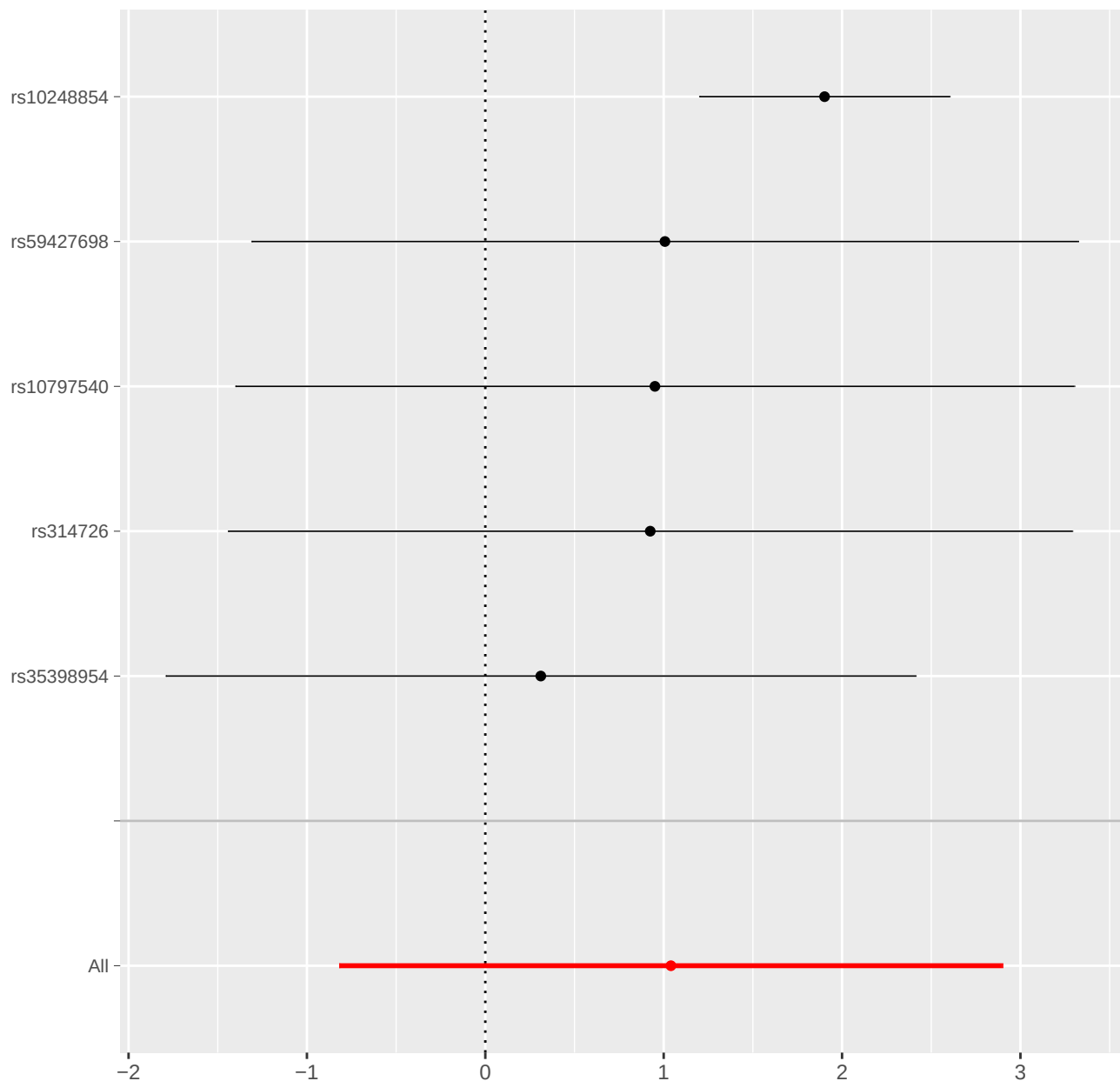




MR effect size for
'Gut microbiota abundance (genus Eubacterium hallii group id.11338)' on 'Ulcerative colitis (strict) with PSC'

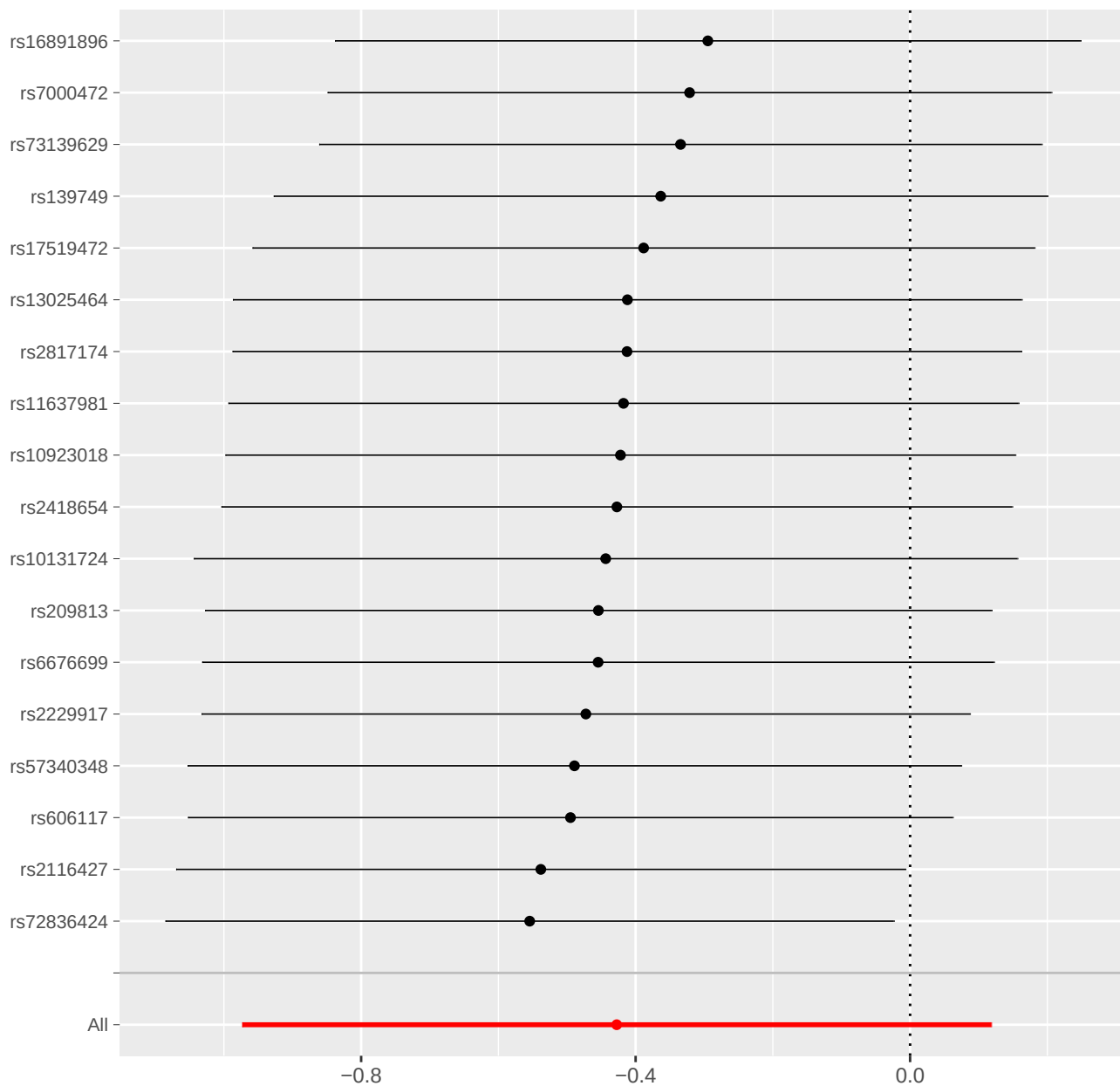




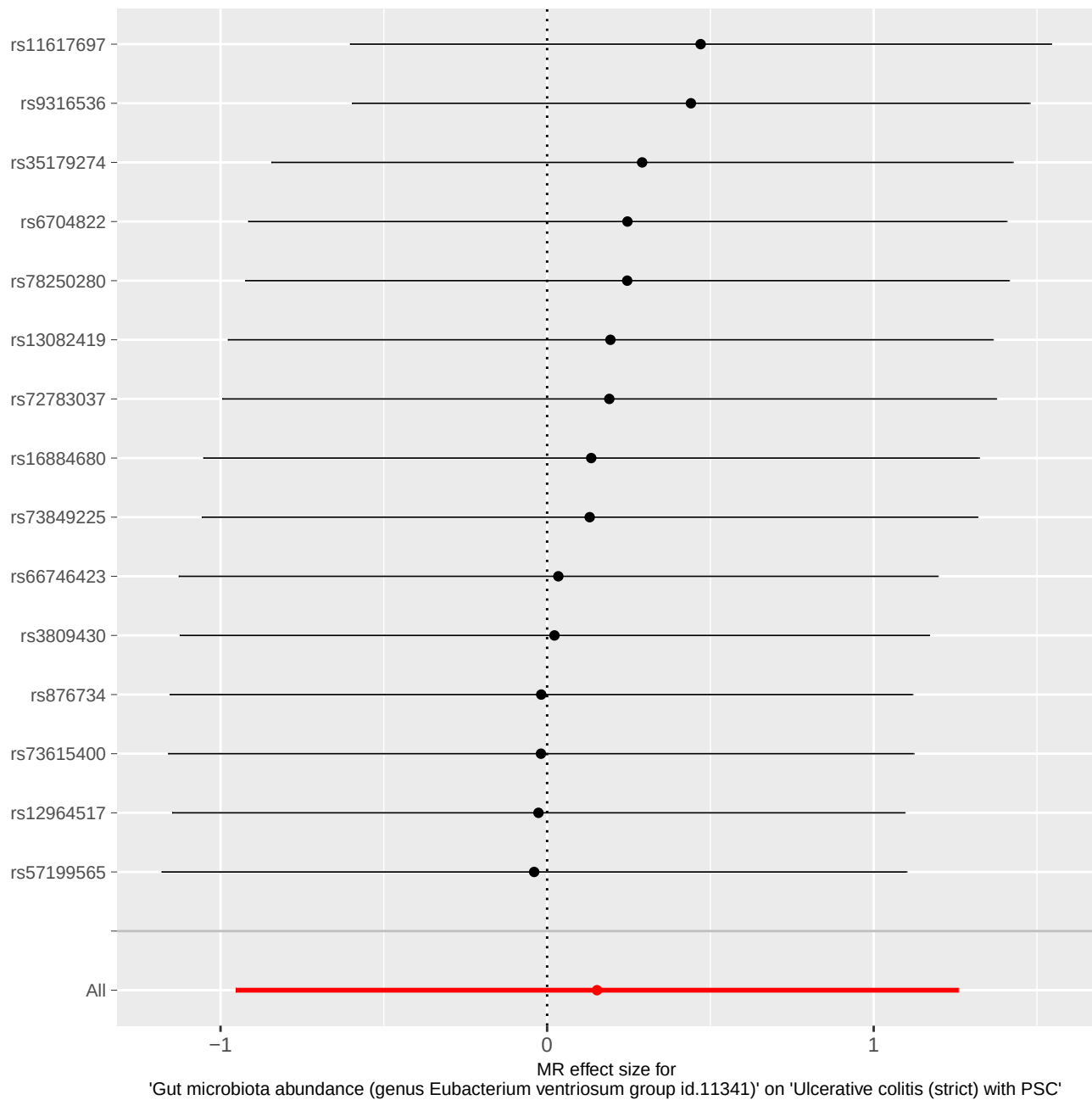


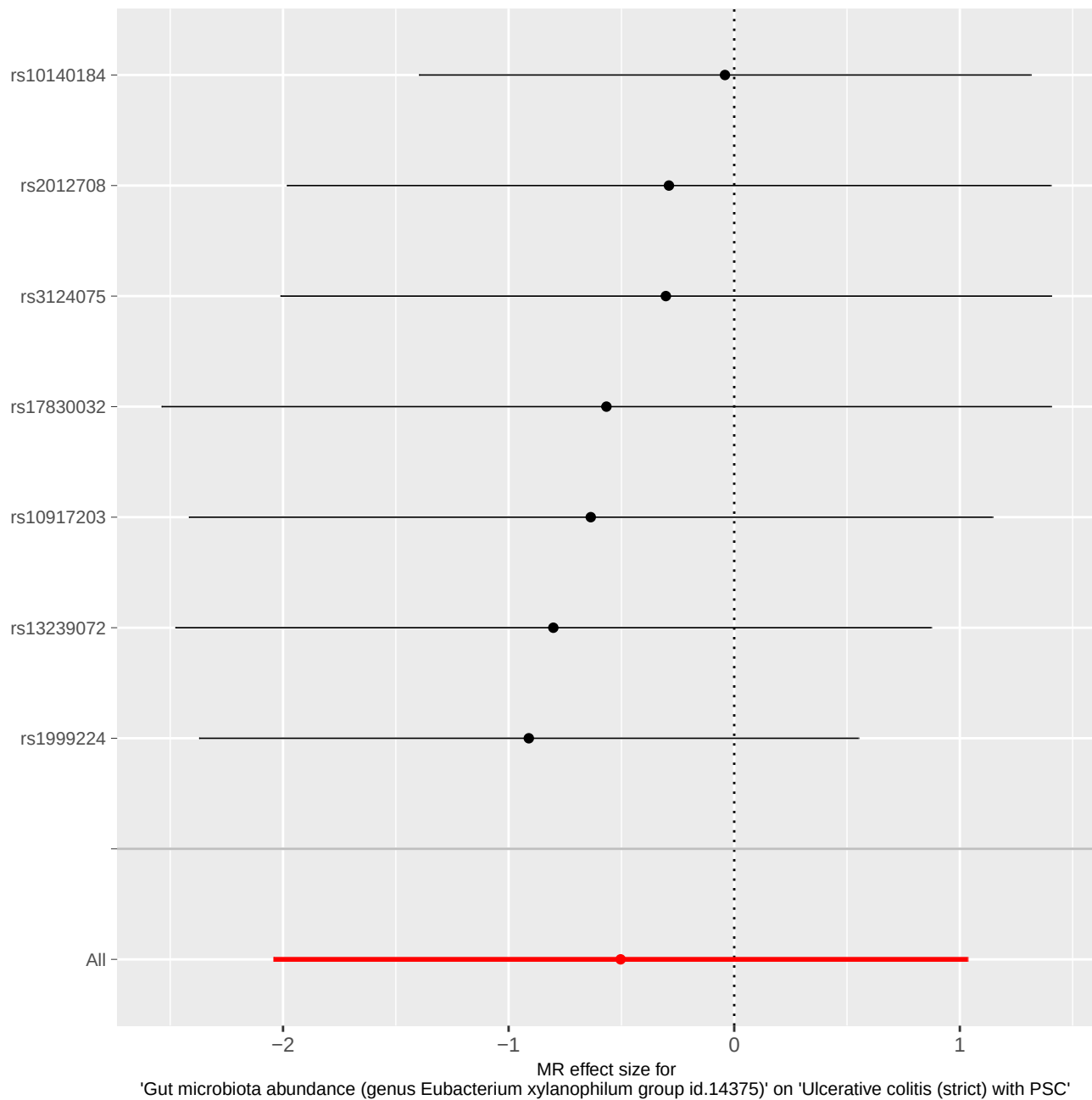
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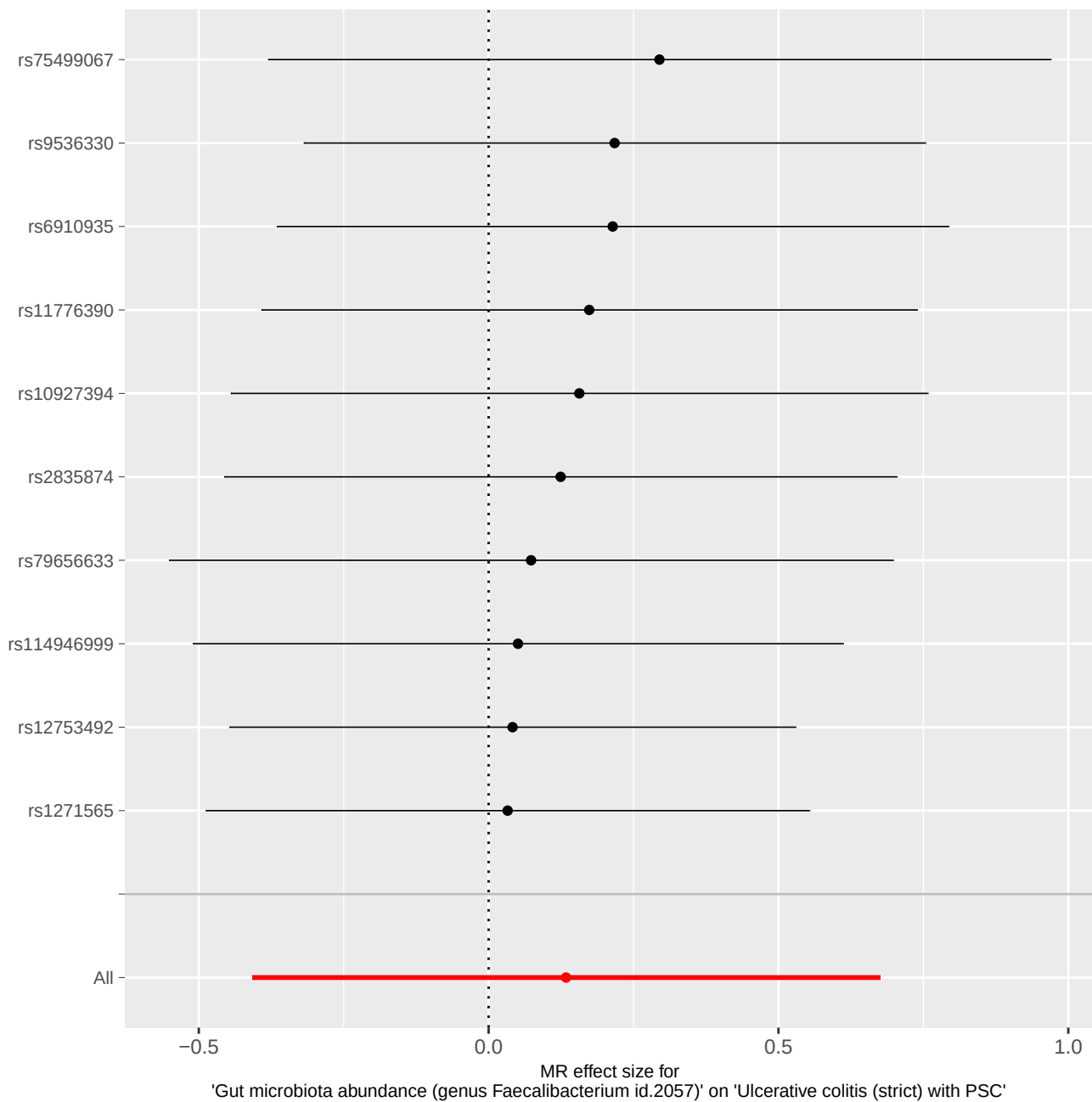
'Gut microbiota abundance (genus Eubacterium rectale group id.14374)' on 'Ulcerative colitis (strict) with PSC'

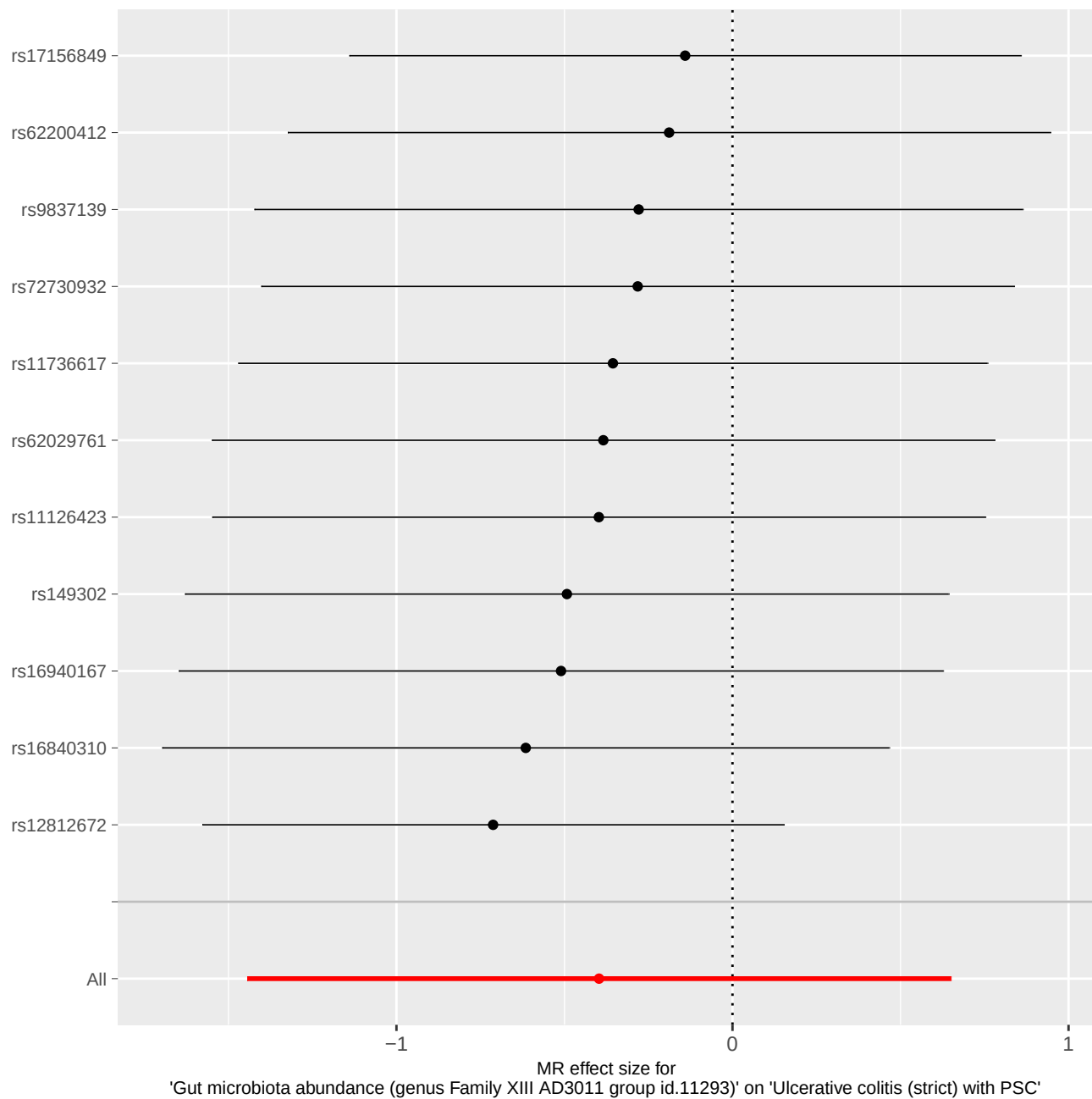


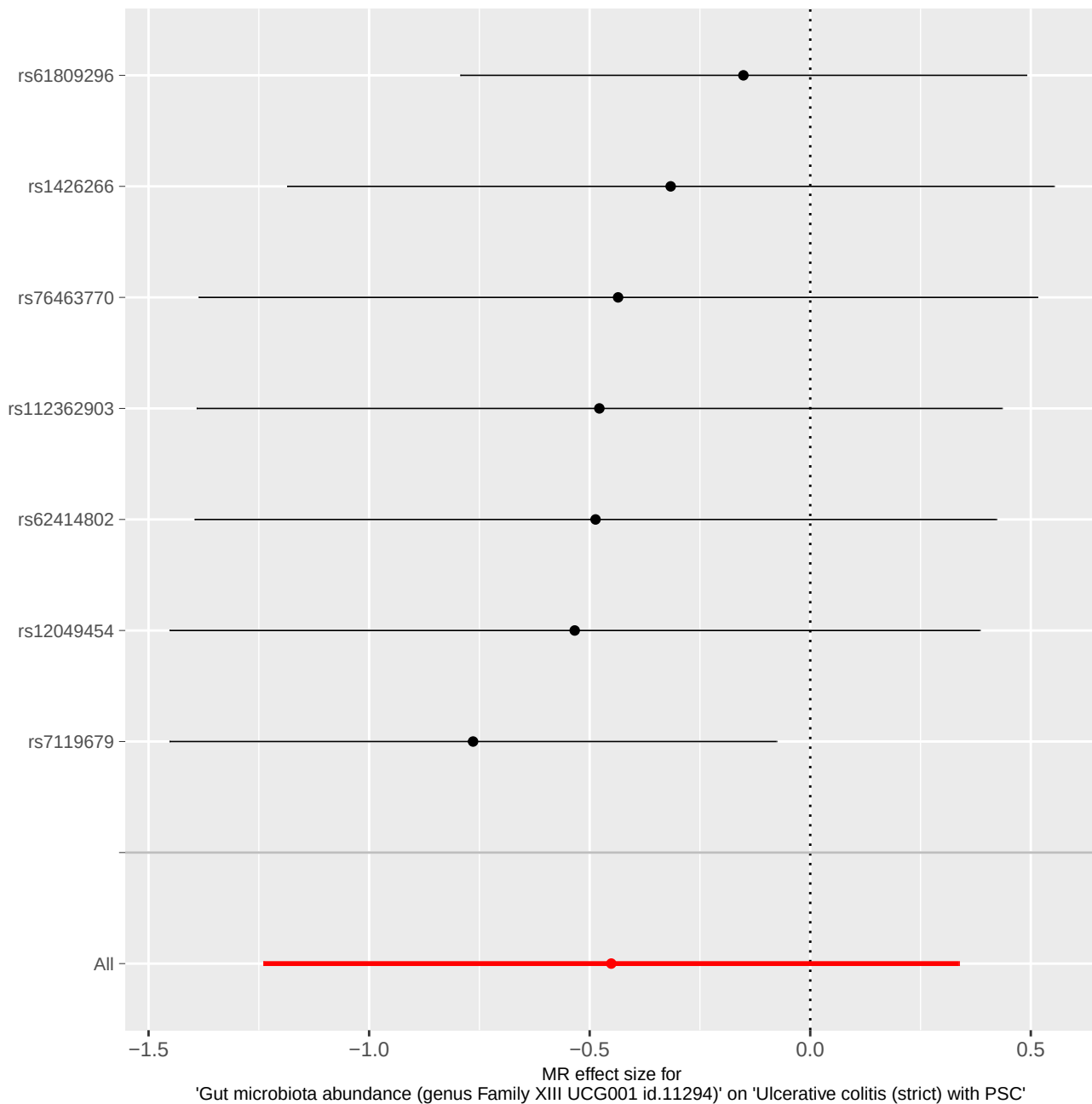
MR effect size for
'Gut microbiota abundance (genus Eubacterium ruminantium group id.11340)' on 'Ulcerative colitis (strict) with PSC'

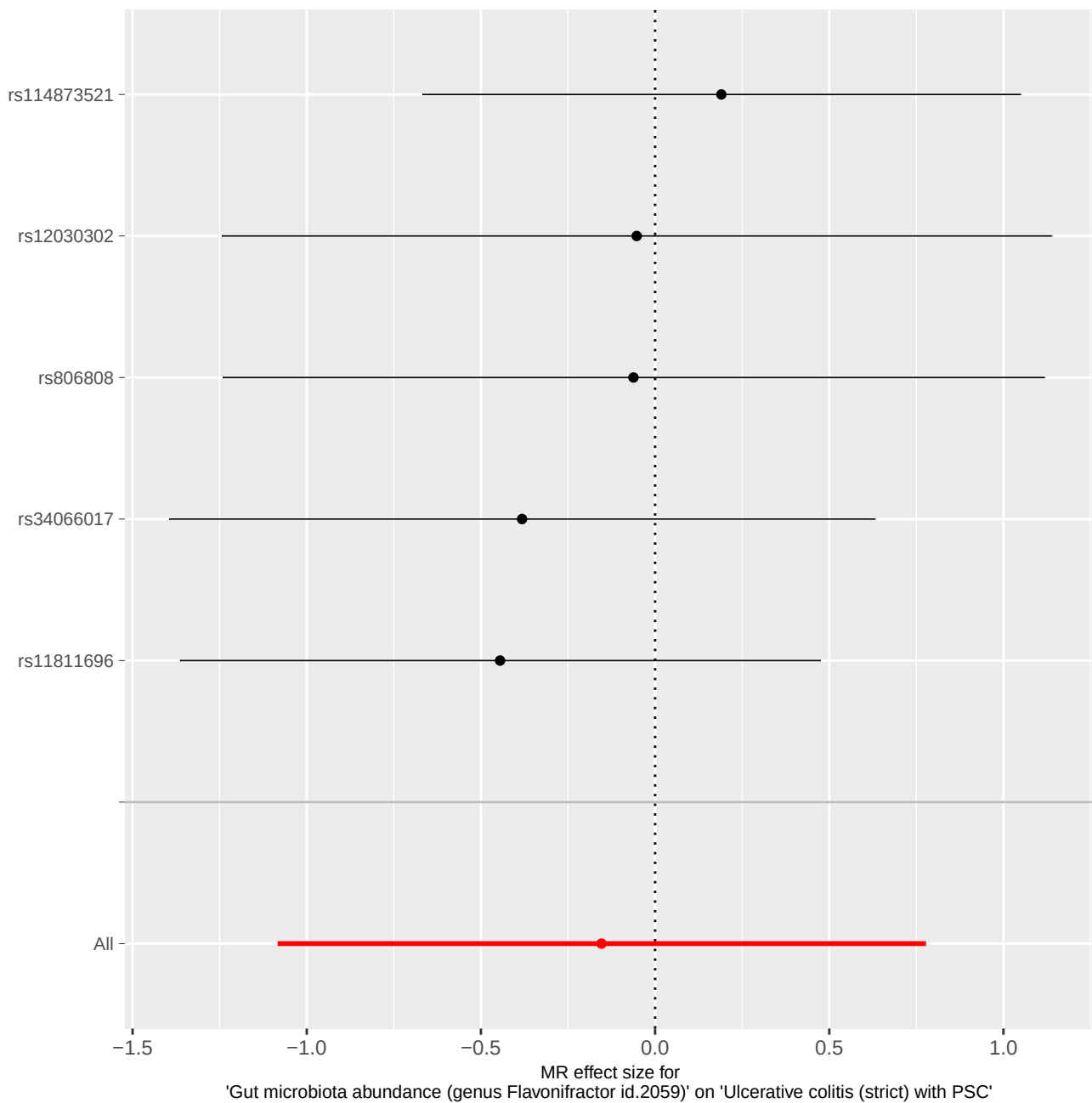


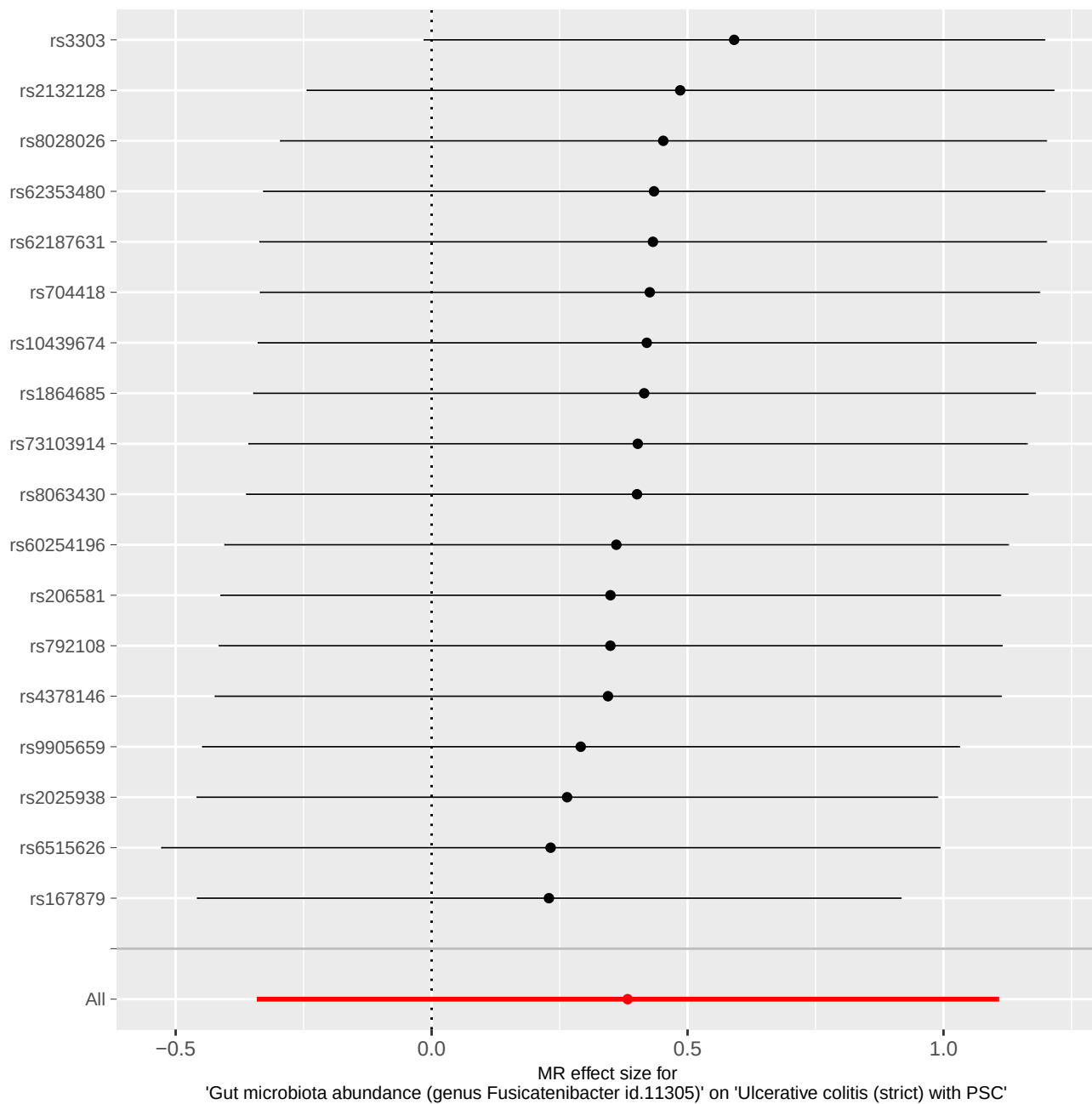


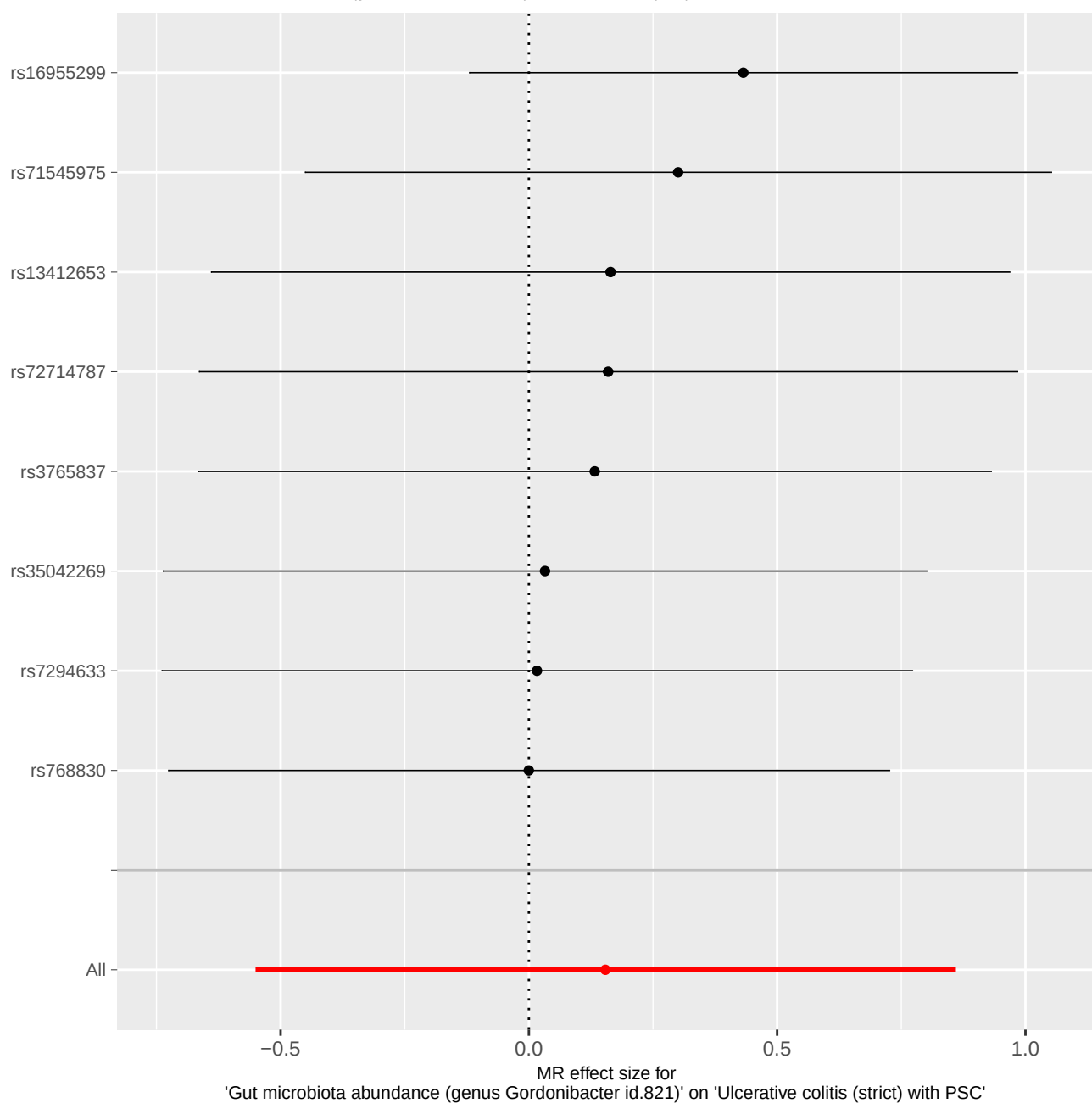


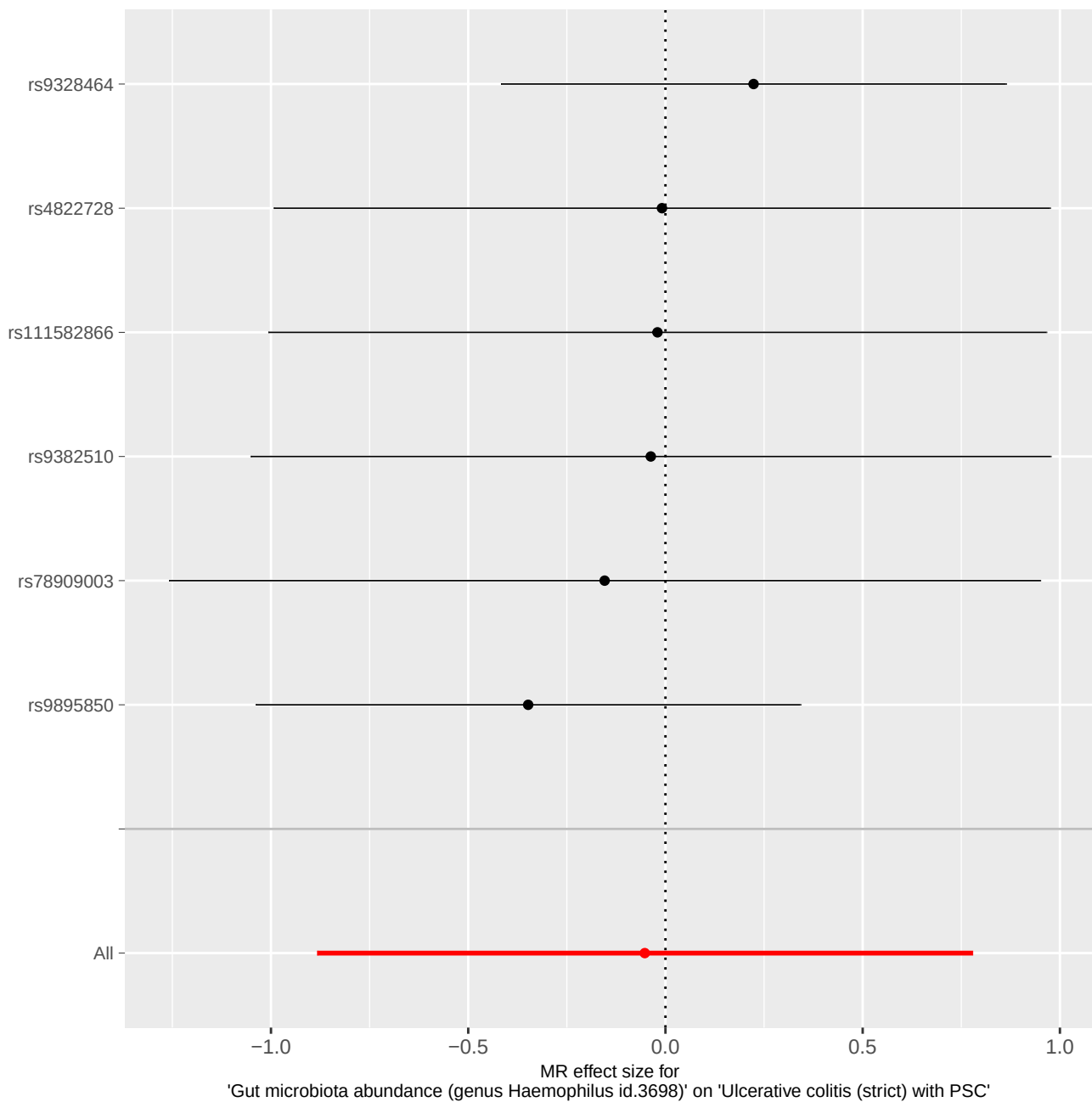


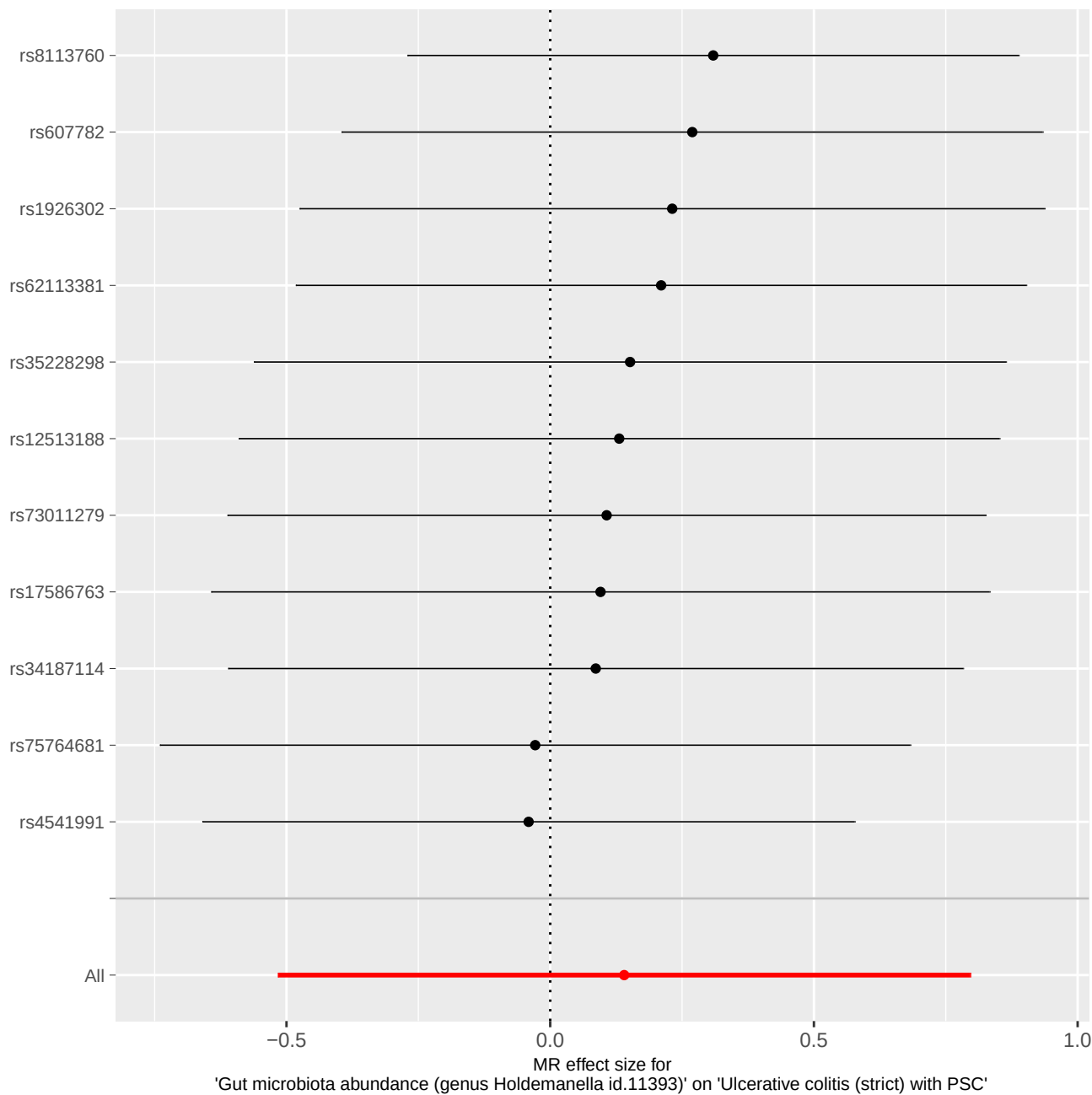




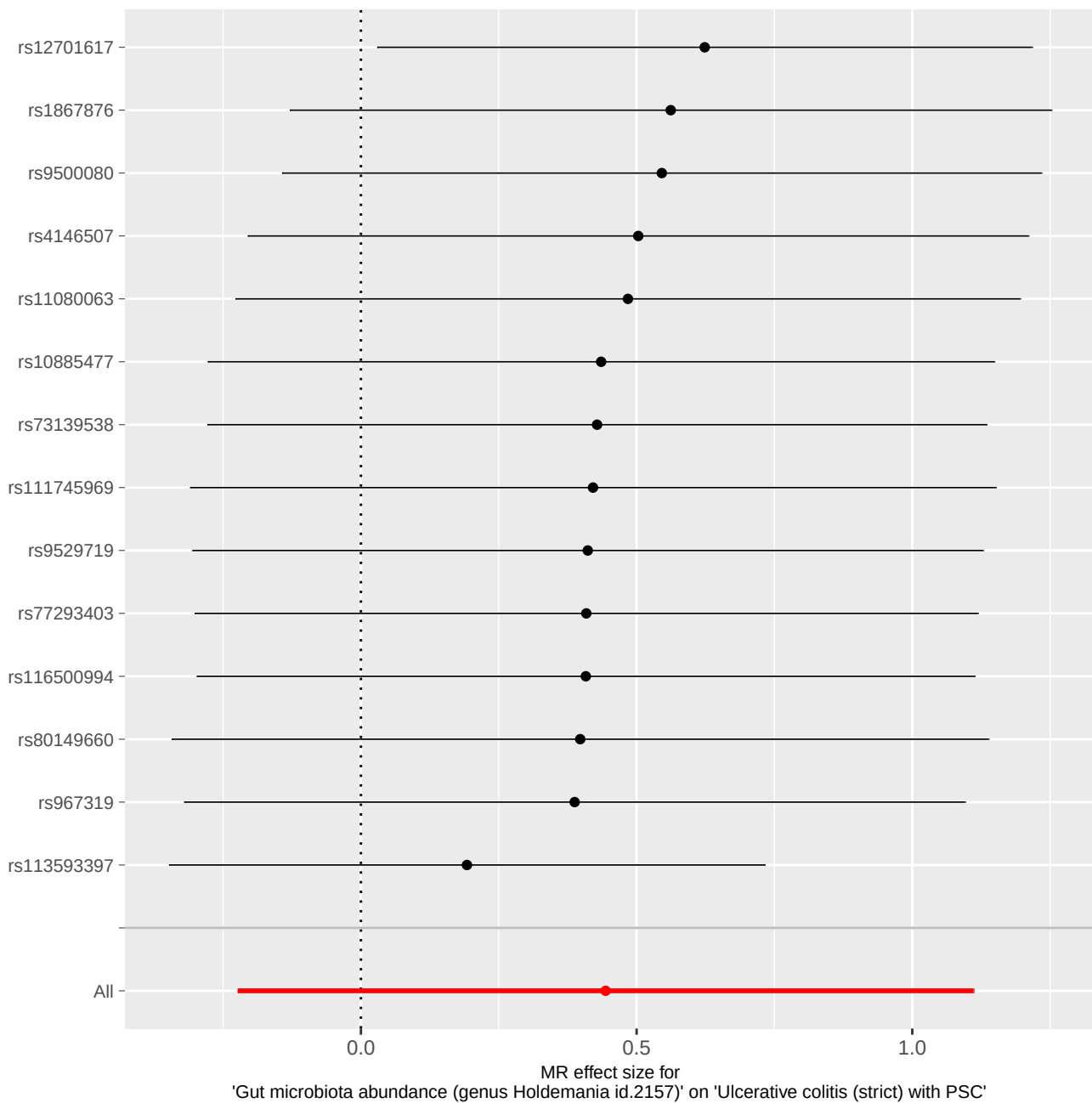


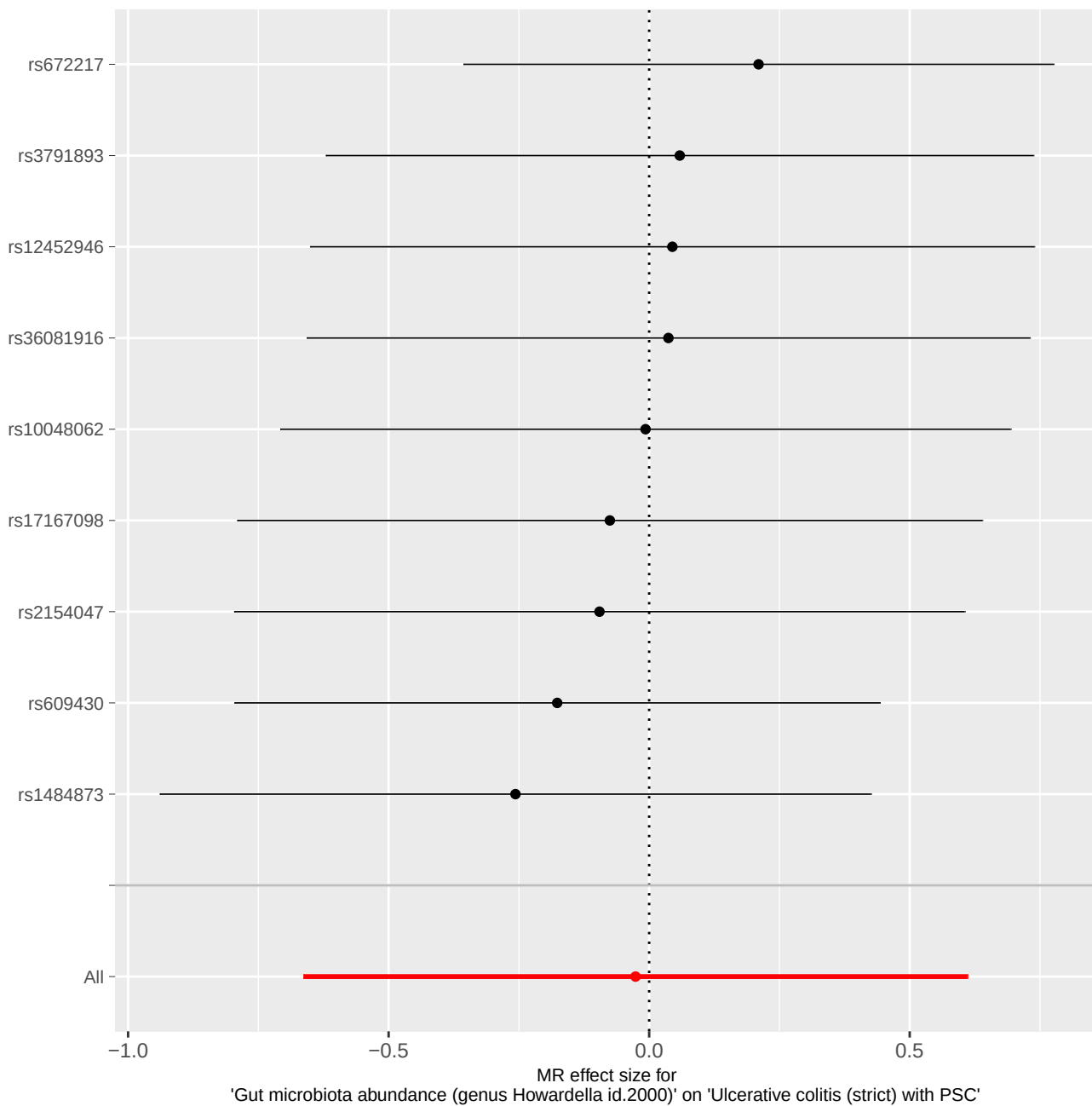




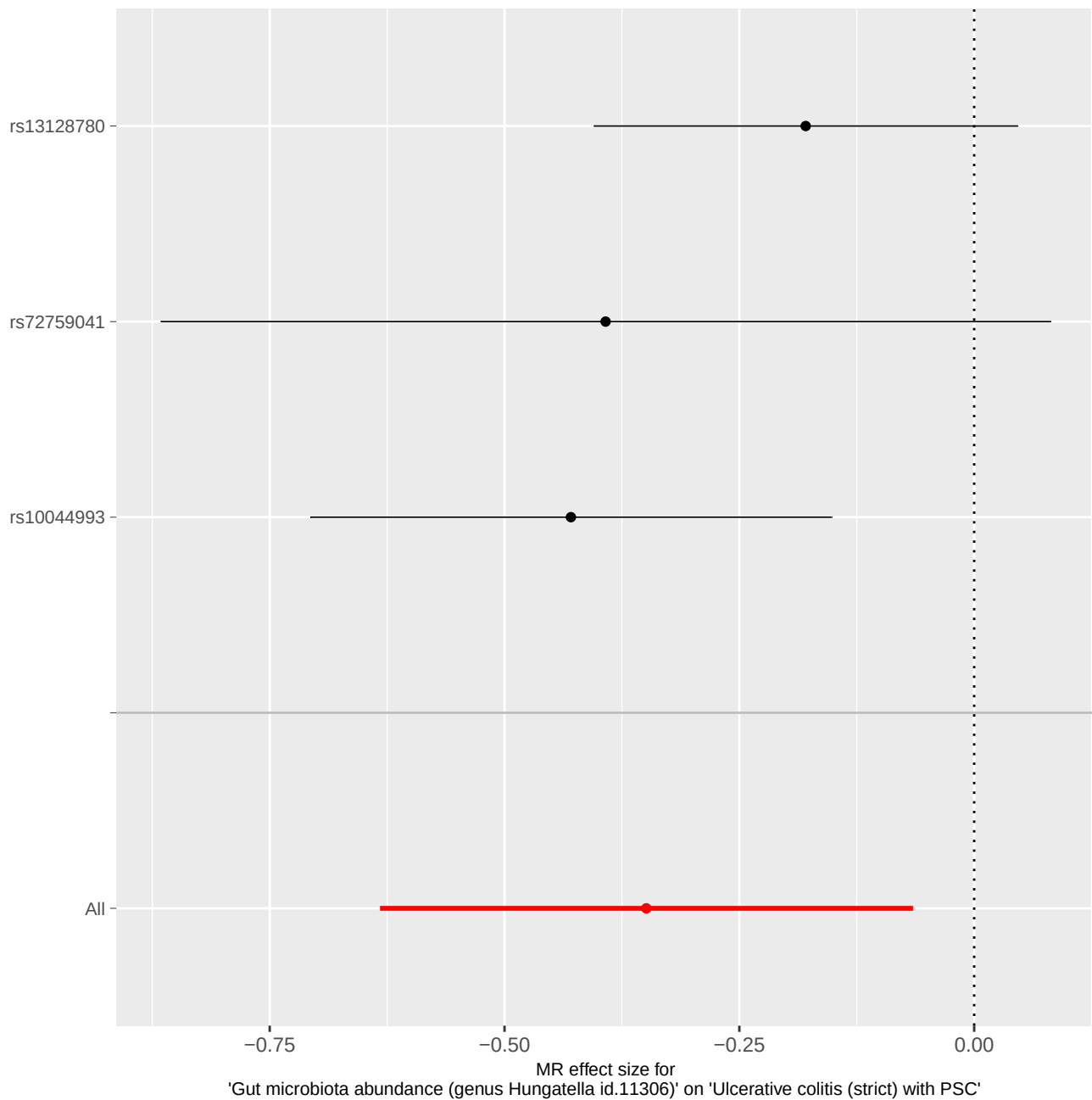


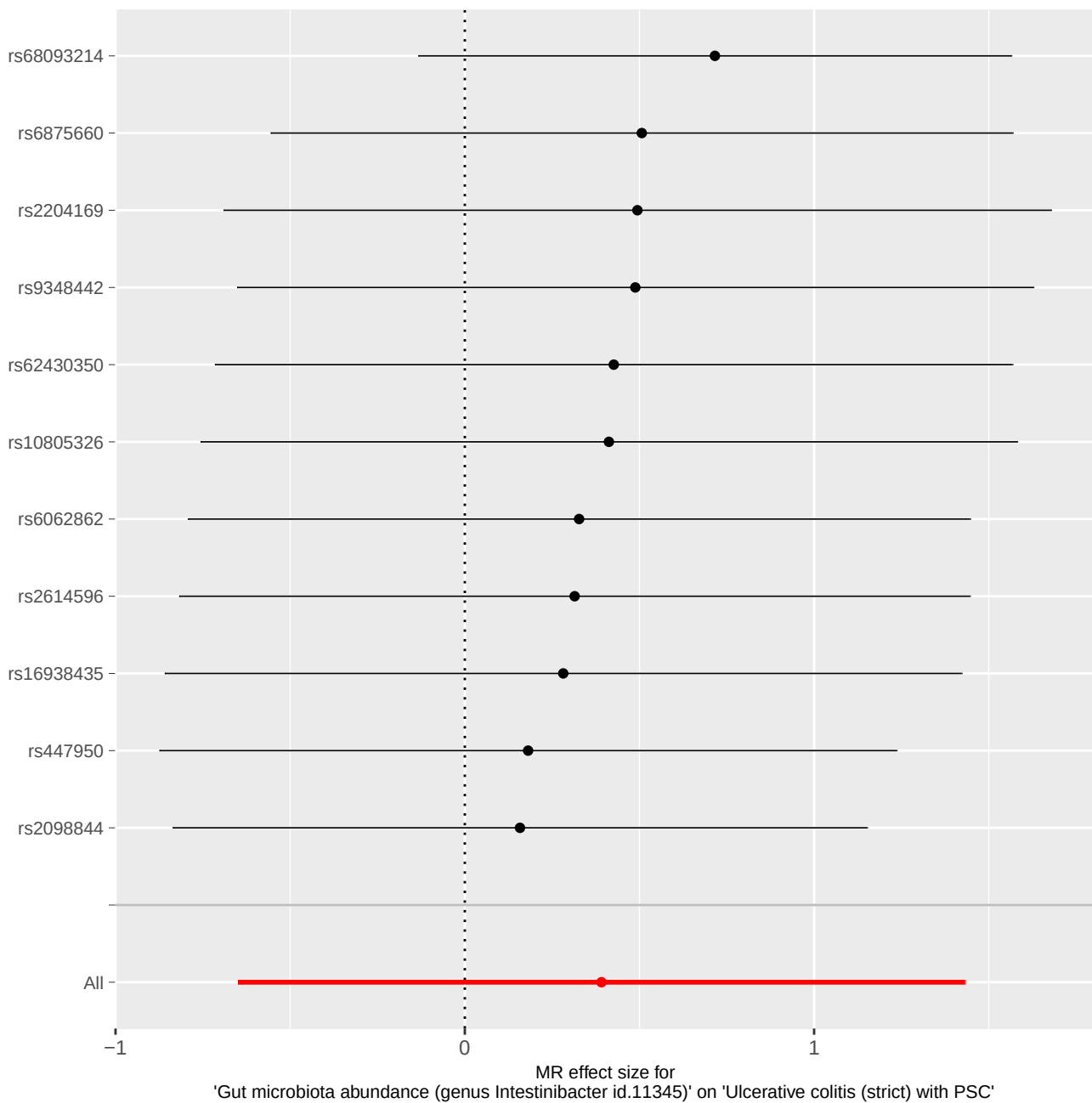
MR effect size for
'Gut microbiota abundance (genus Holdemanella id.11393)' on 'Ulcerative colitis (strict) with PSC'

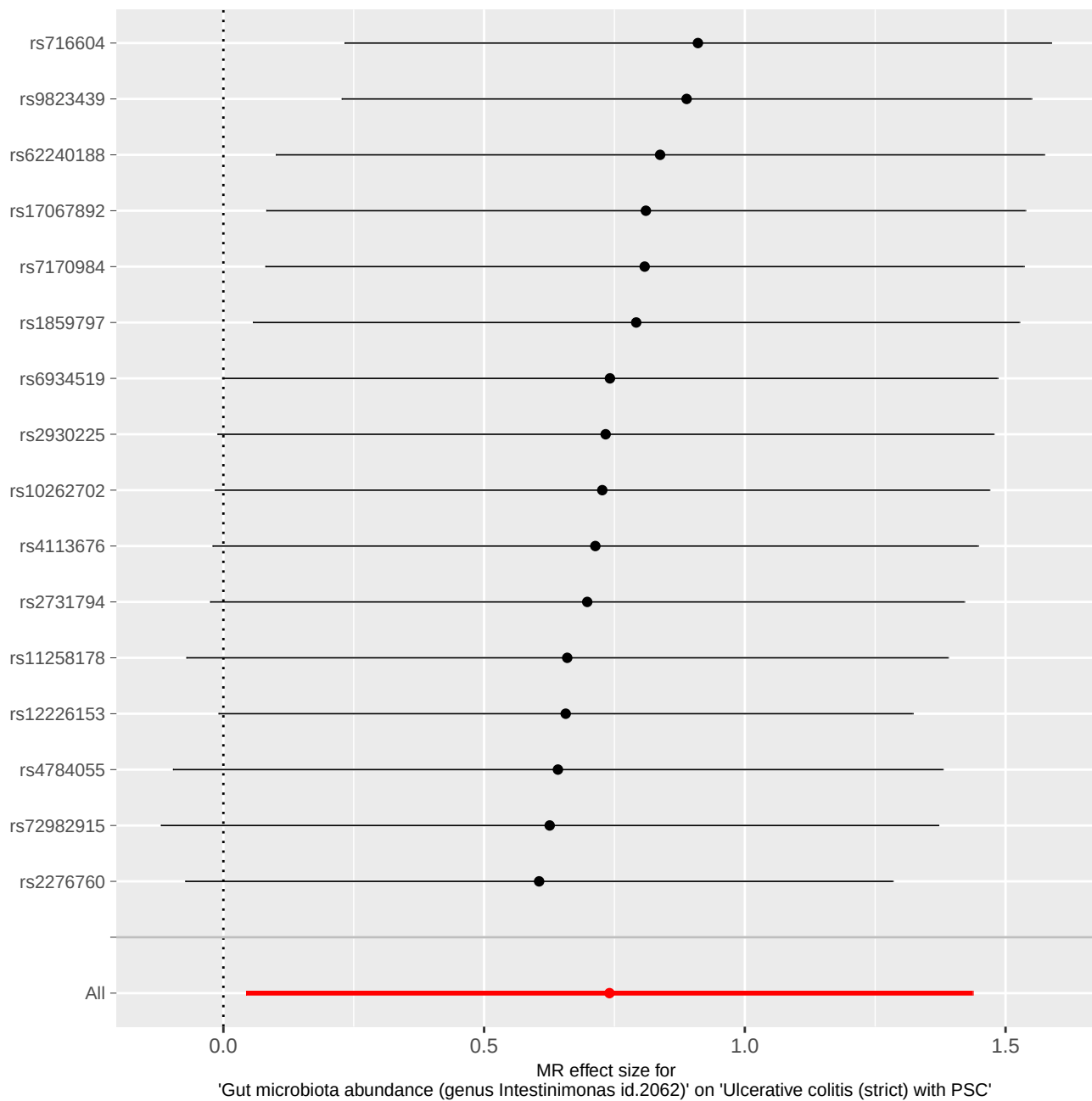


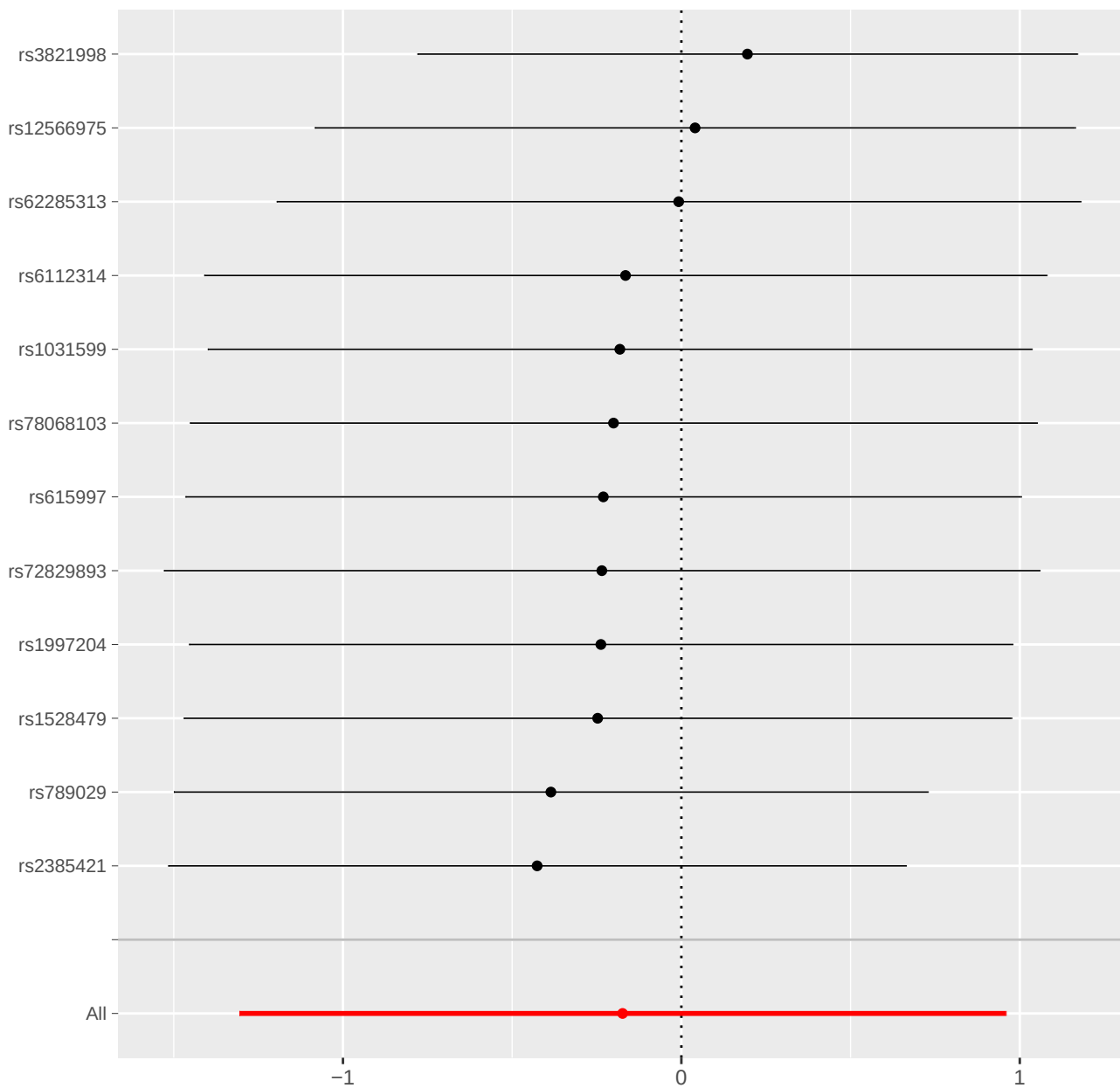


MR effect size for
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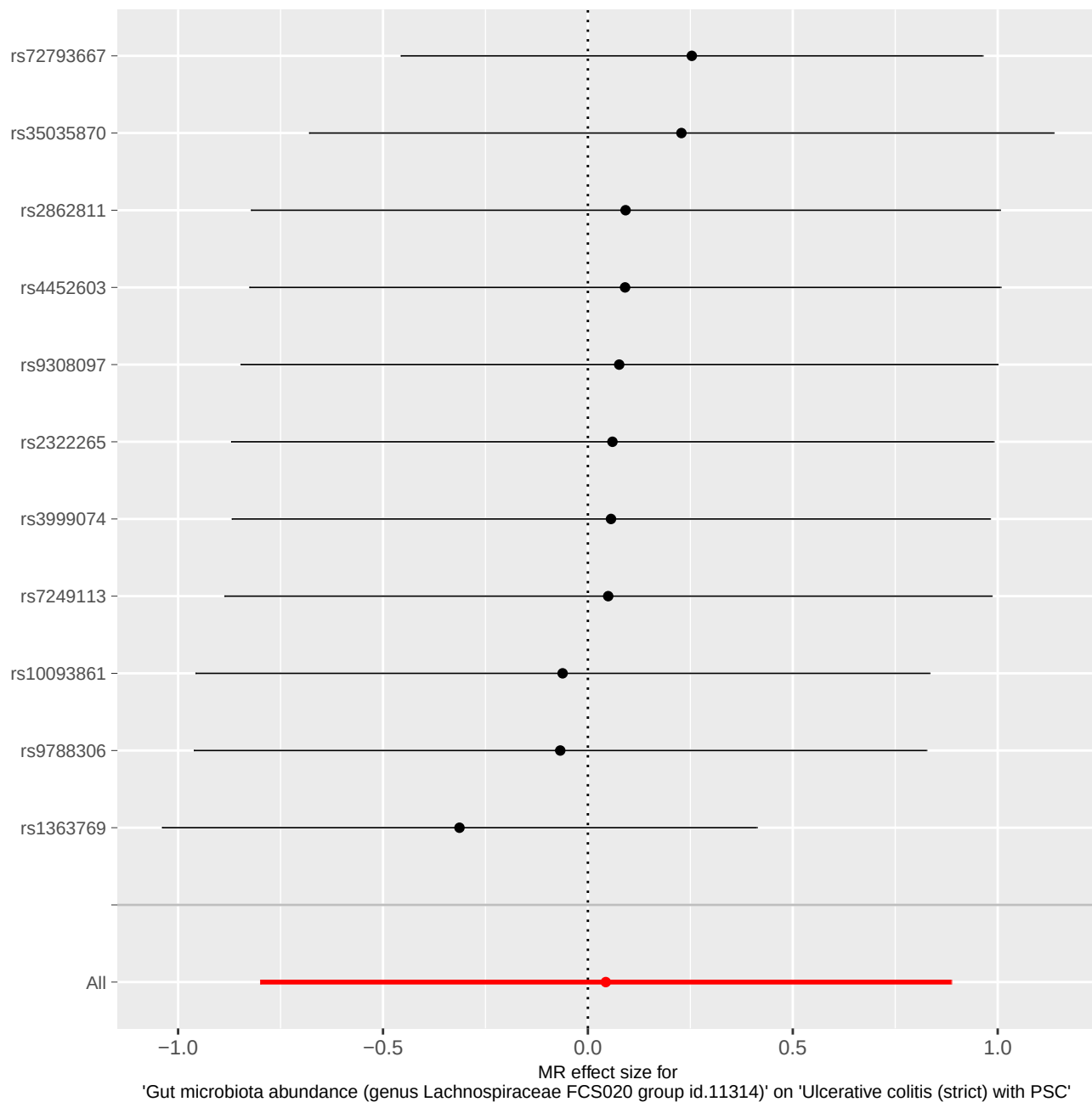


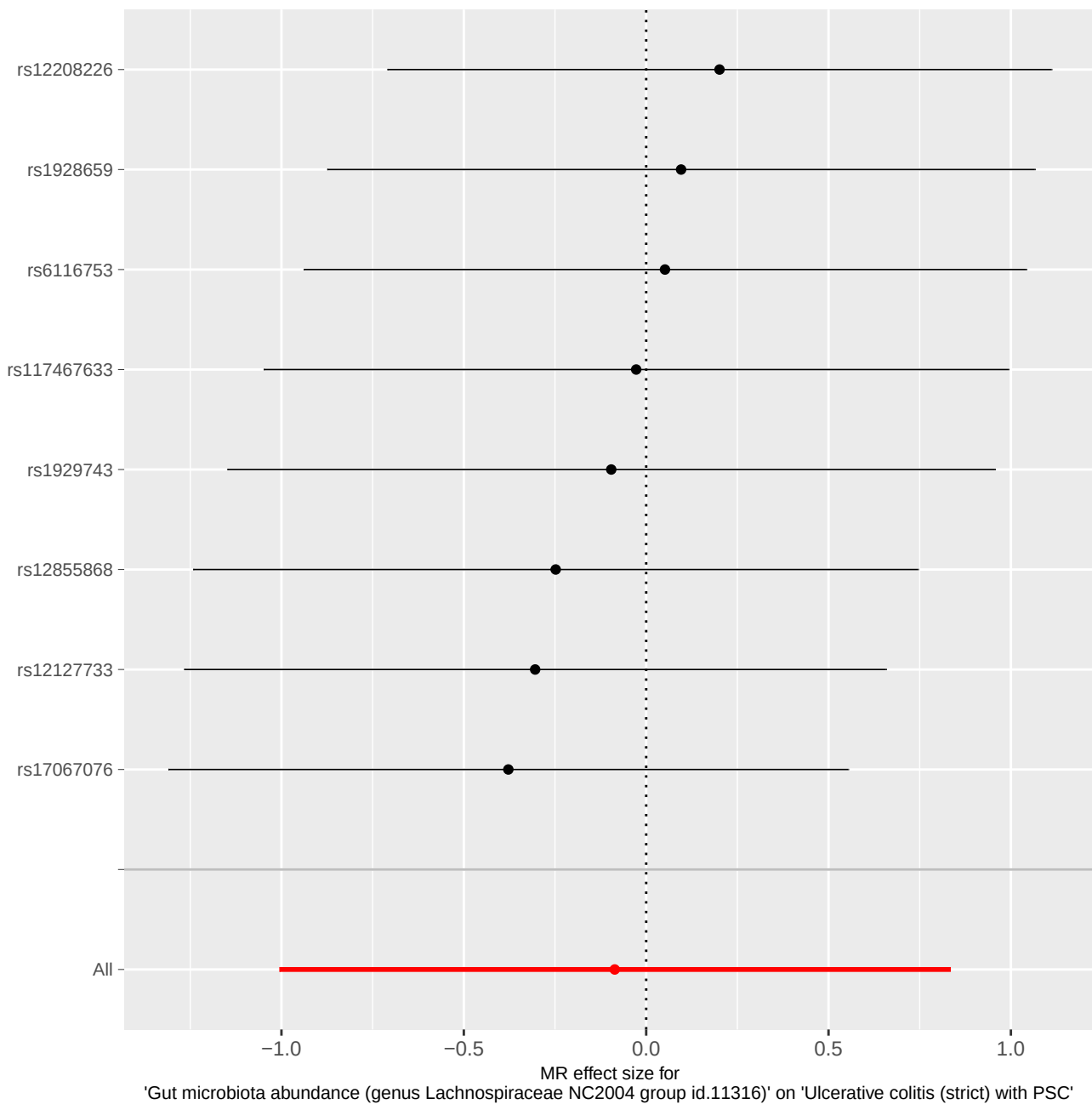


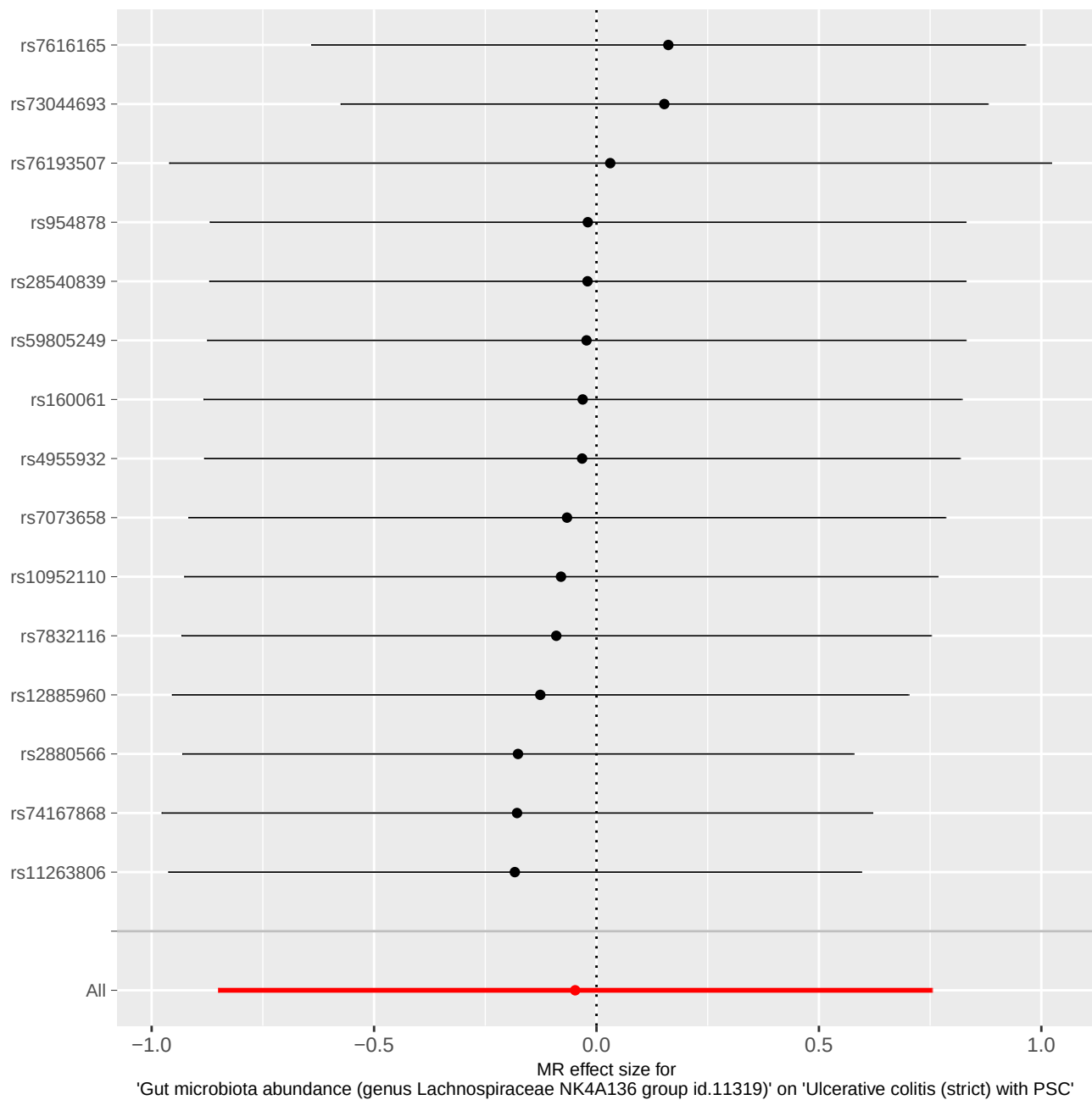


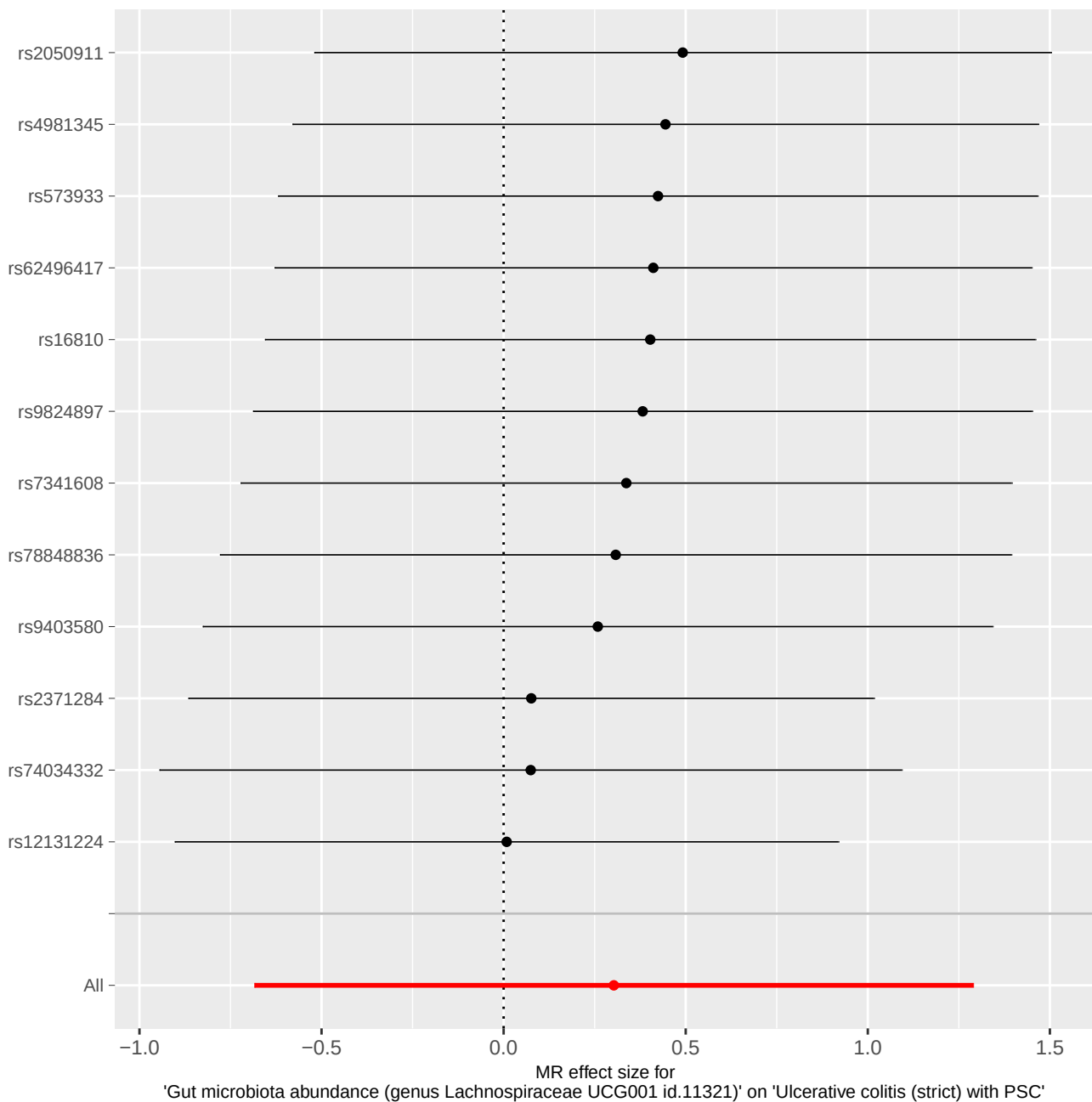
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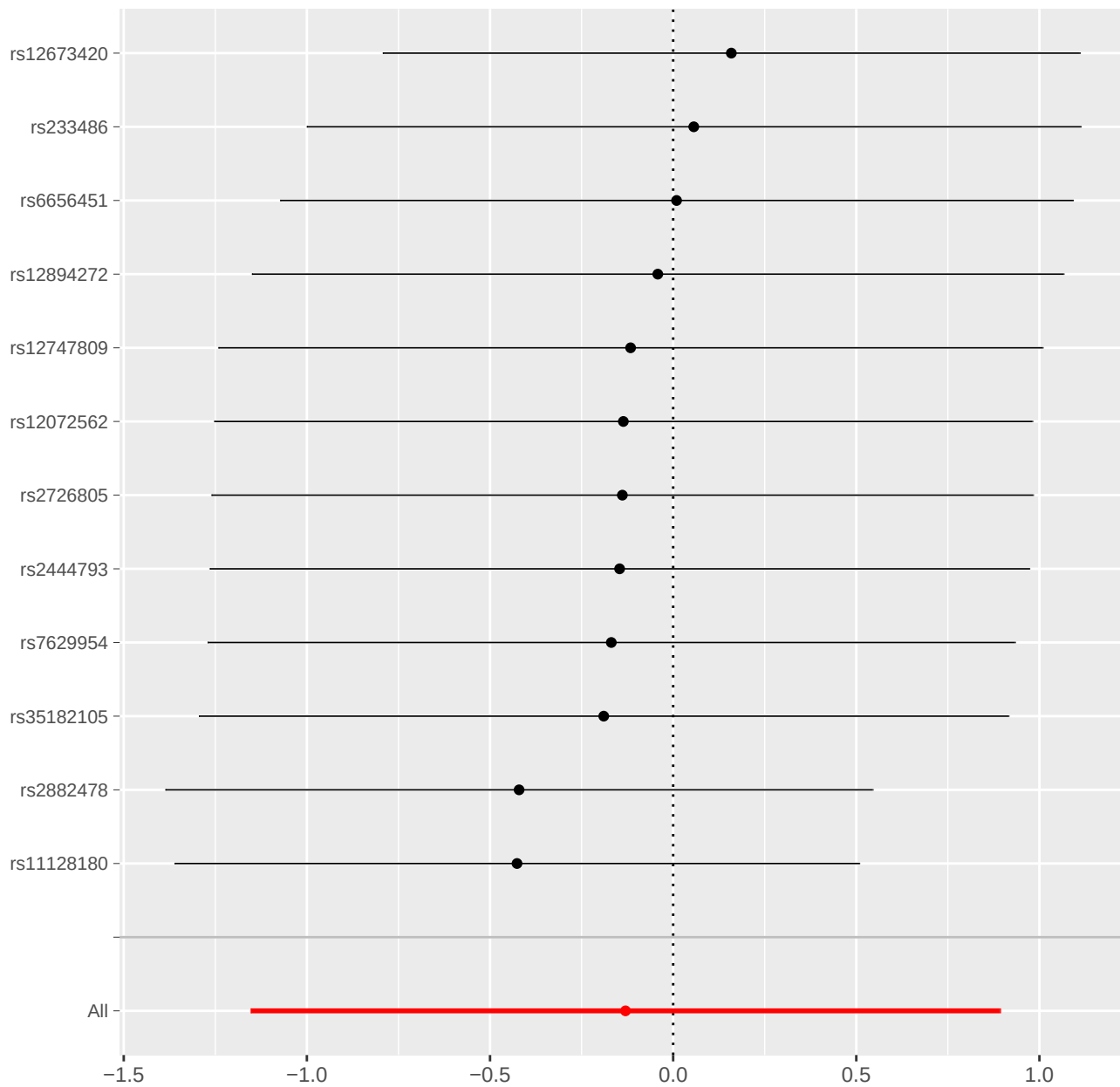
'Gut microbiota abundance (genus Lachnoclostridium id.11308)' on 'Ulcerative colitis (strict) with PSC'



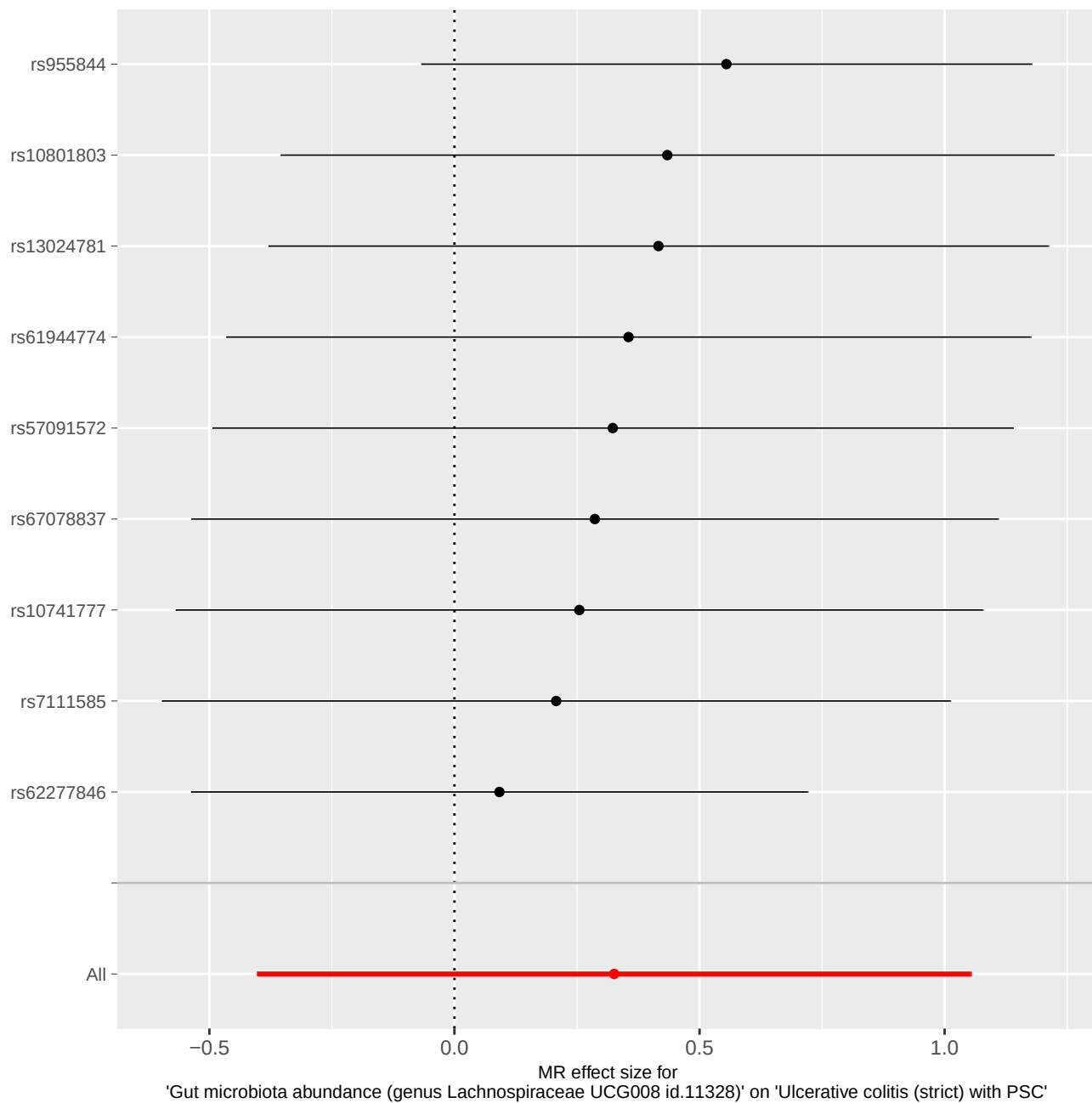


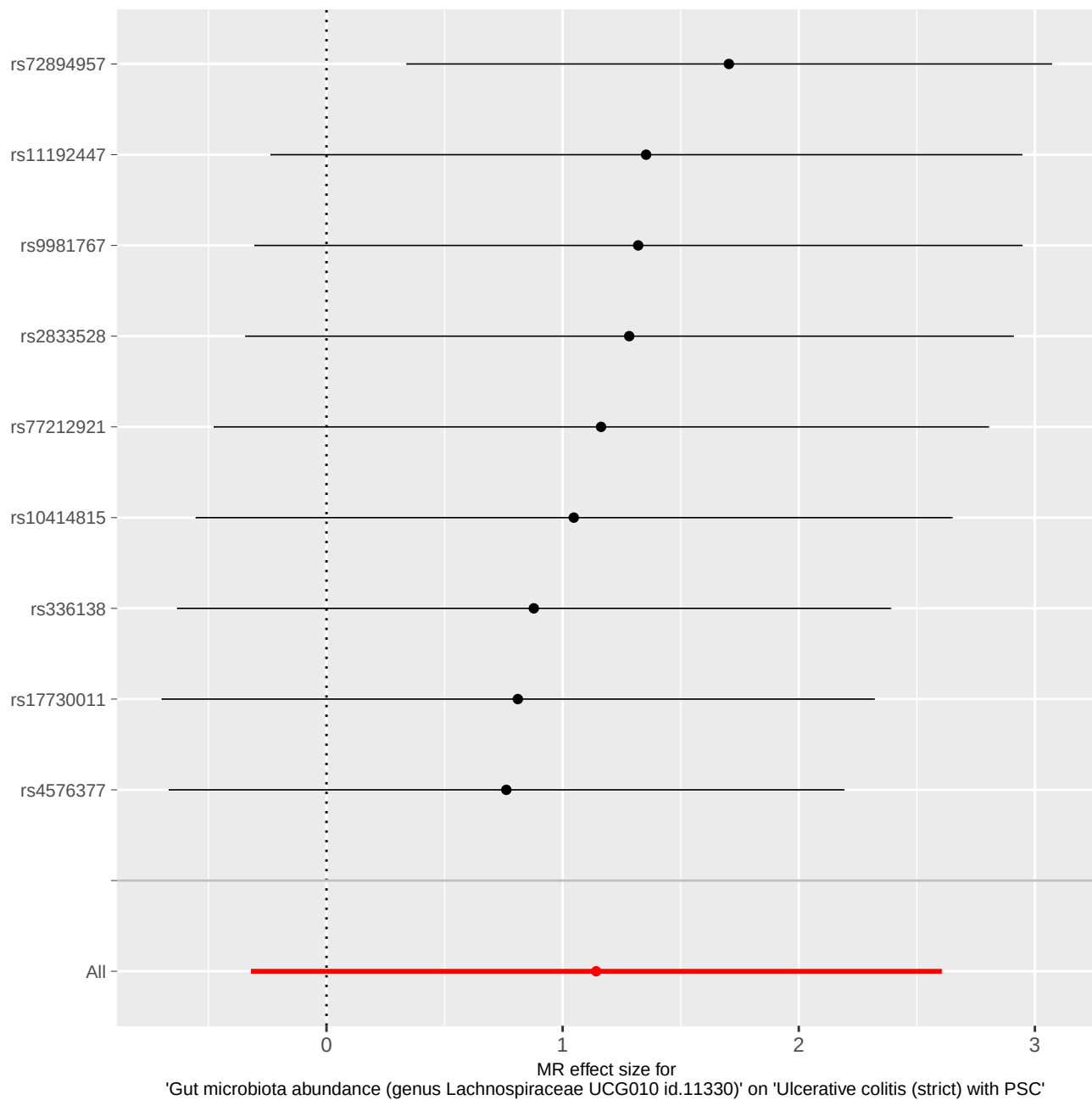




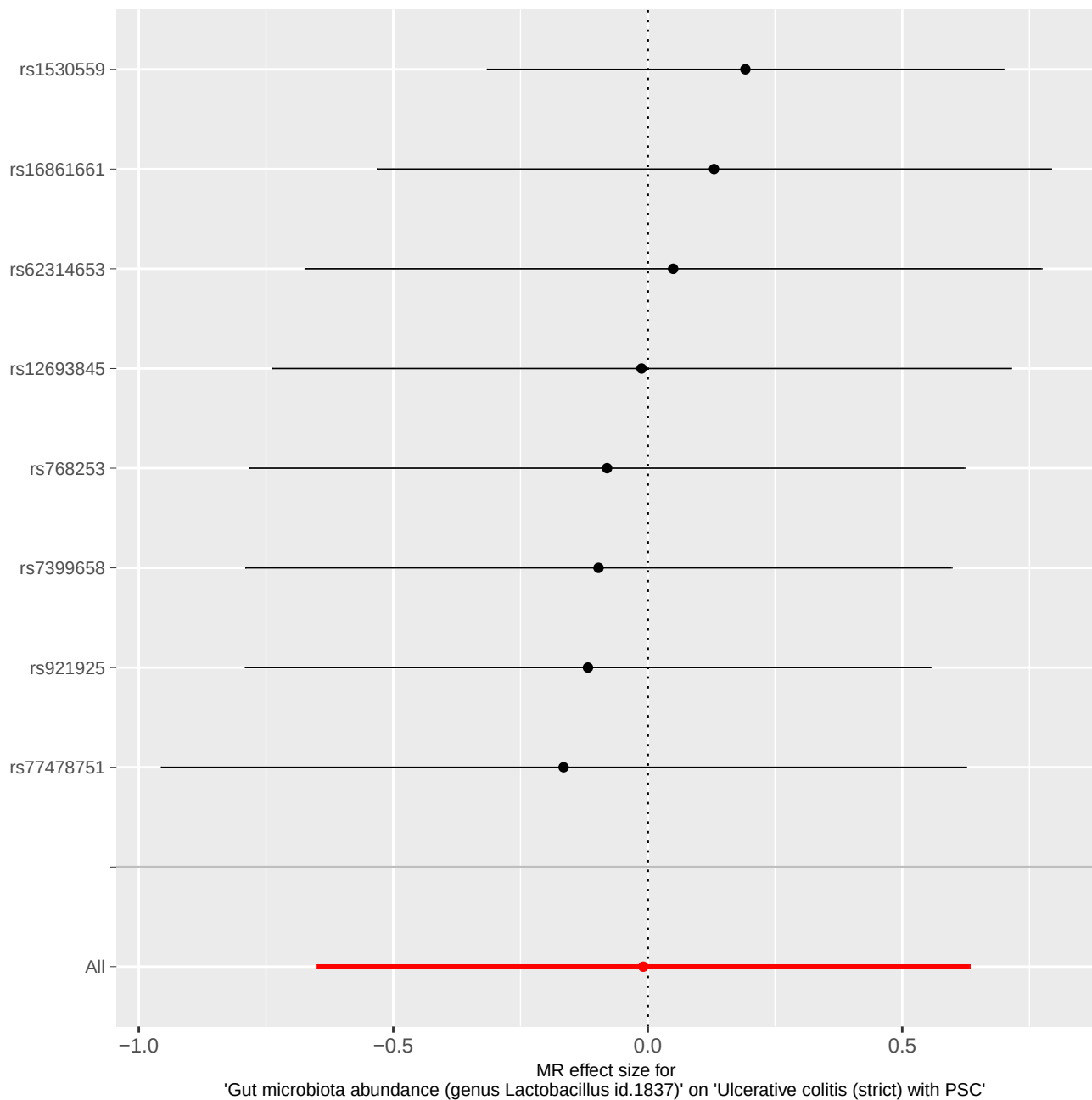


MR effect size for
'Gut microbiota abundance (genus Lachnospiraceae UCG004 id.11324)' on 'Ulcerative colitis (strict) with PSC'

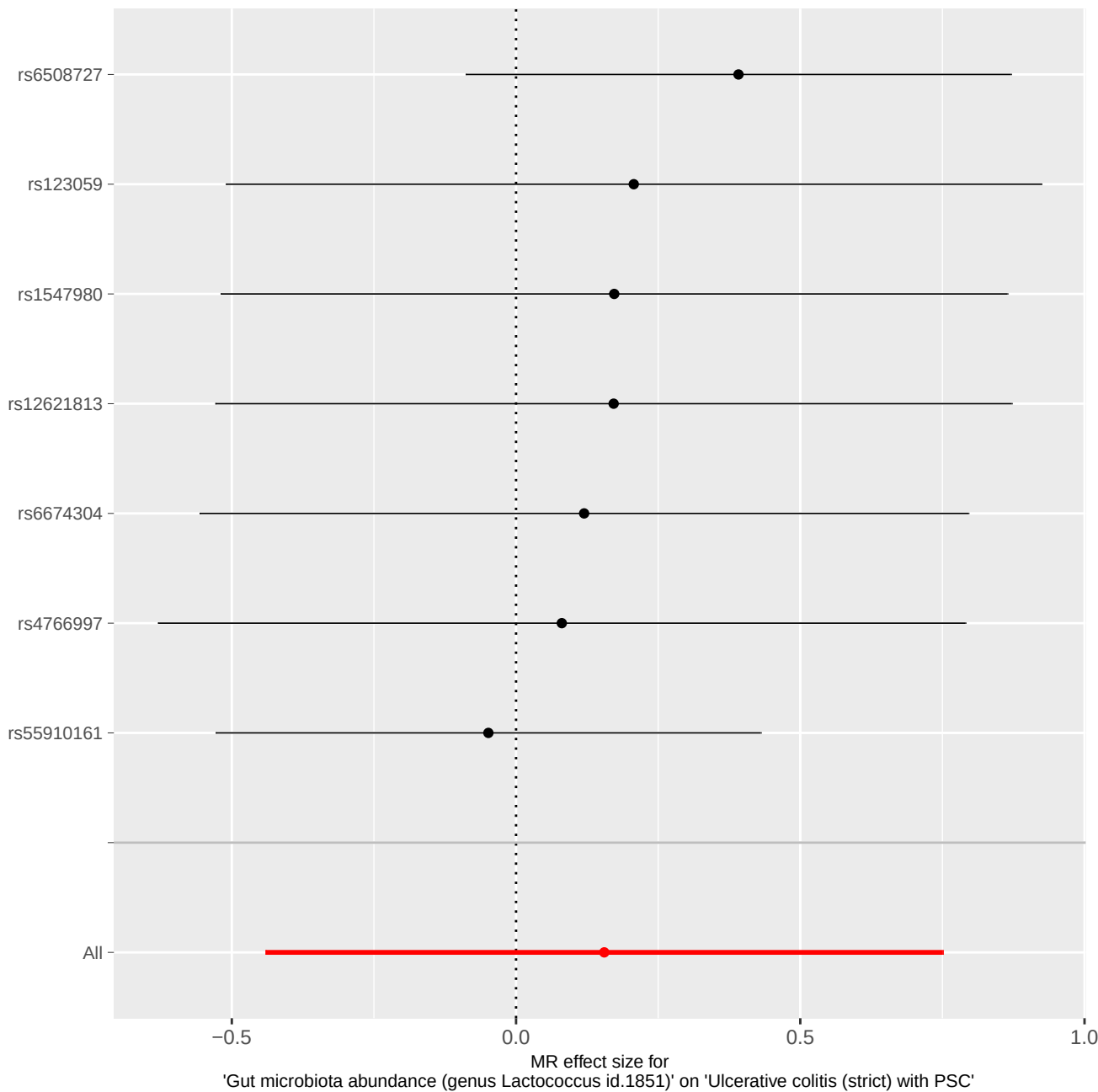


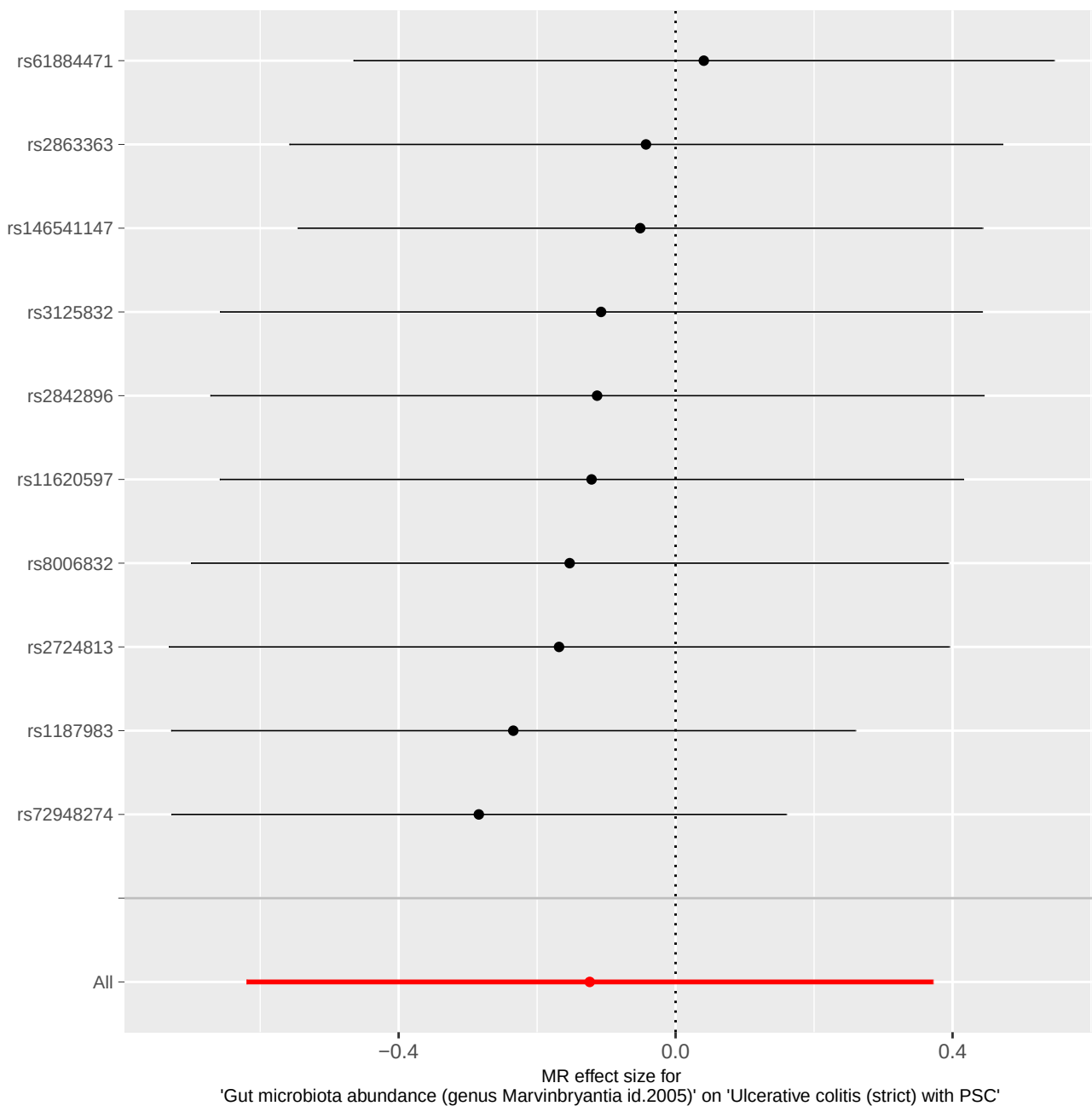


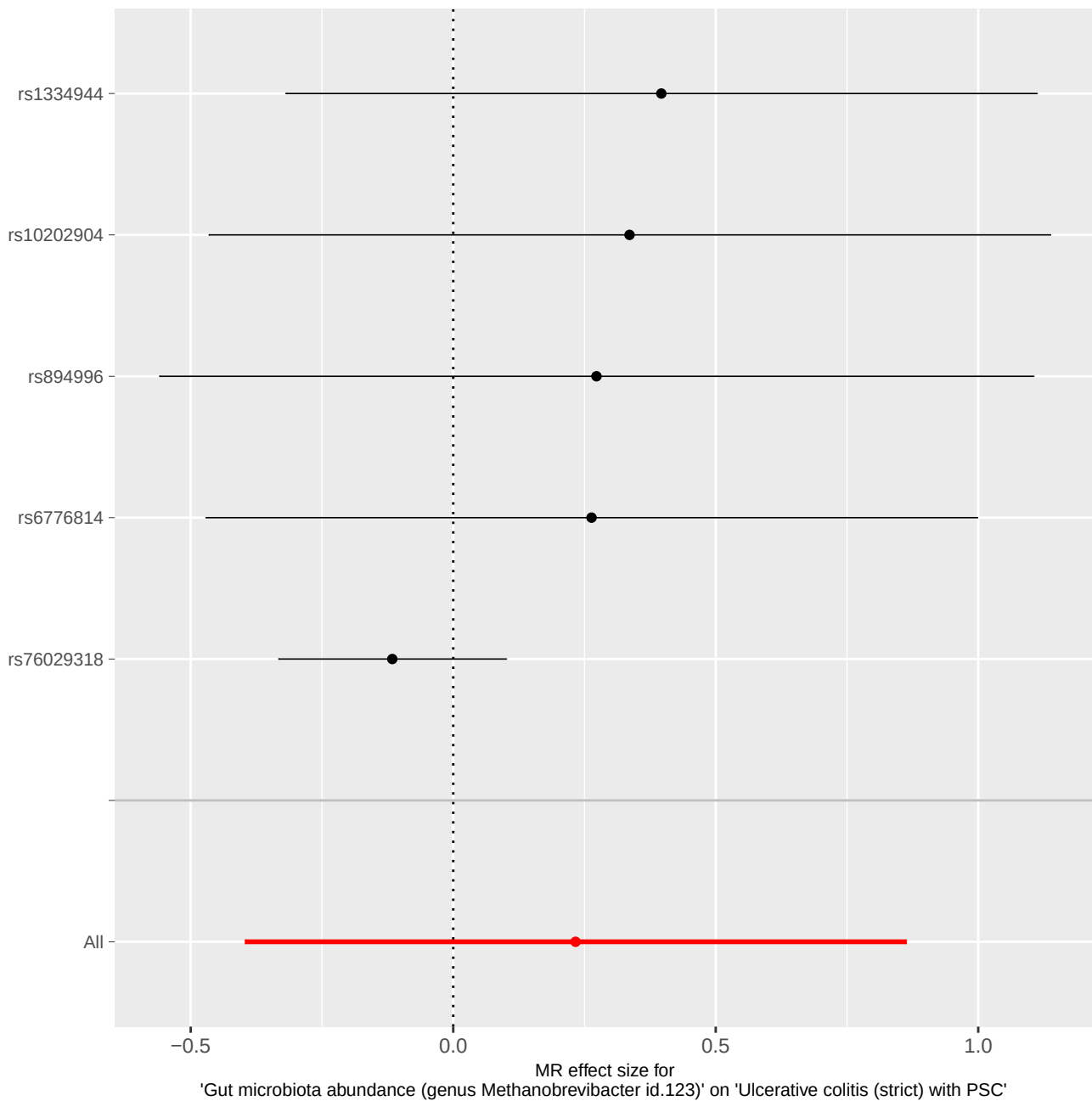
MR effect size for
'Gut microbiota abundance (genus Lachnospiraceae UCG010 id.11330)' on 'Ulcerative colitis (strict) with PSC'

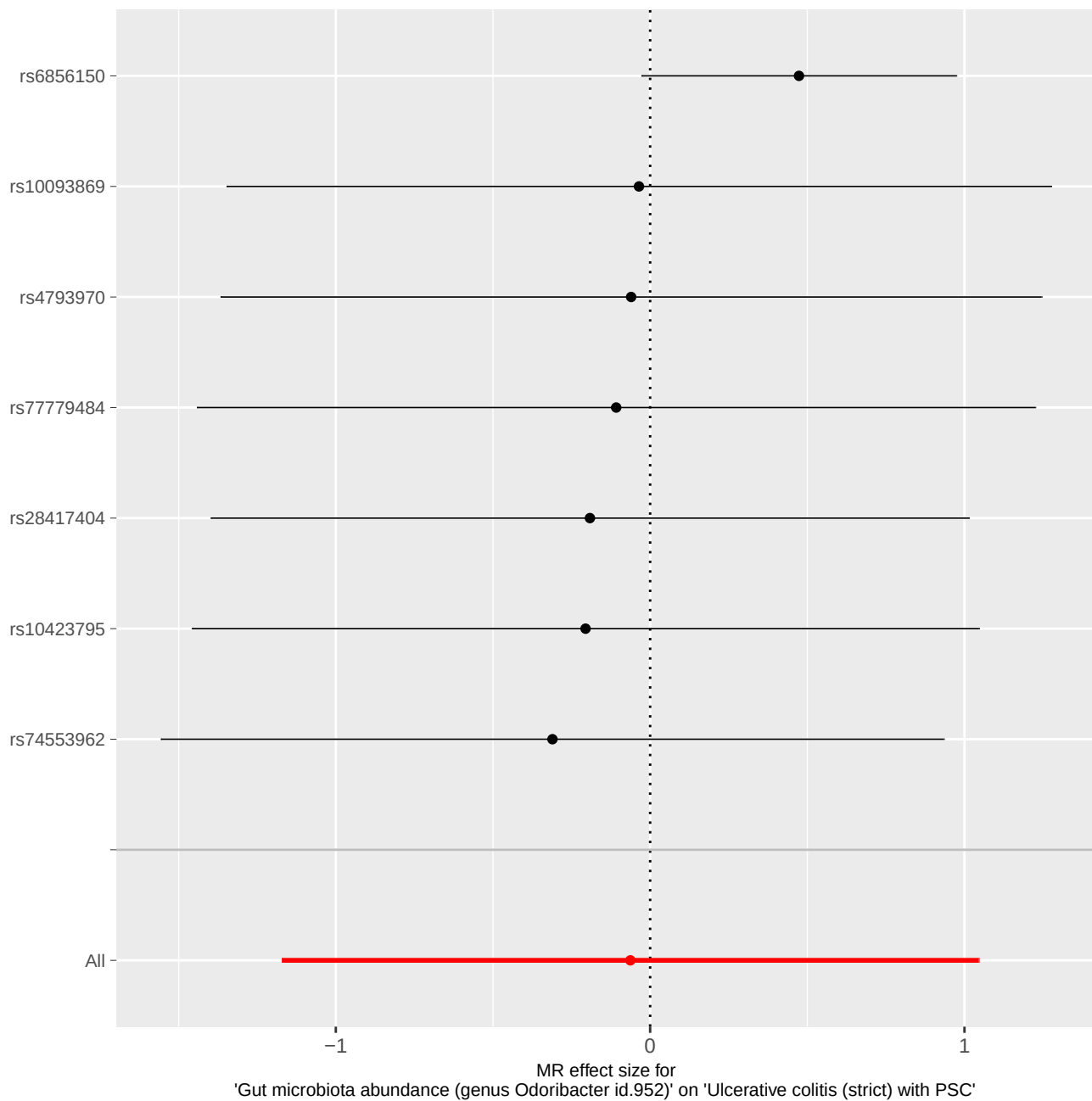


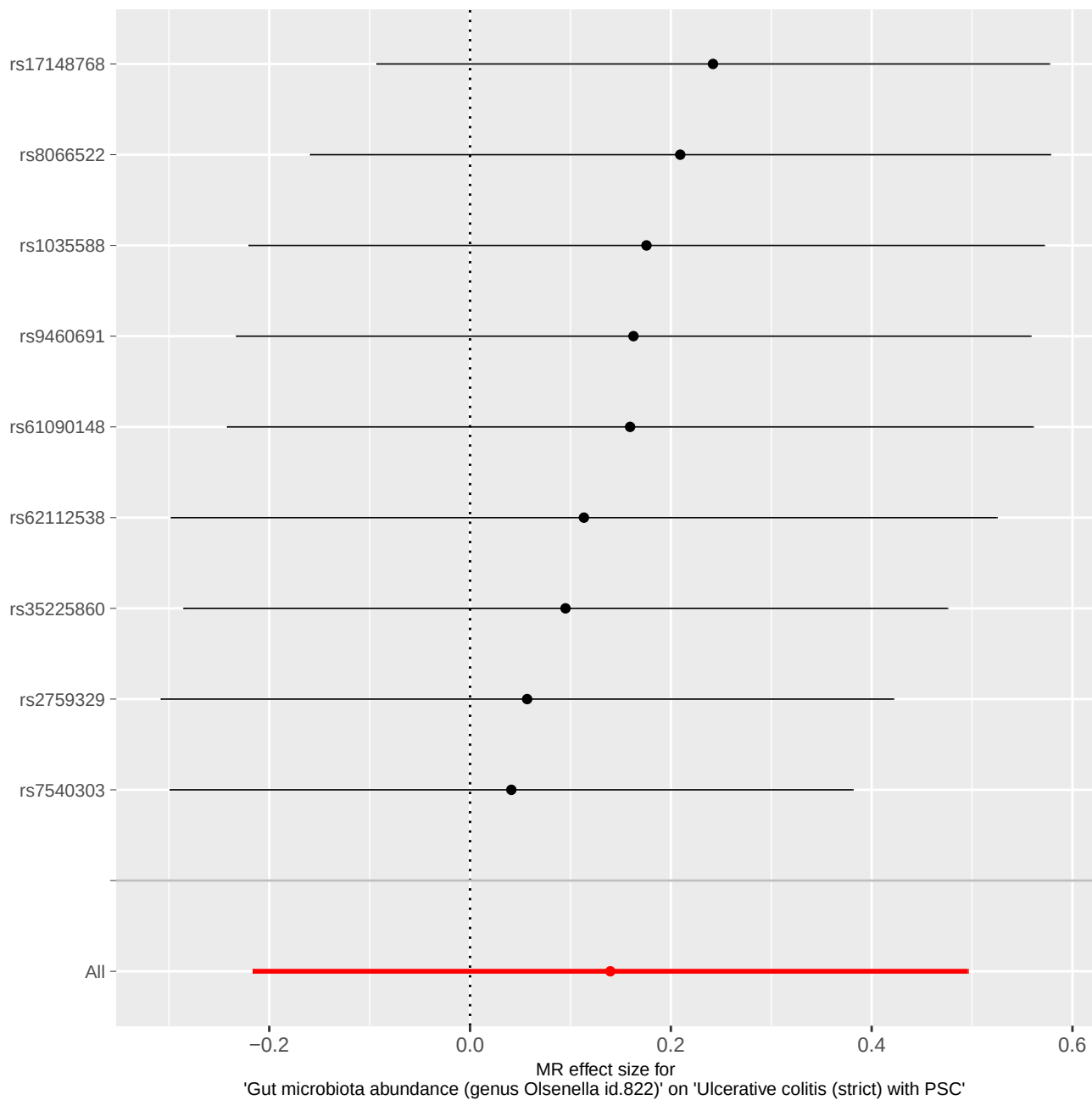
MR effect size for
'Gut microbiota abundance (genus Lactobacillus id.1837)' on 'Ulcerative colitis (strict) with PSC'

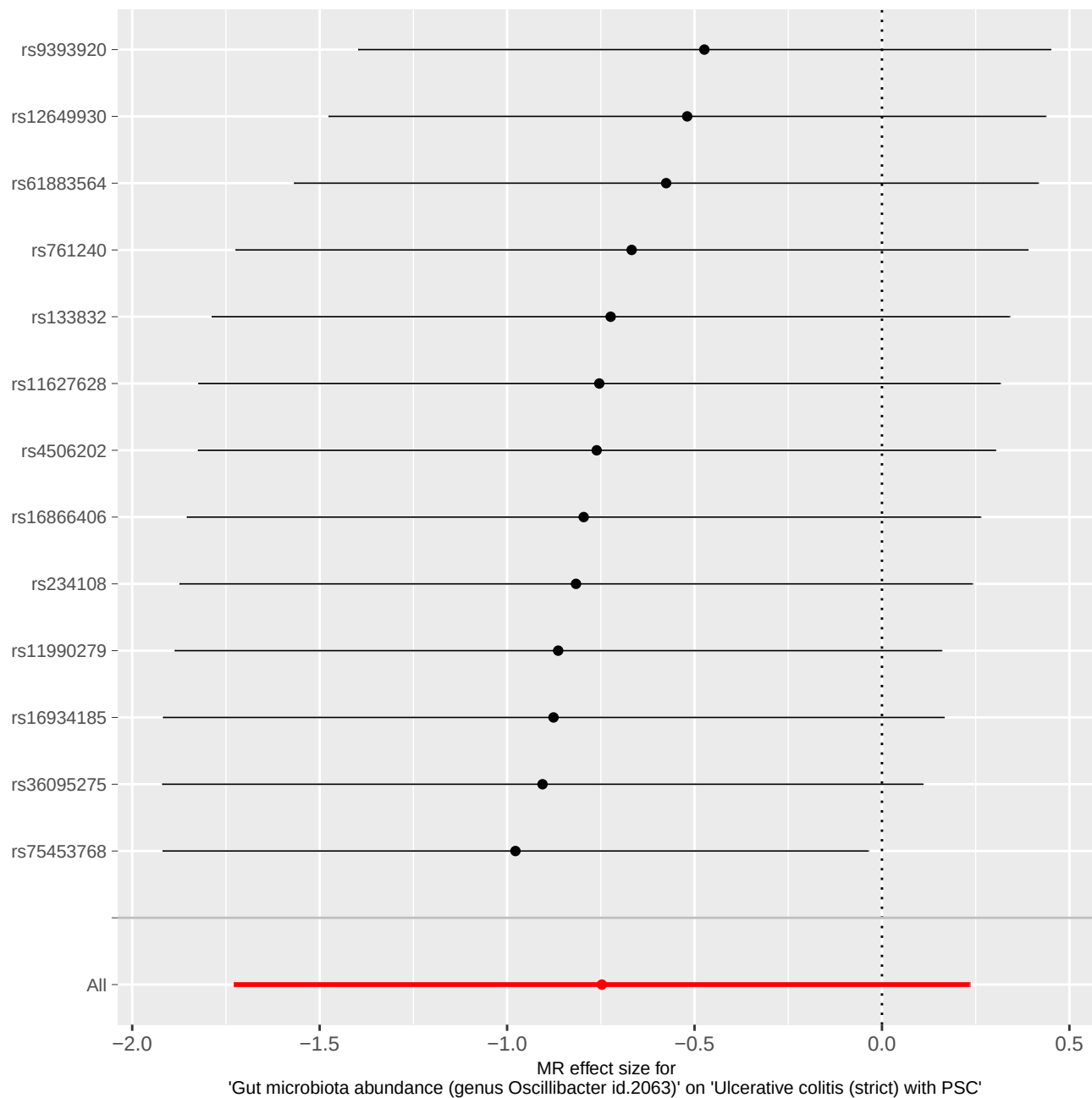


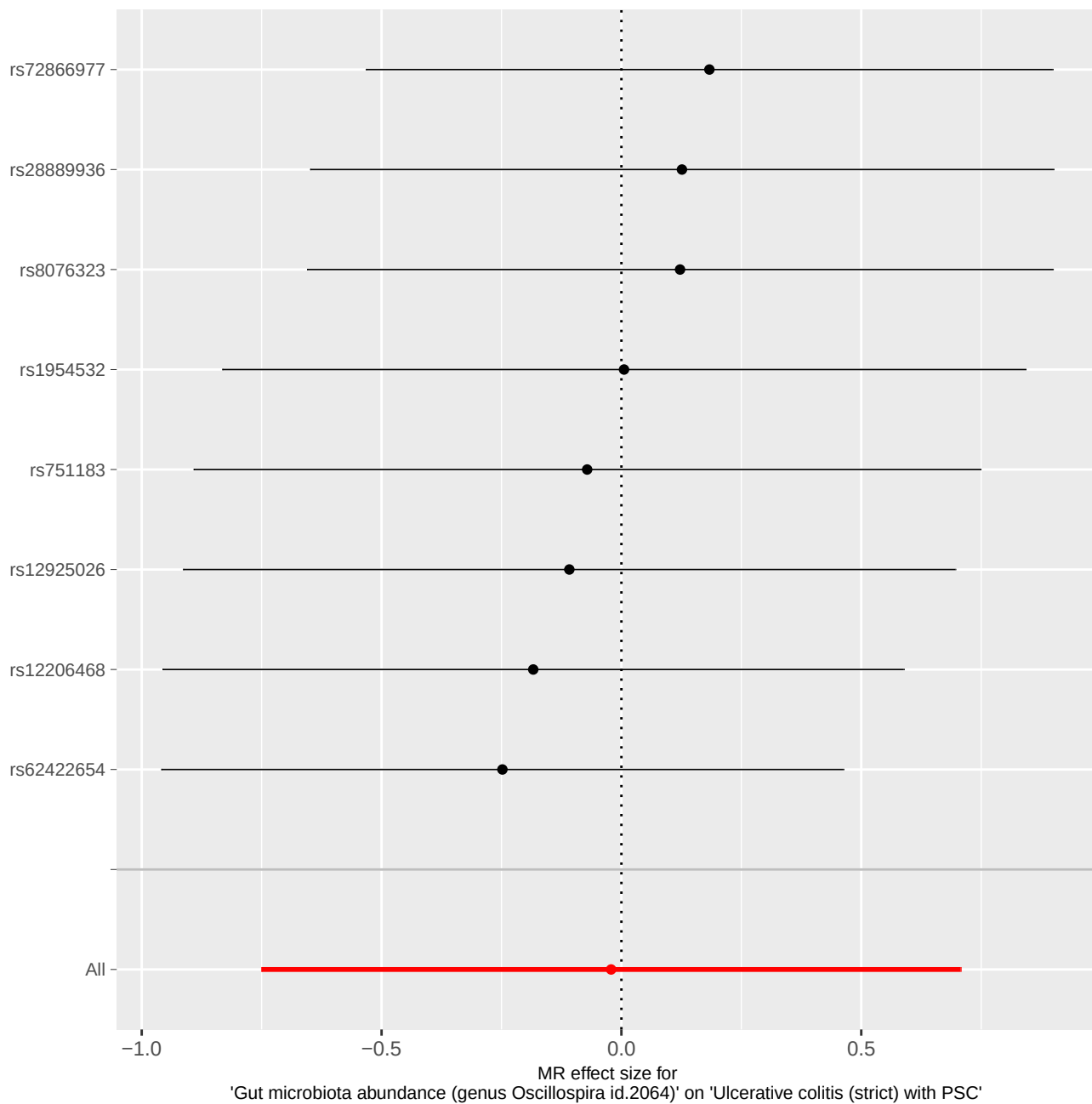


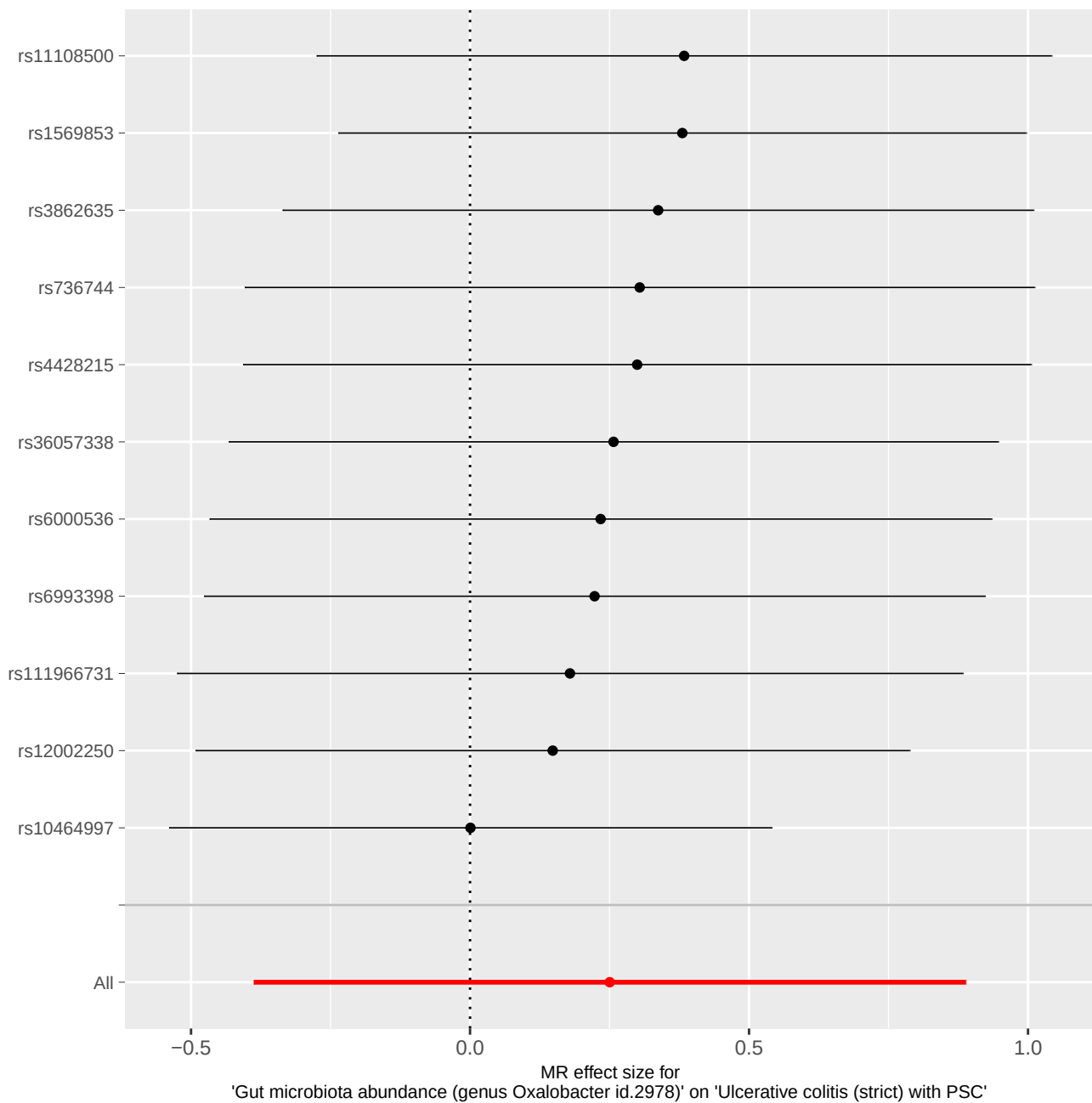




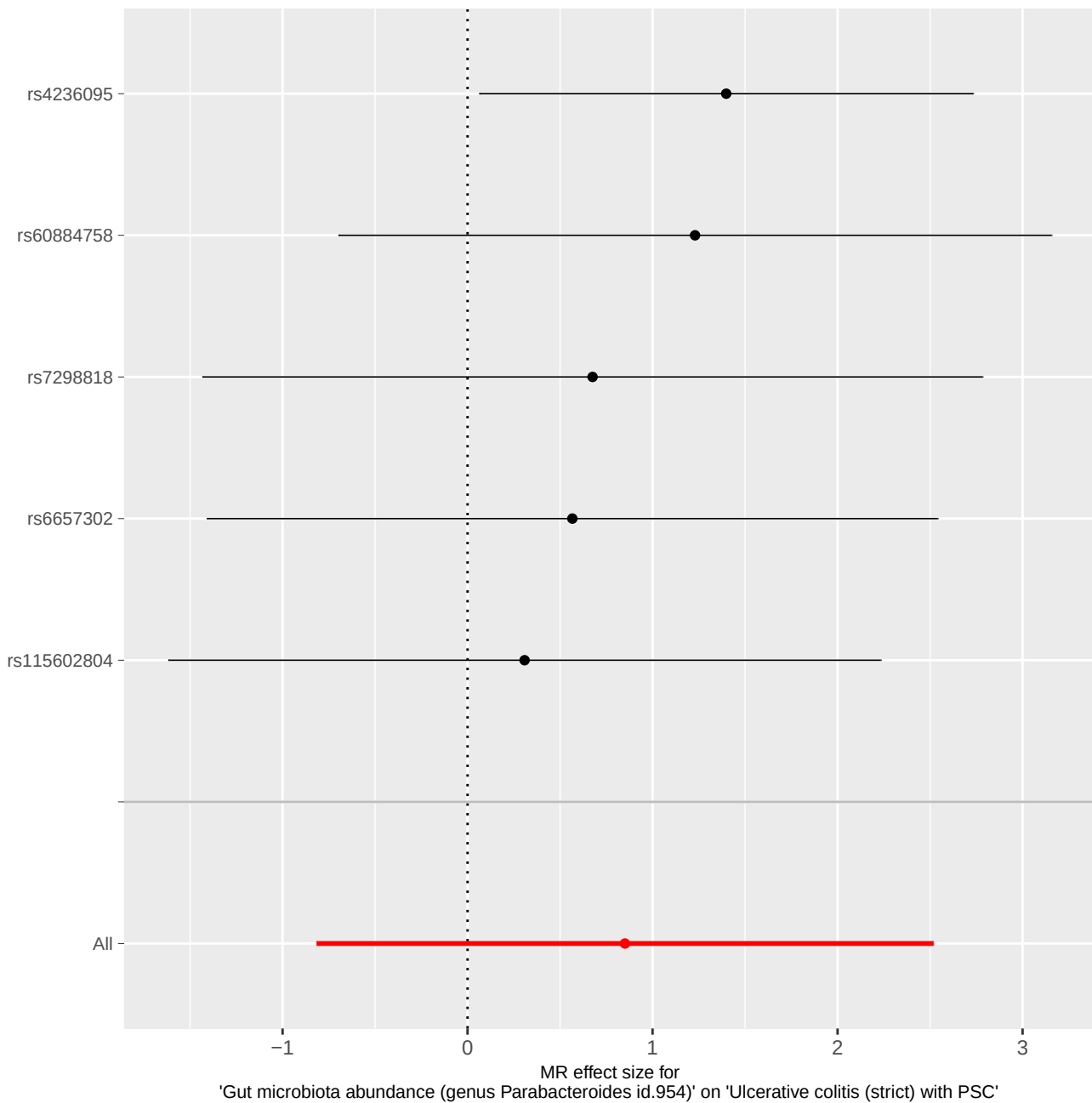




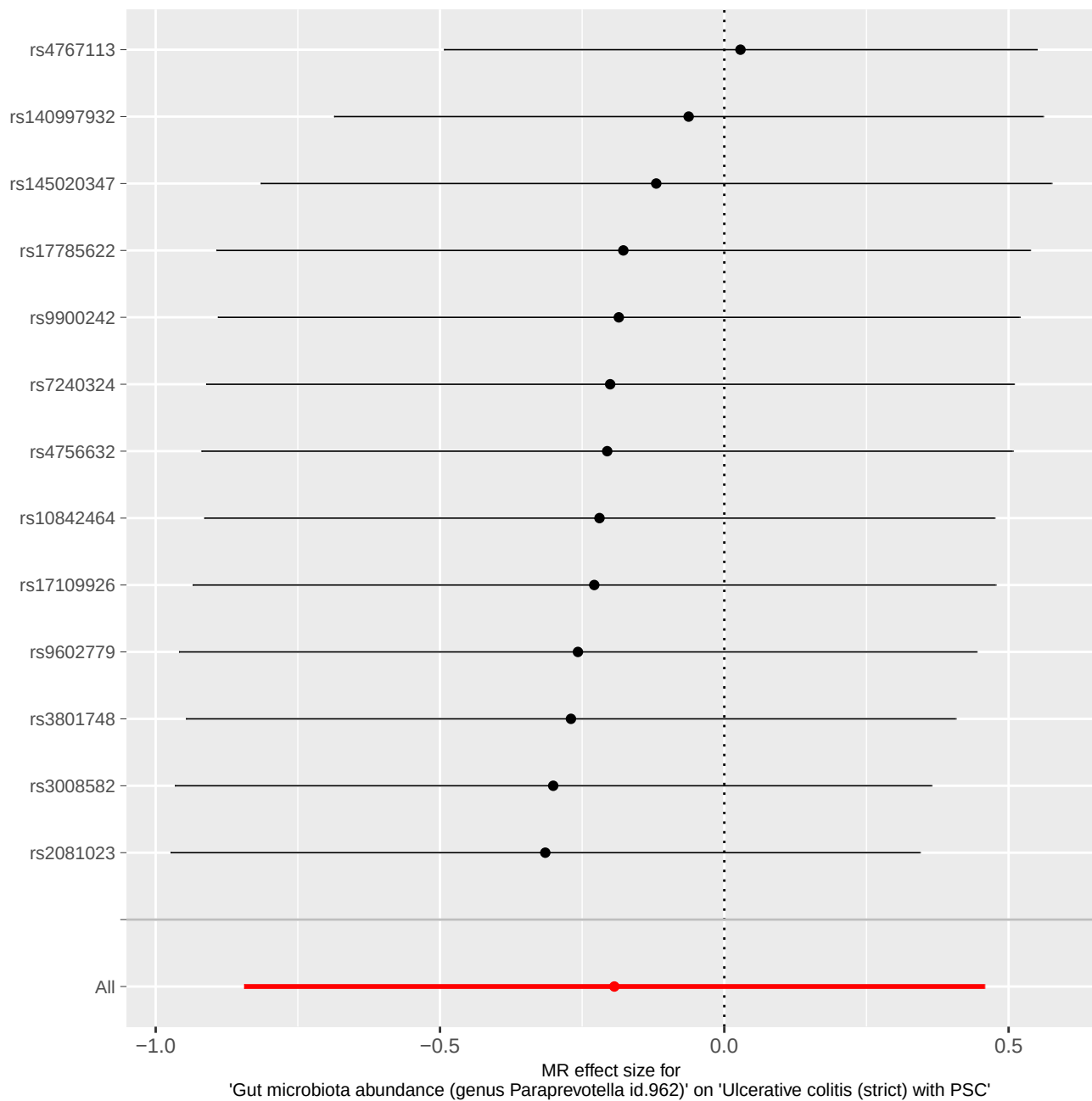


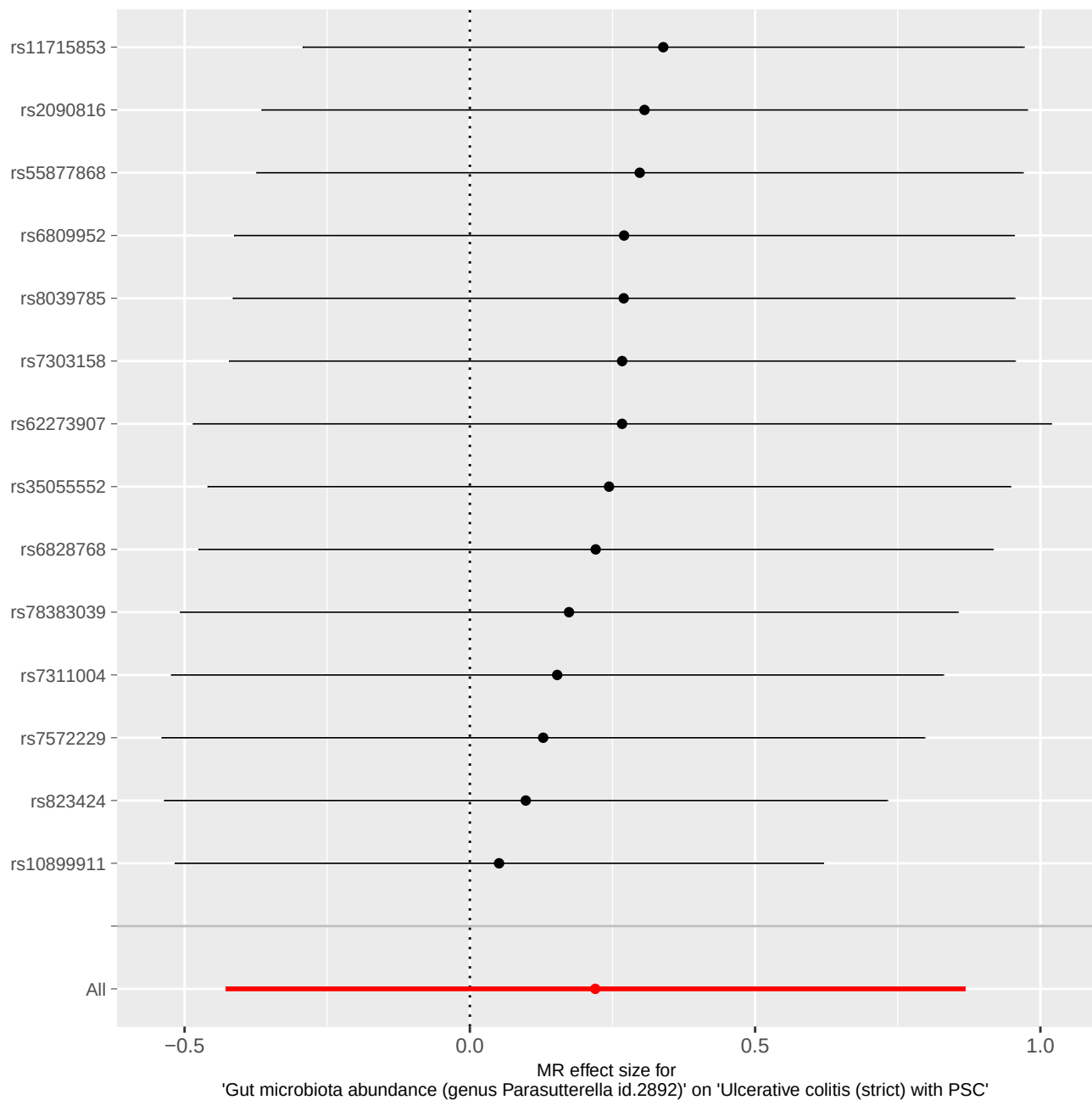


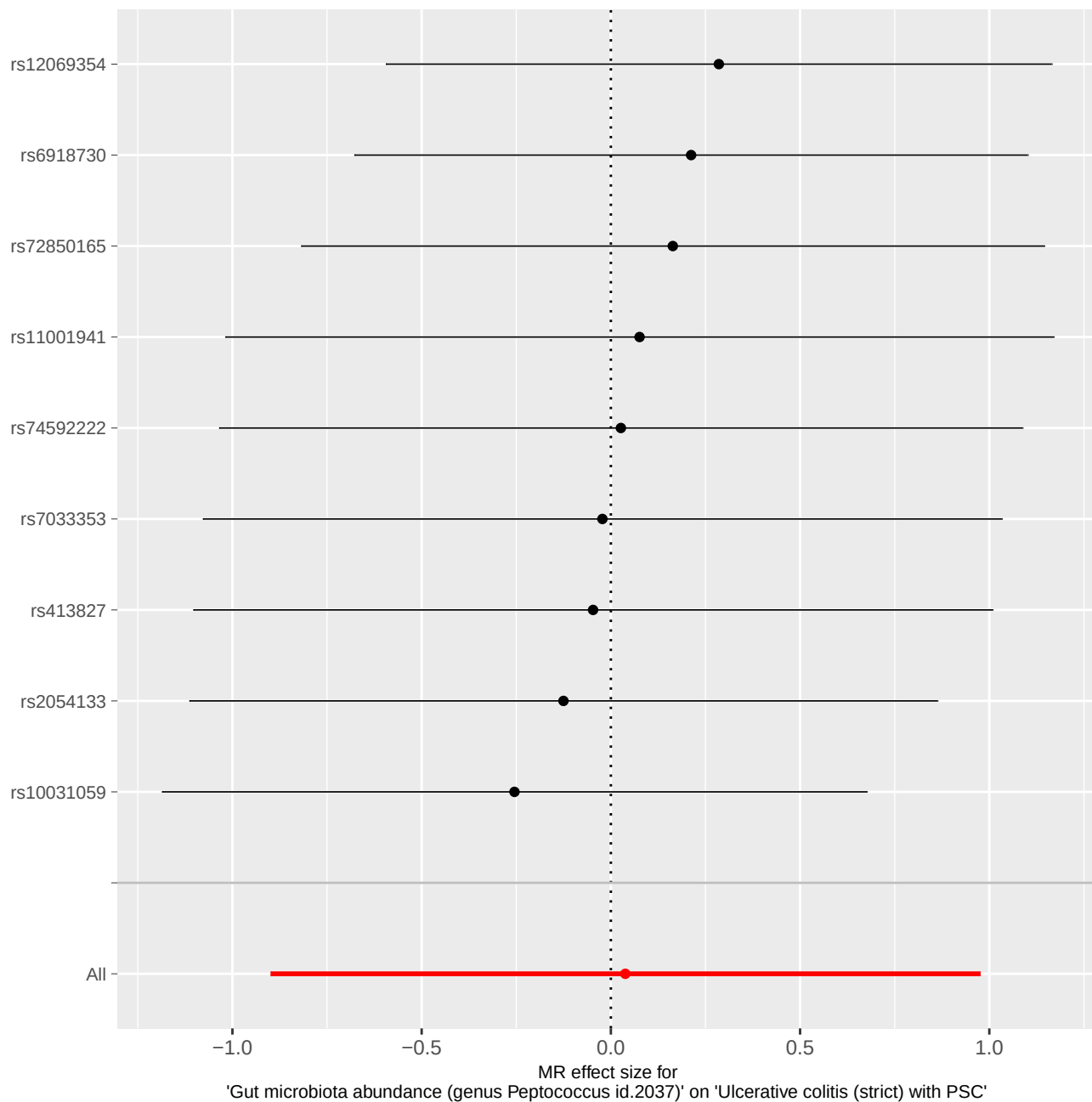
MR effect size for
'Gut microbiota abundance (genus Oxalobacter id.2978)' on 'Ulcerative colitis (strict) with PSC'

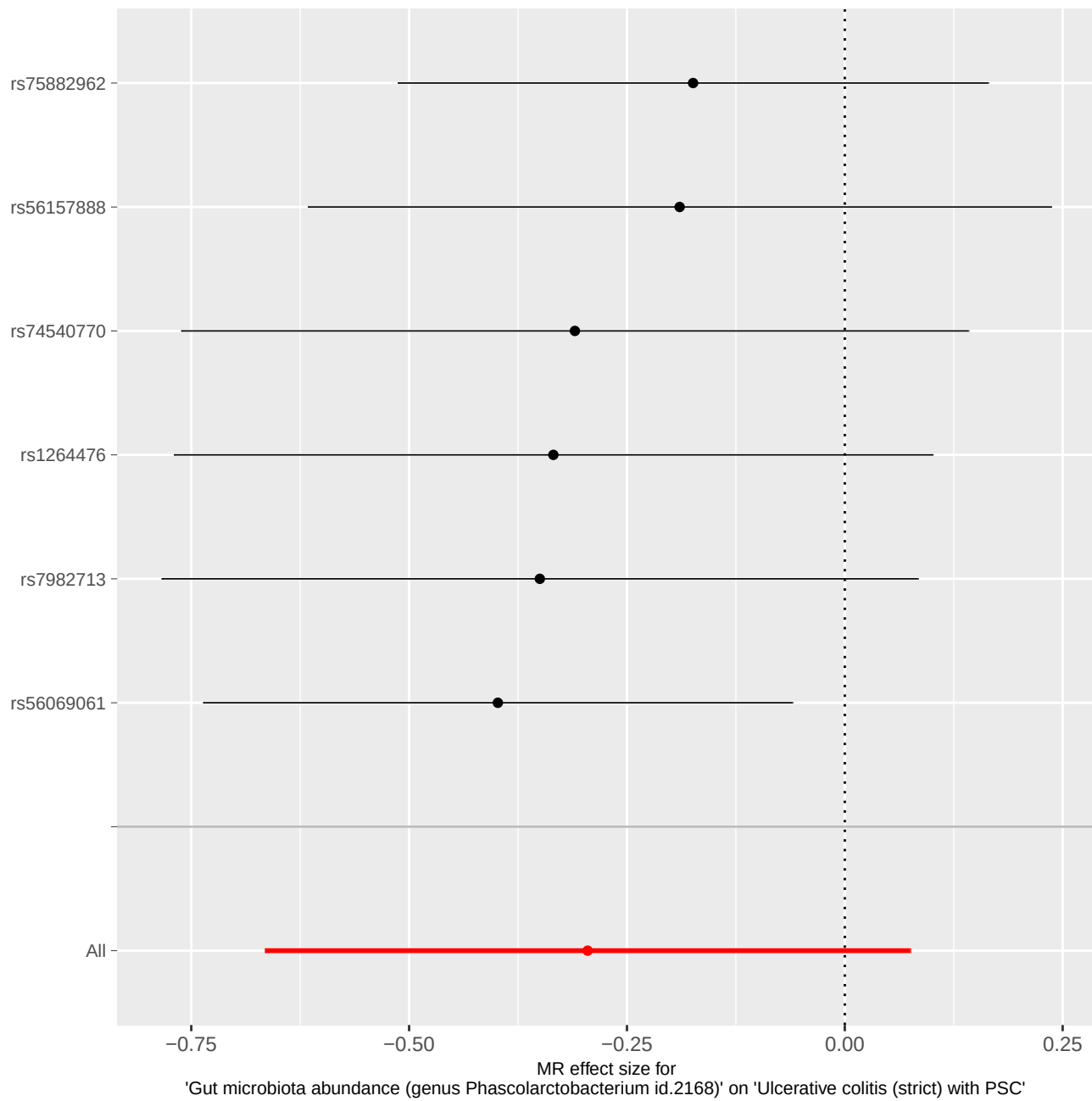


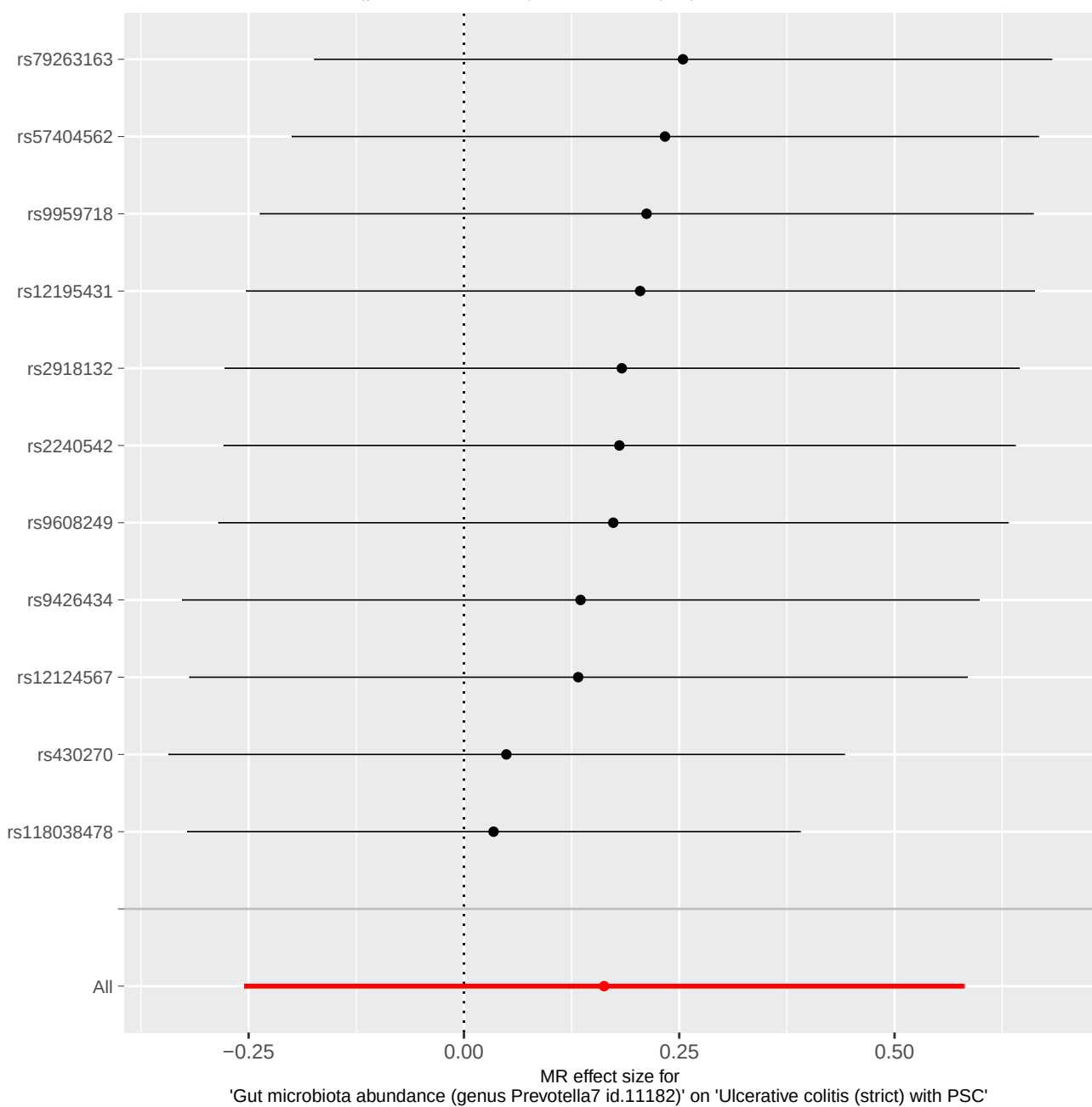
Batch 714 : Gut microbiota abundance (genus Paraprevotella id.962) on Ulcerative colitis (strict) with PSC

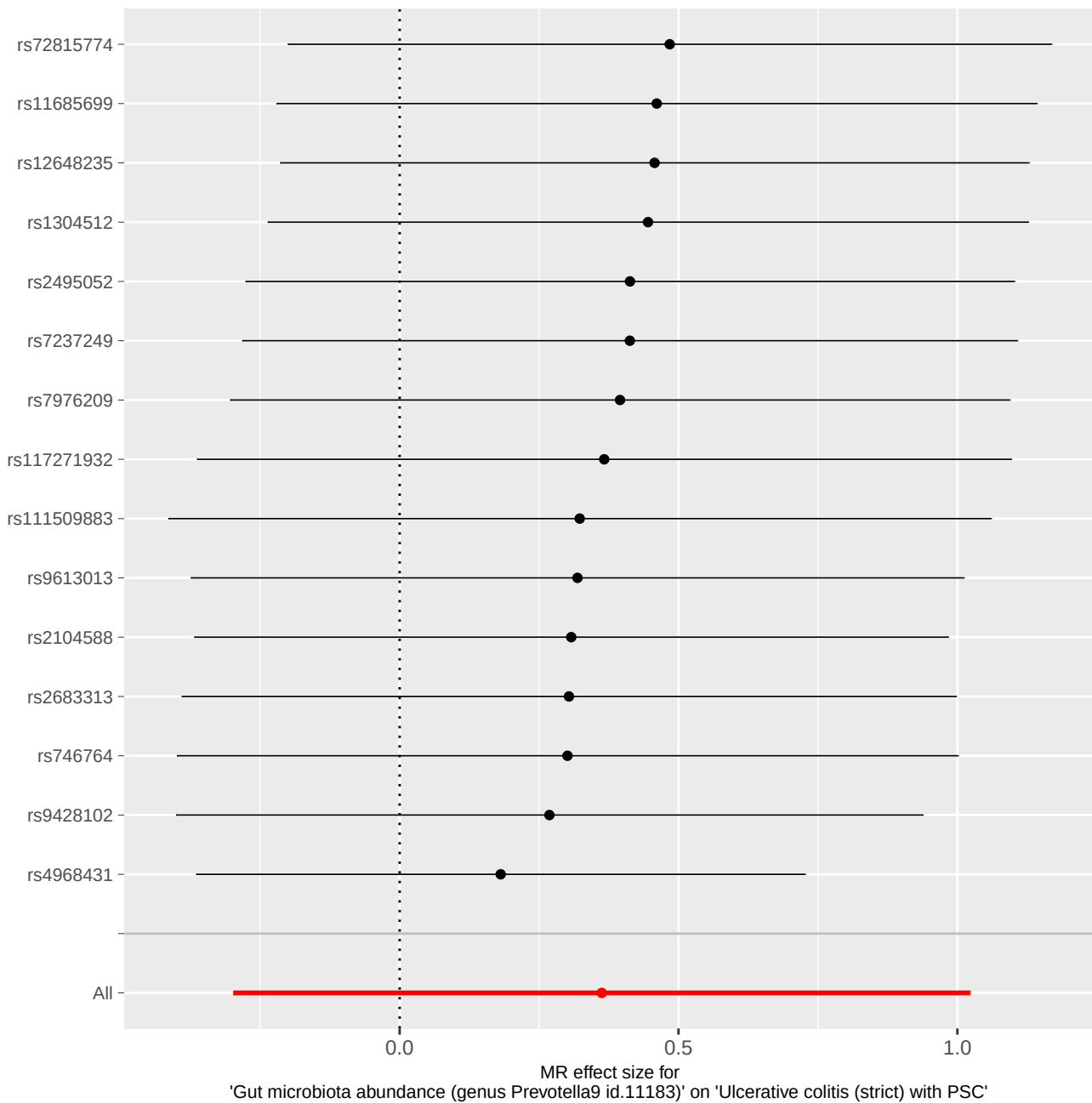


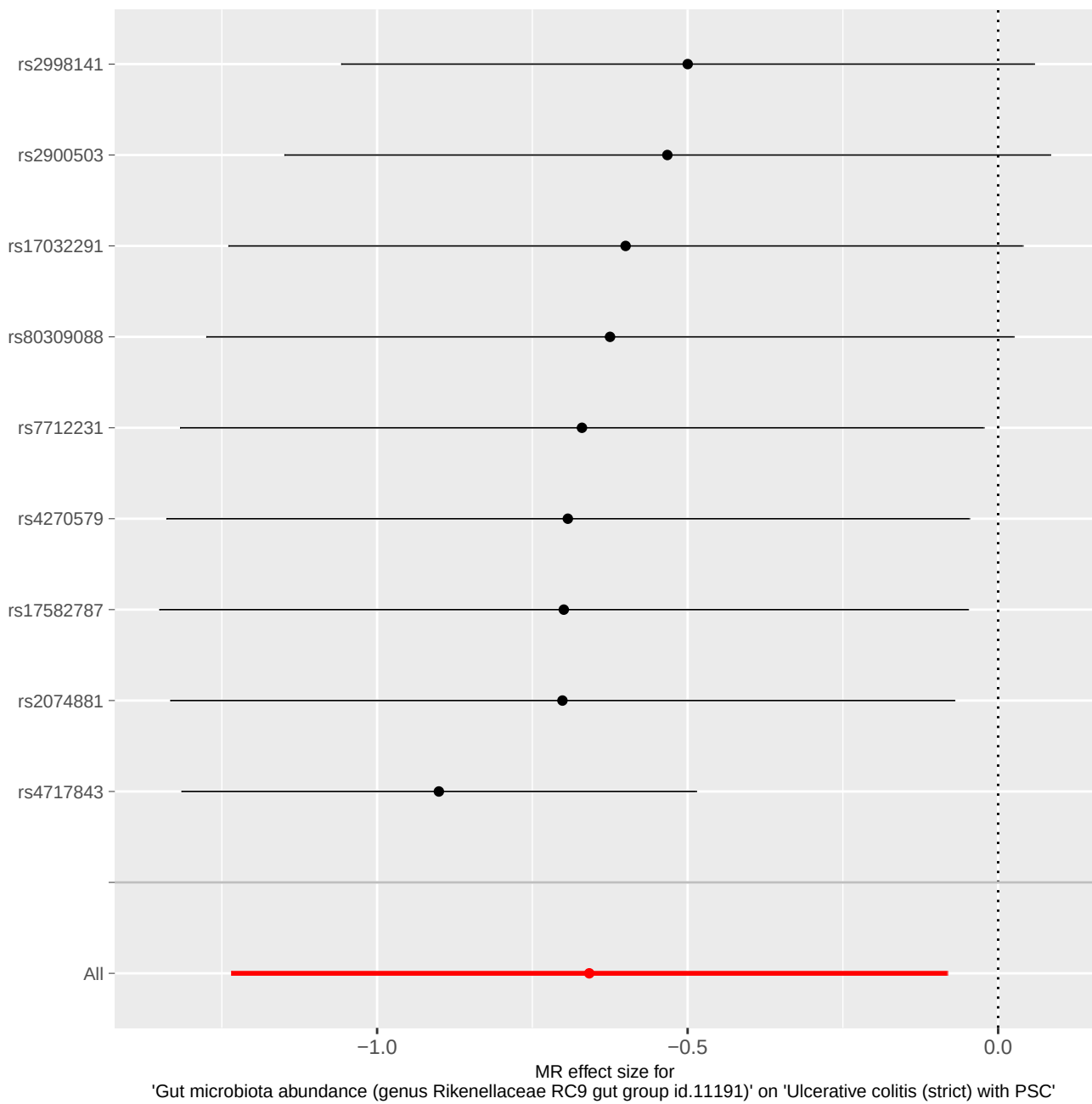


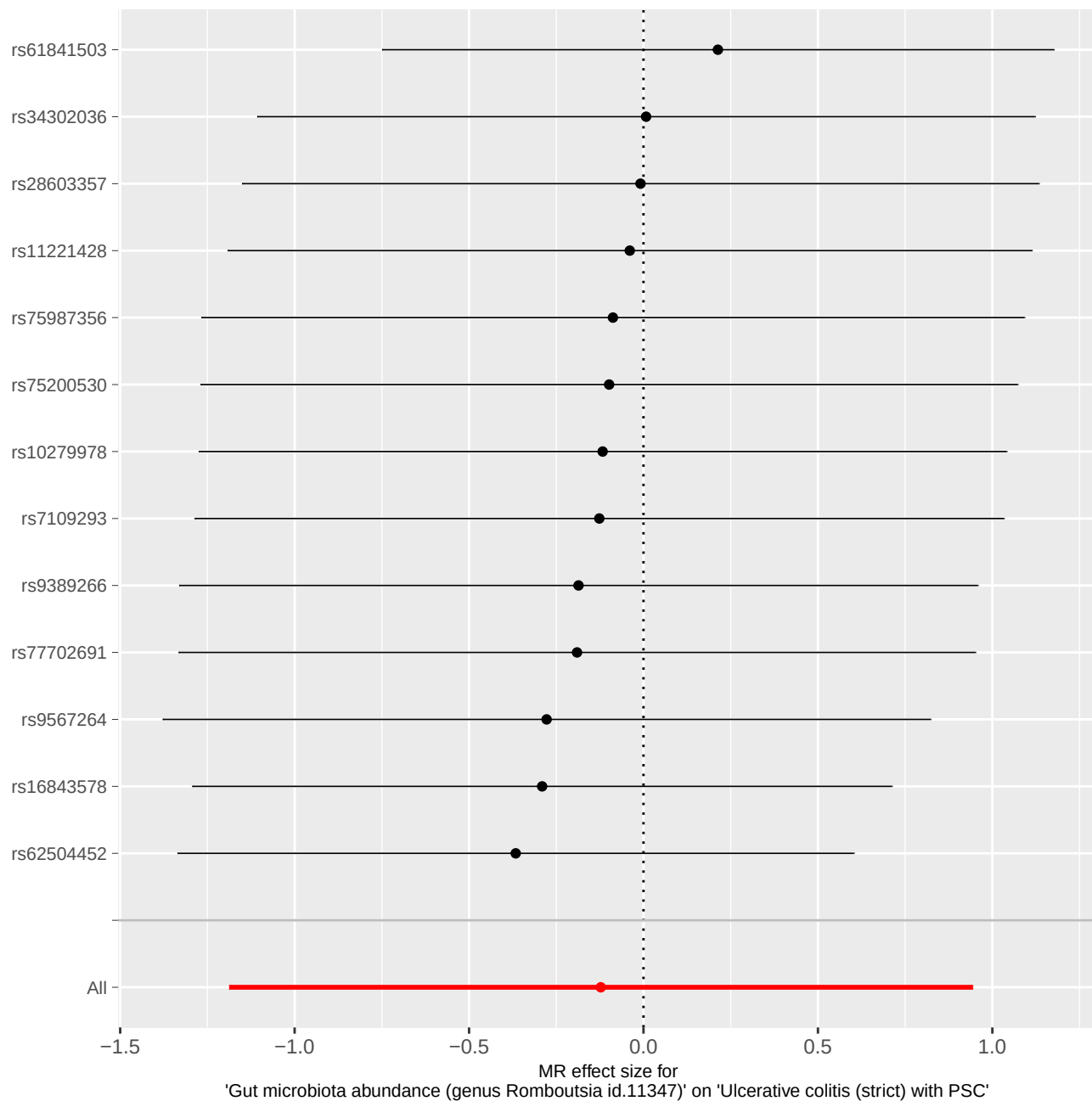


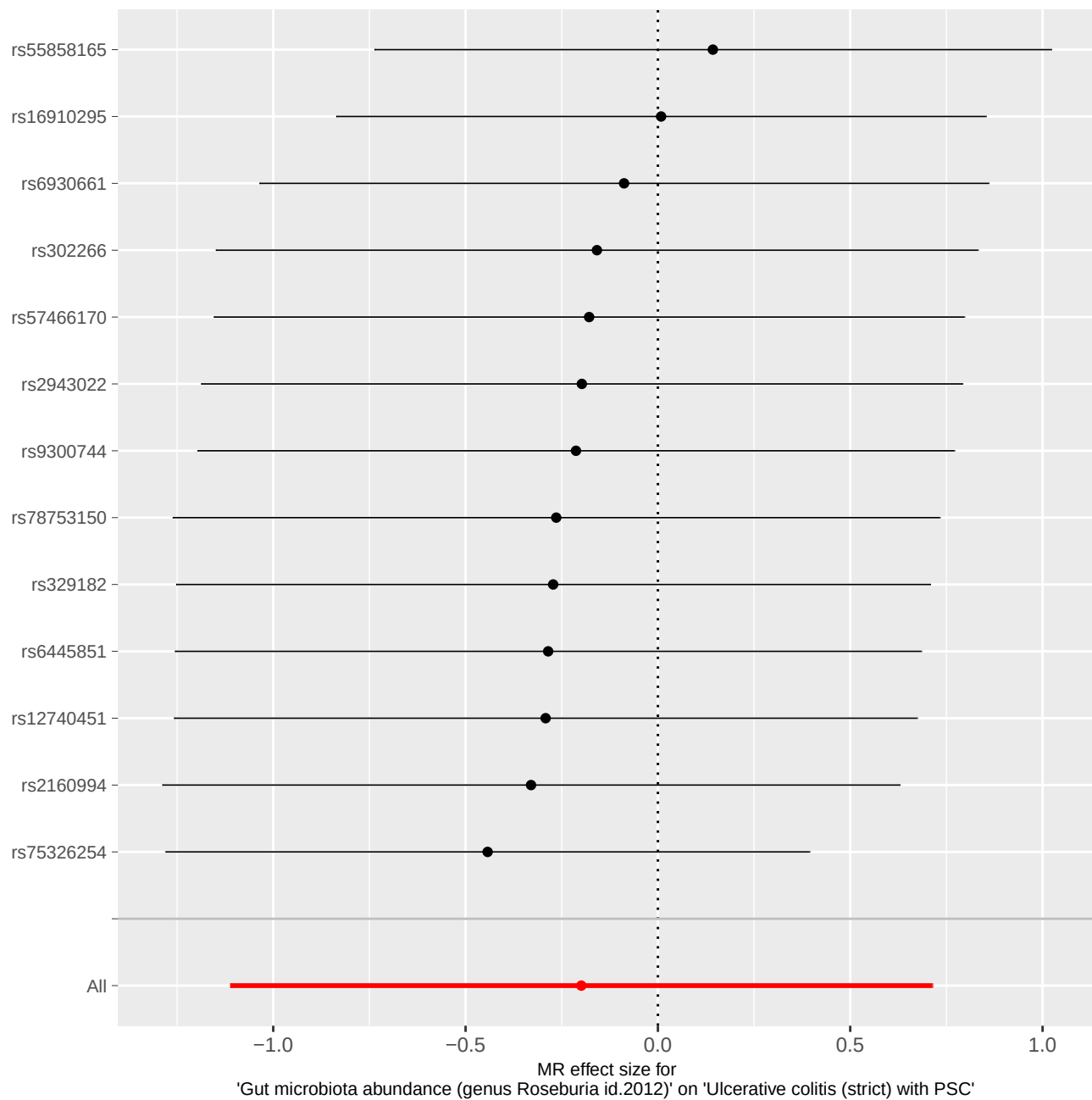


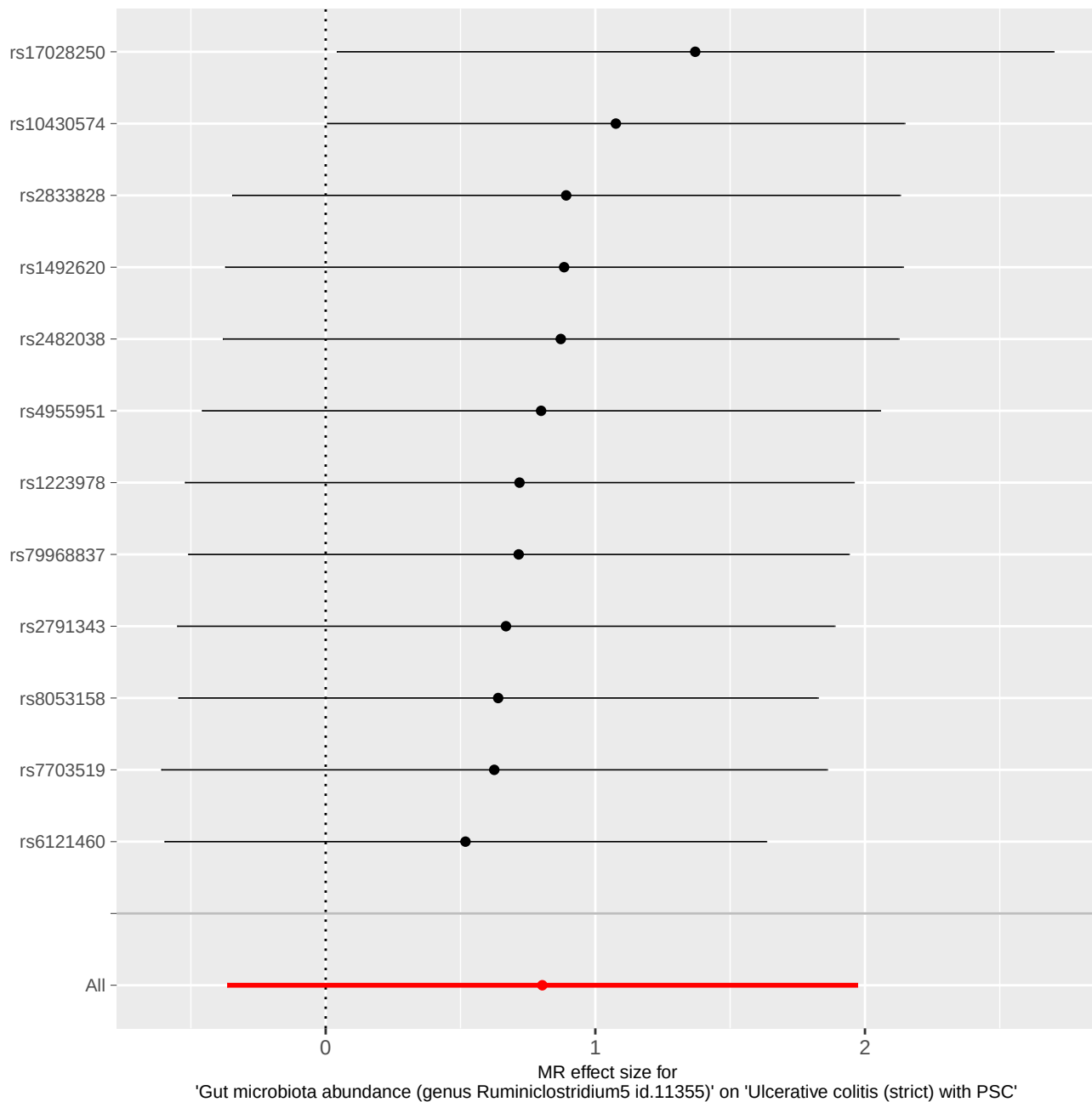


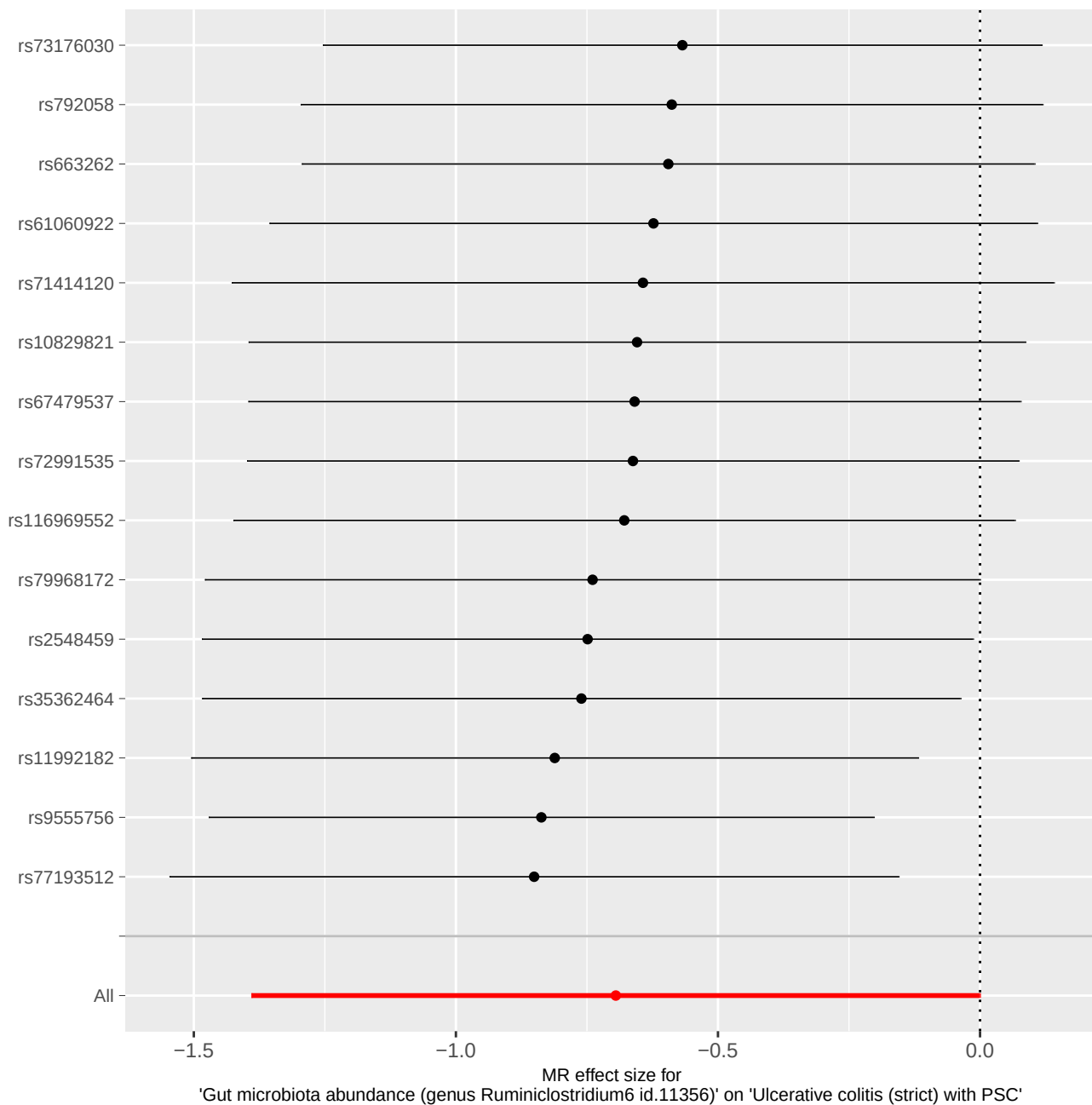


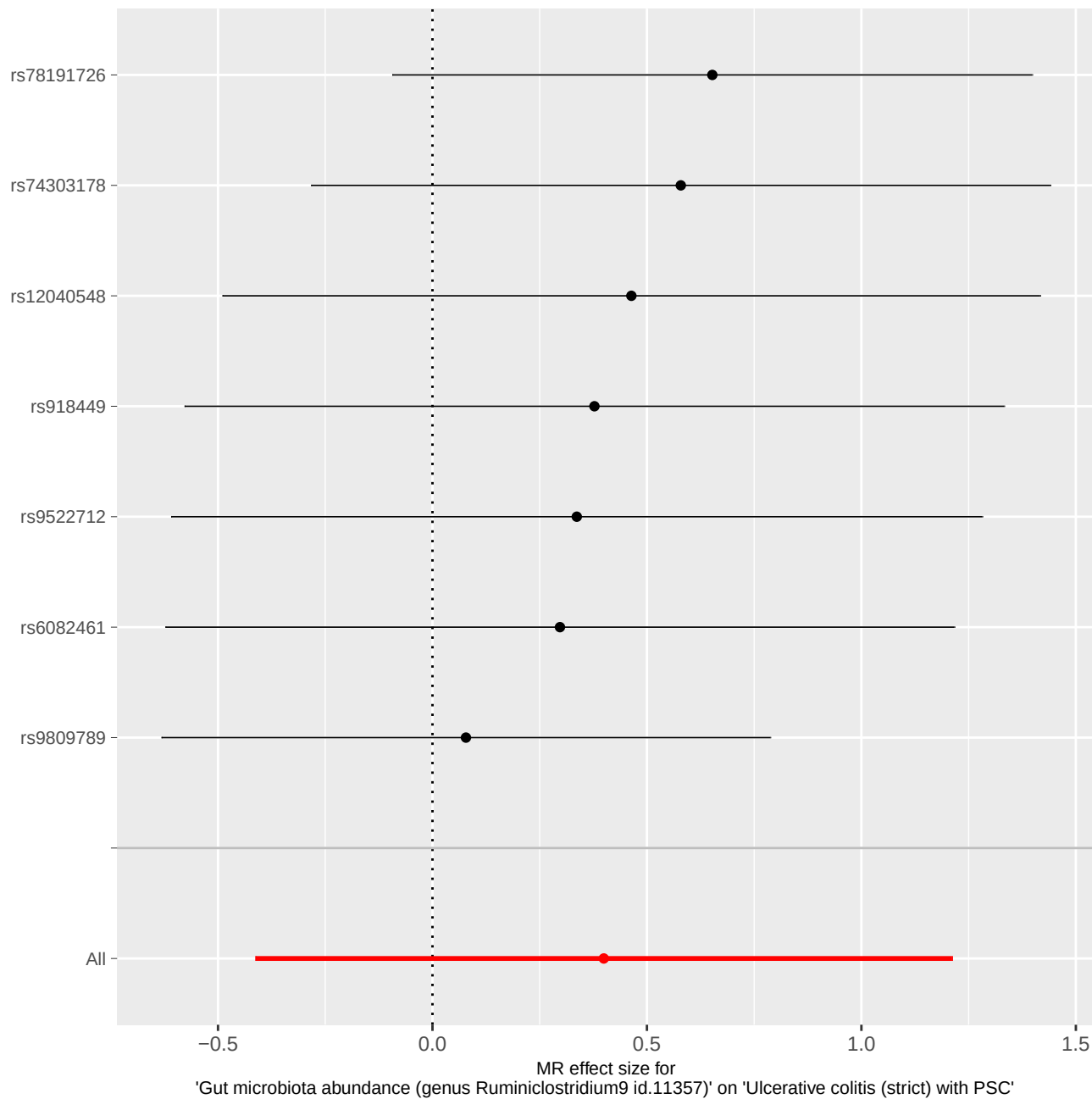


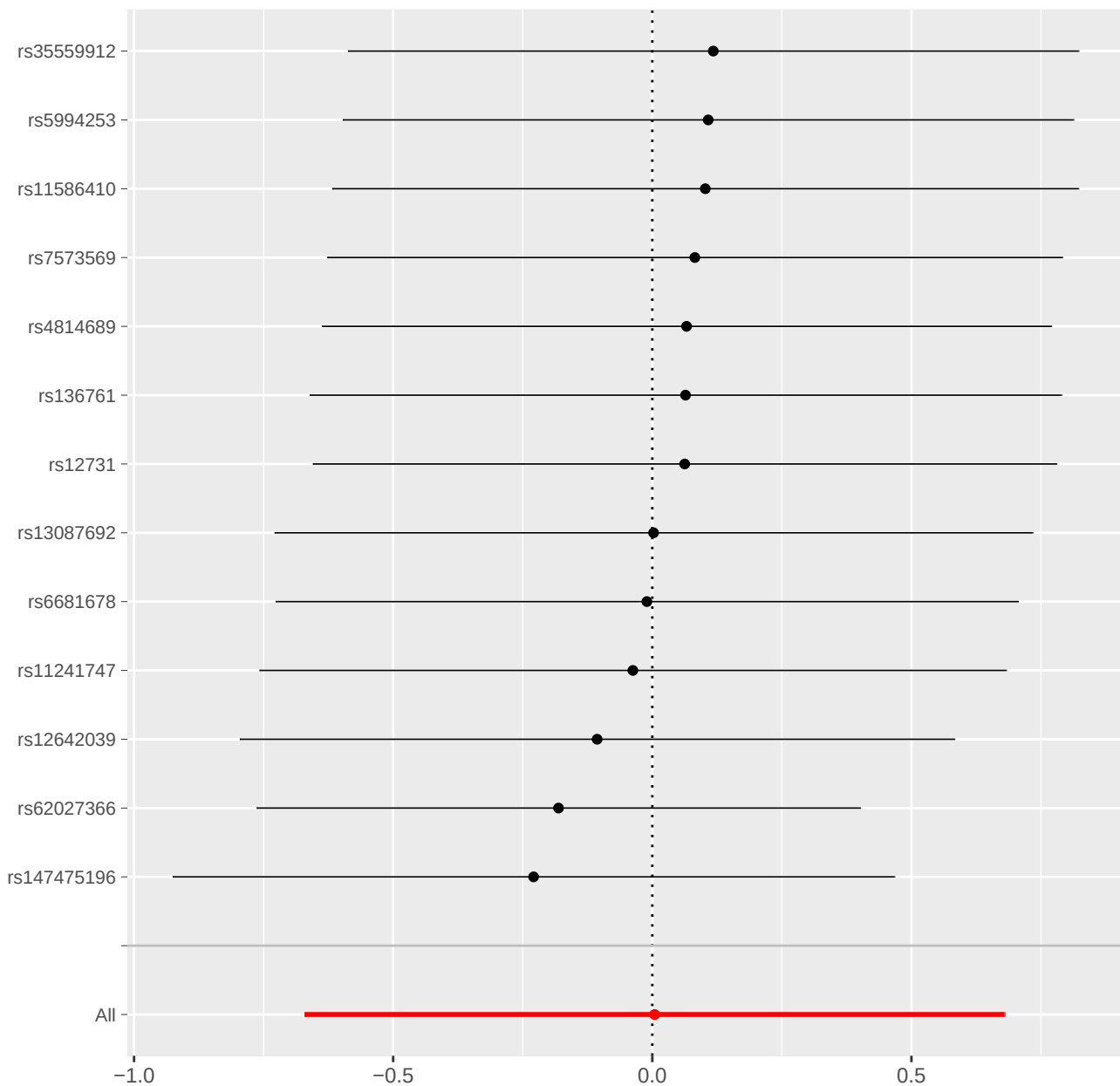




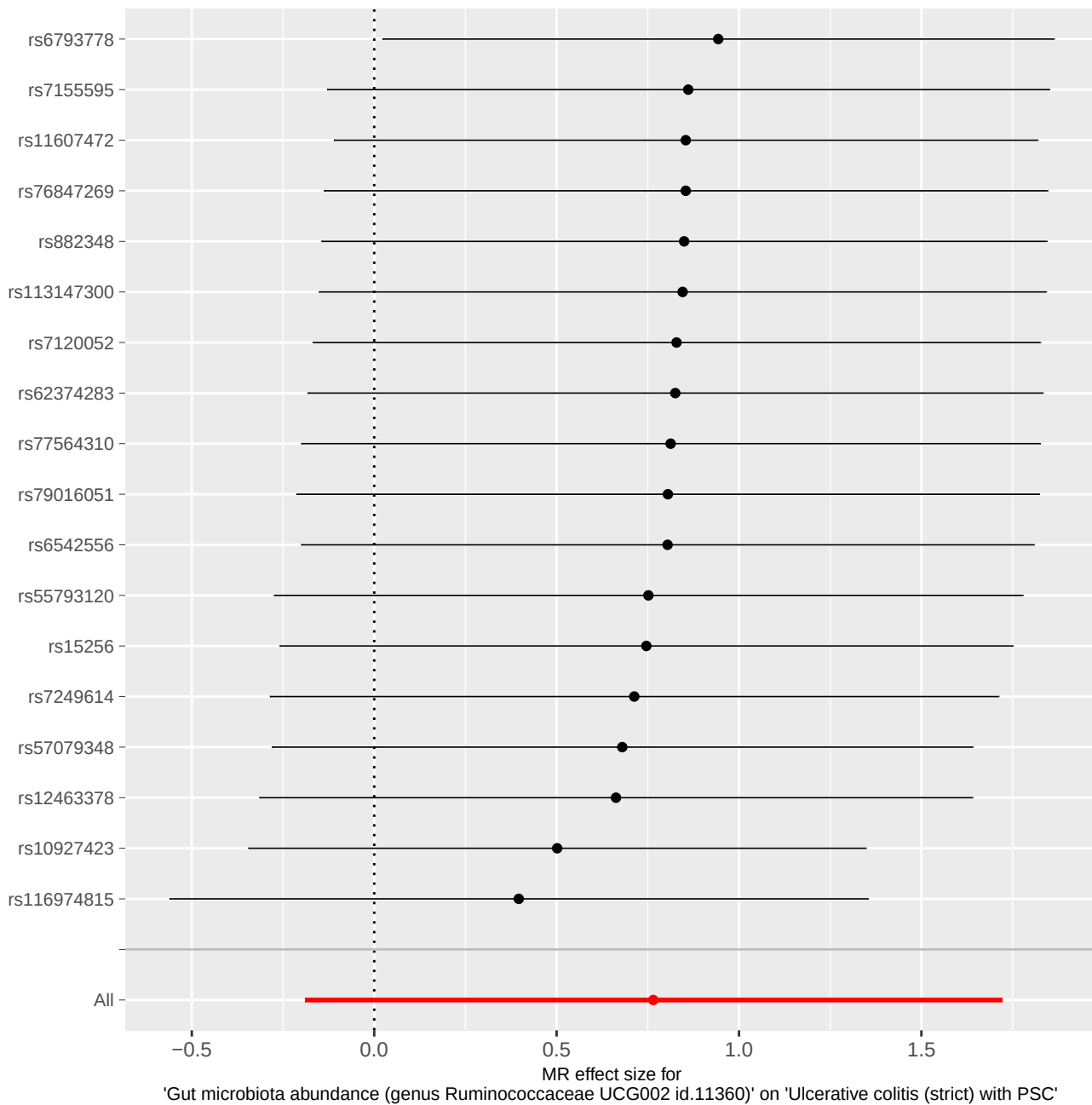


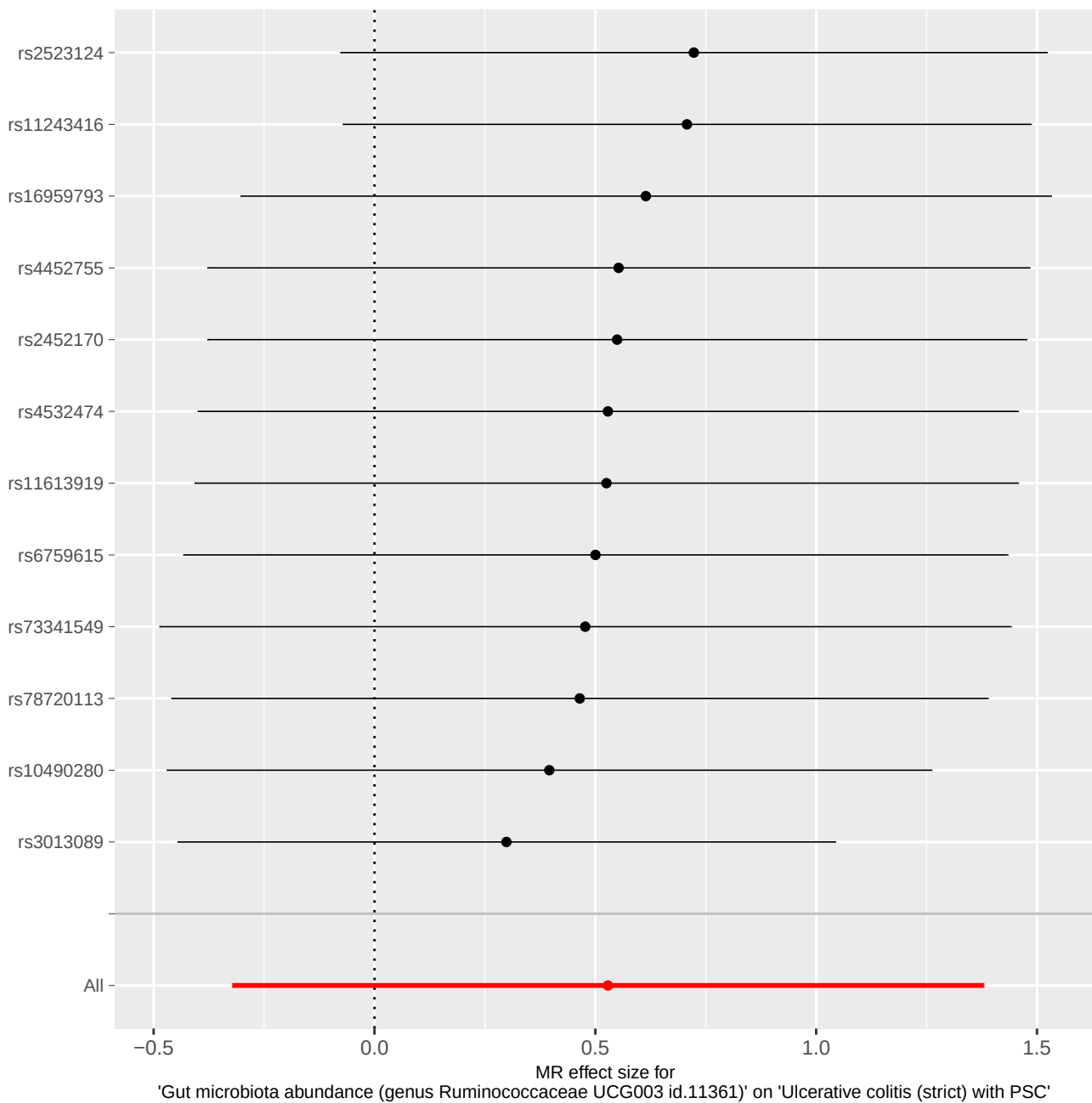


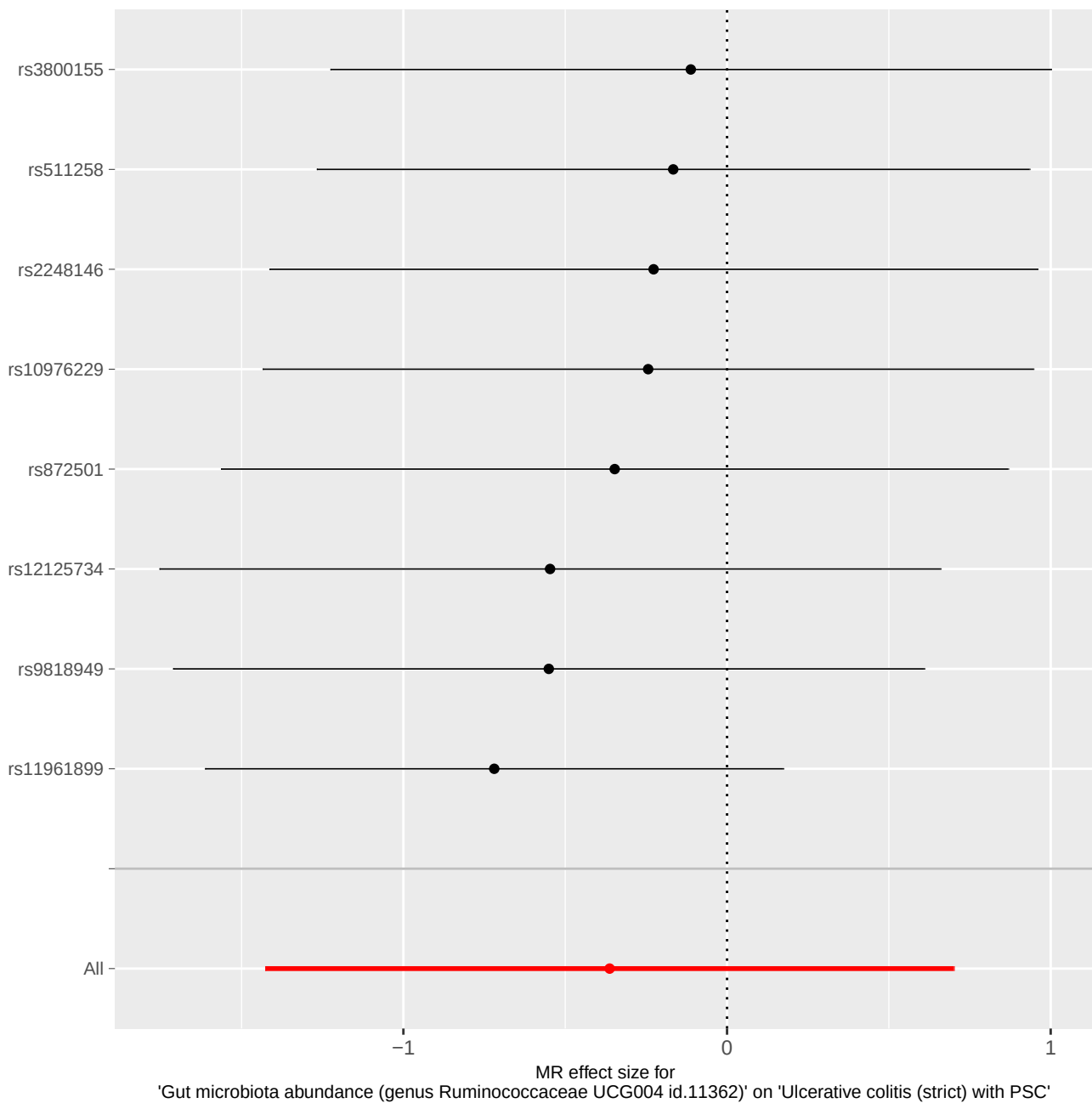


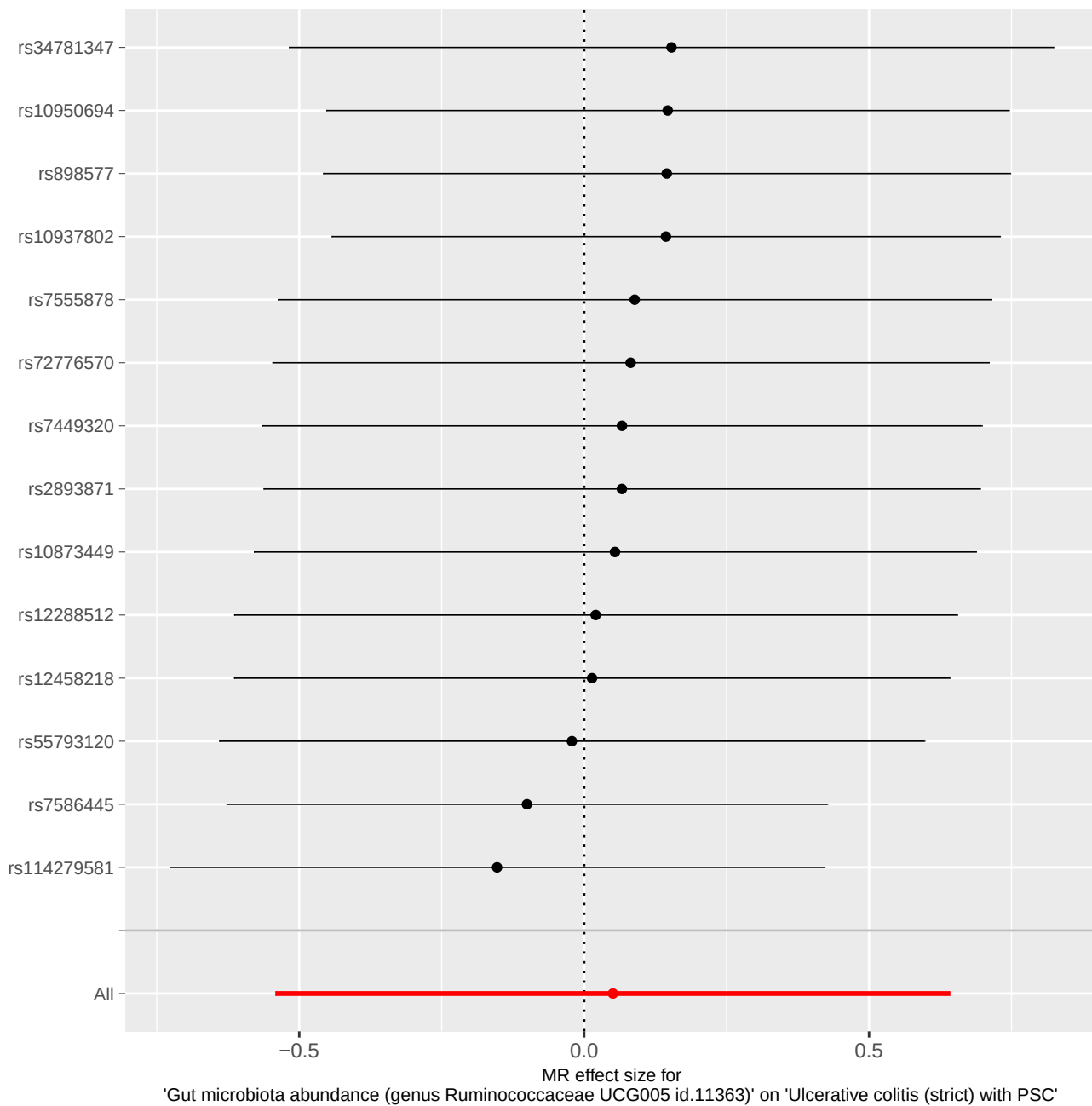


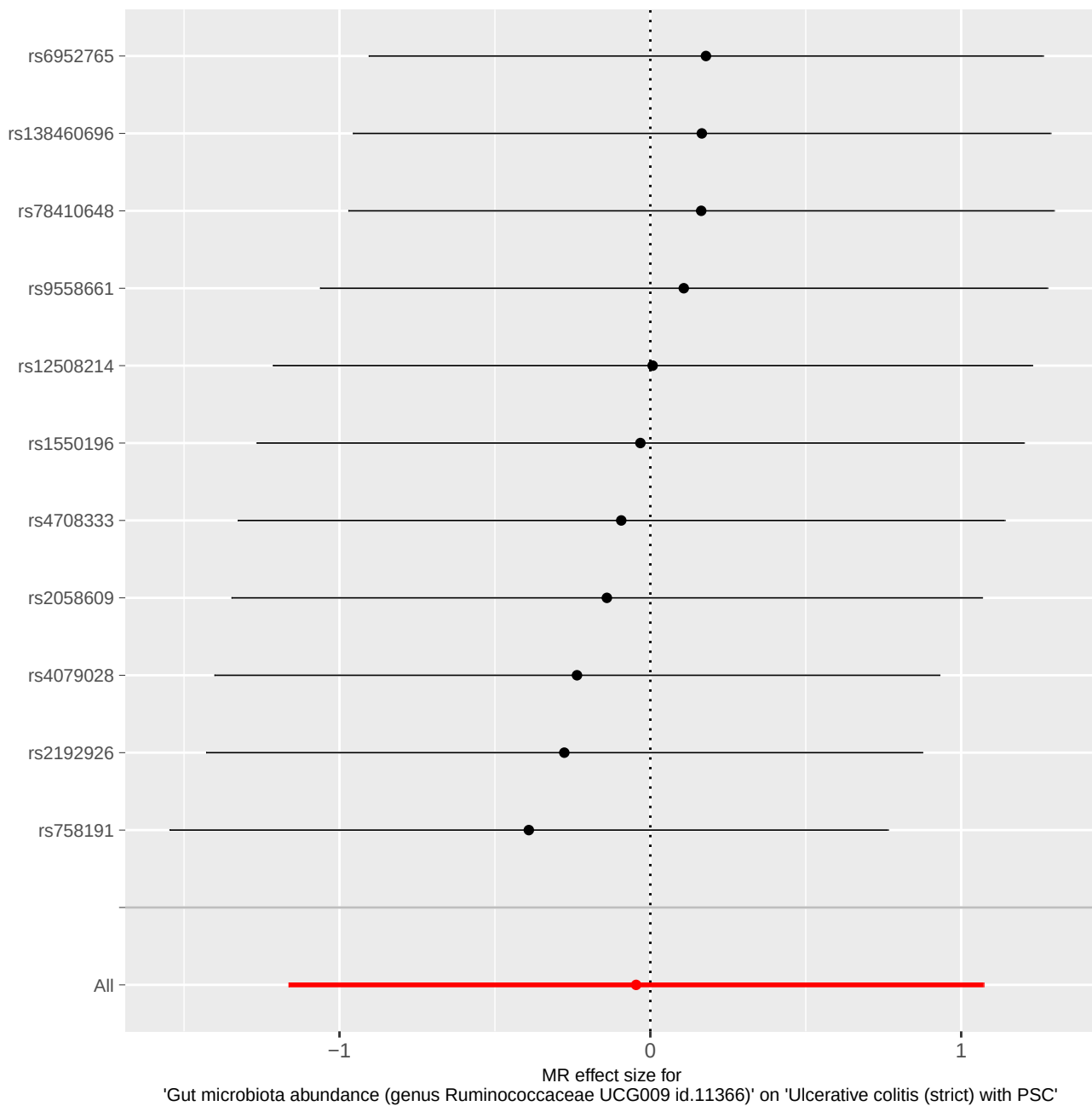
MR effect size for
'Gut microbiota abundance (genus Ruminococcaceae NK4A214 group id.11358)' on 'Ulcerative colitis (strict) with PSC'

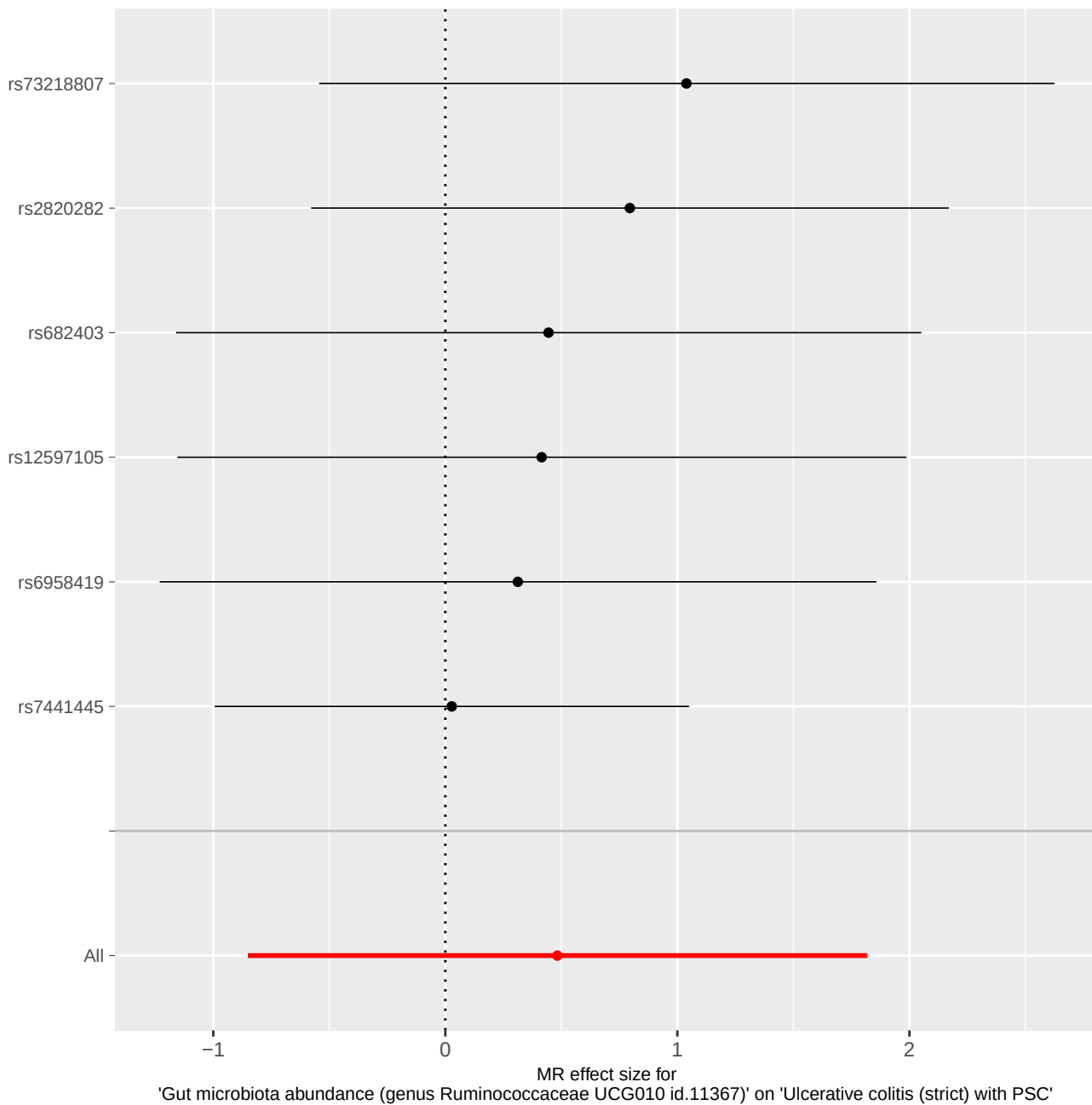


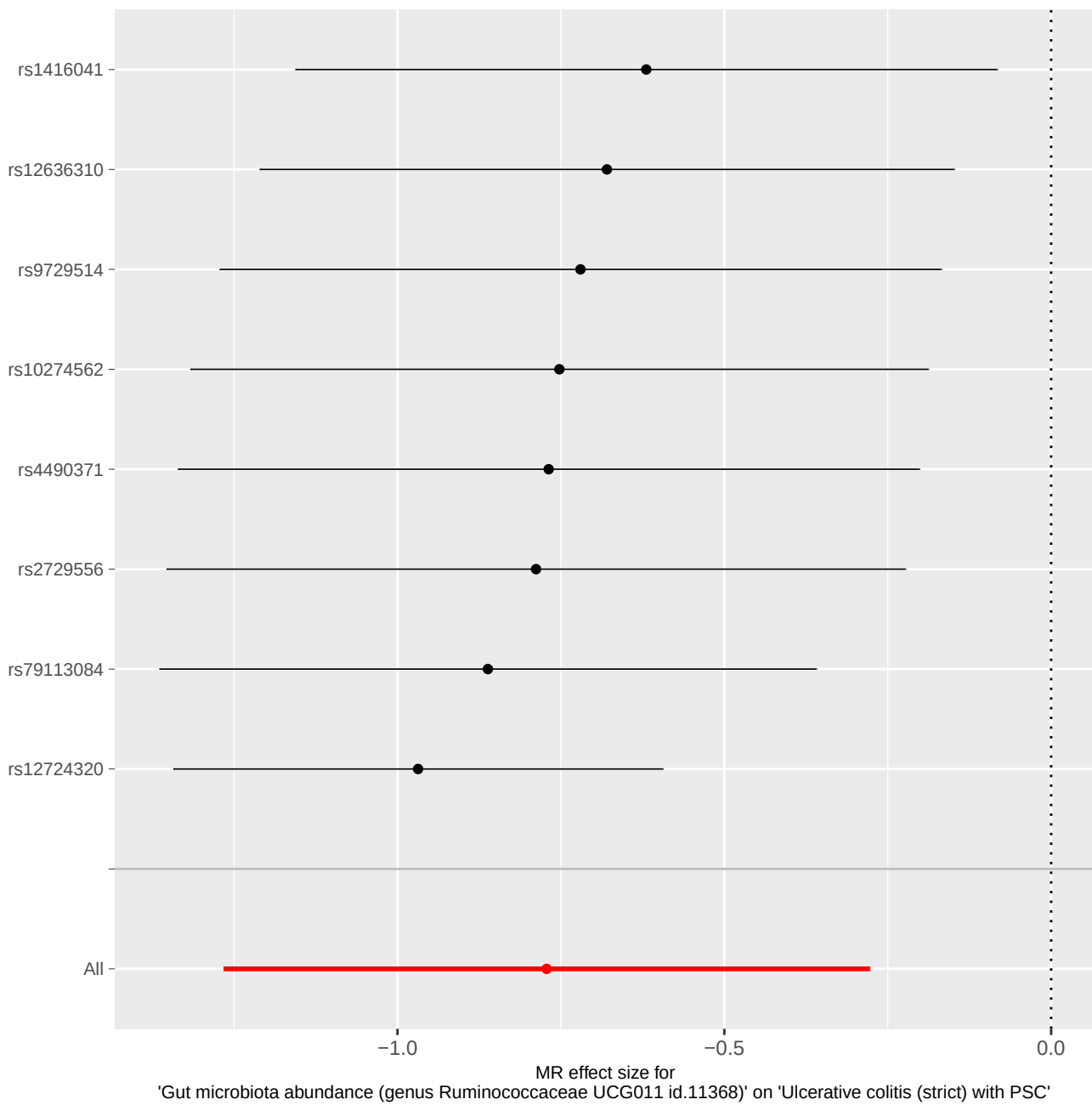


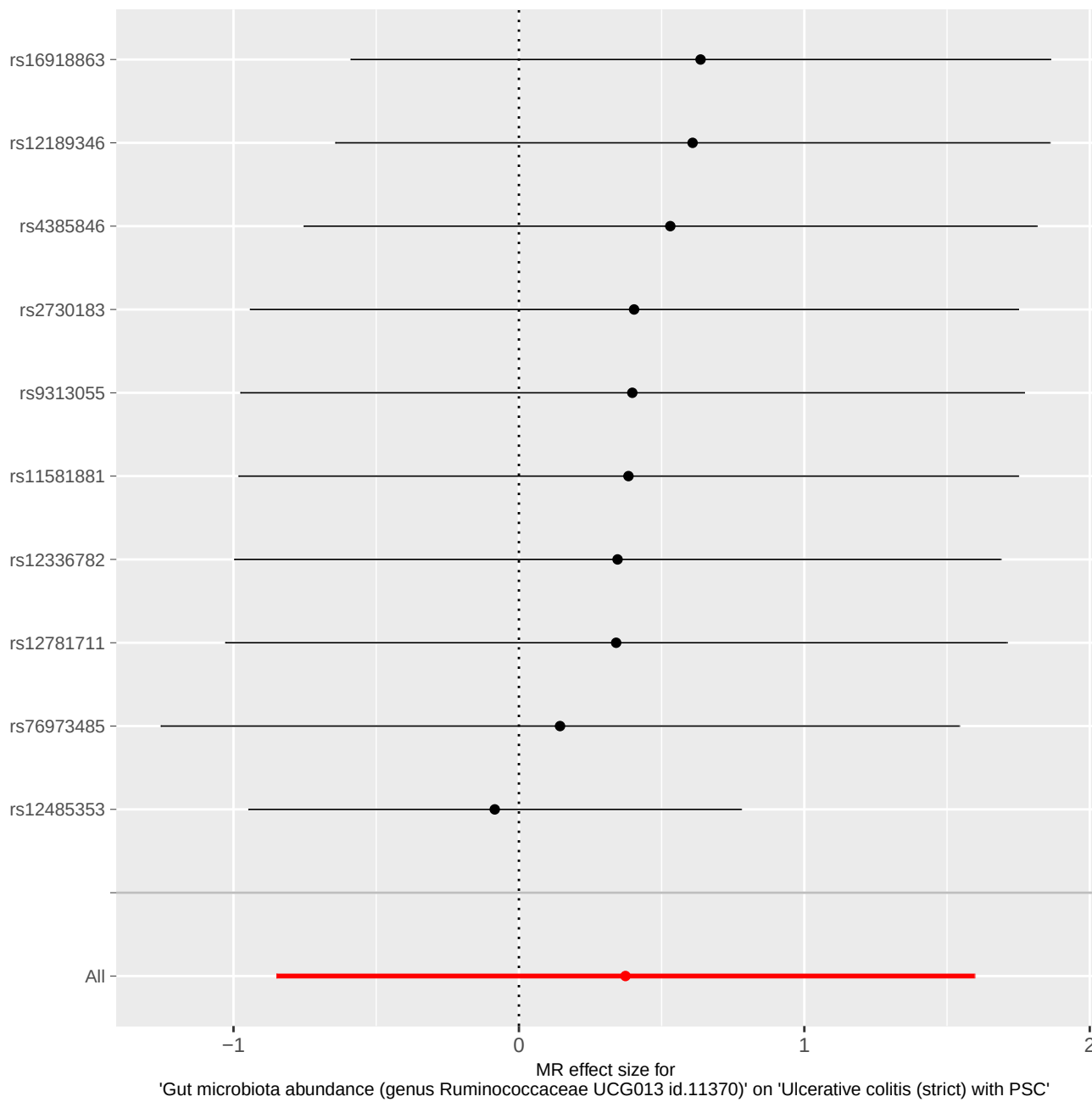


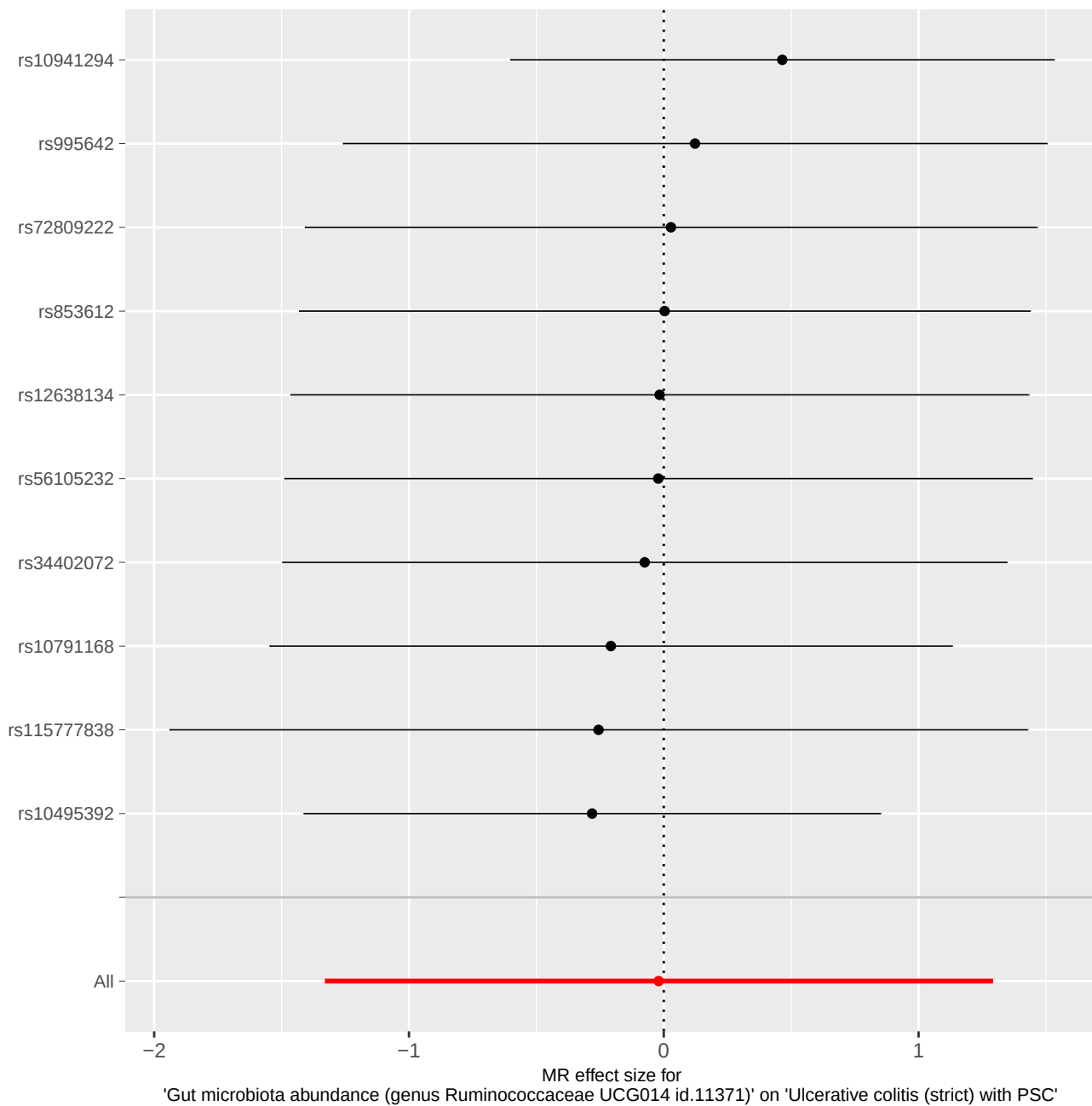


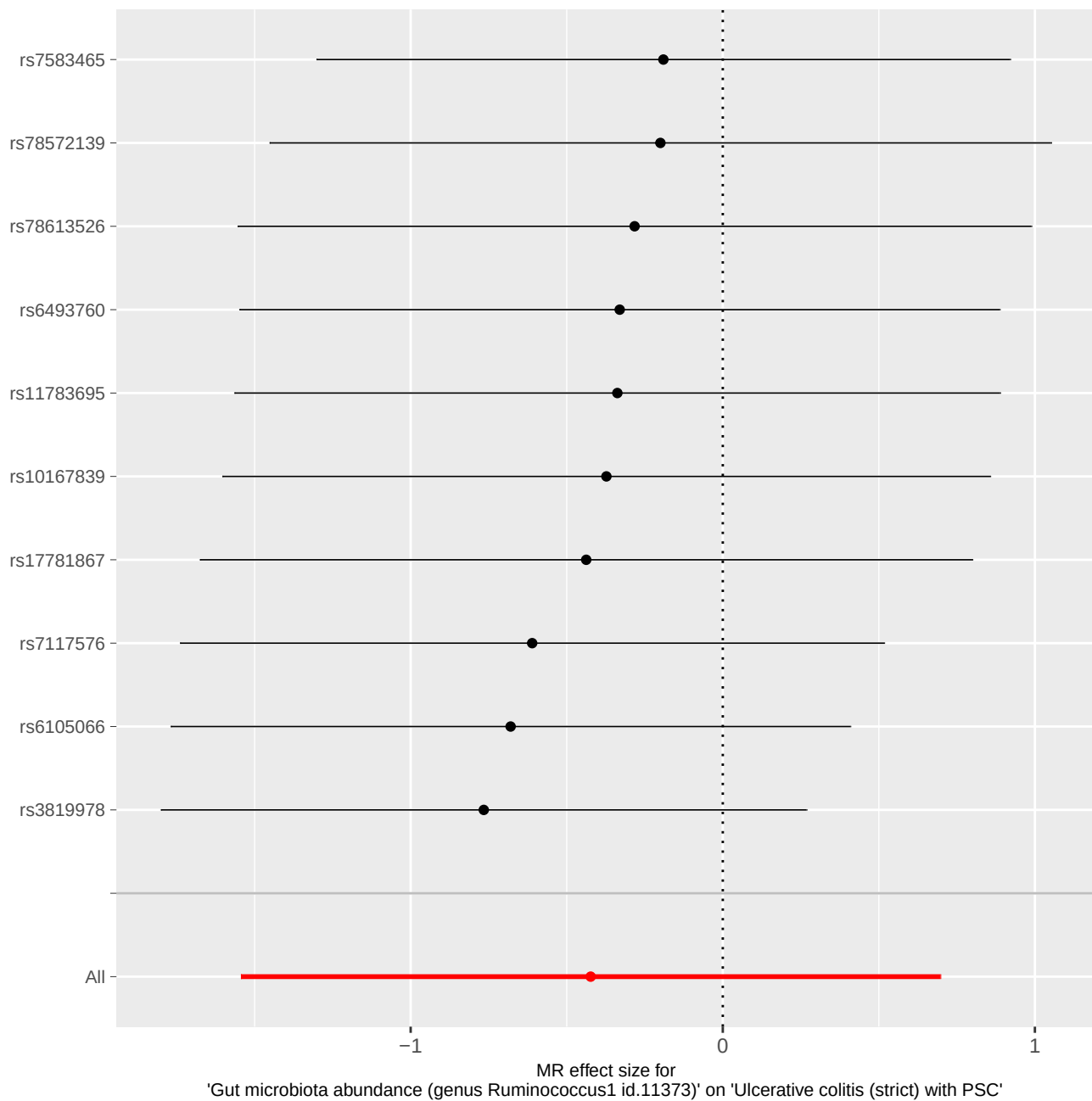


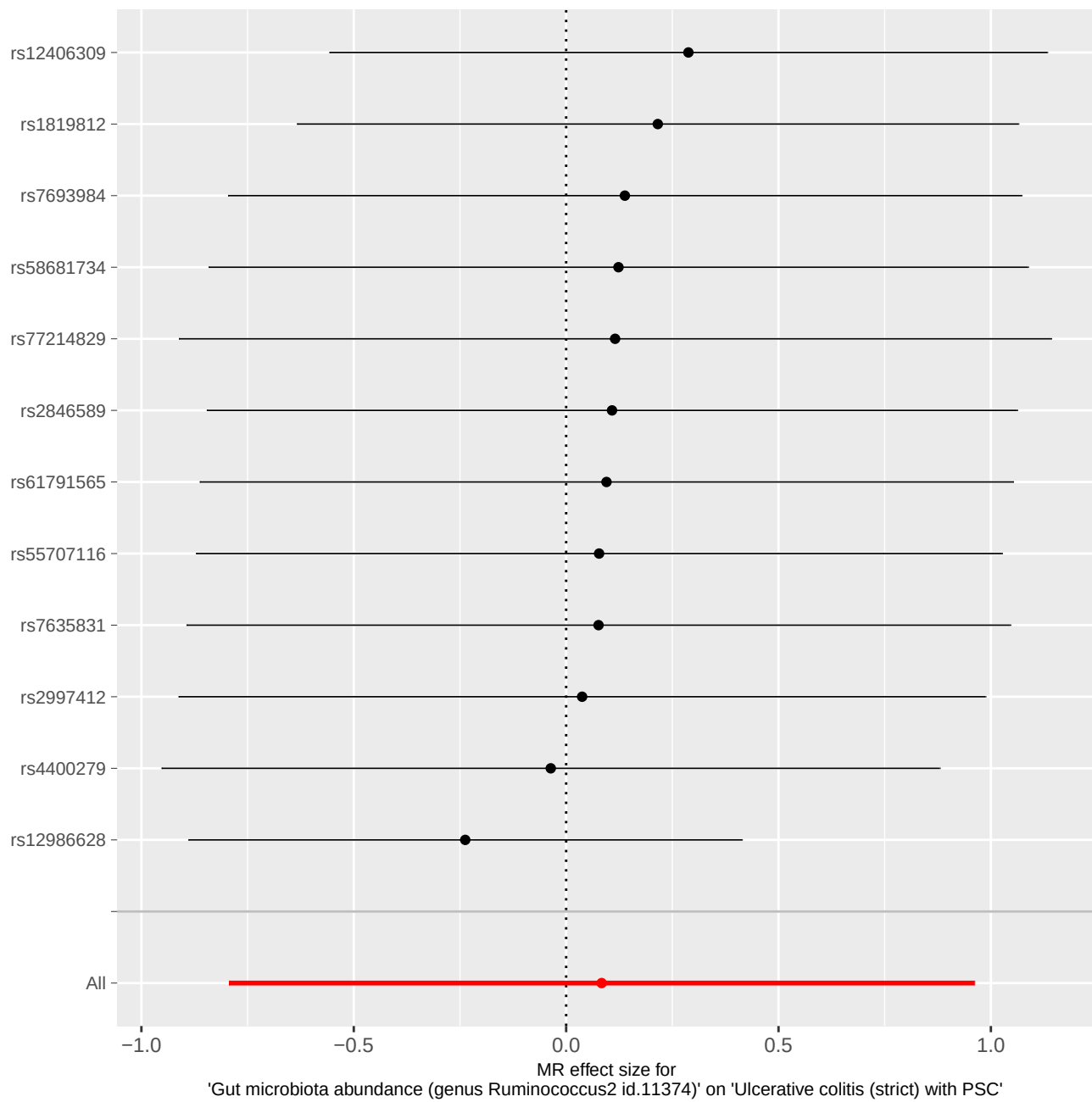


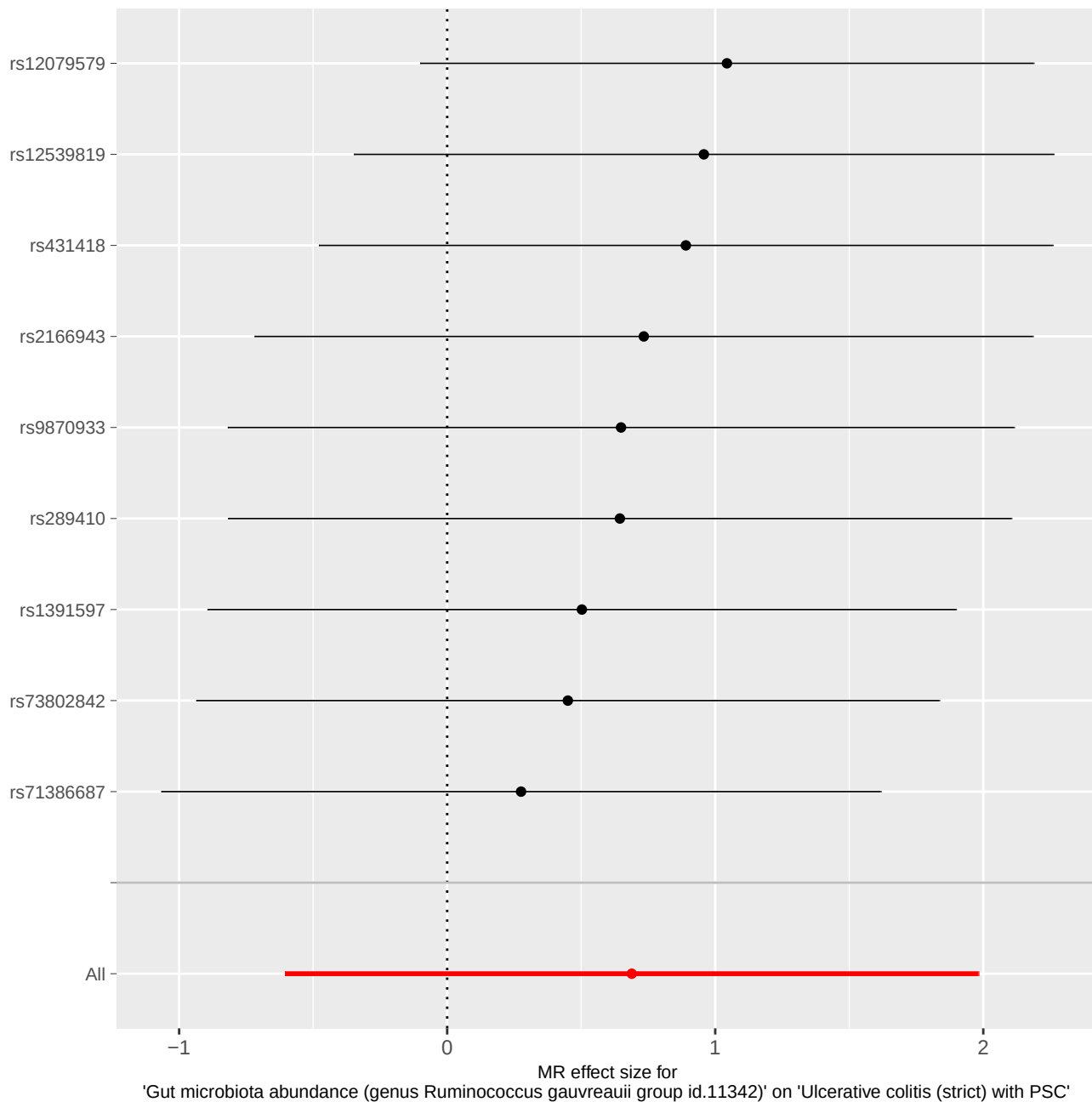


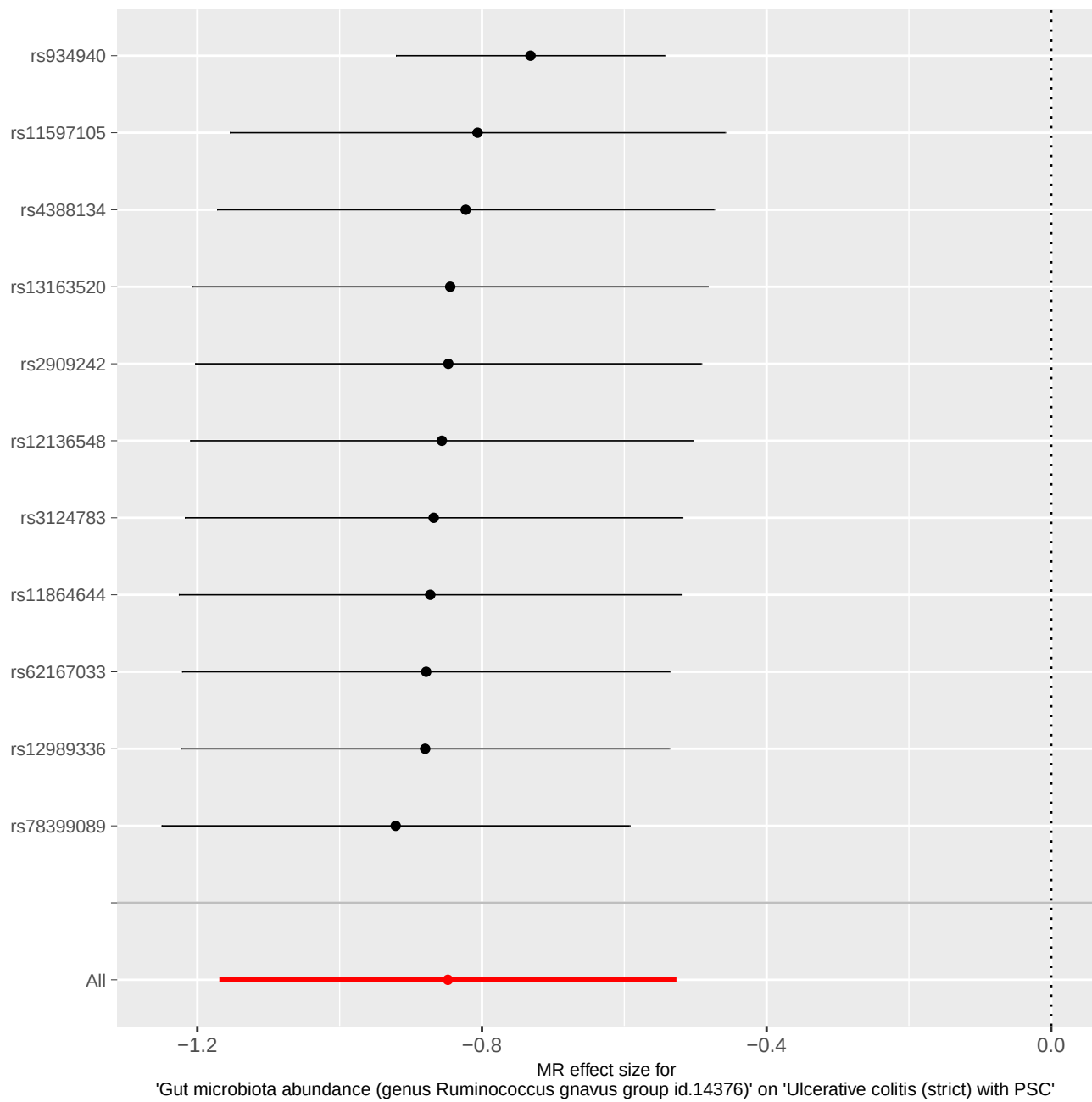


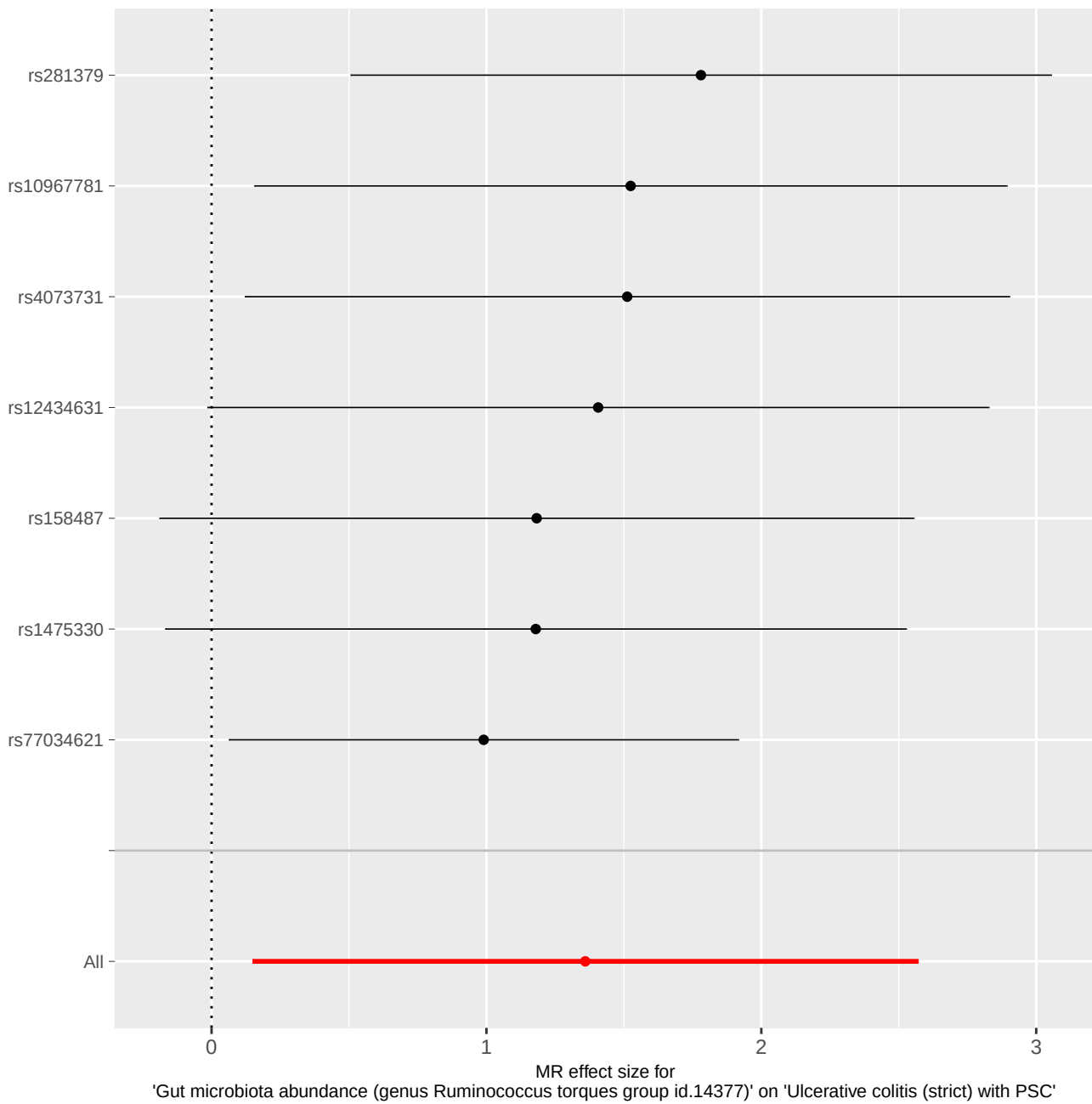


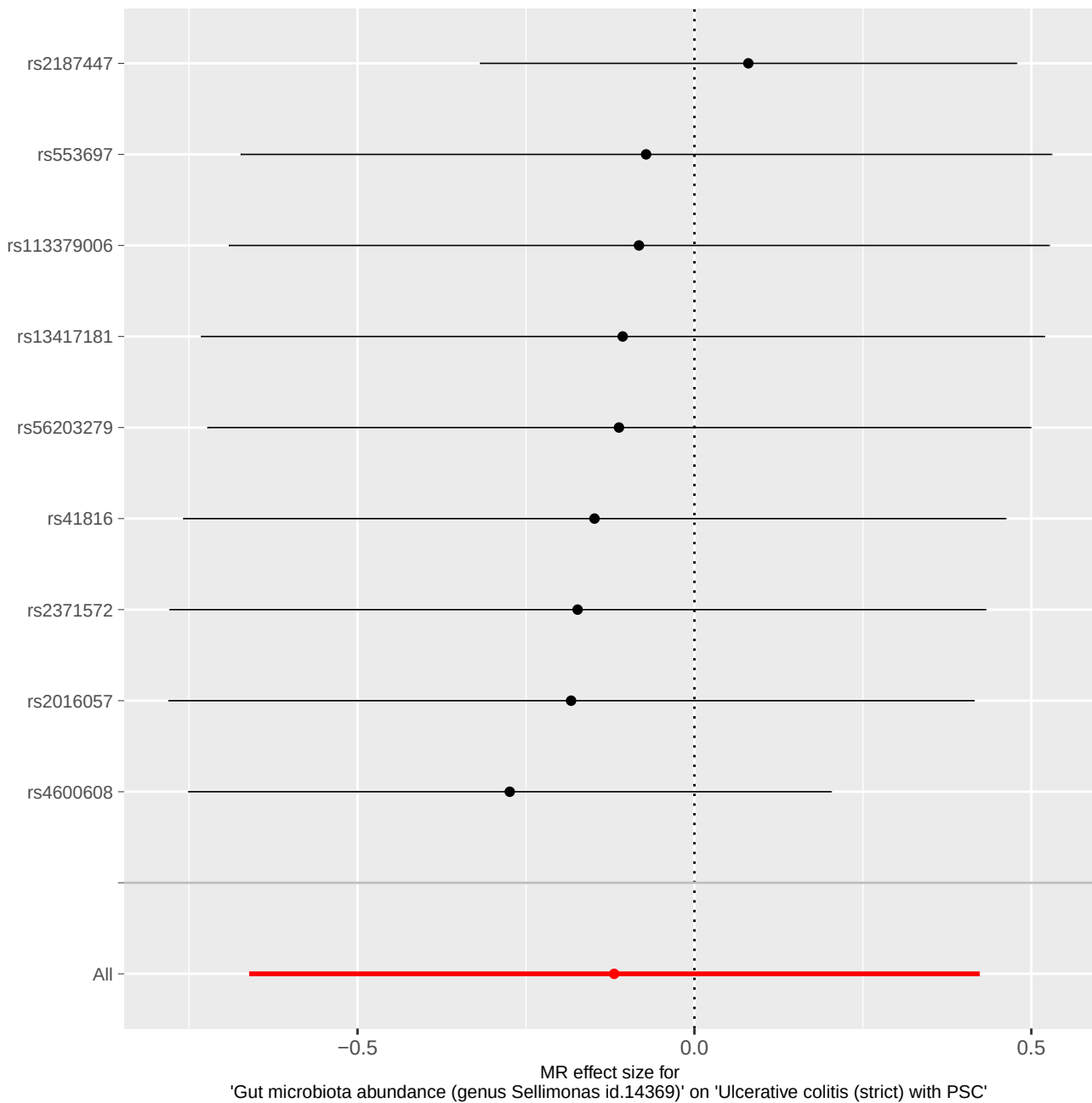


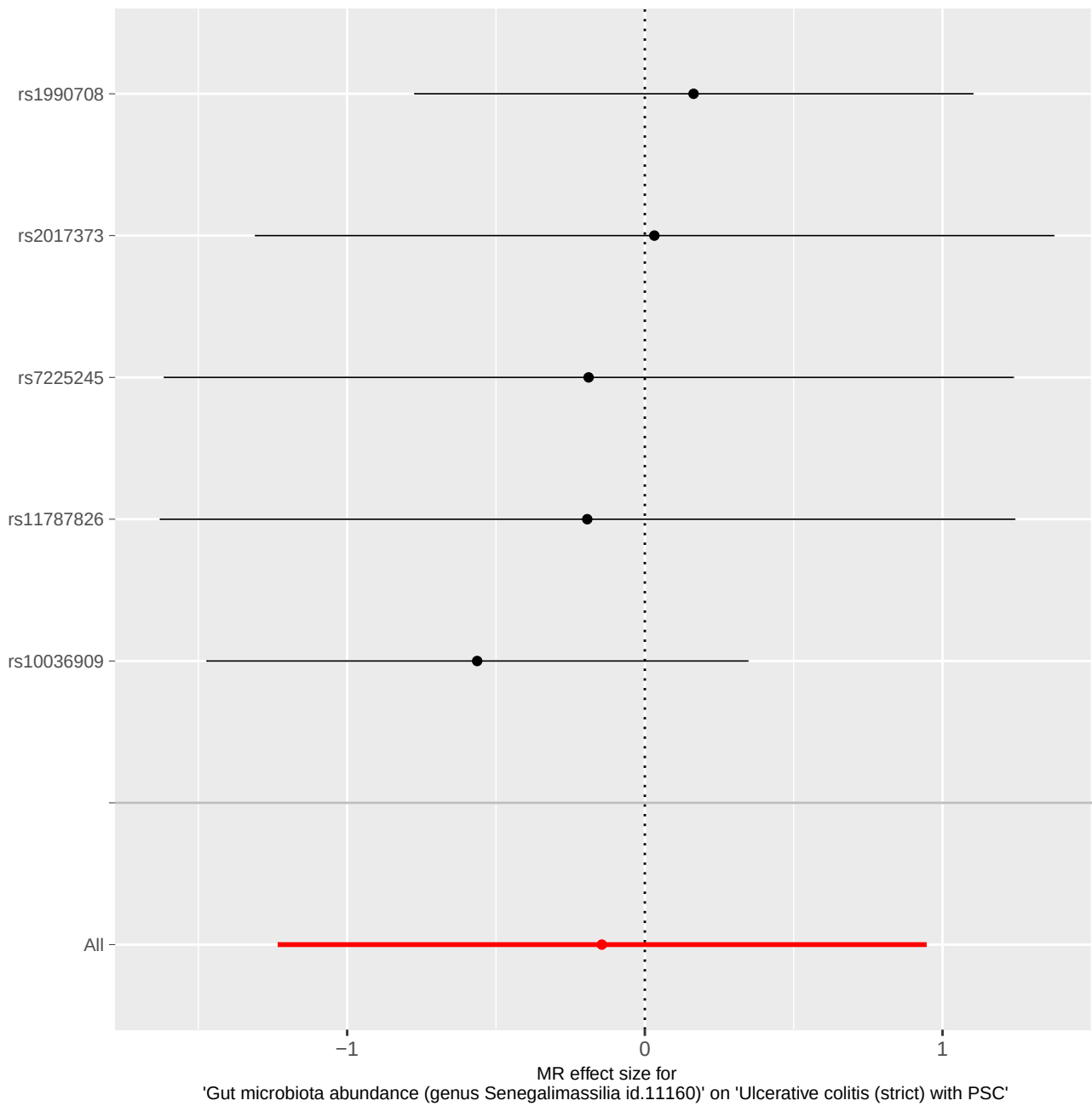


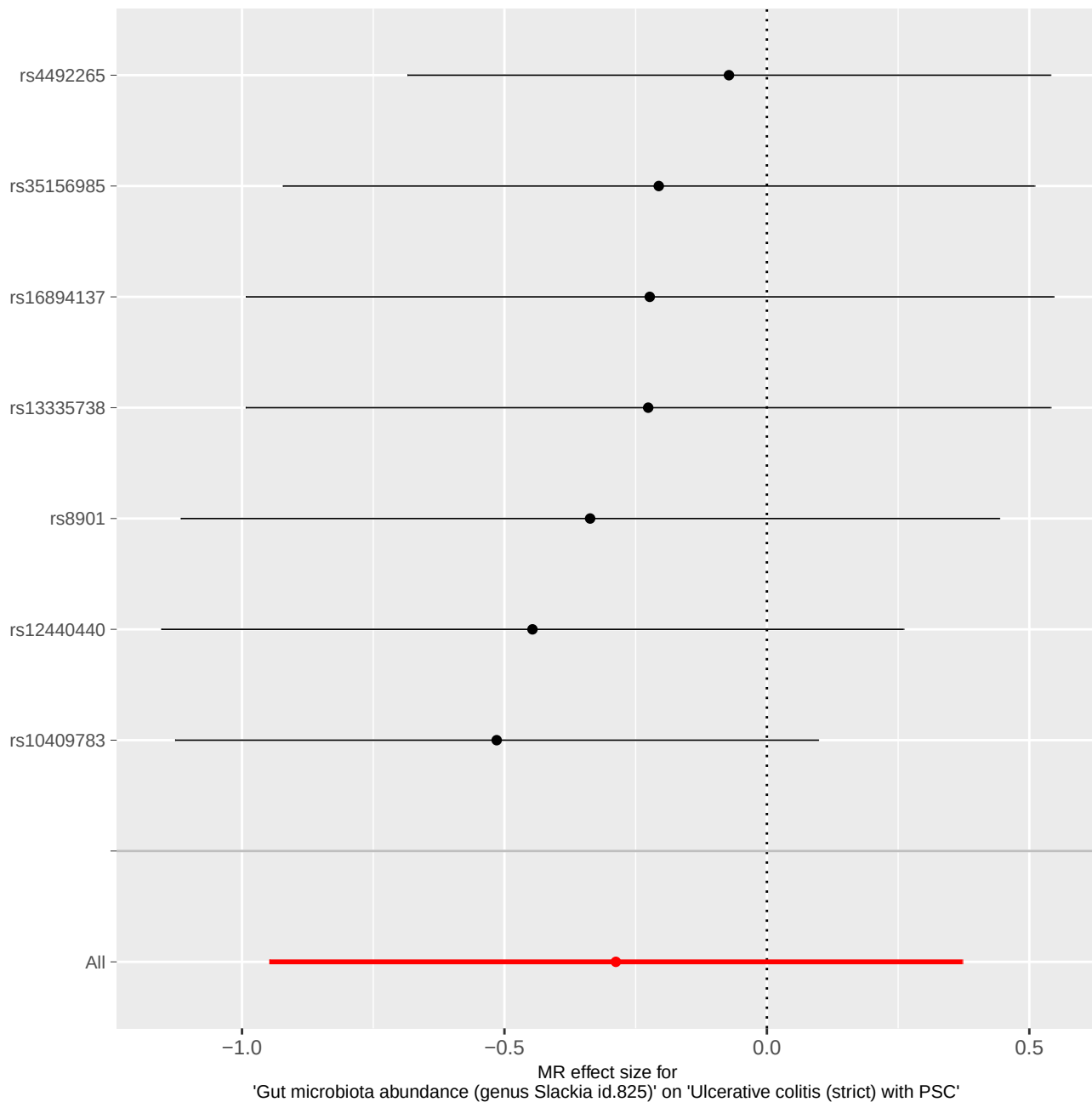


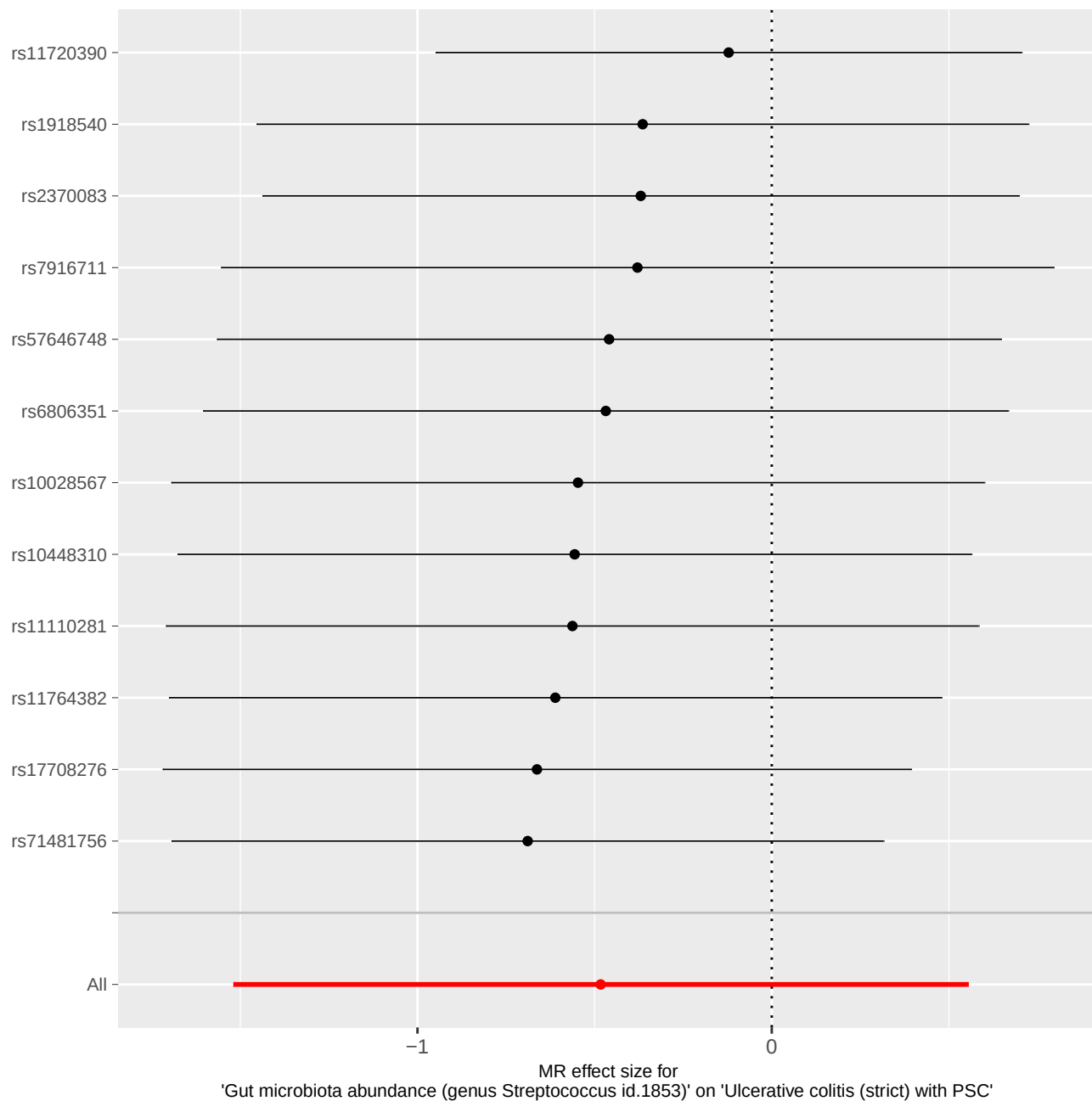




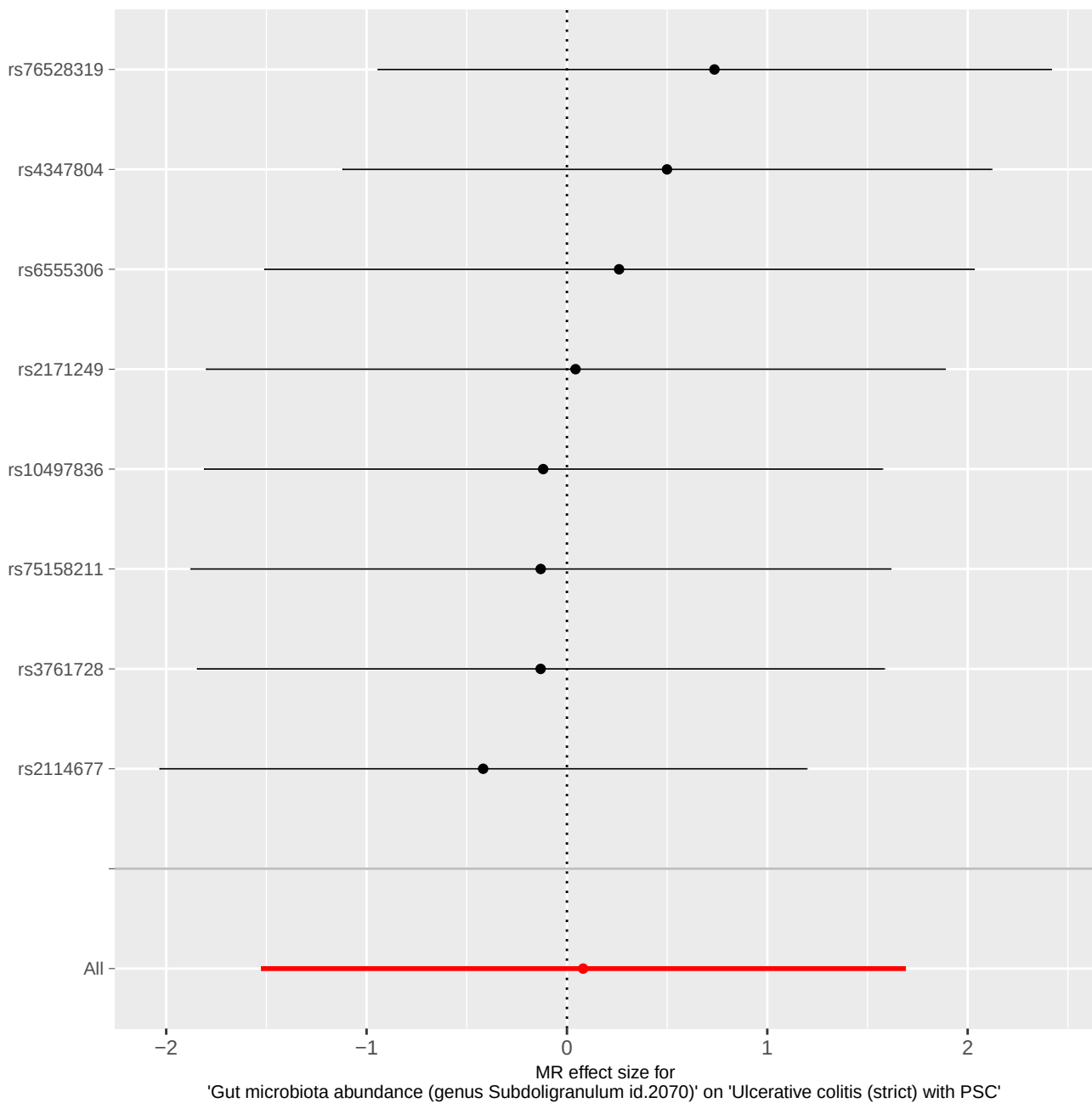


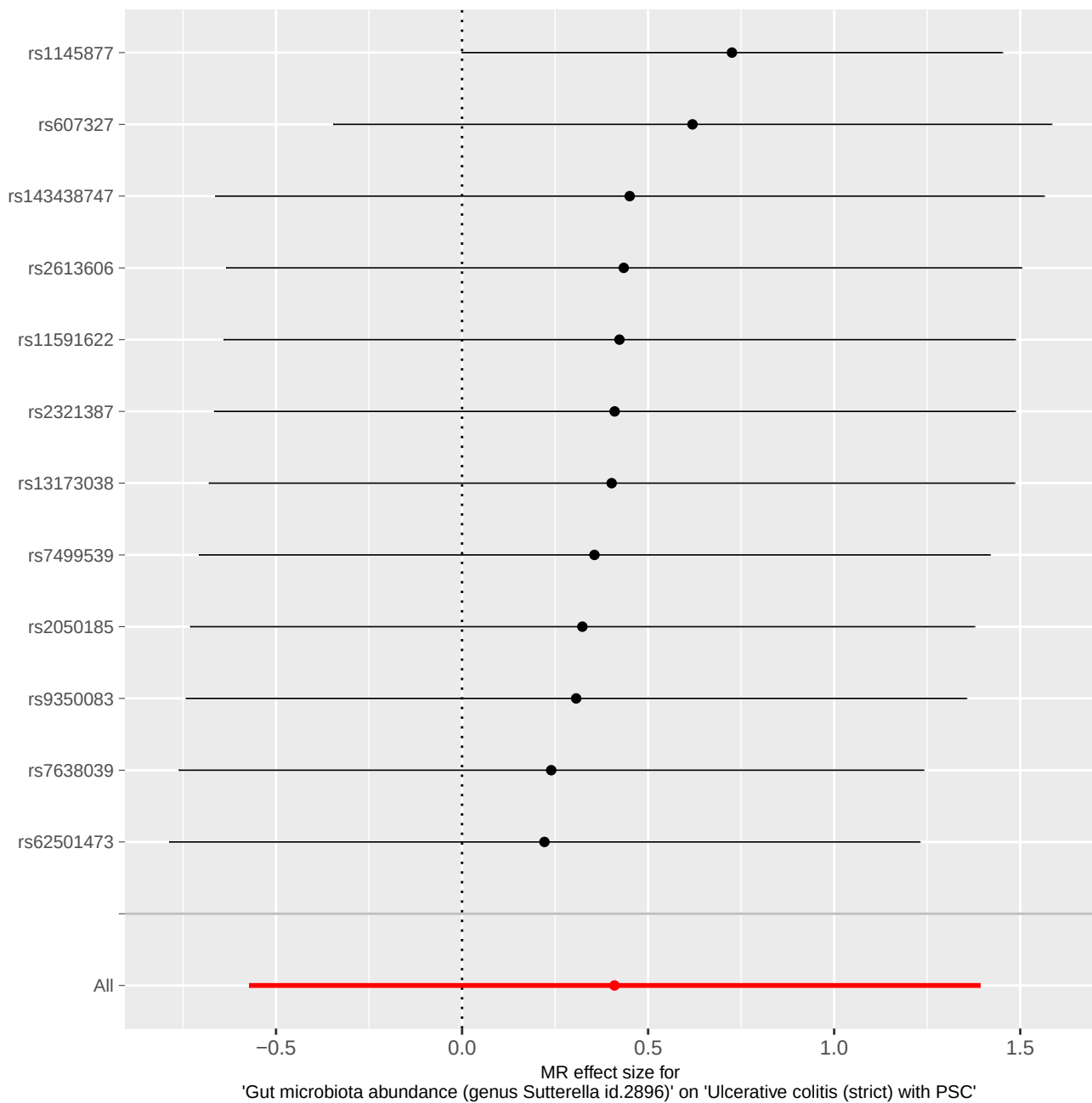


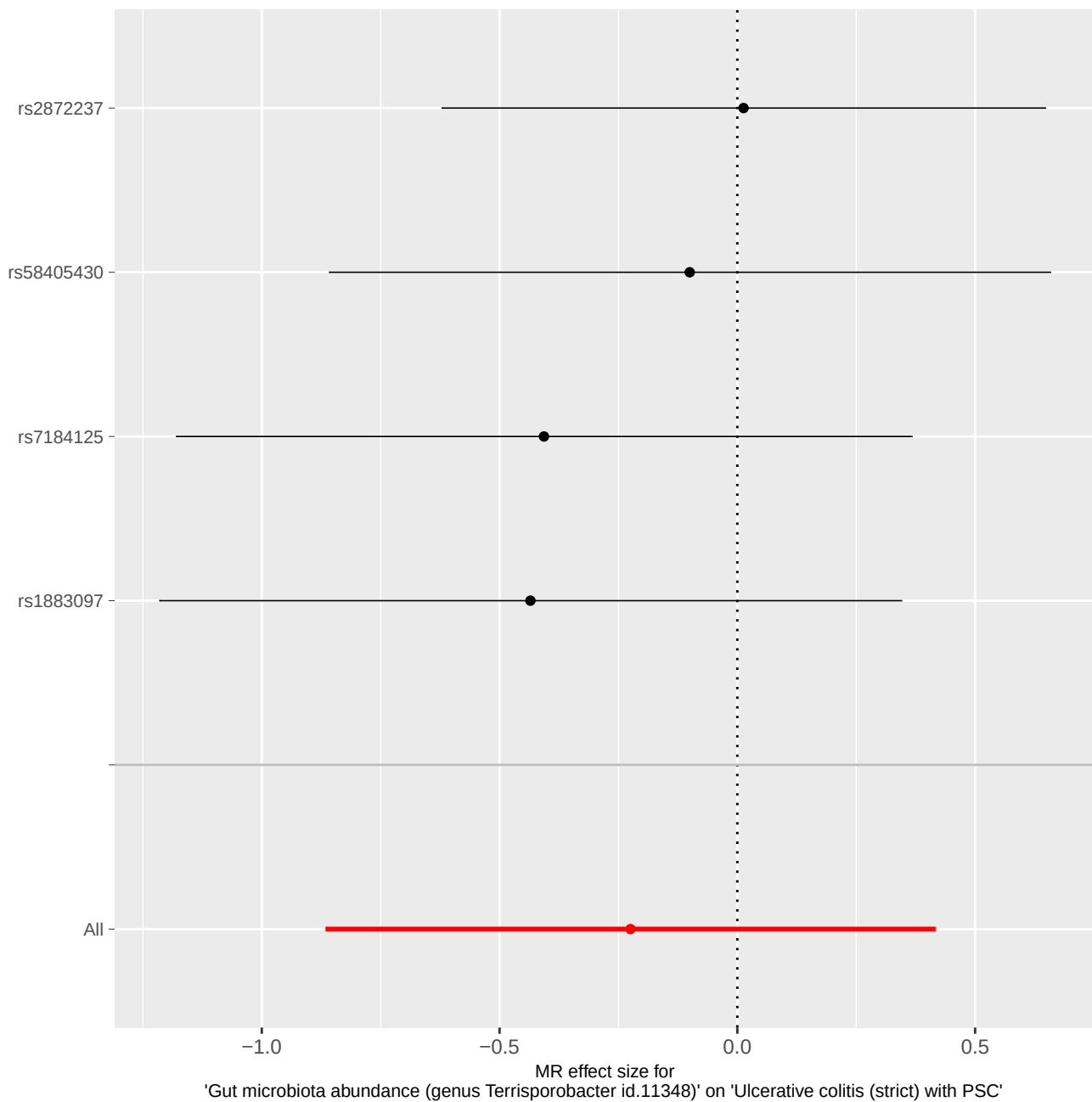


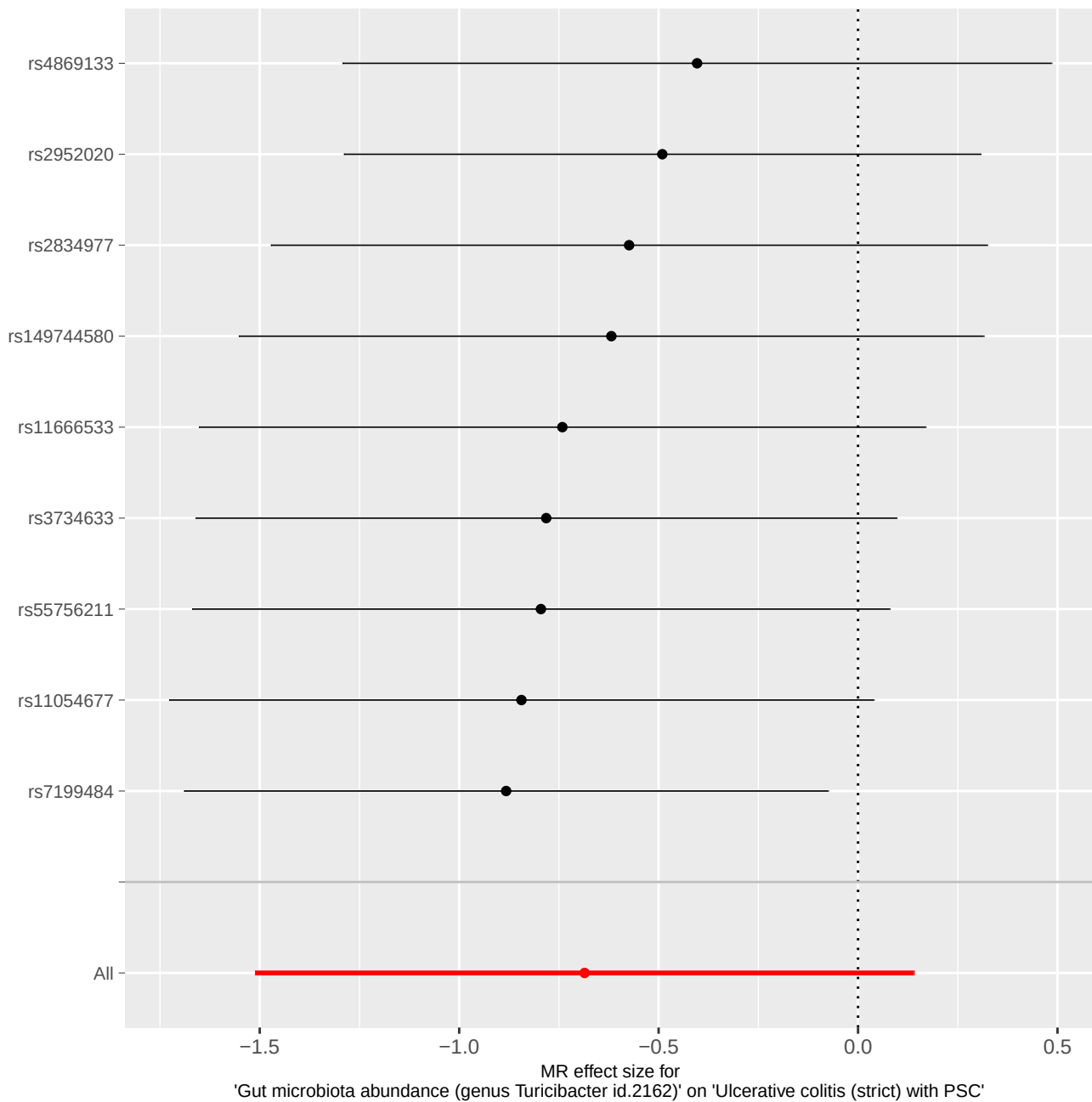


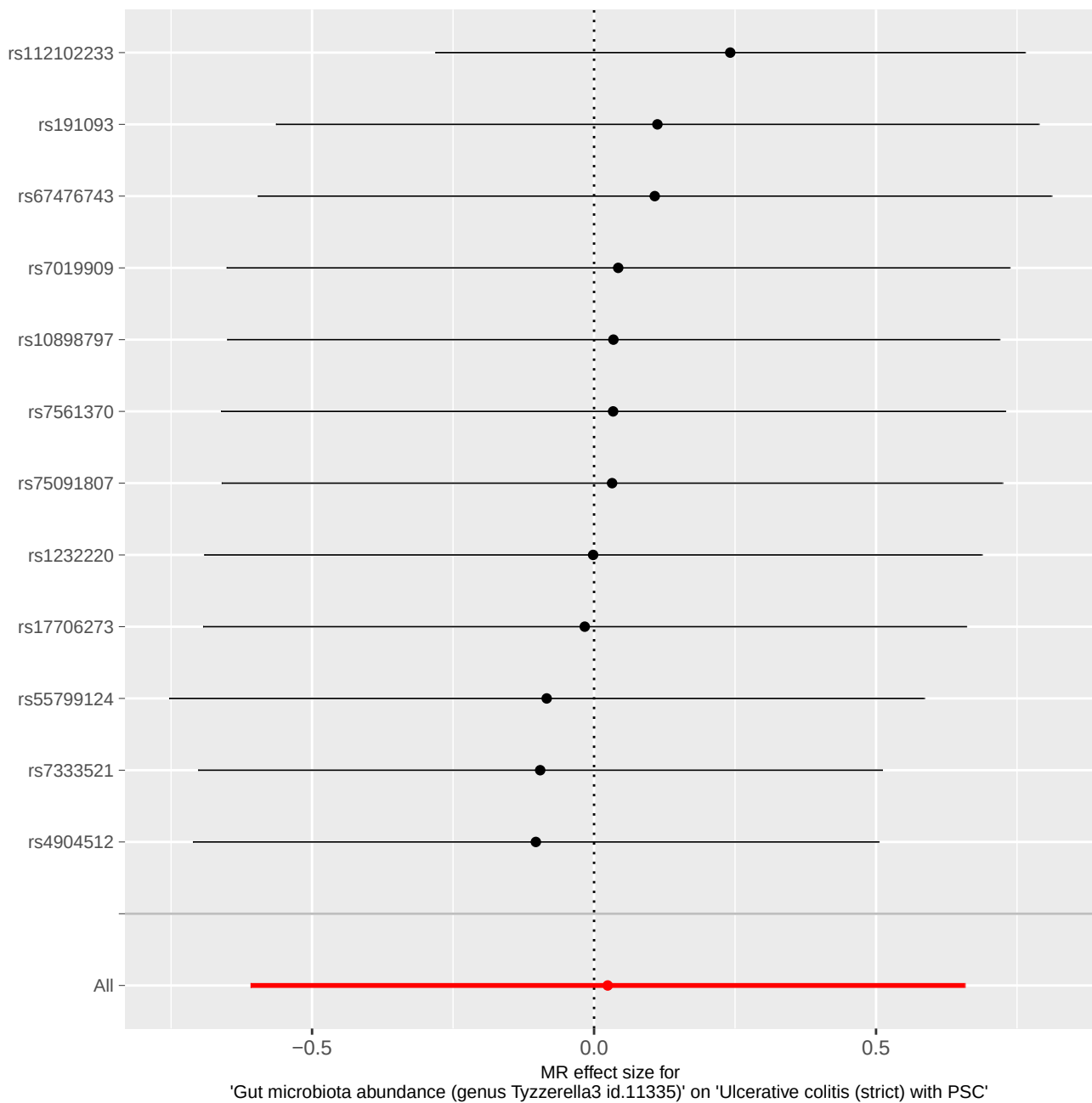
MR effect size for
'Gut microbiota abundance (genus Streptococcus id.1853)' on 'Ulcerative colitis (strict) with PSC'

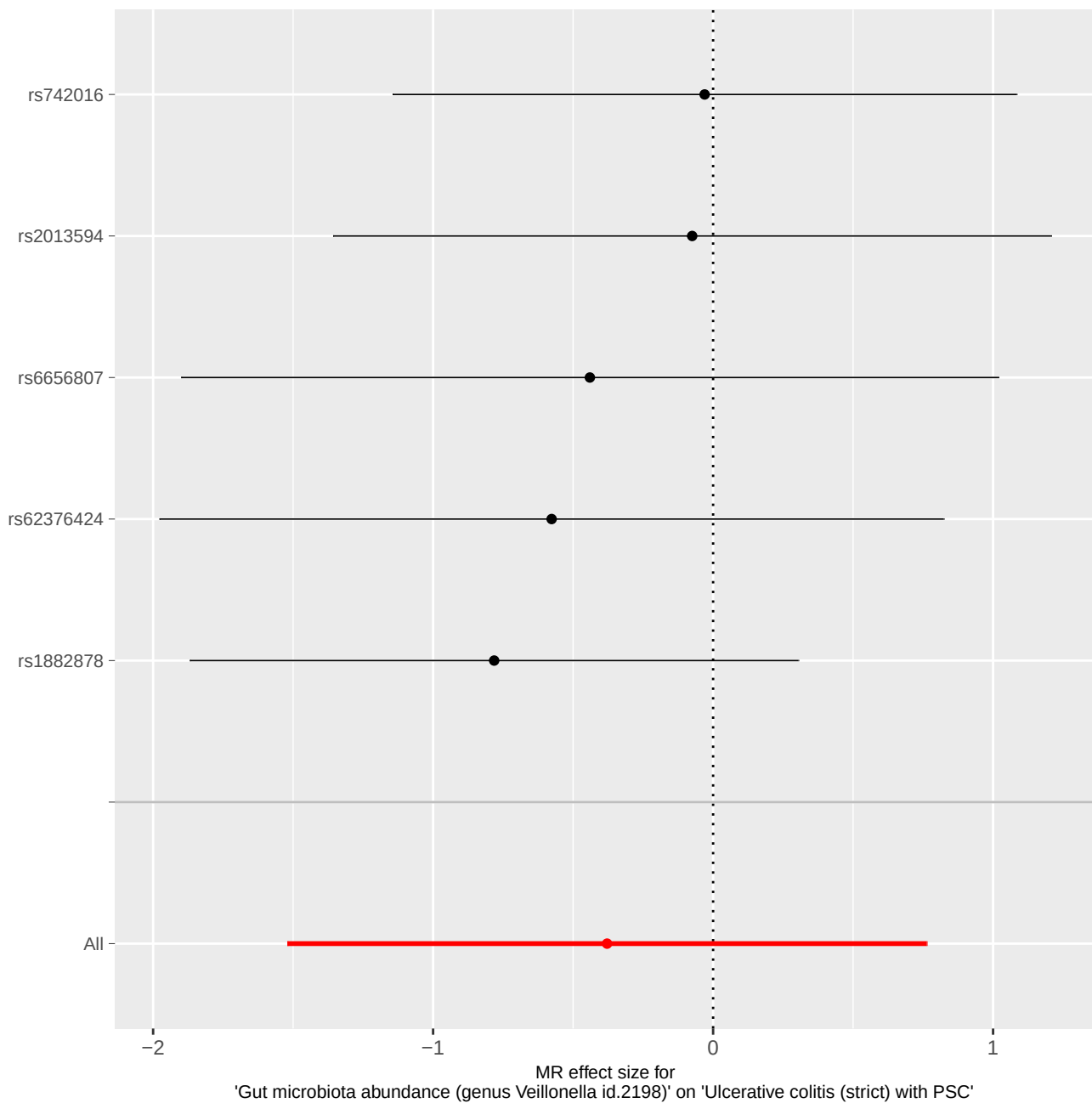


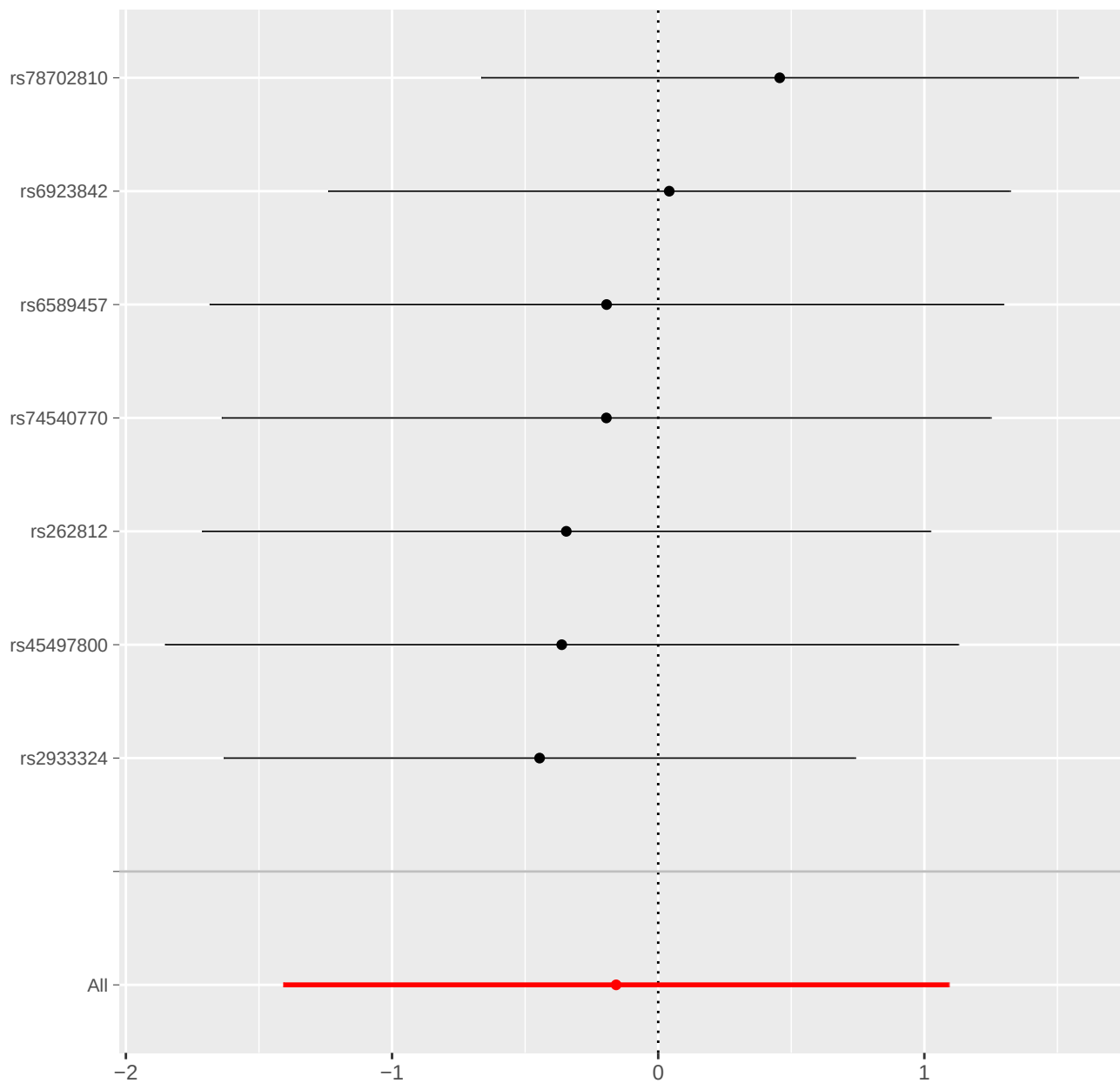




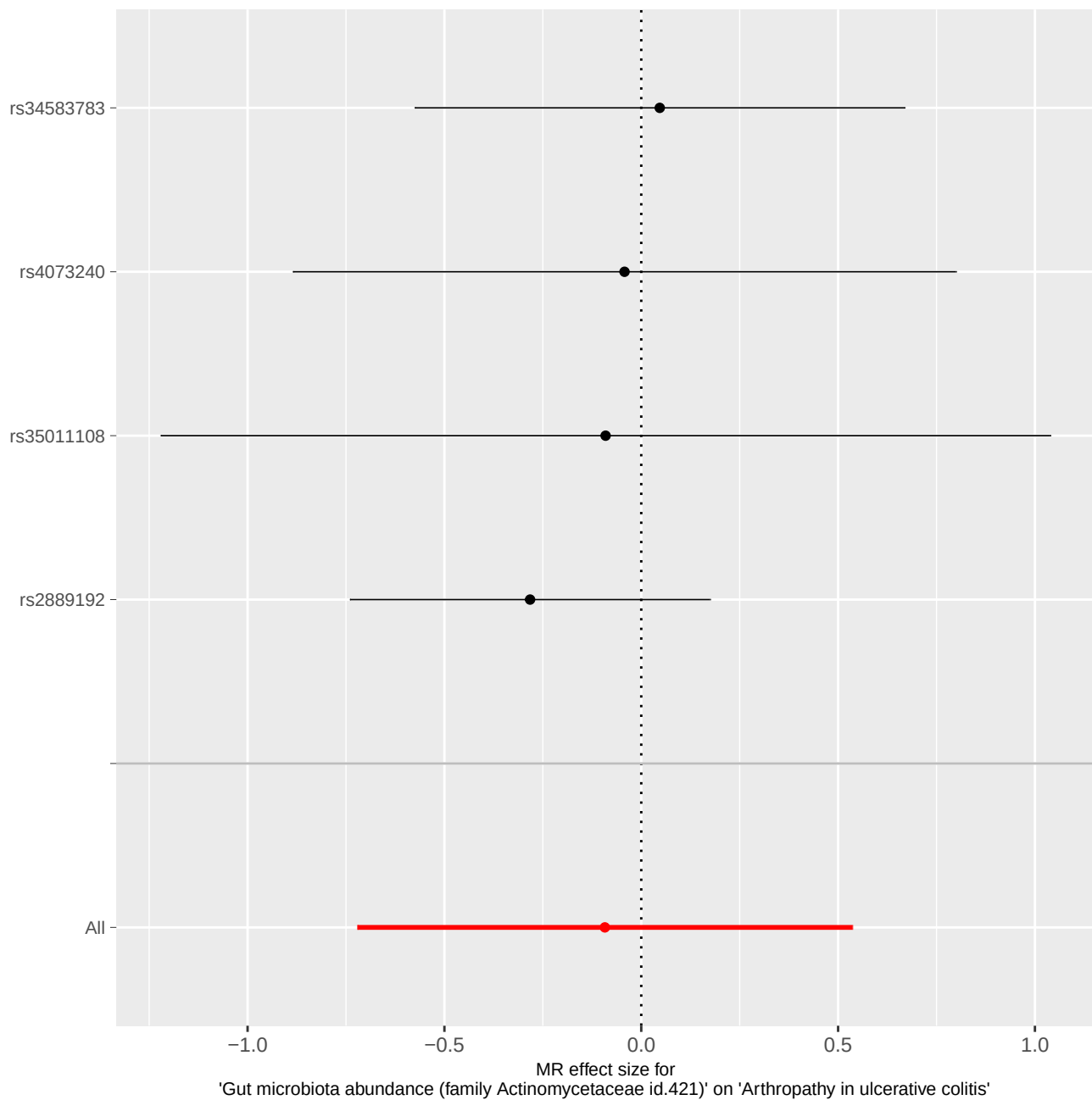


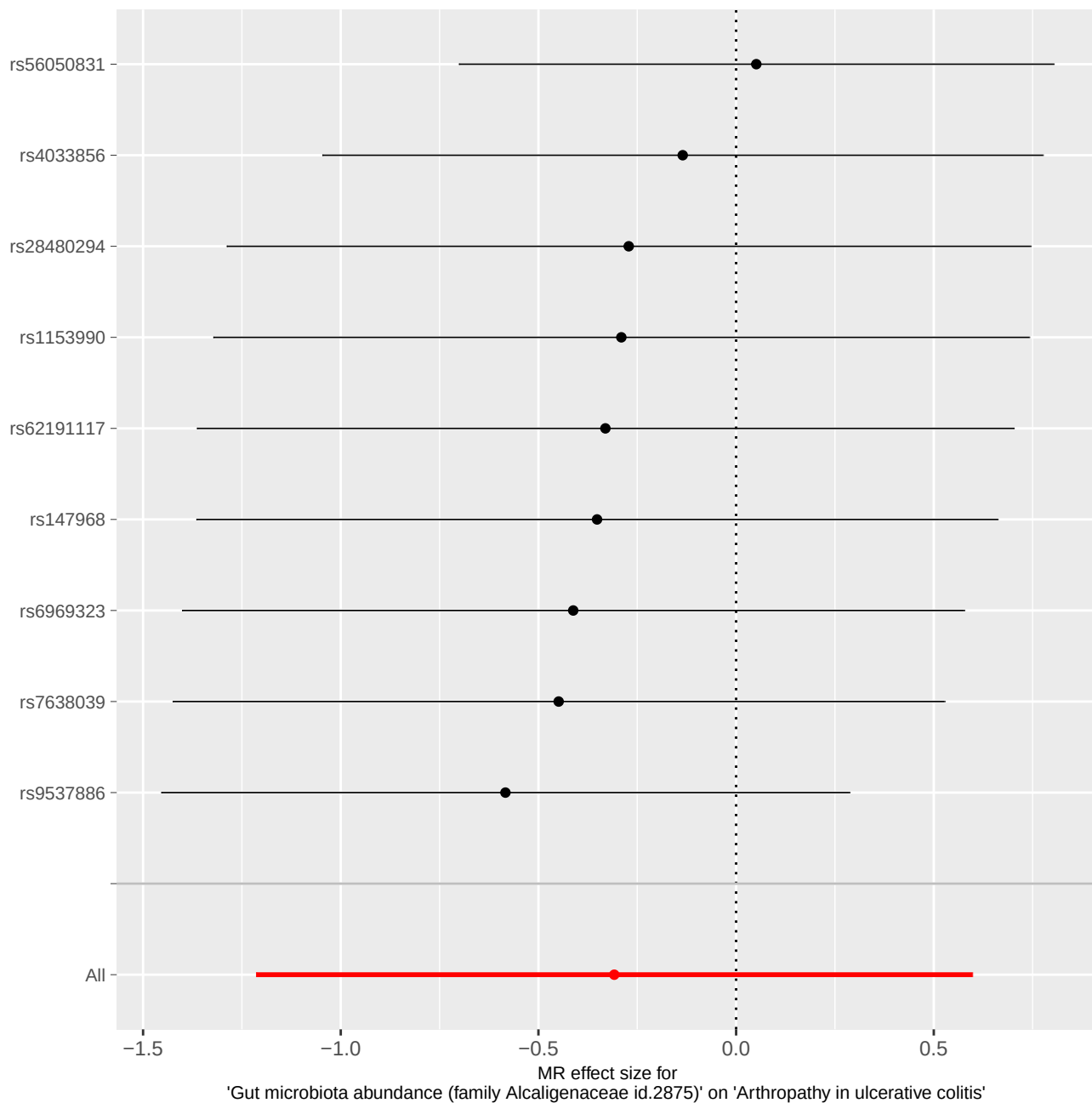


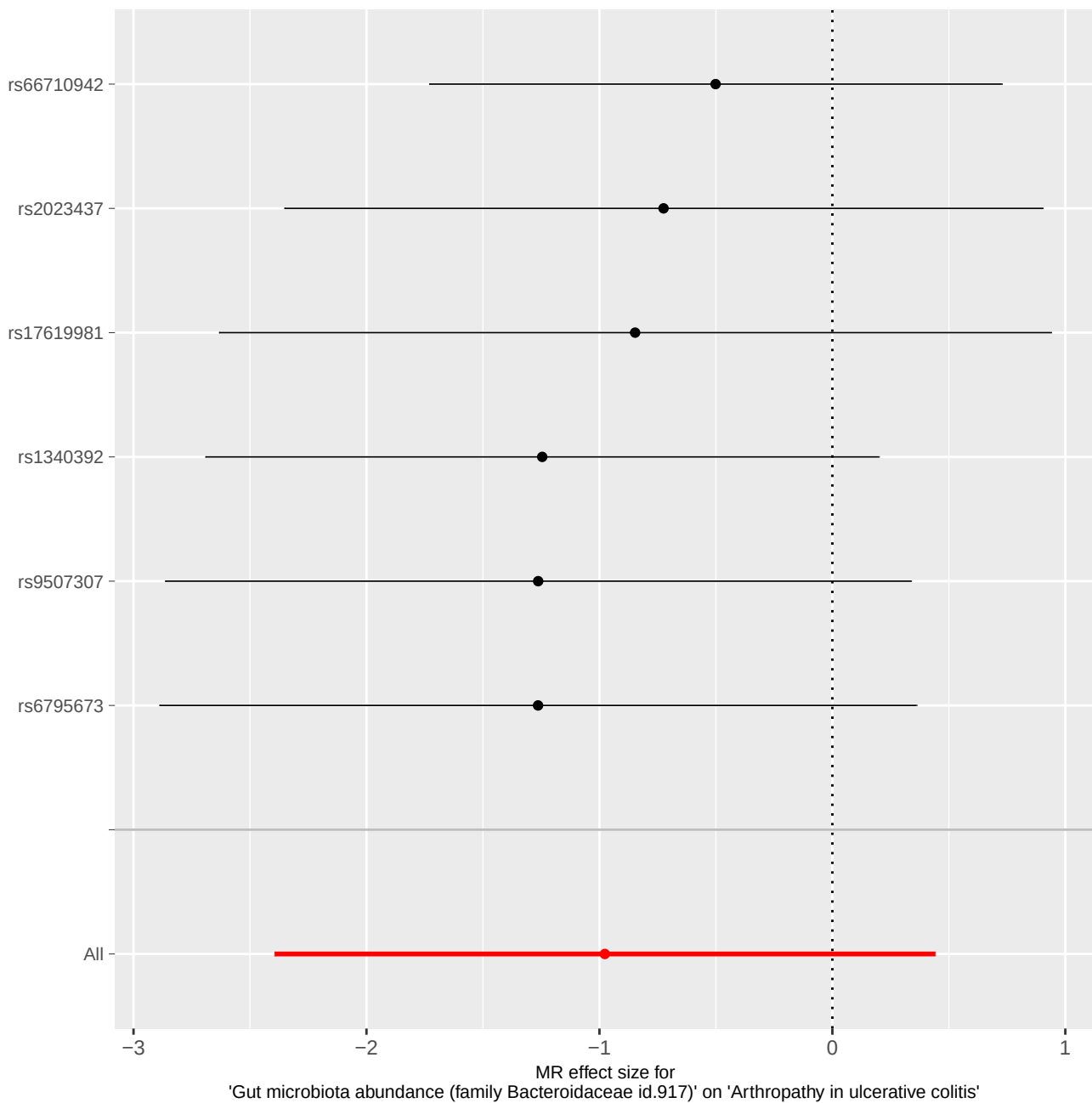


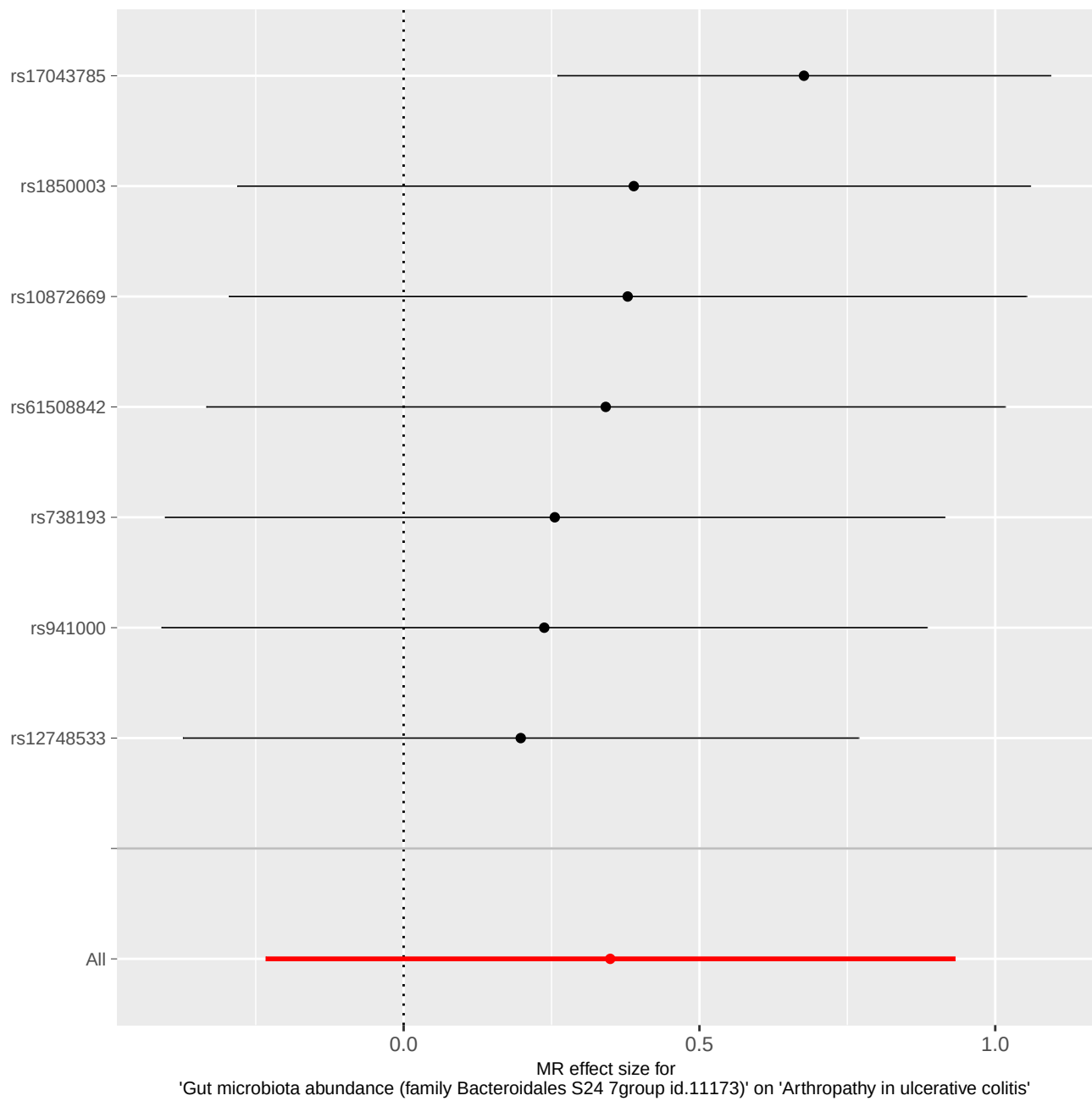


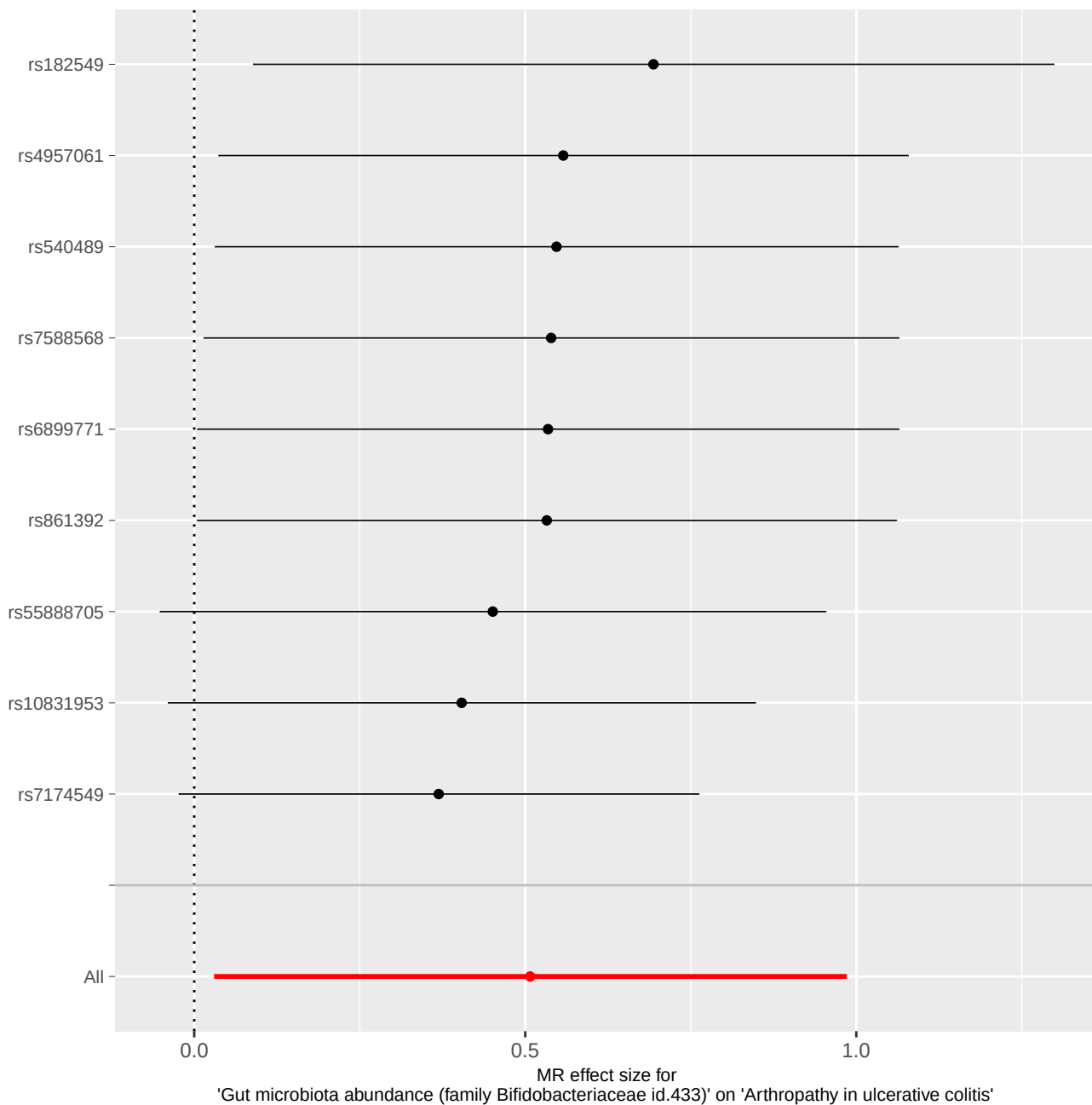
MR effect size for
'Gut microbiota abundance (family Acidaminococcaceae id.2166)' on 'Arthropathy in ulcerative colitis'

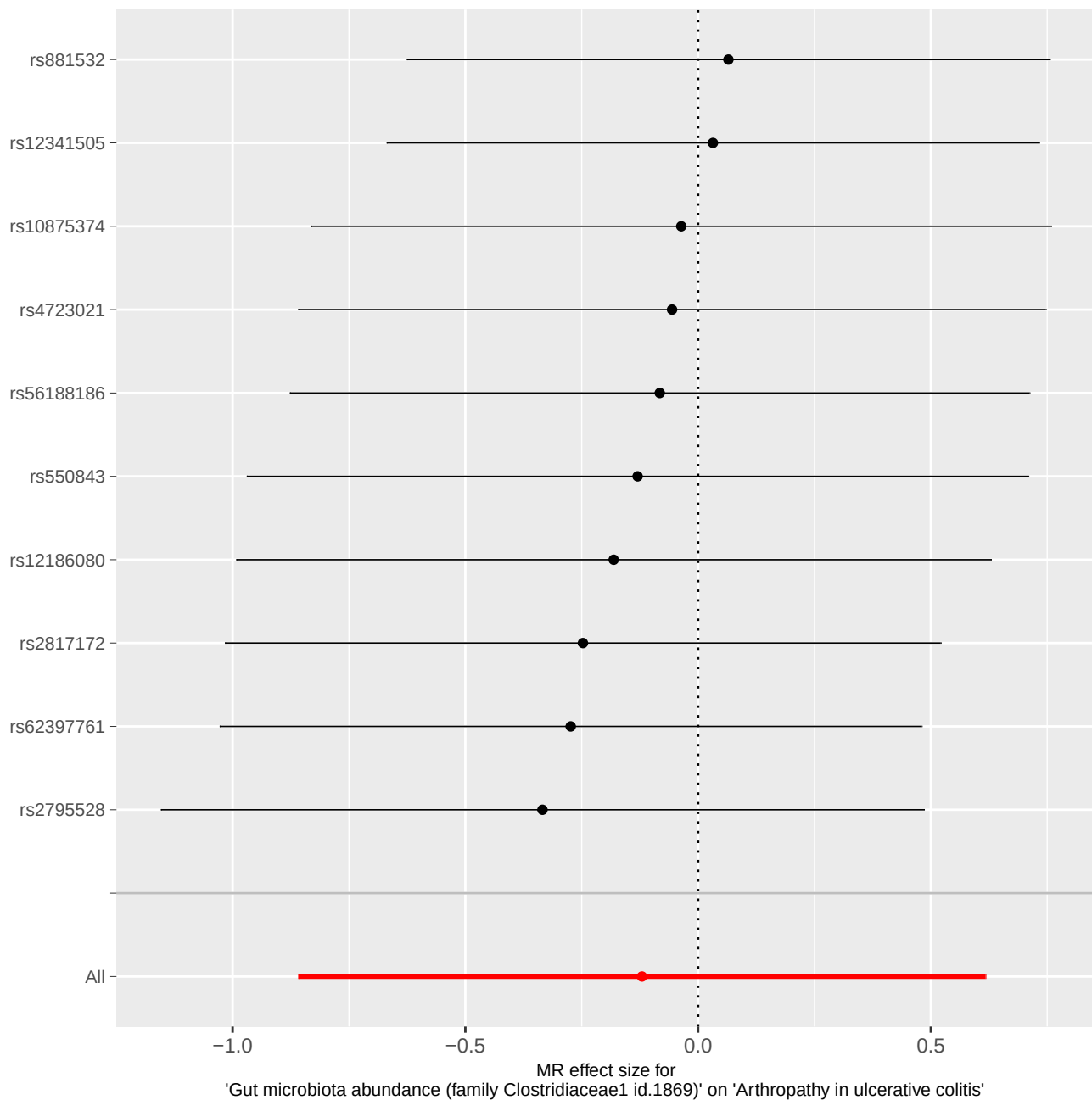


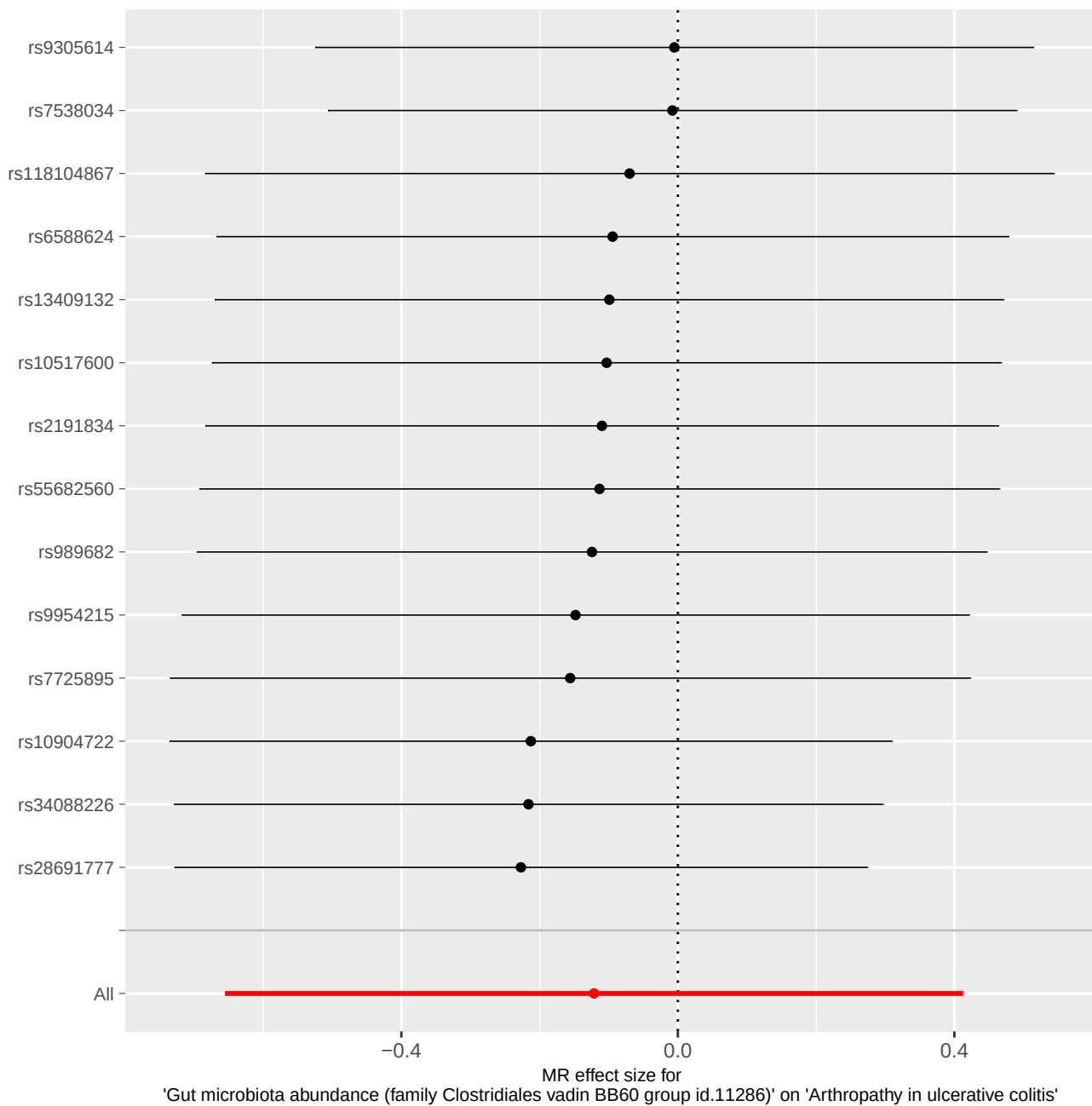


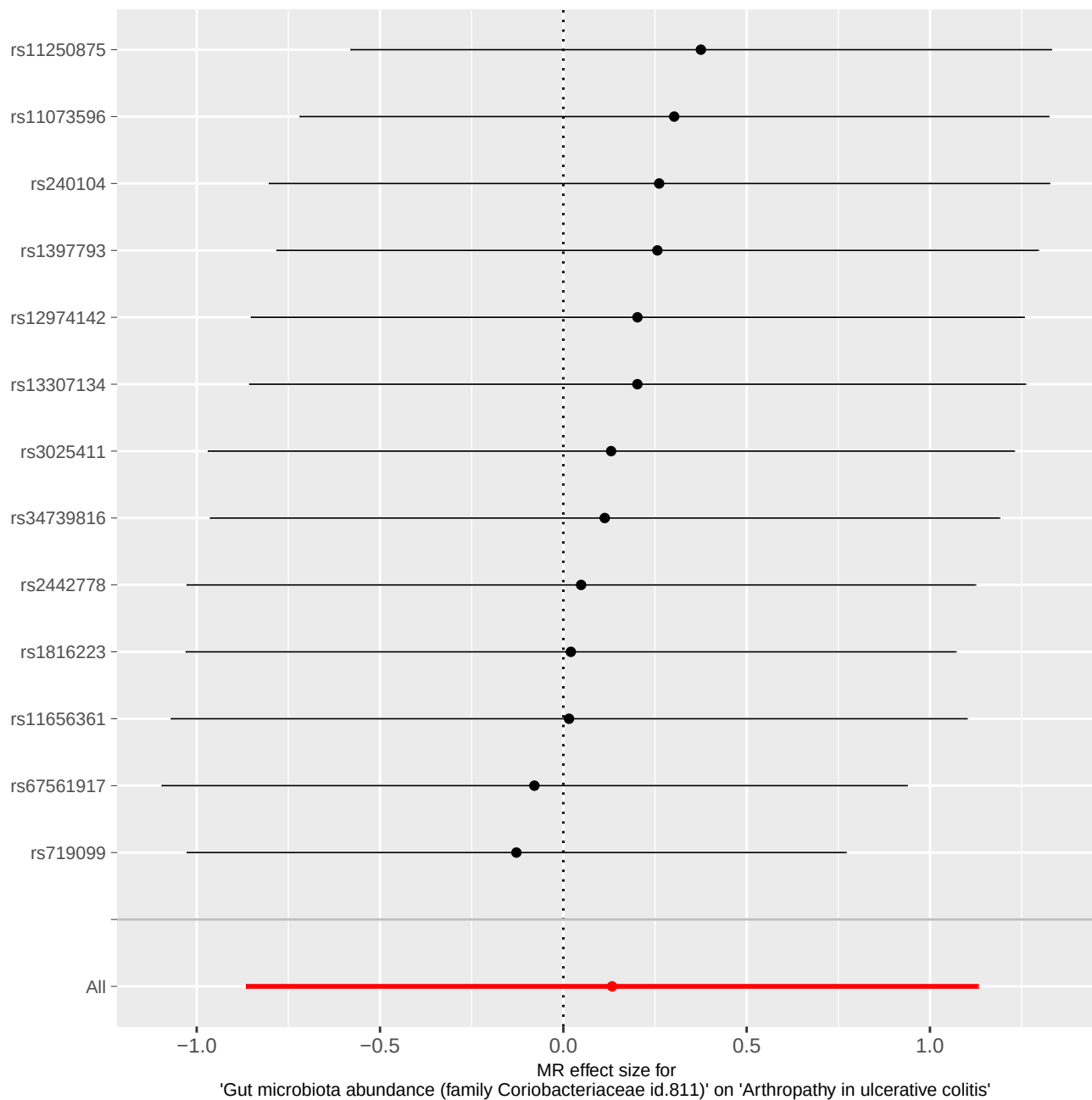


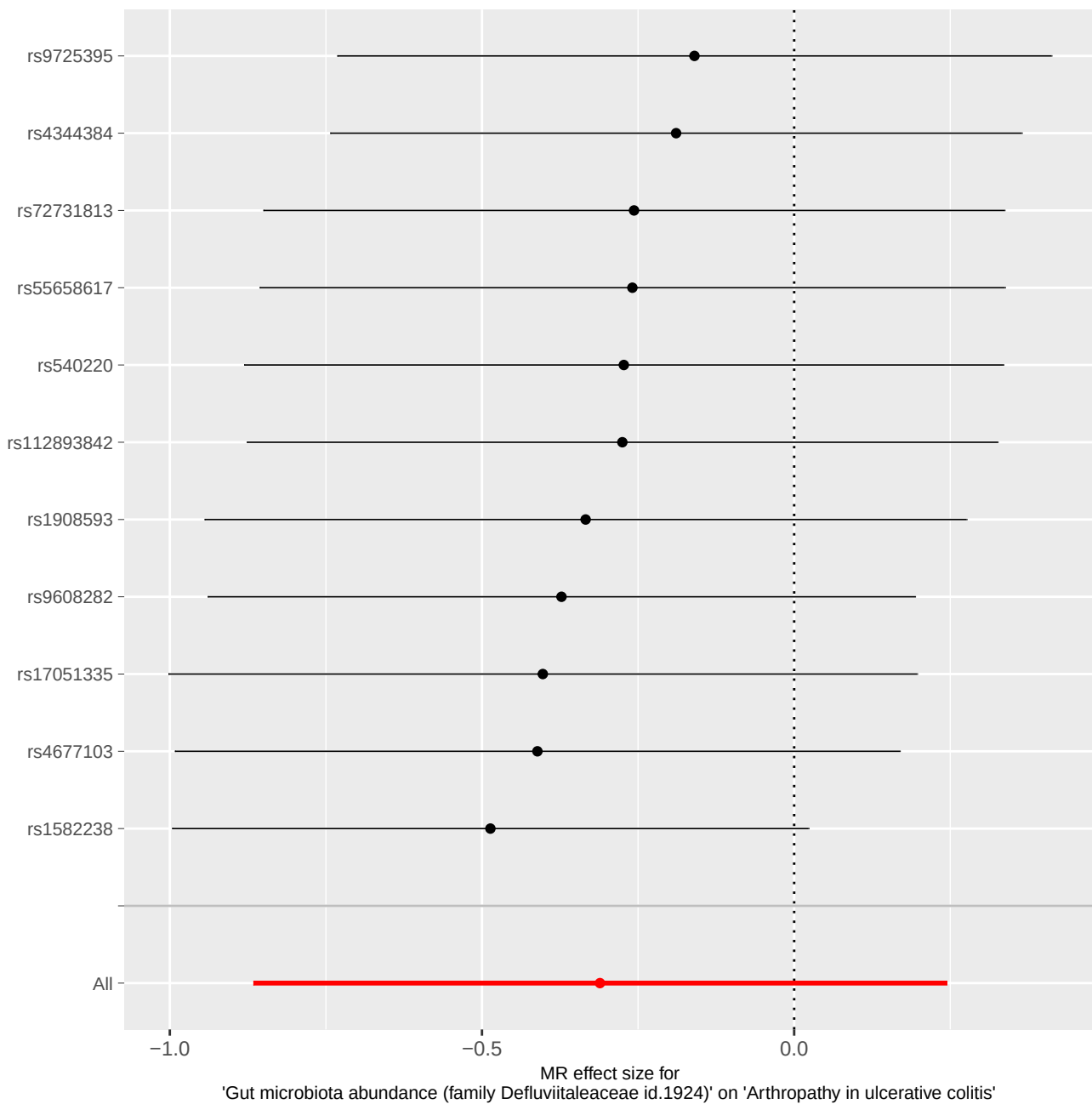


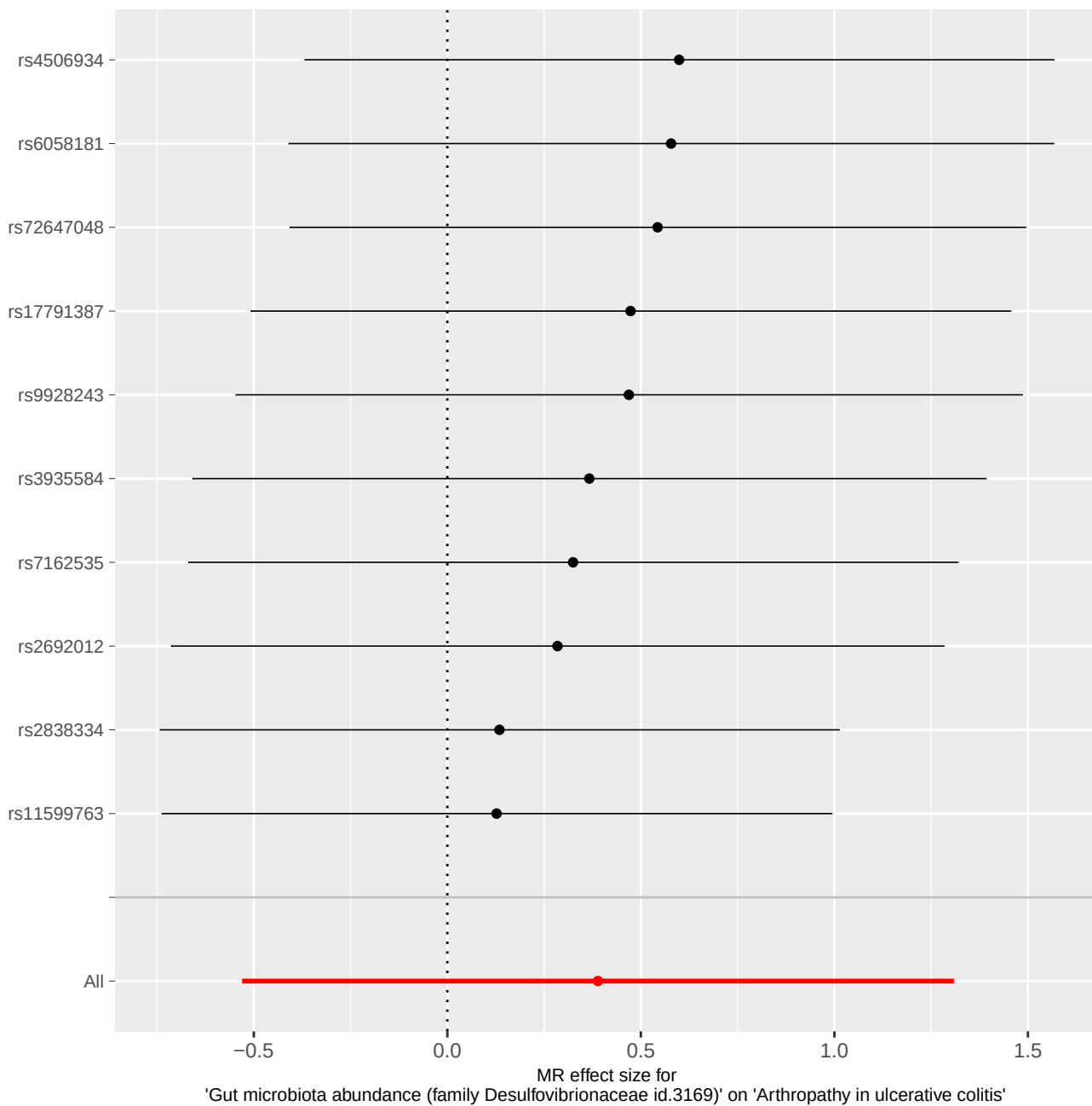




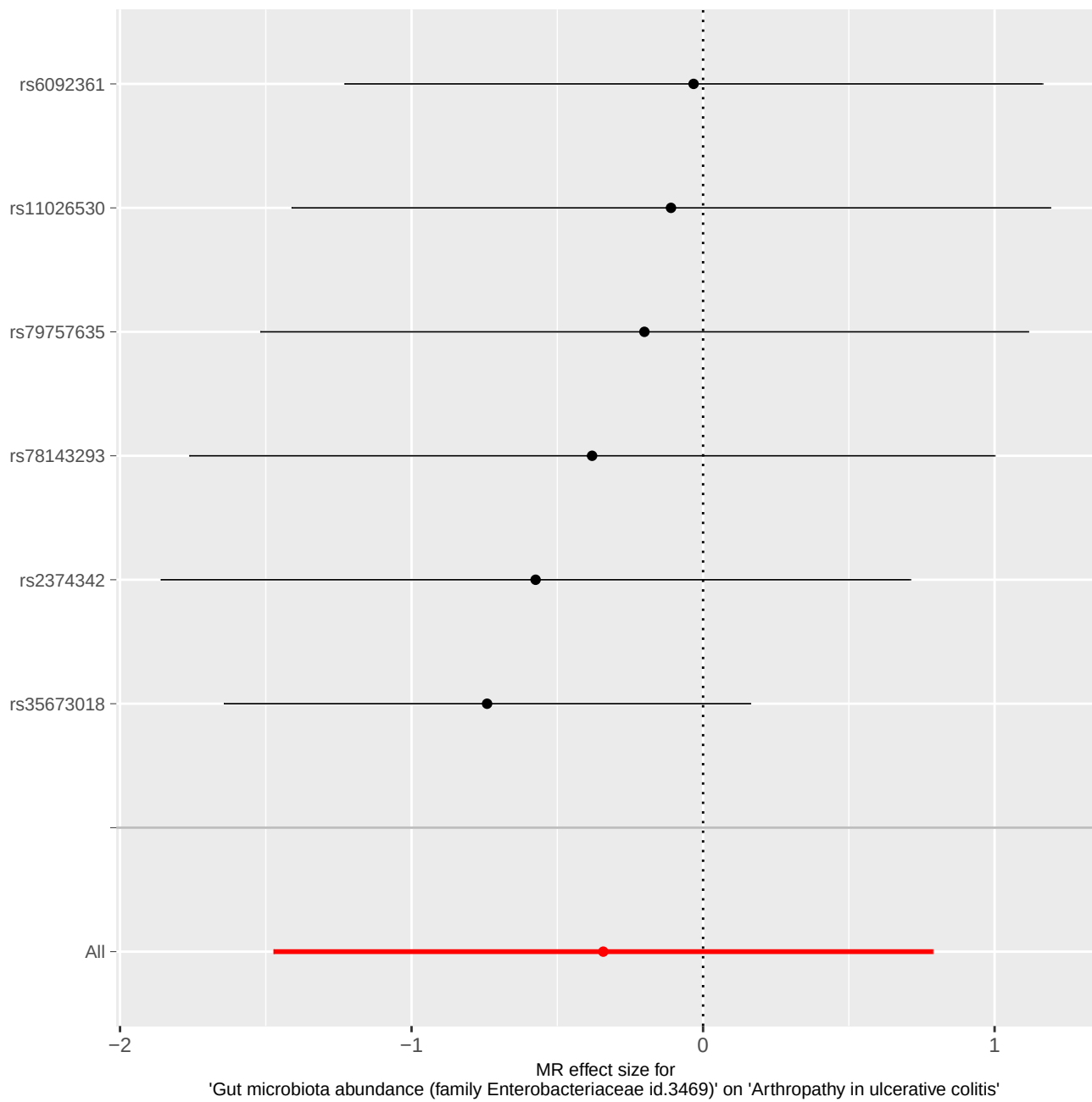


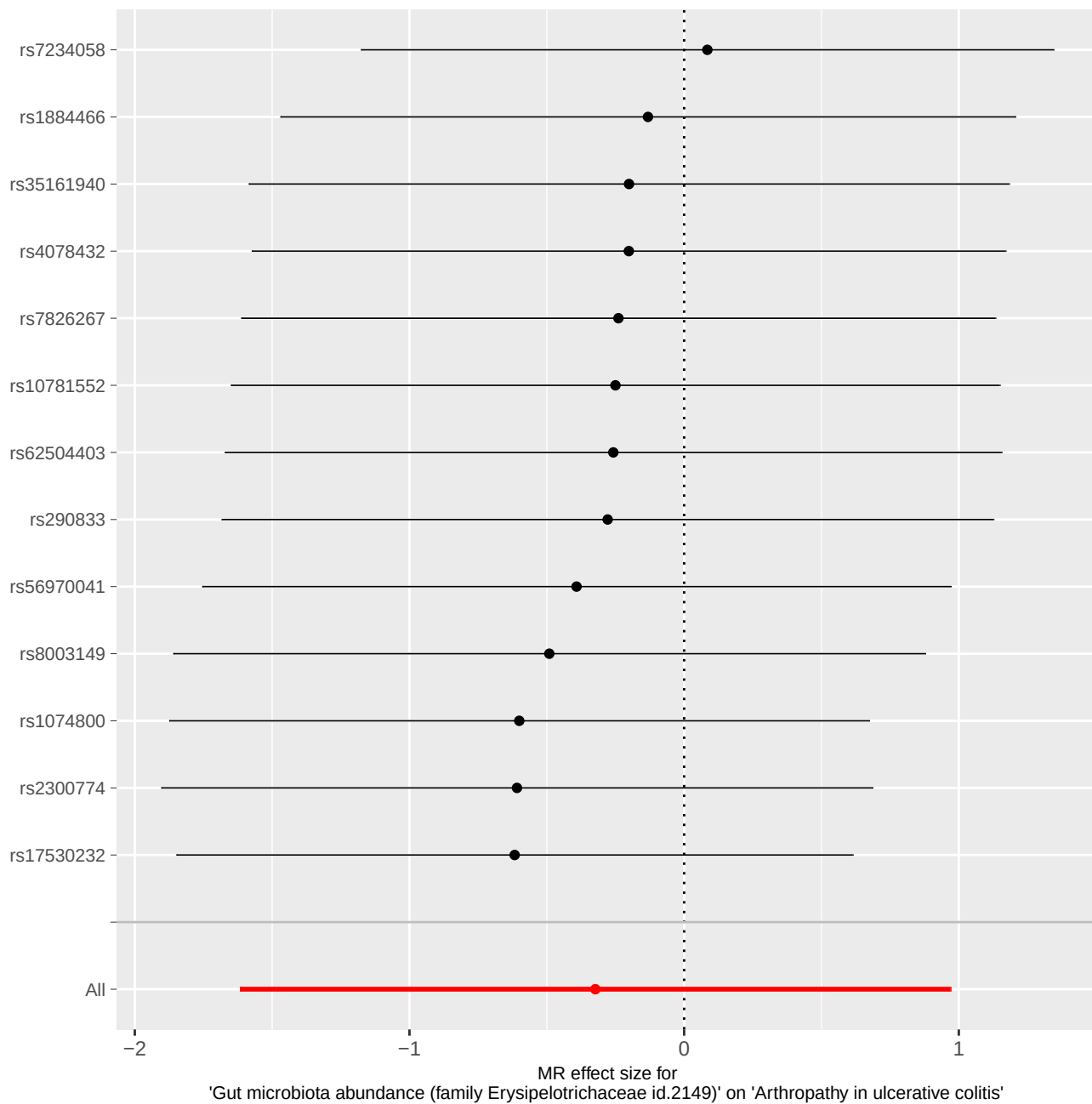


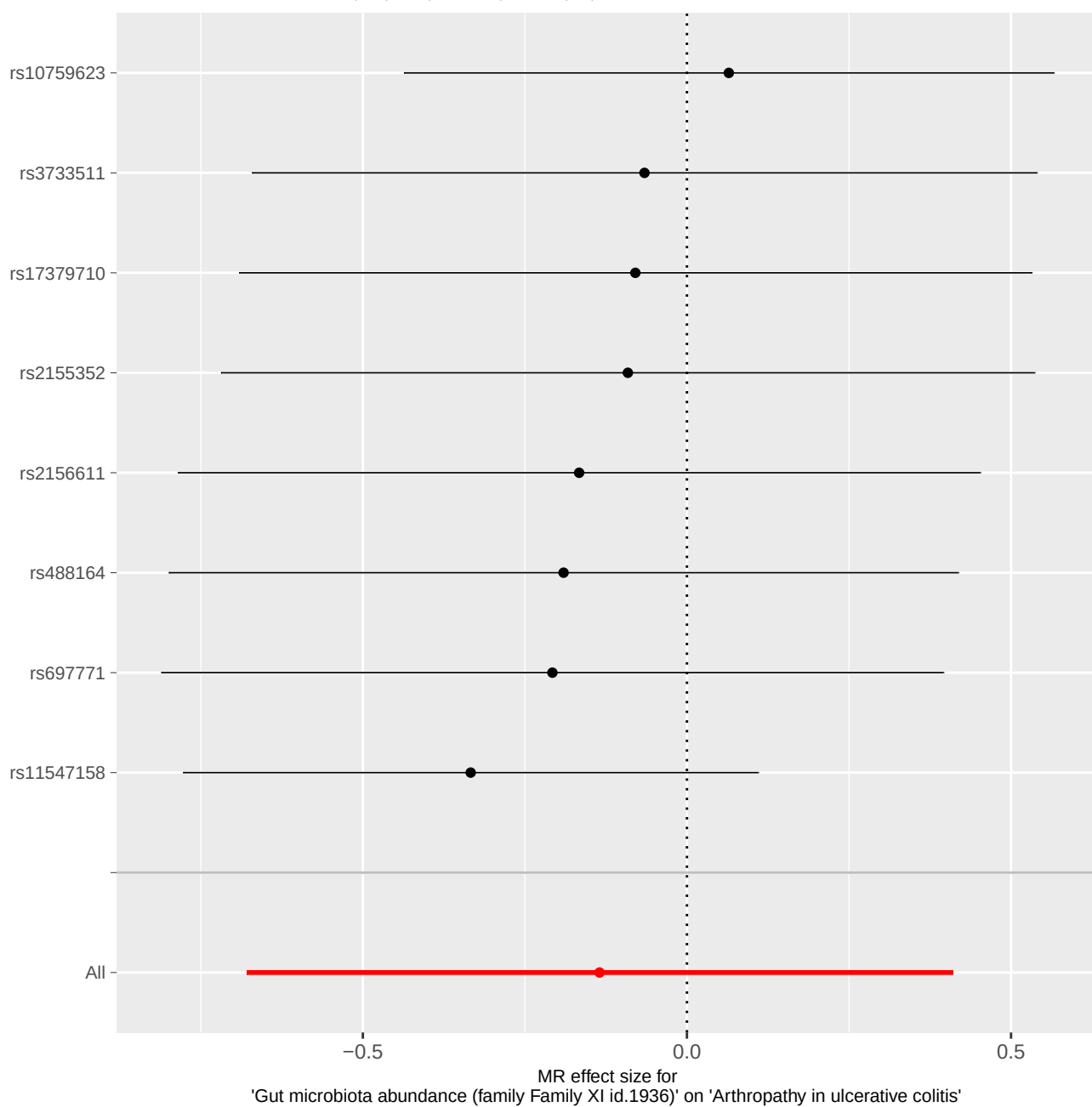


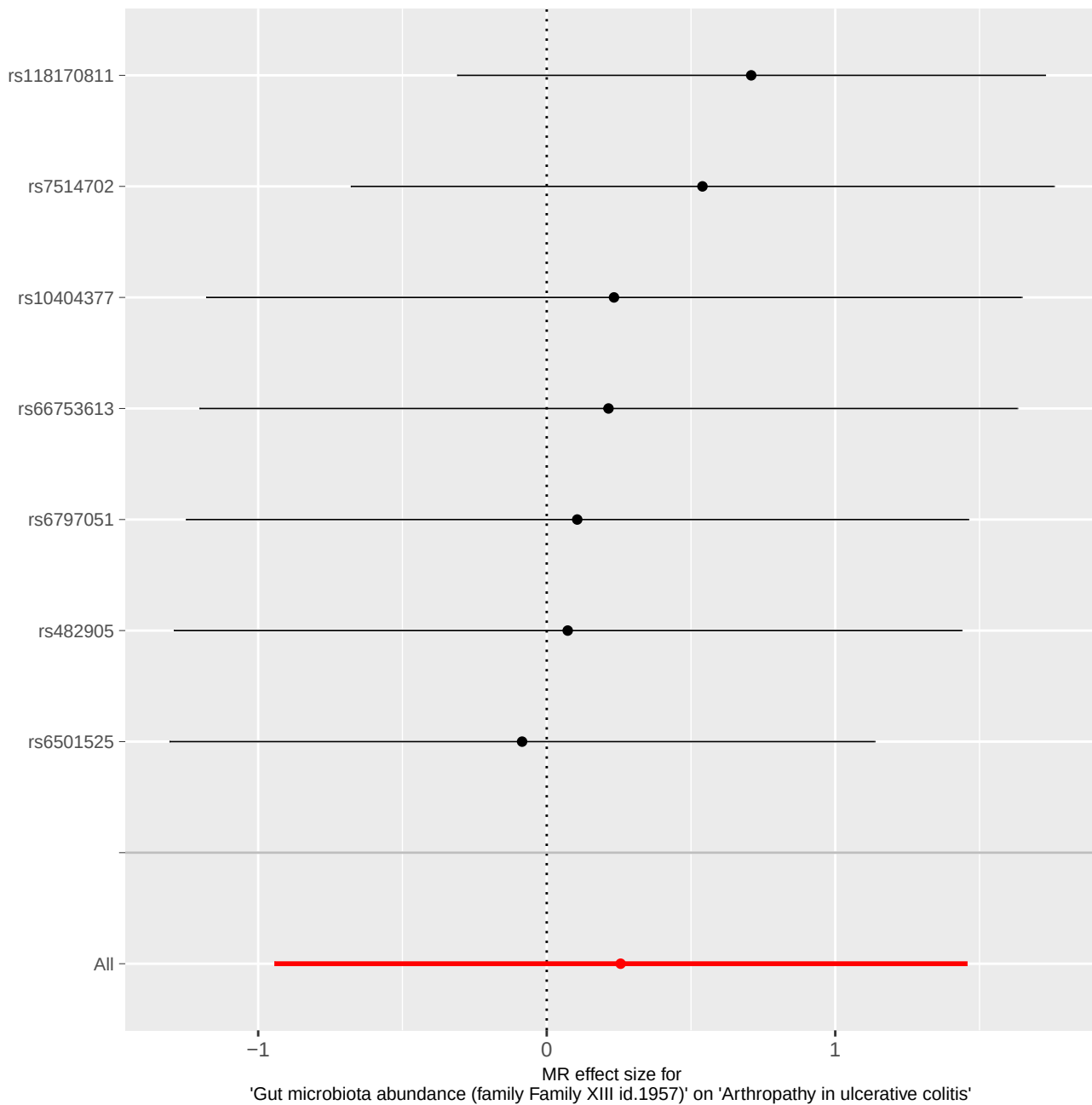


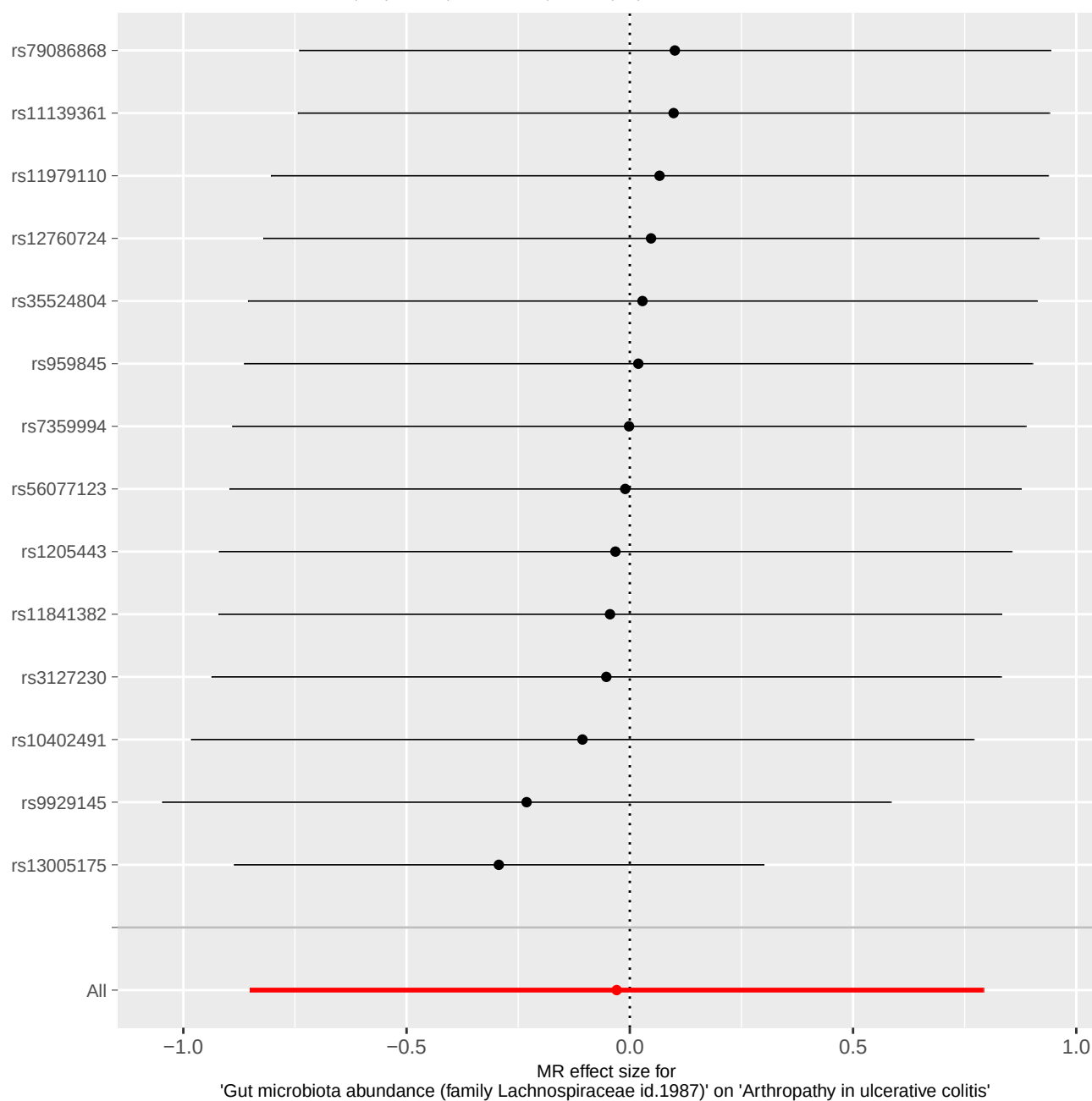
Batch 763 : Gut microbiota abundance (family Enterobacteriaceae id.3469) on Arthropathy in ulcerative colitis

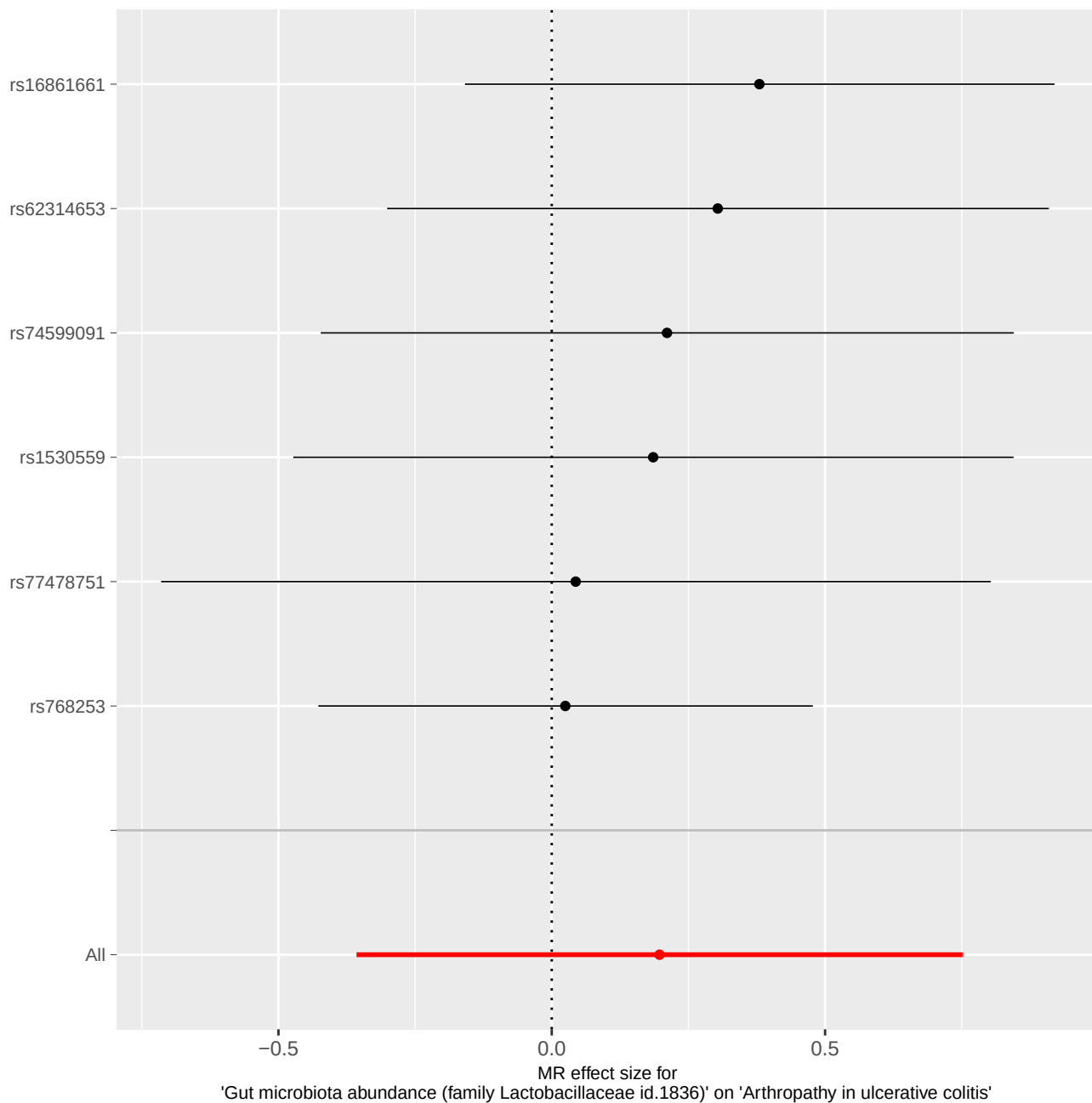


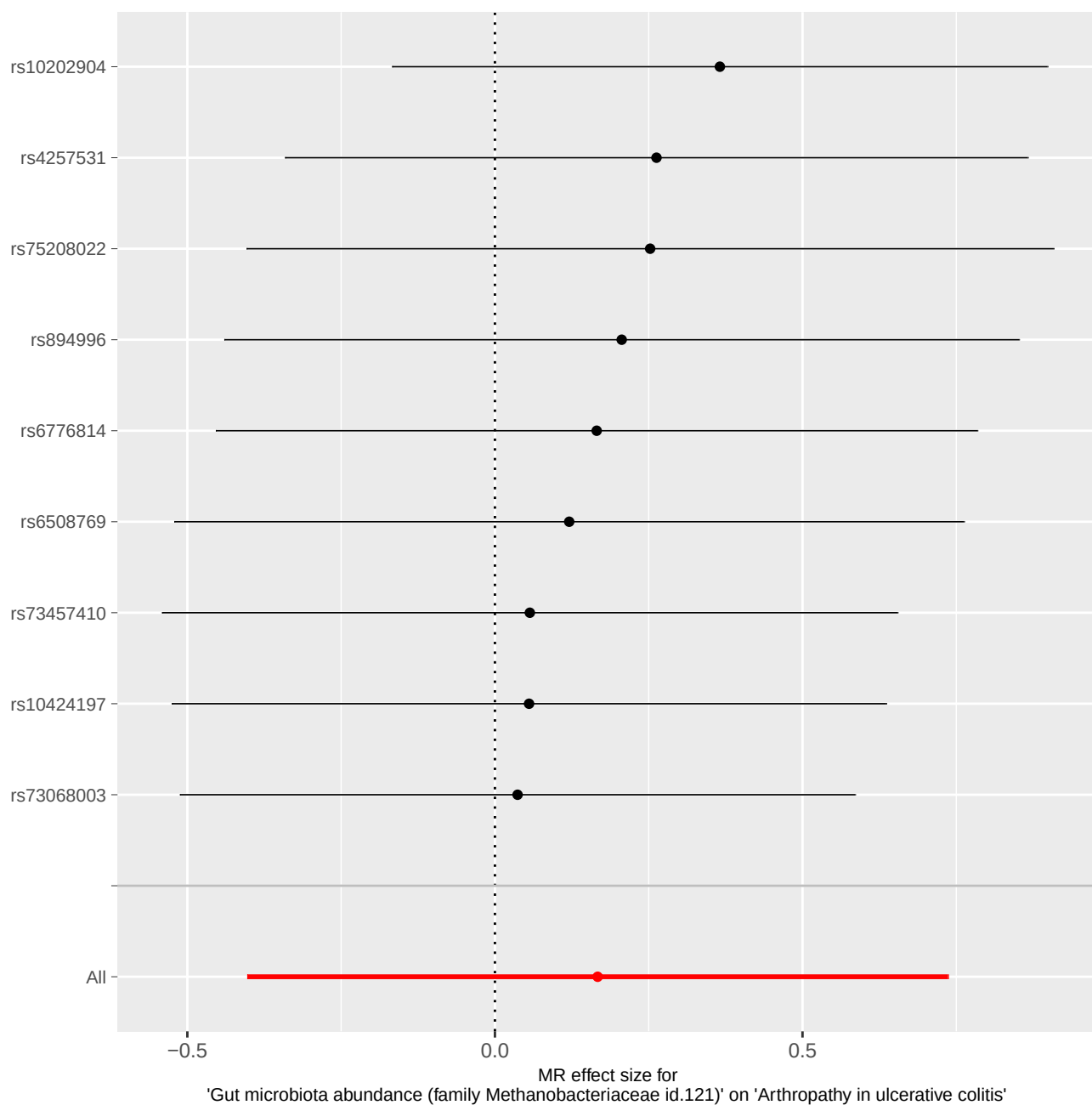


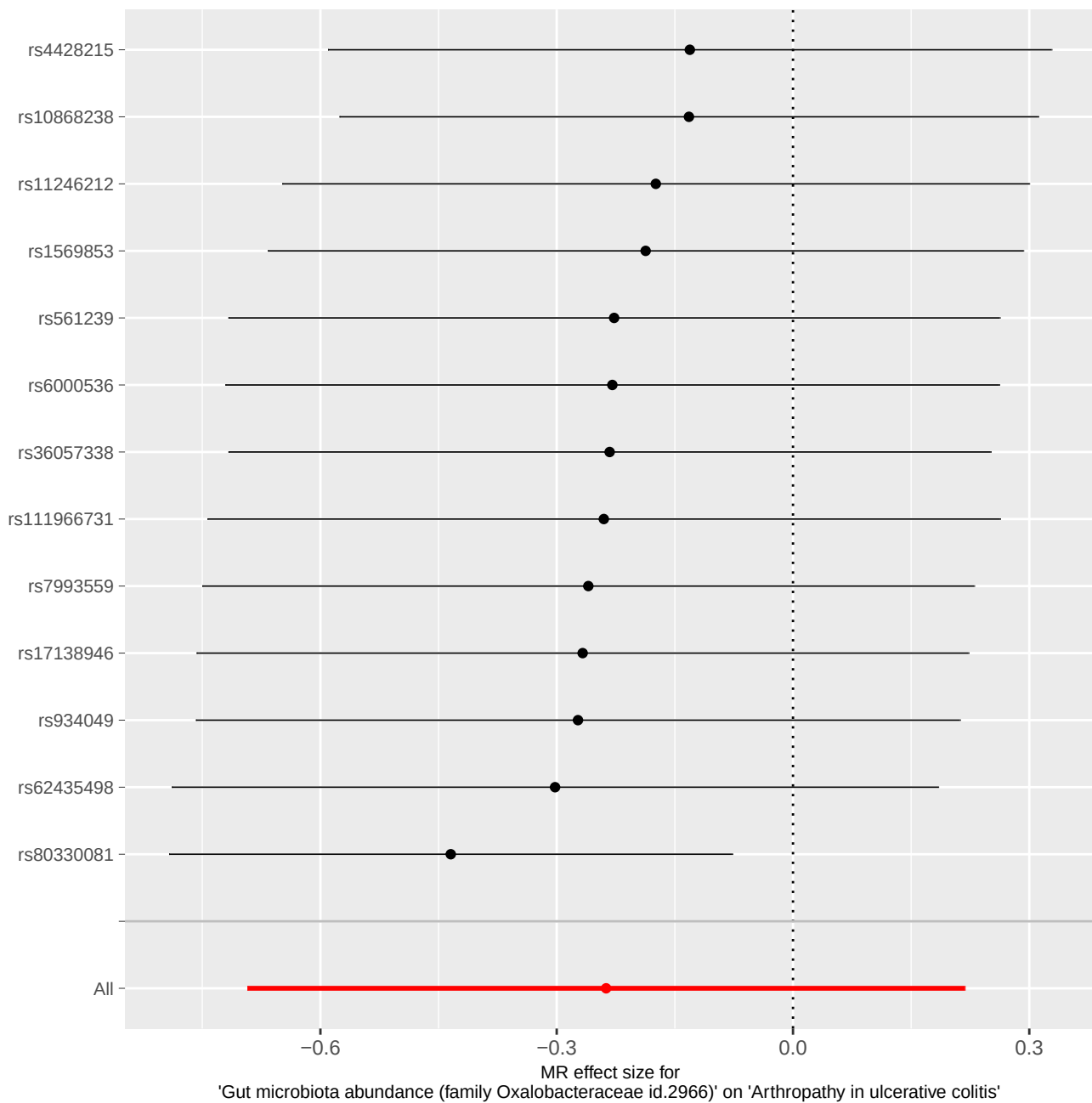




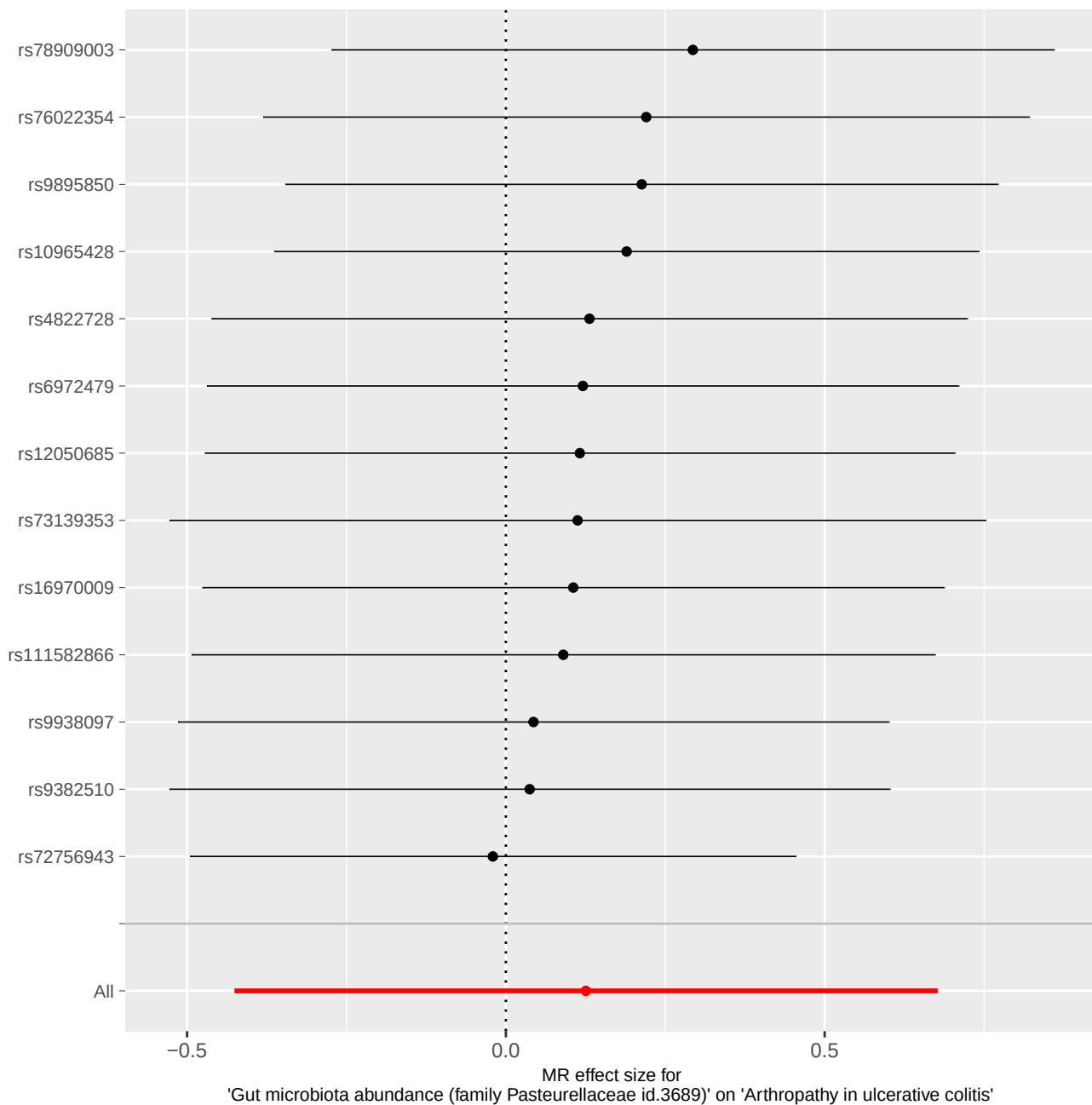


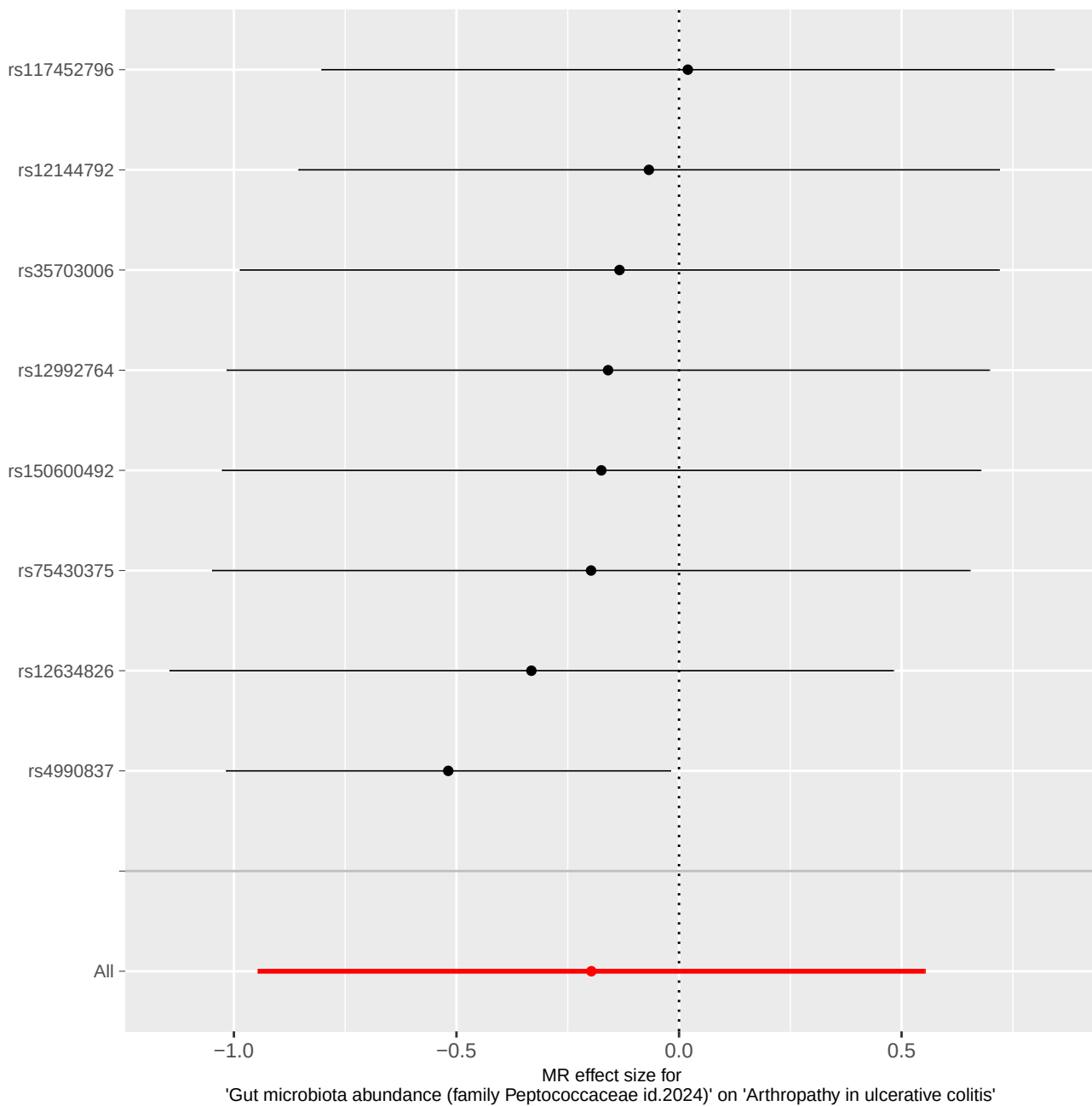


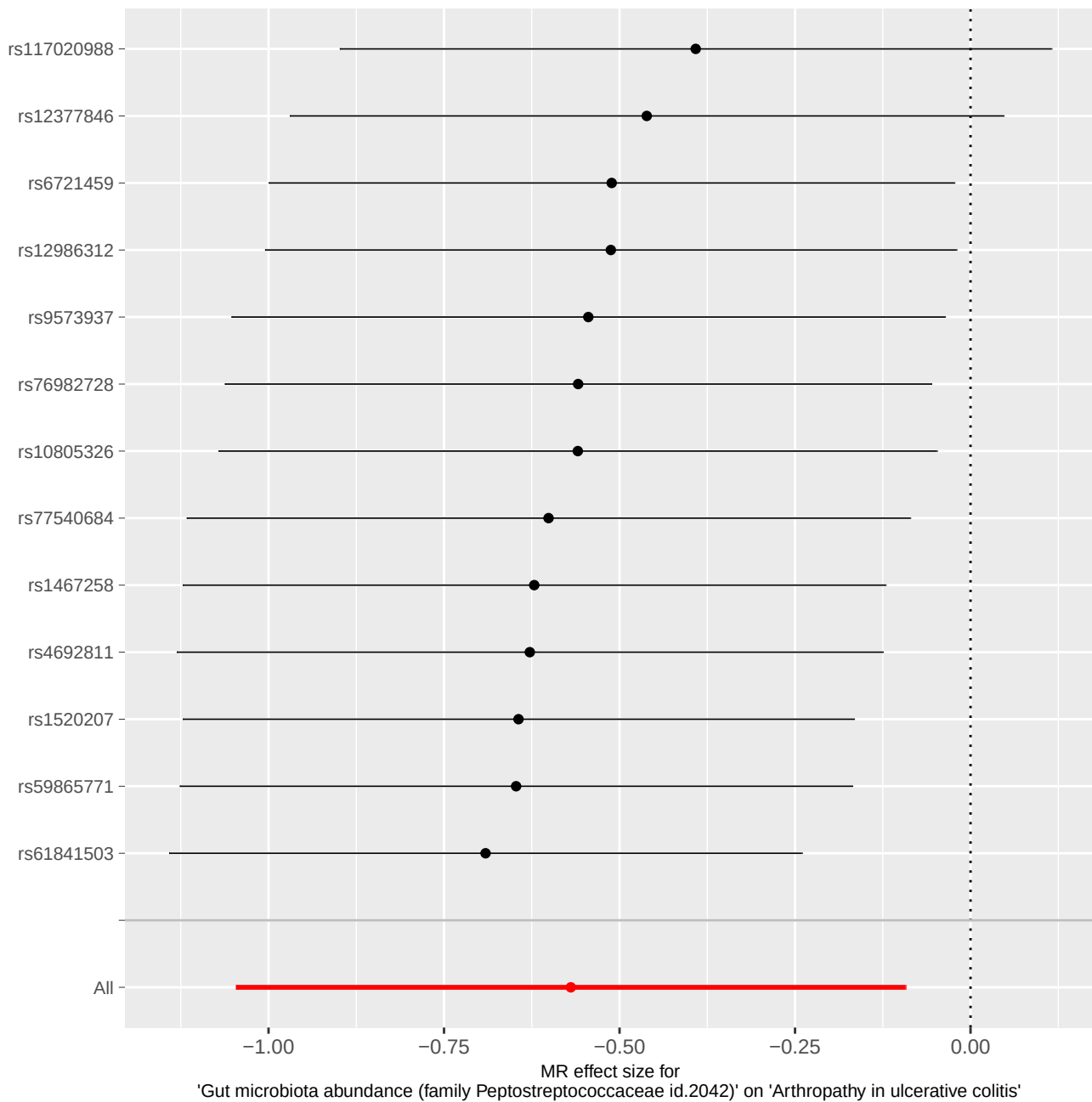


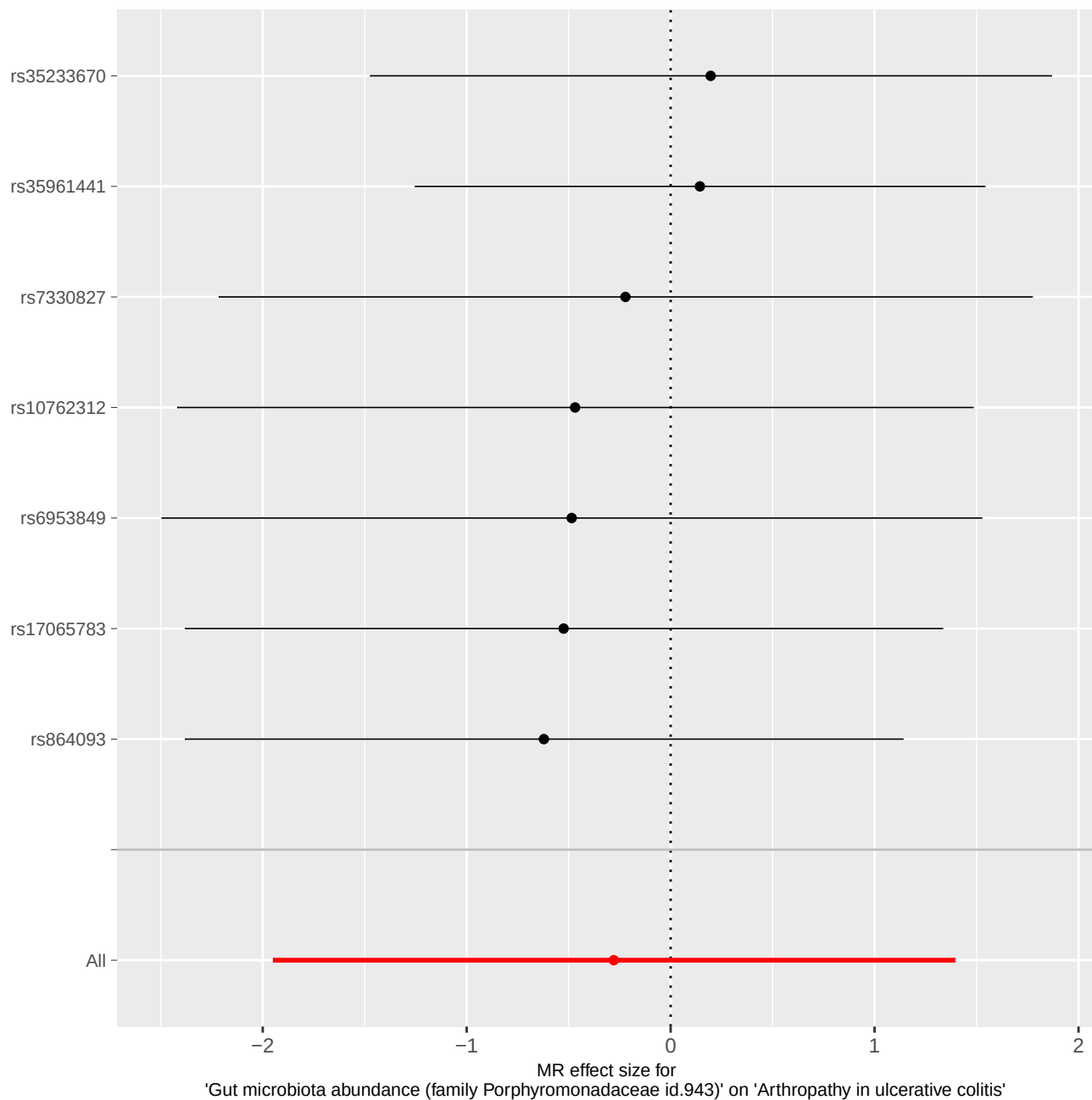


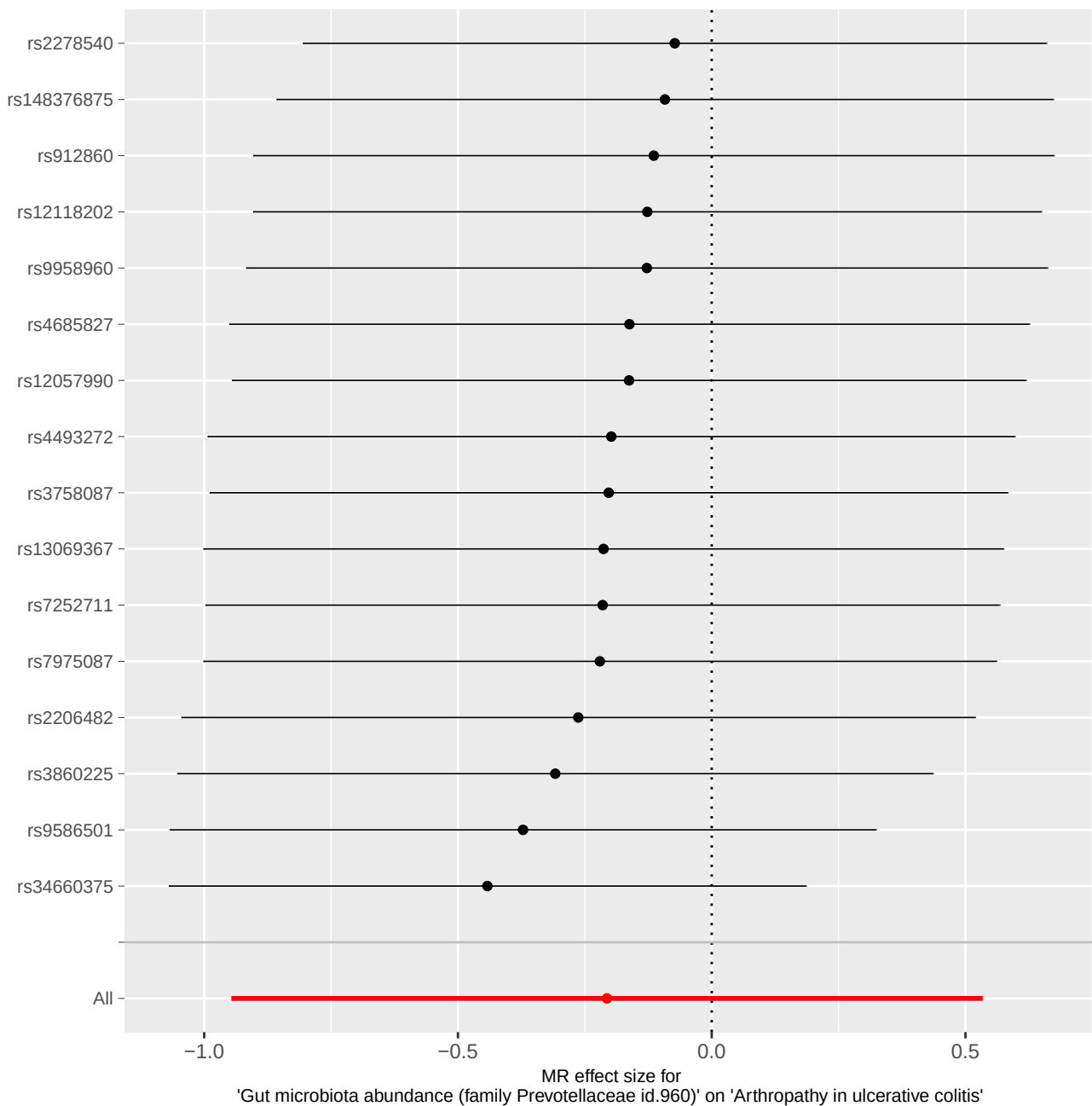
Batch 771 : Gut microbiota abundance (family Pasteurellaceae id.3689) on Arthropathy in ulcerative colitis

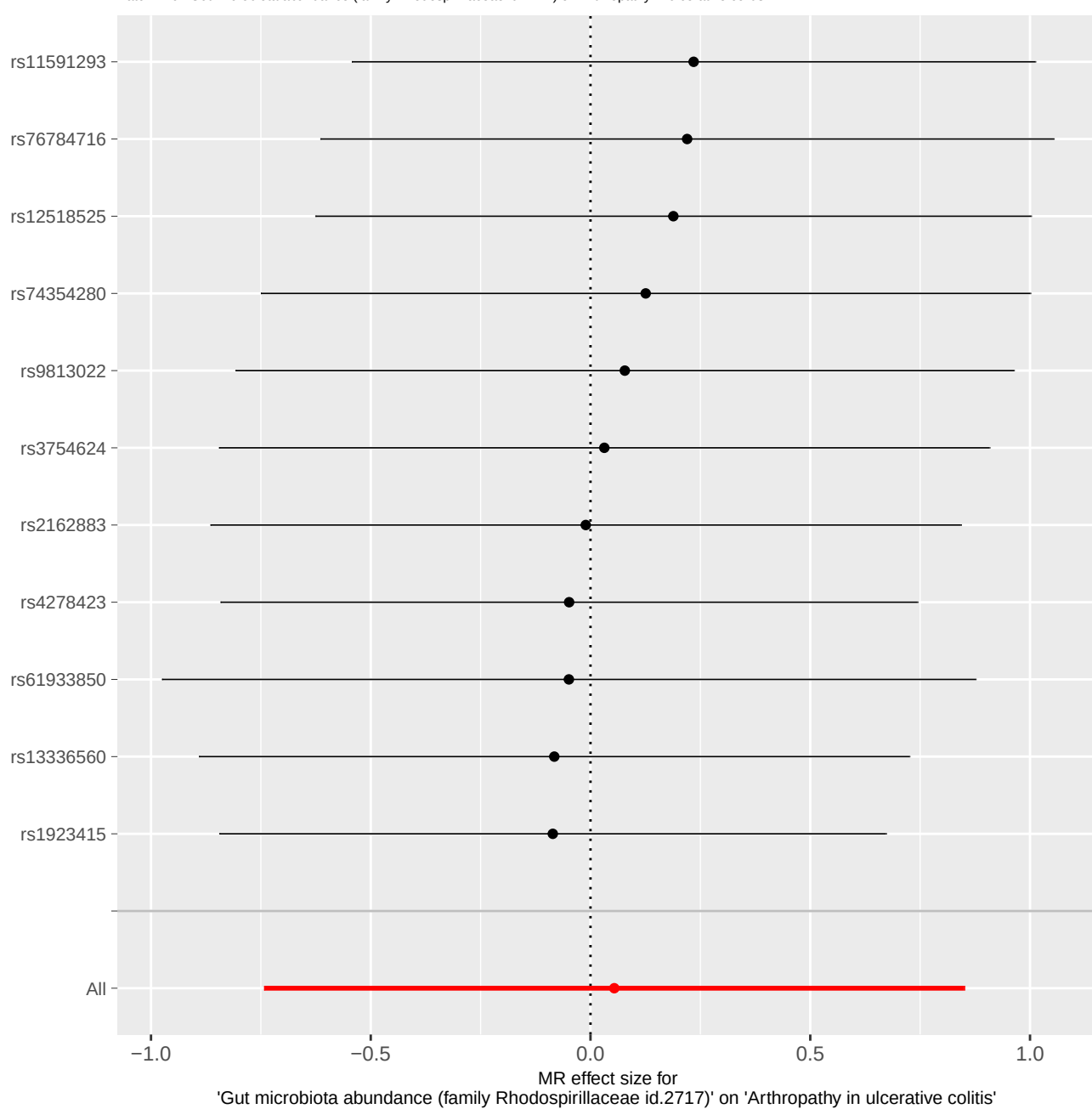




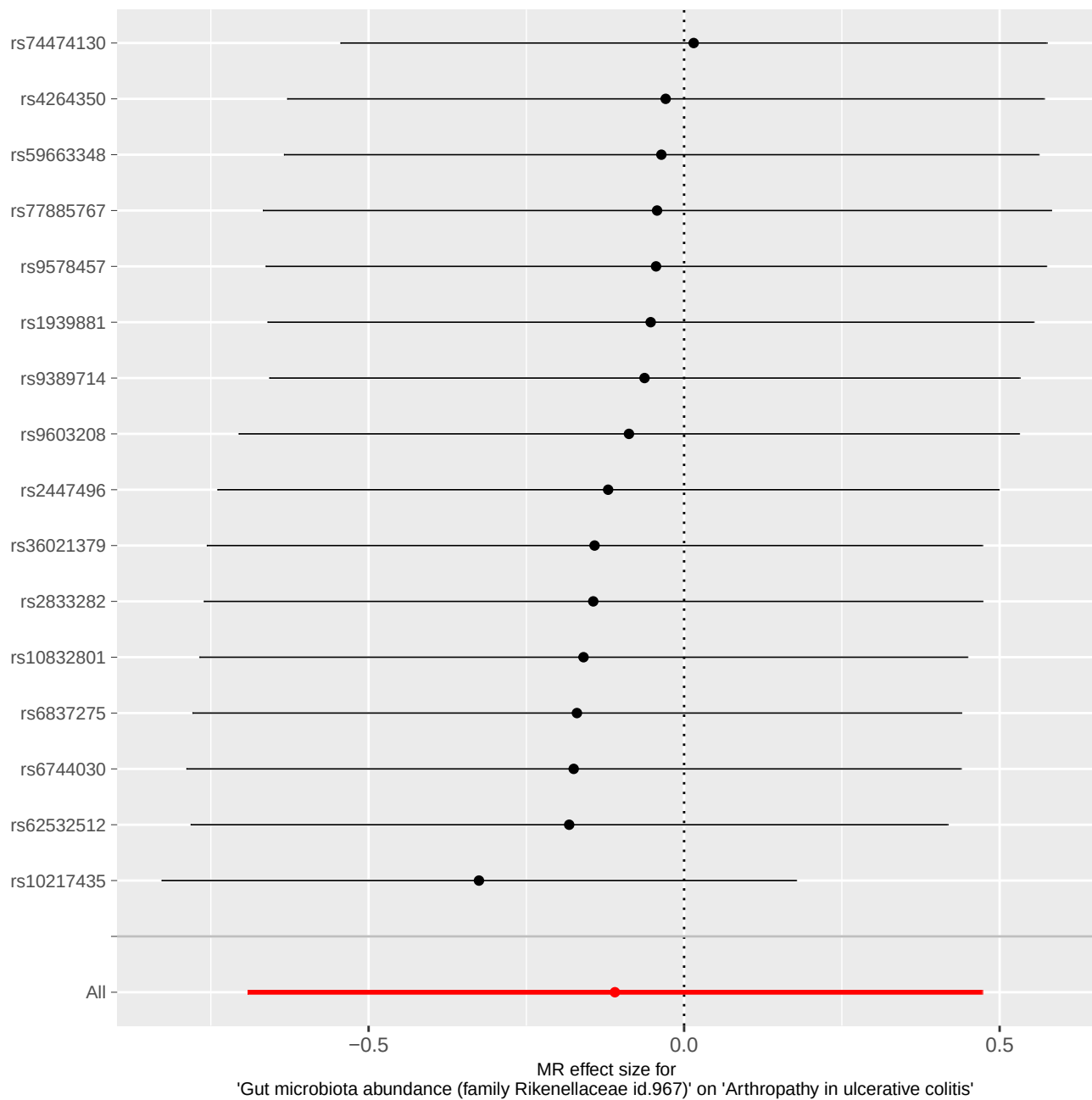


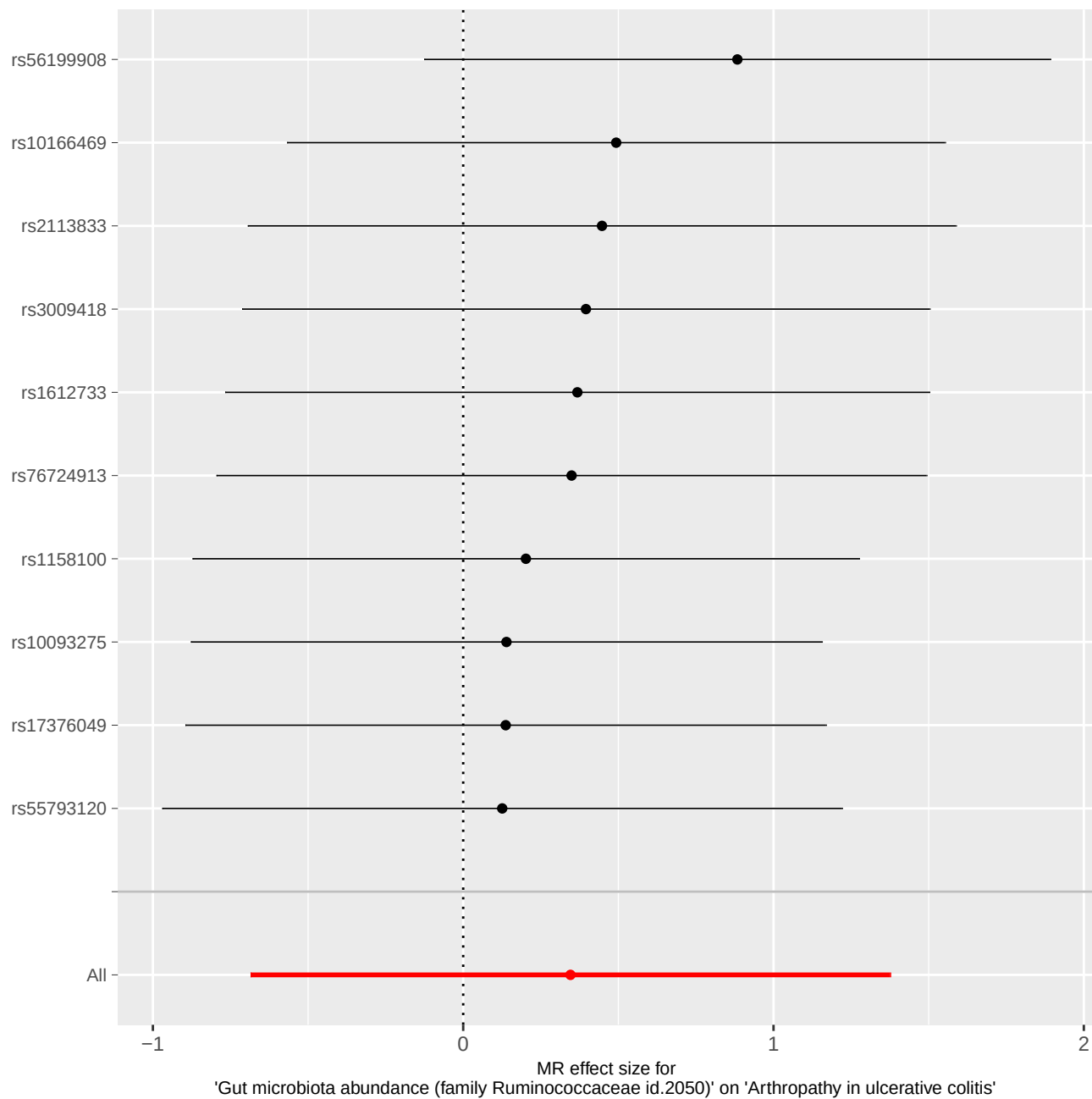


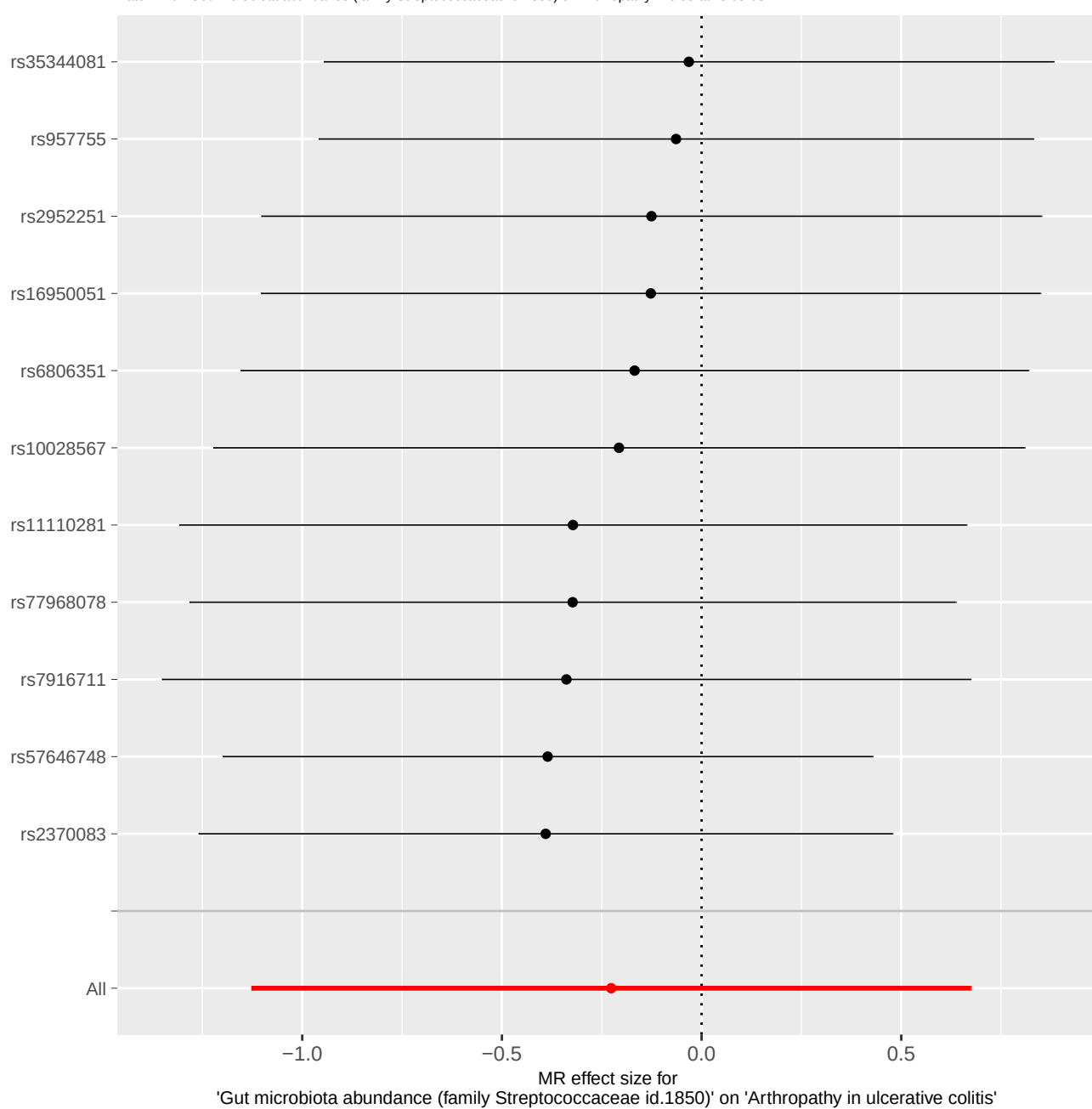


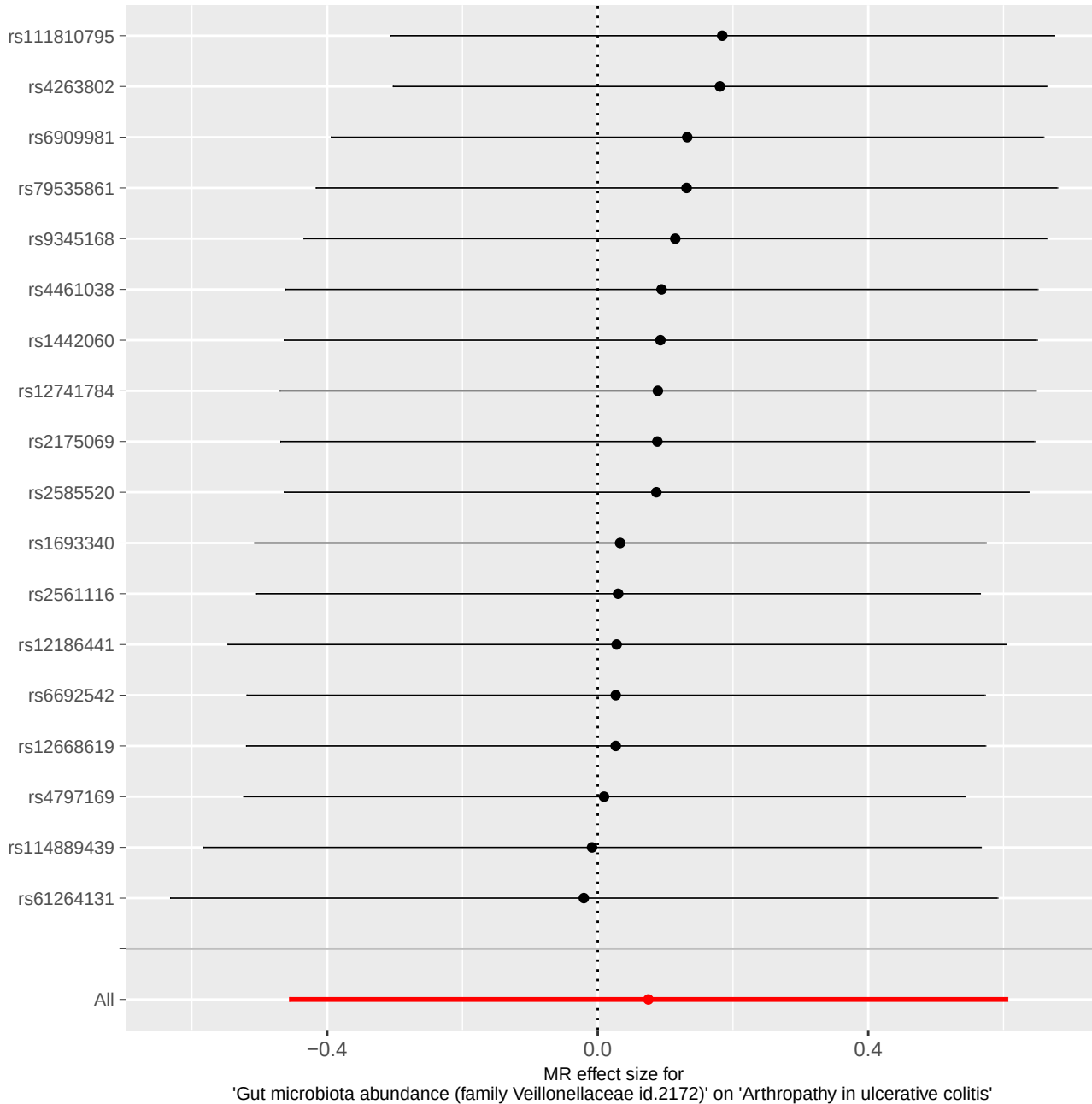


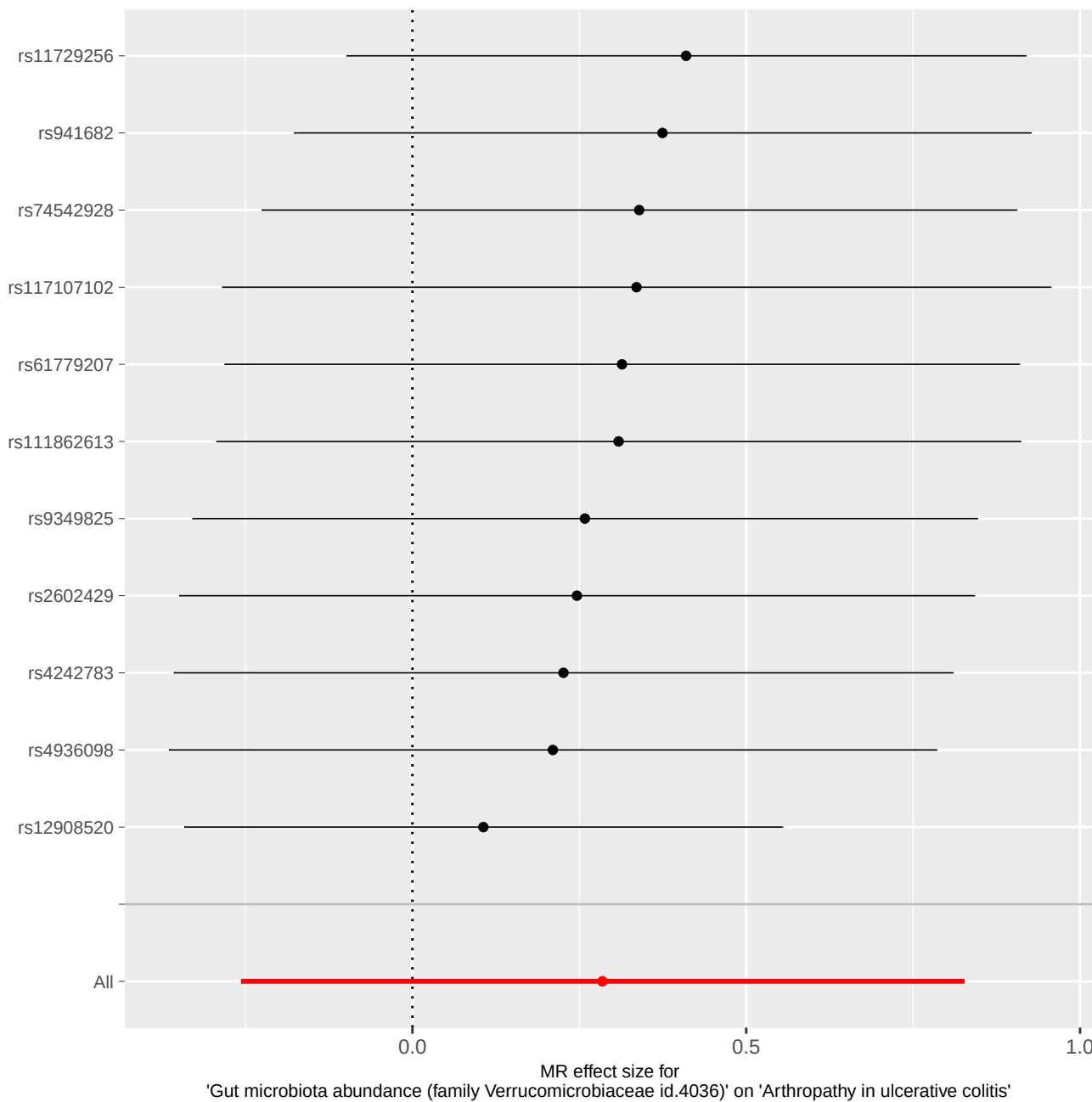
Batch 777 : Gut microbiota abundance (family Rikenellaceae id.967) on Arthropathy in ulcerative colitis

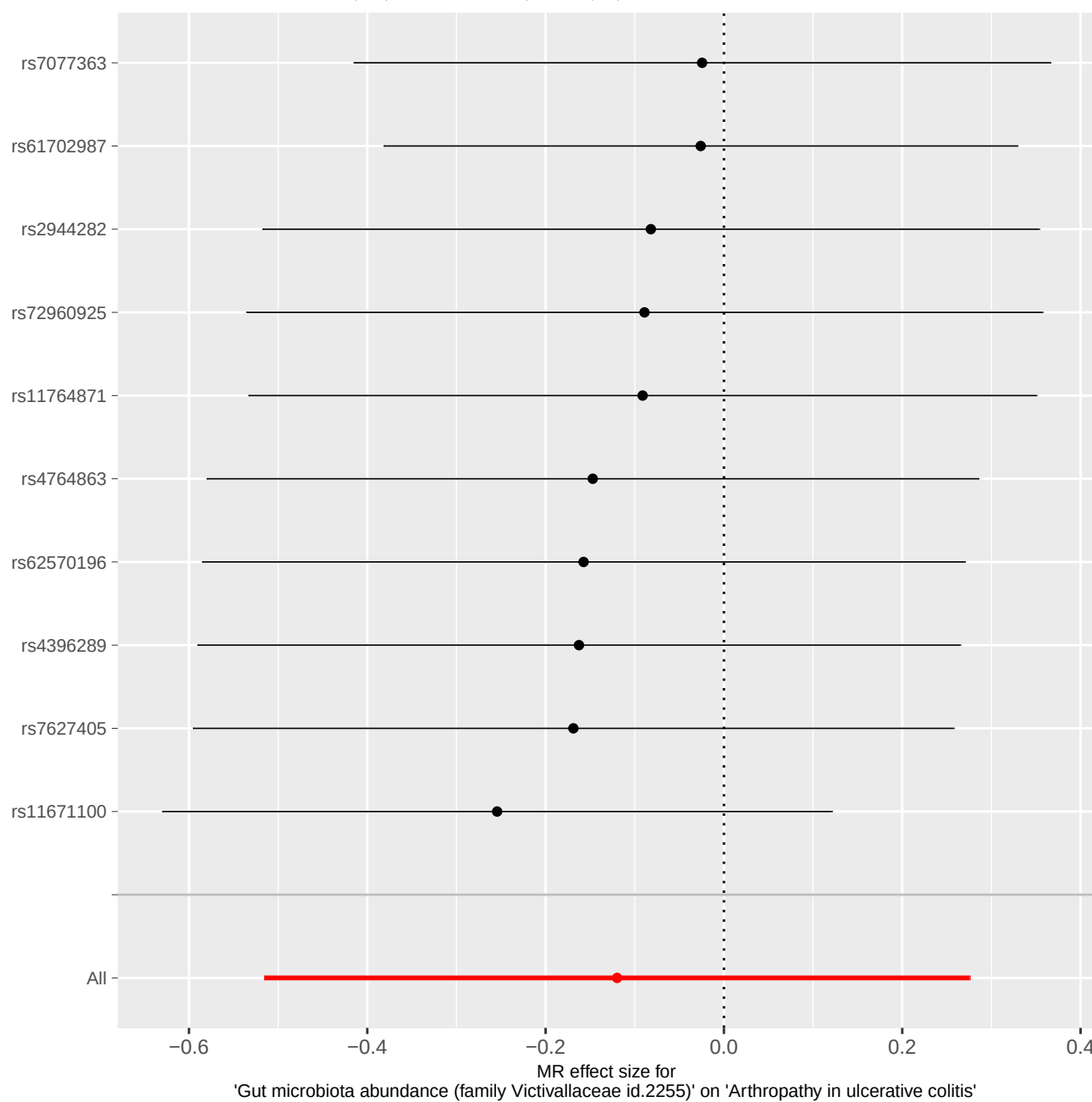


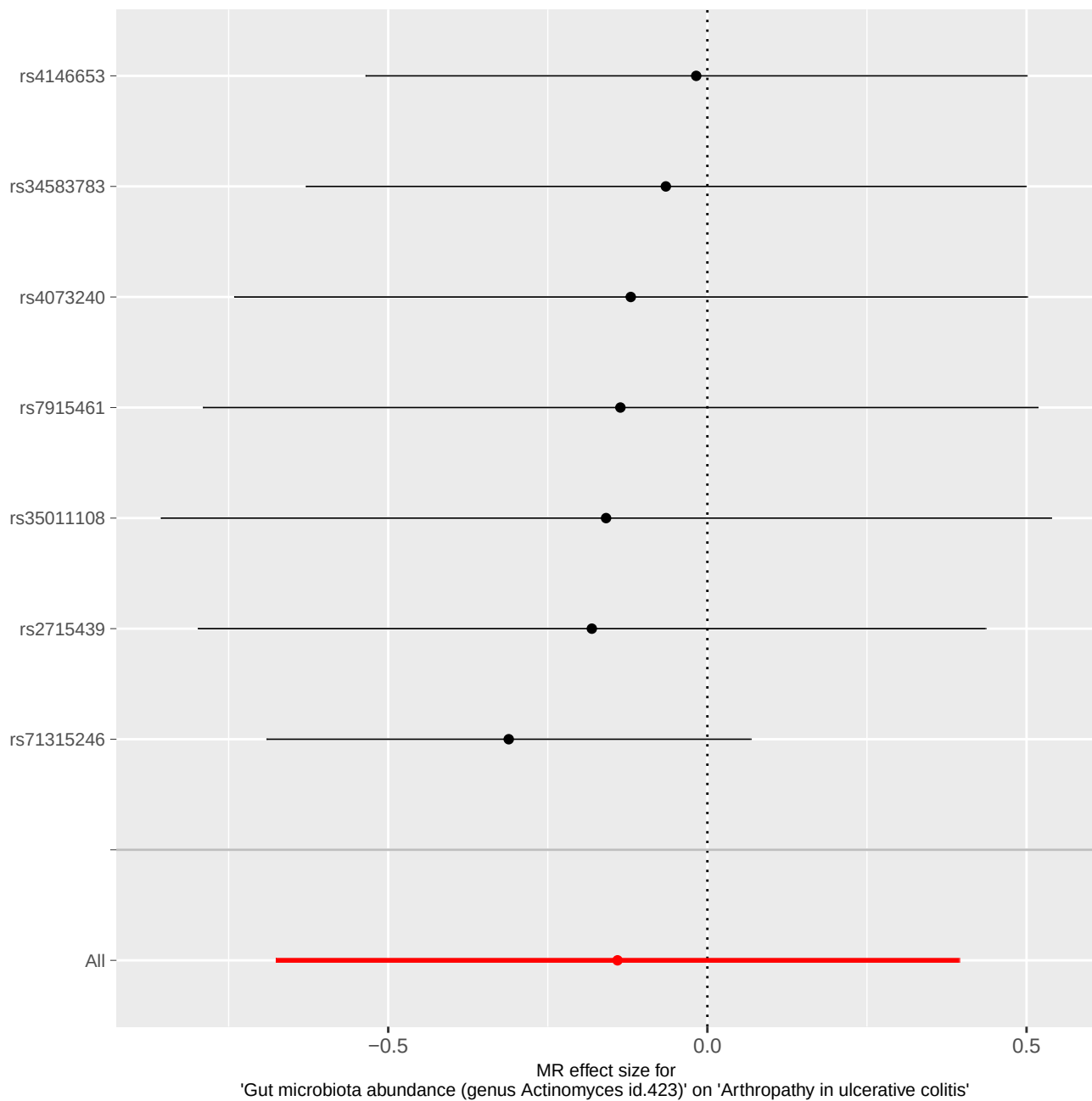




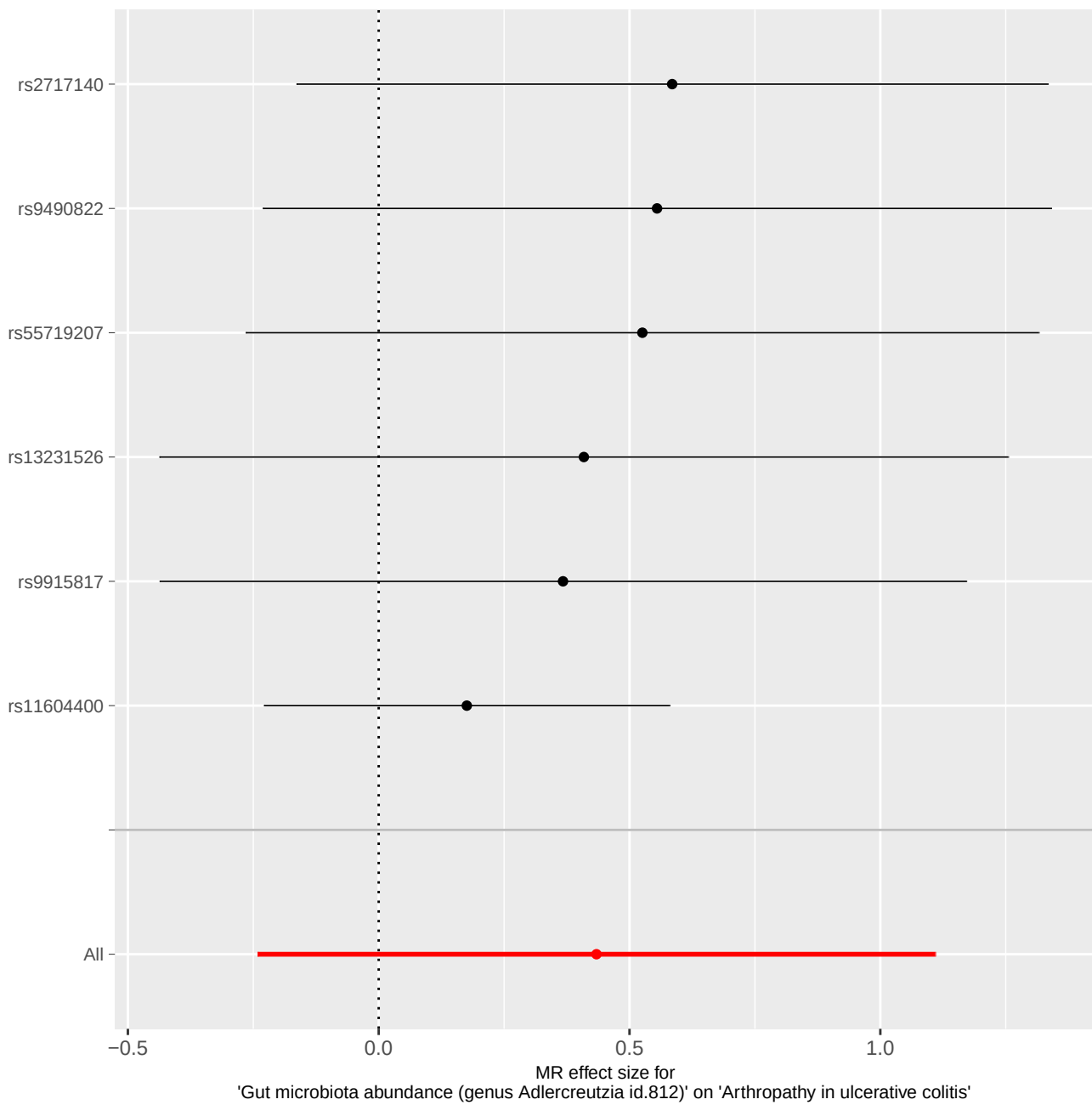


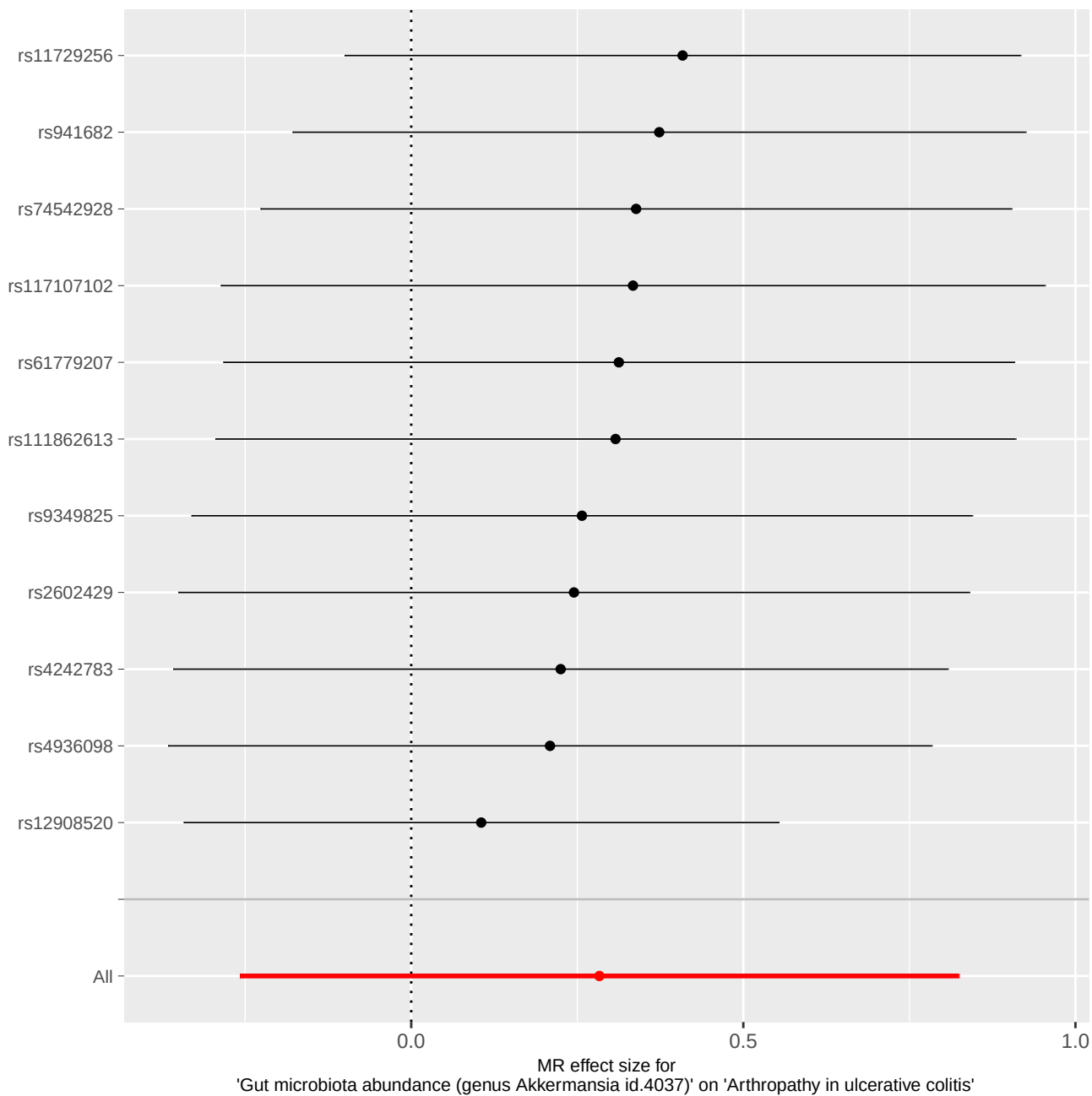




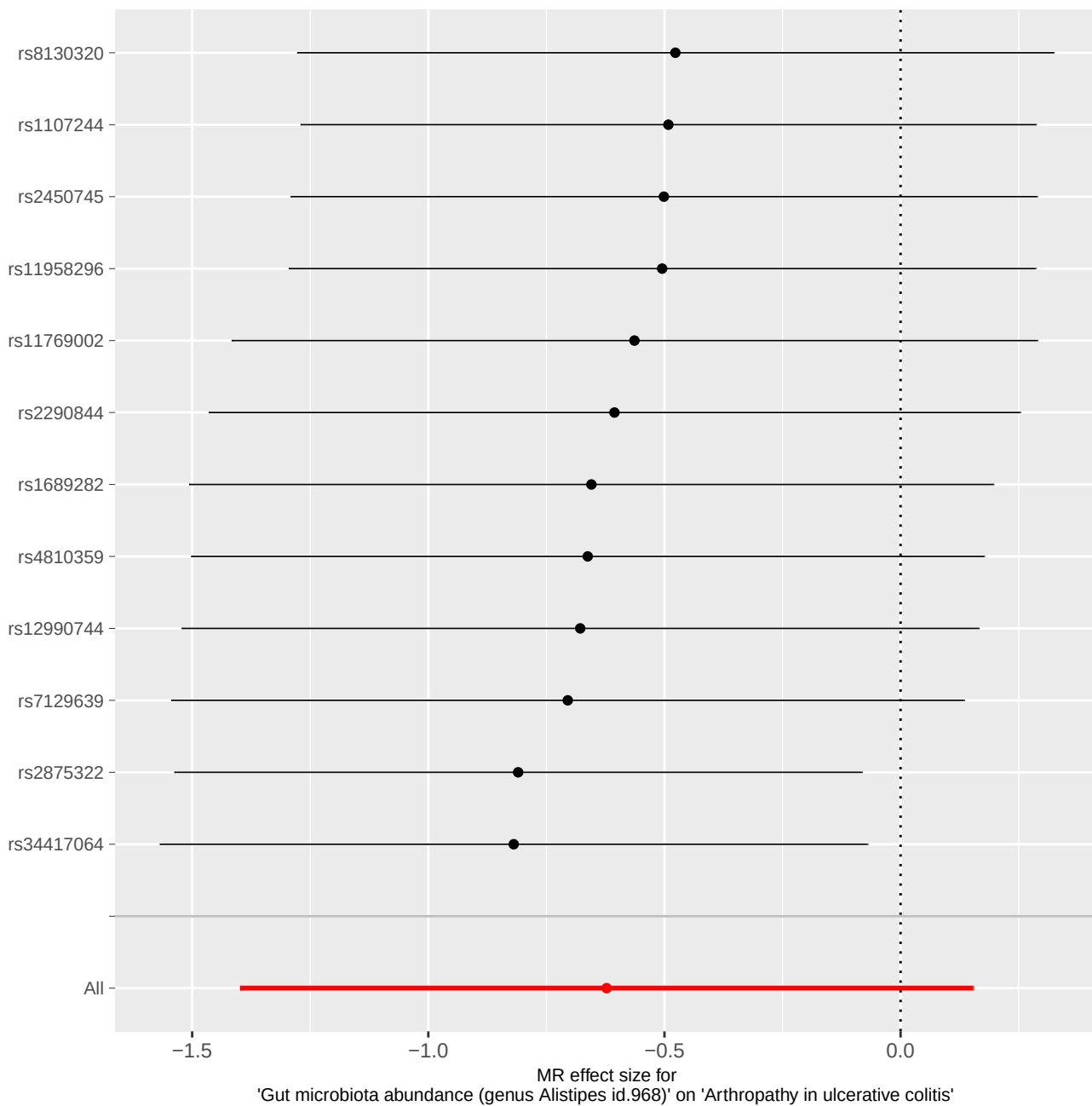


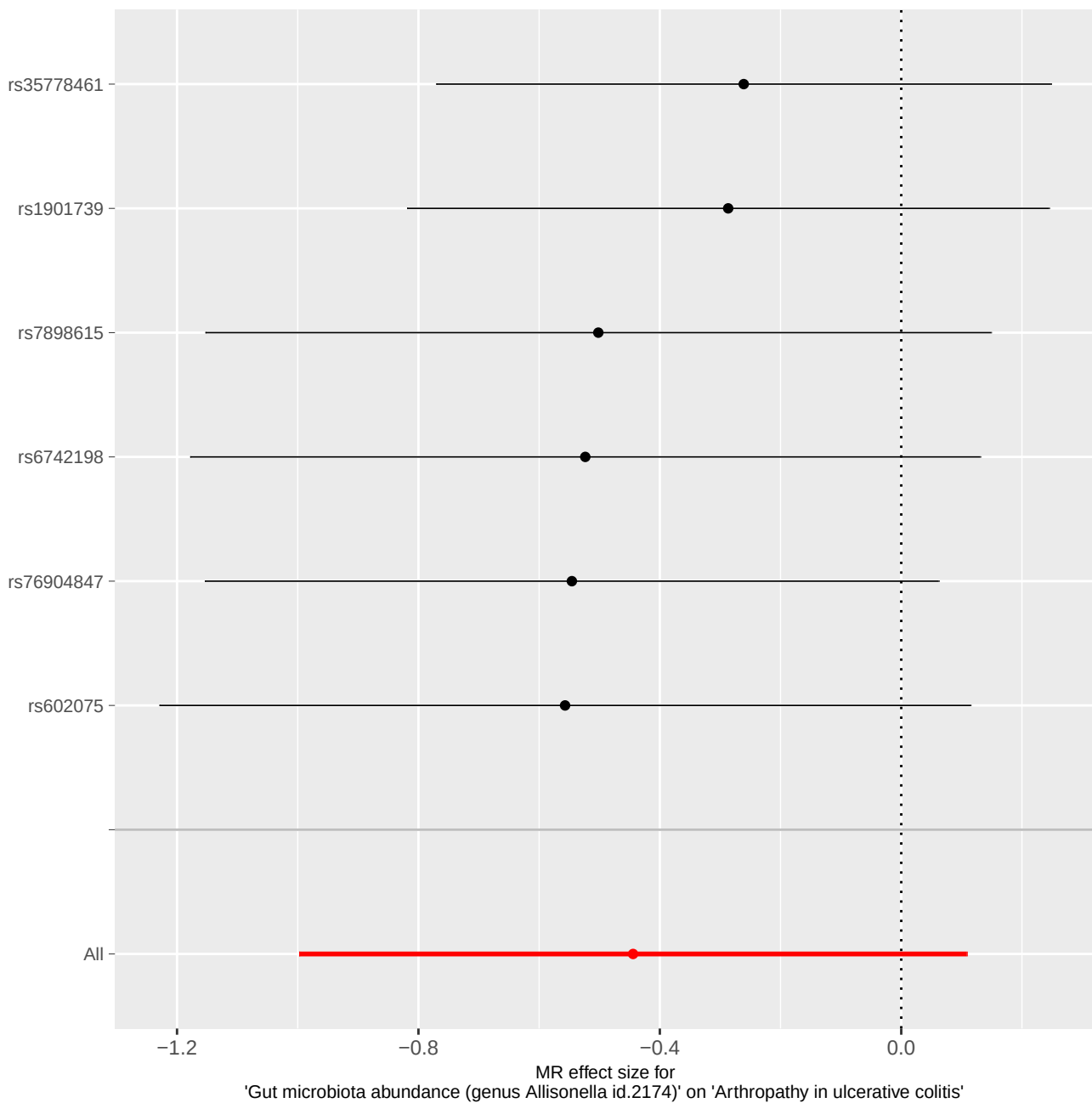
MR effect size for
'Gut microbiota abundance (genus Actinomyces id.423)' on 'Arthropathy in ulcerative colitis'

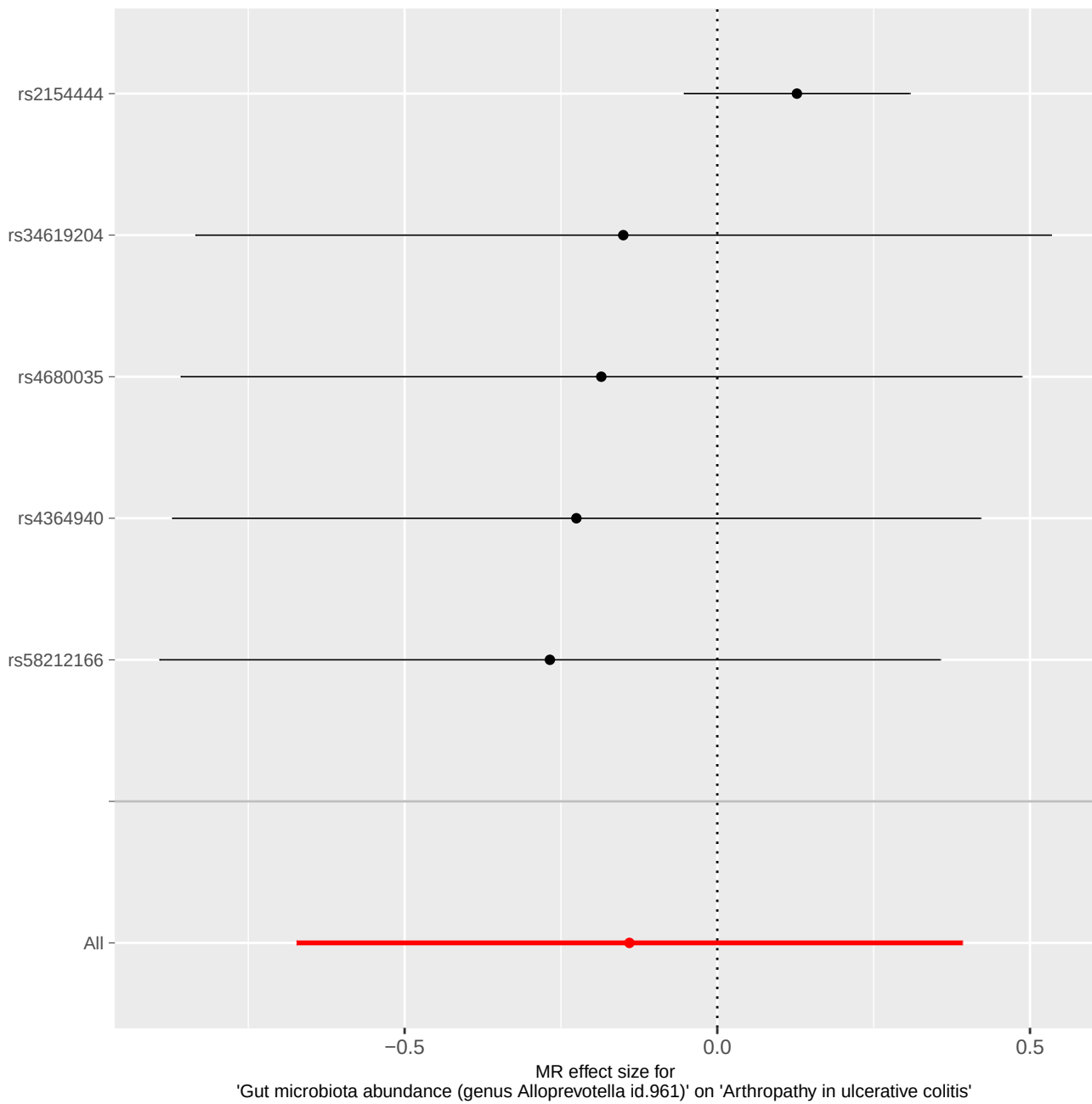


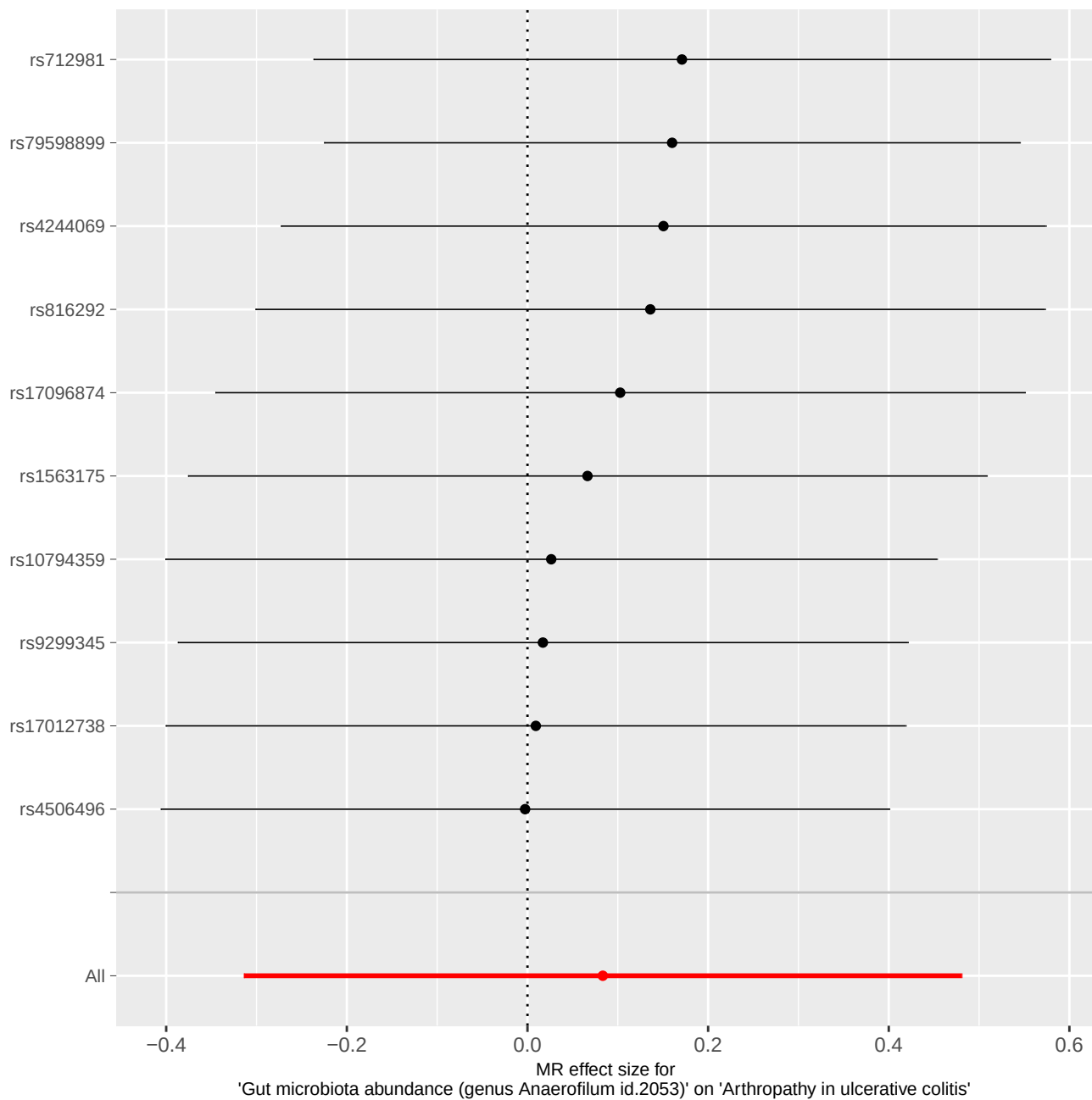


MR effect size for
'Gut microbiota abundance (genus Akkermansia id.4037)' on 'Arthropathy in ulcerative colitis'

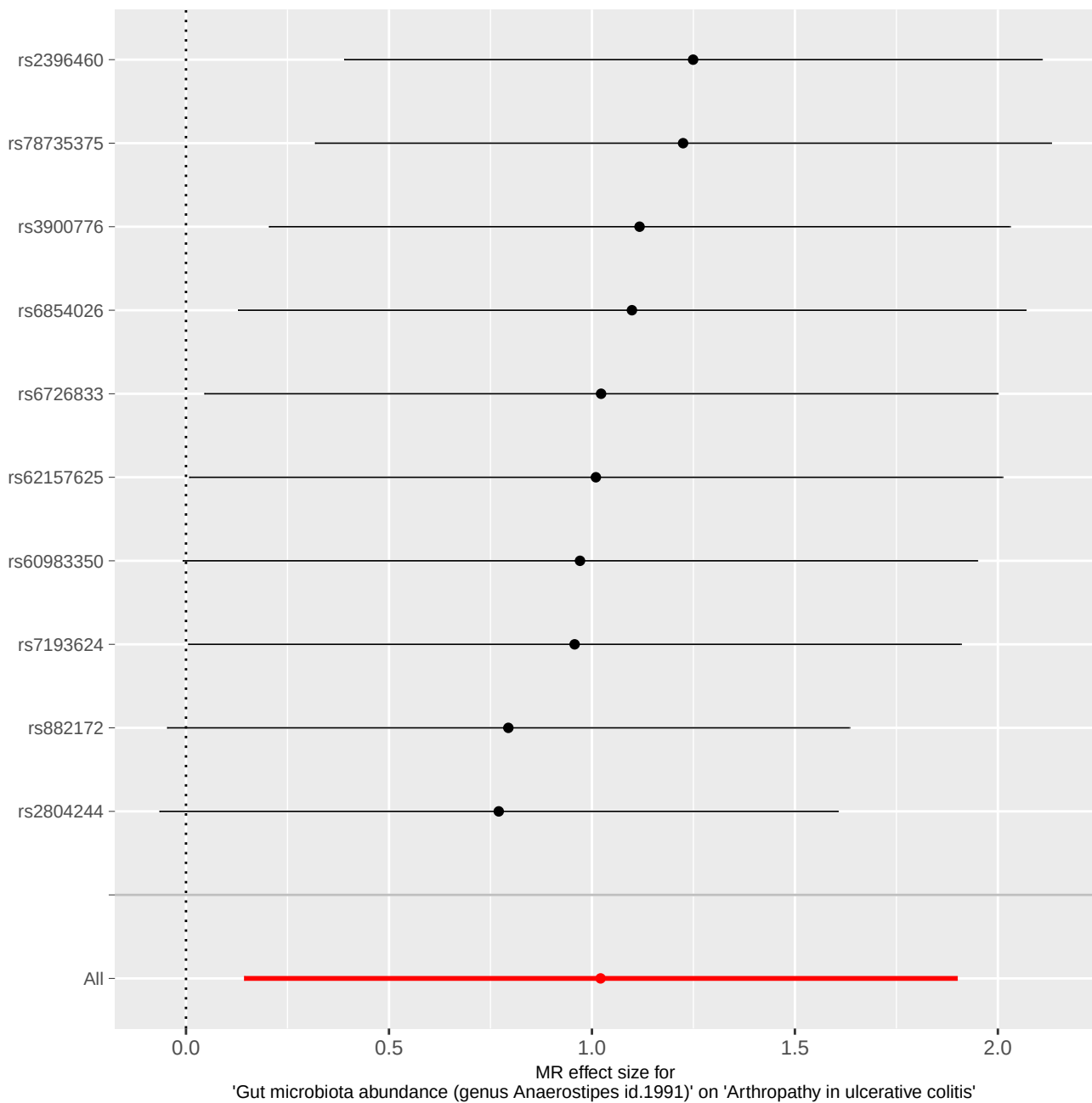


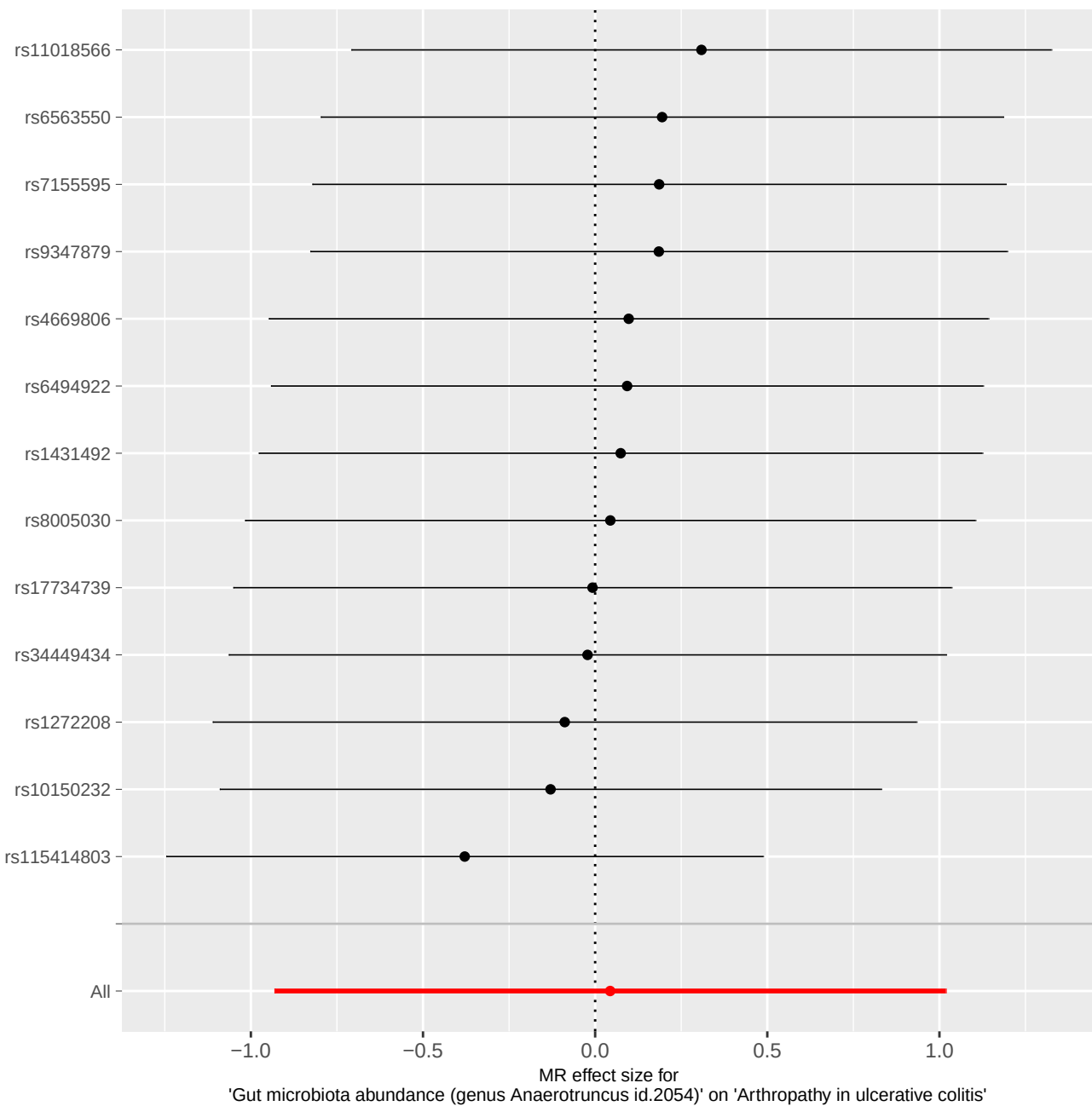


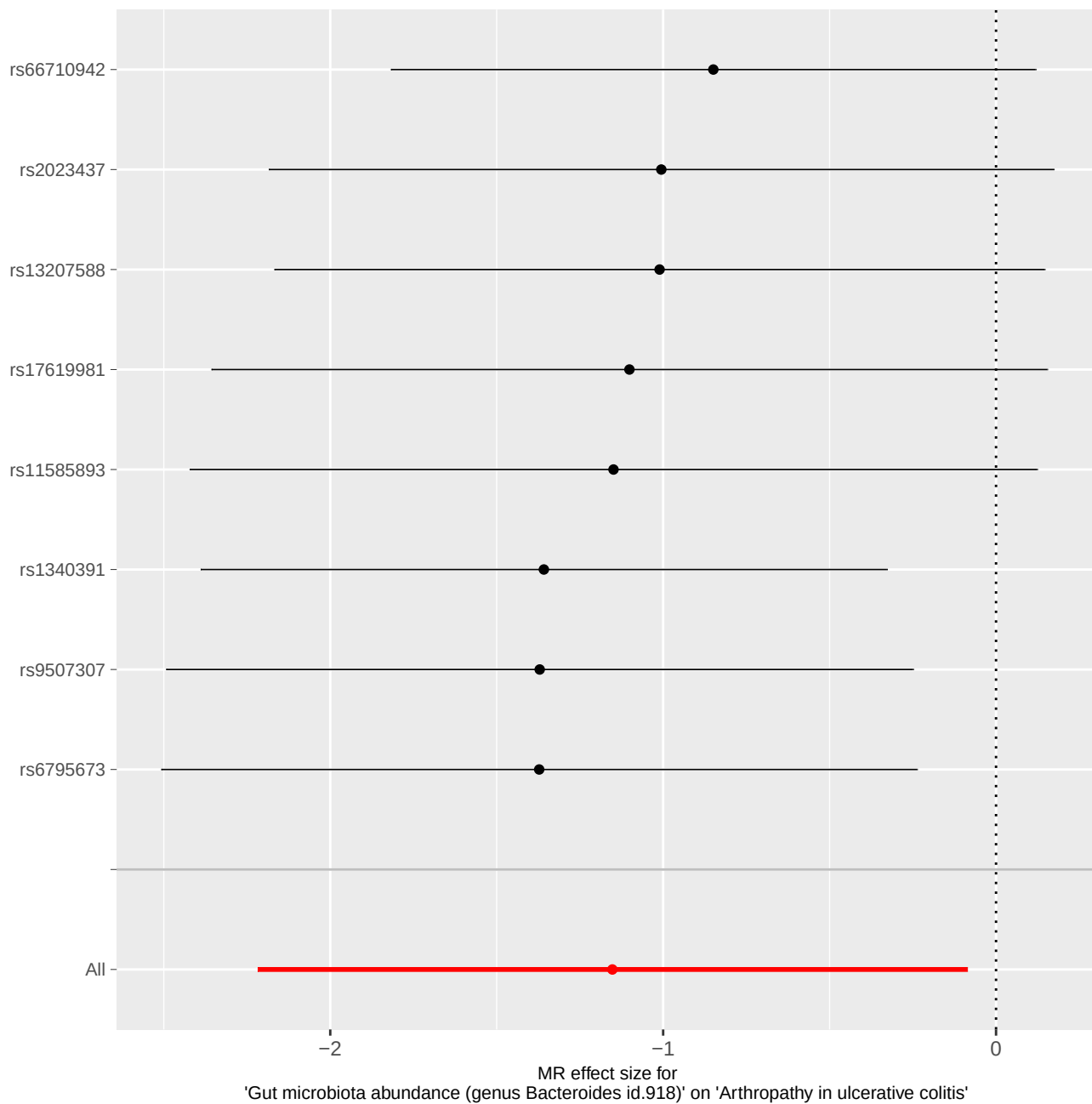


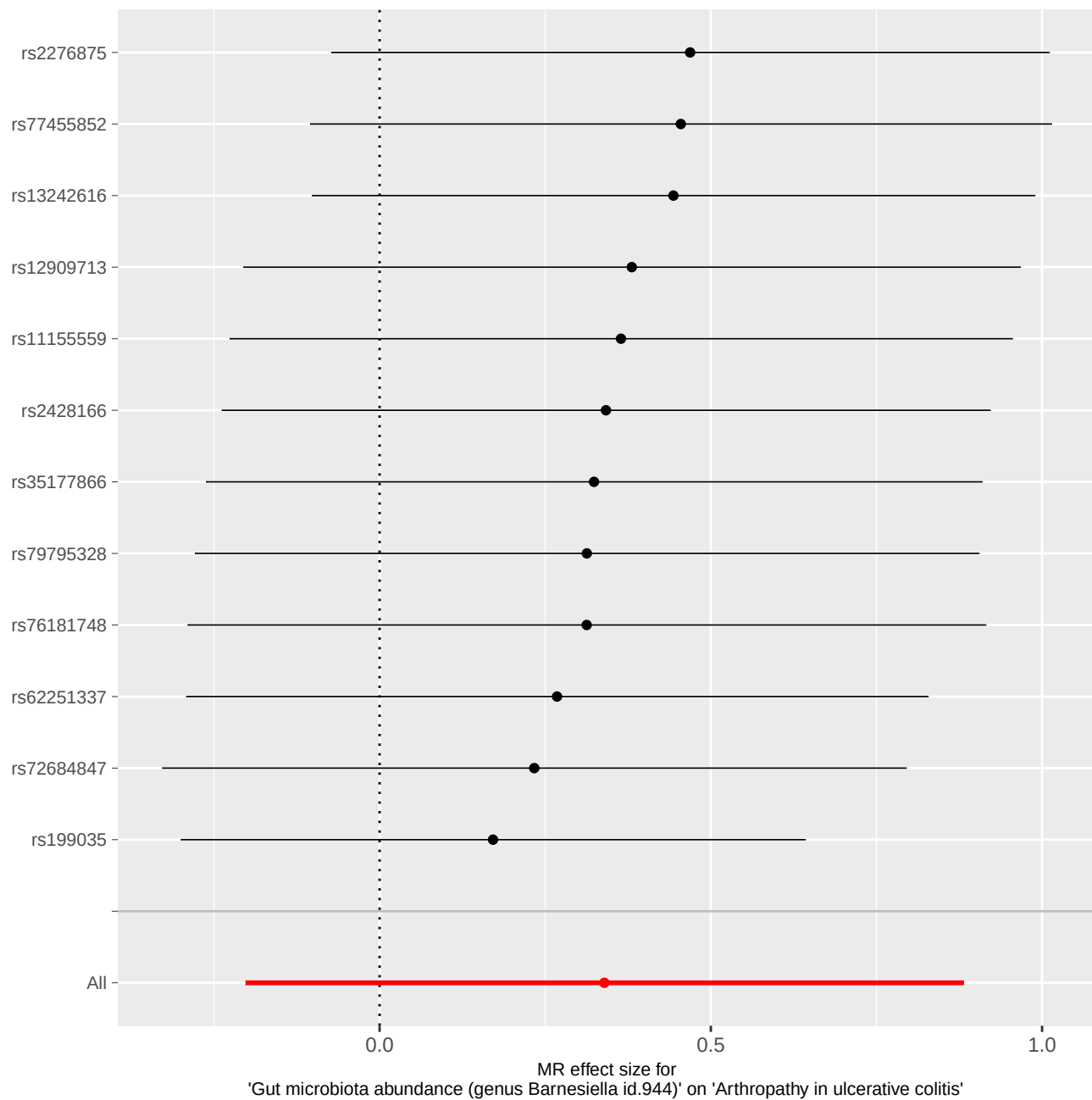


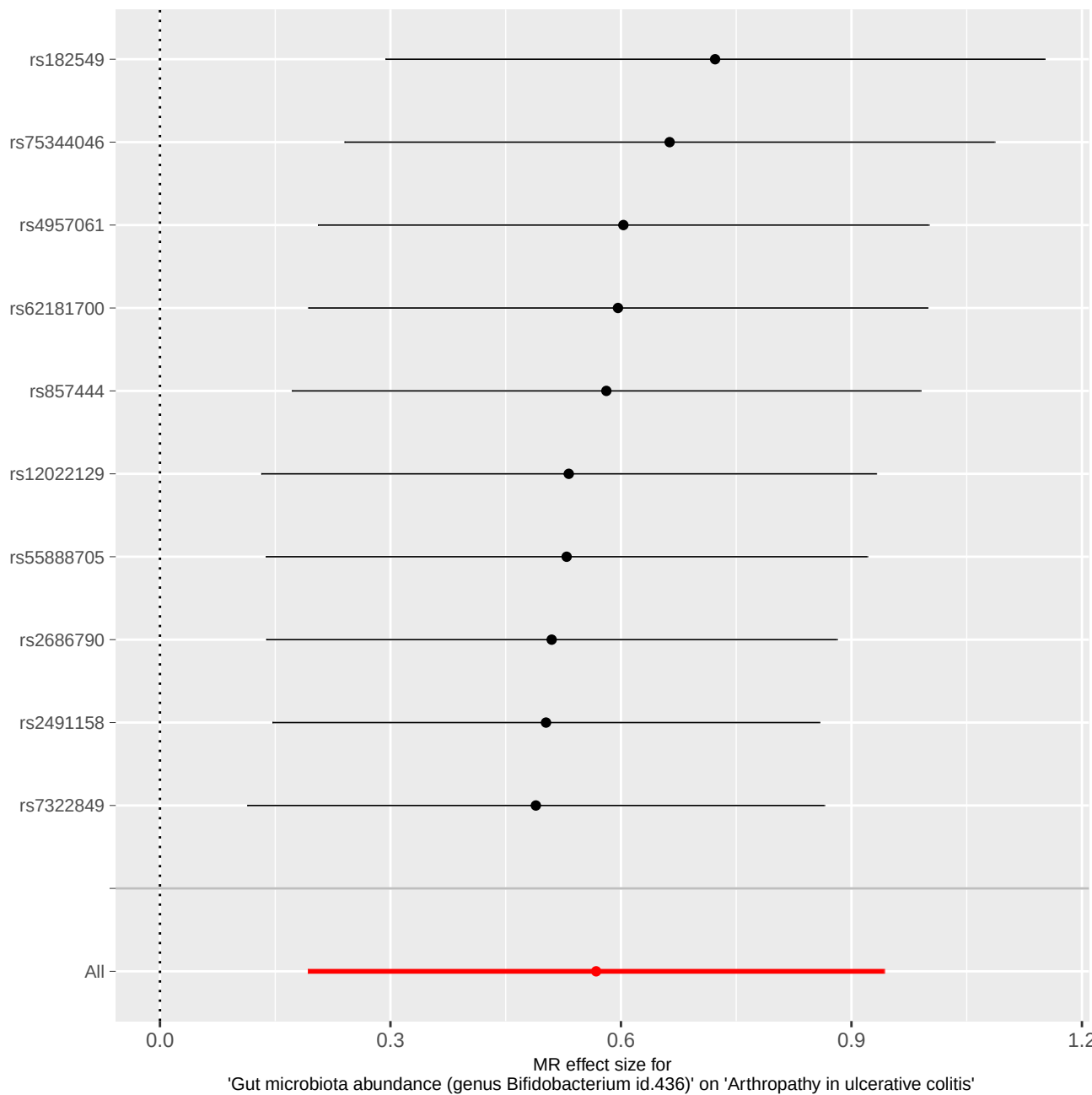
MR effect size for
'Gut microbiota abundance (genus Anaerofilum id.2053)' on 'Arthropathy in ulcerative colitis'



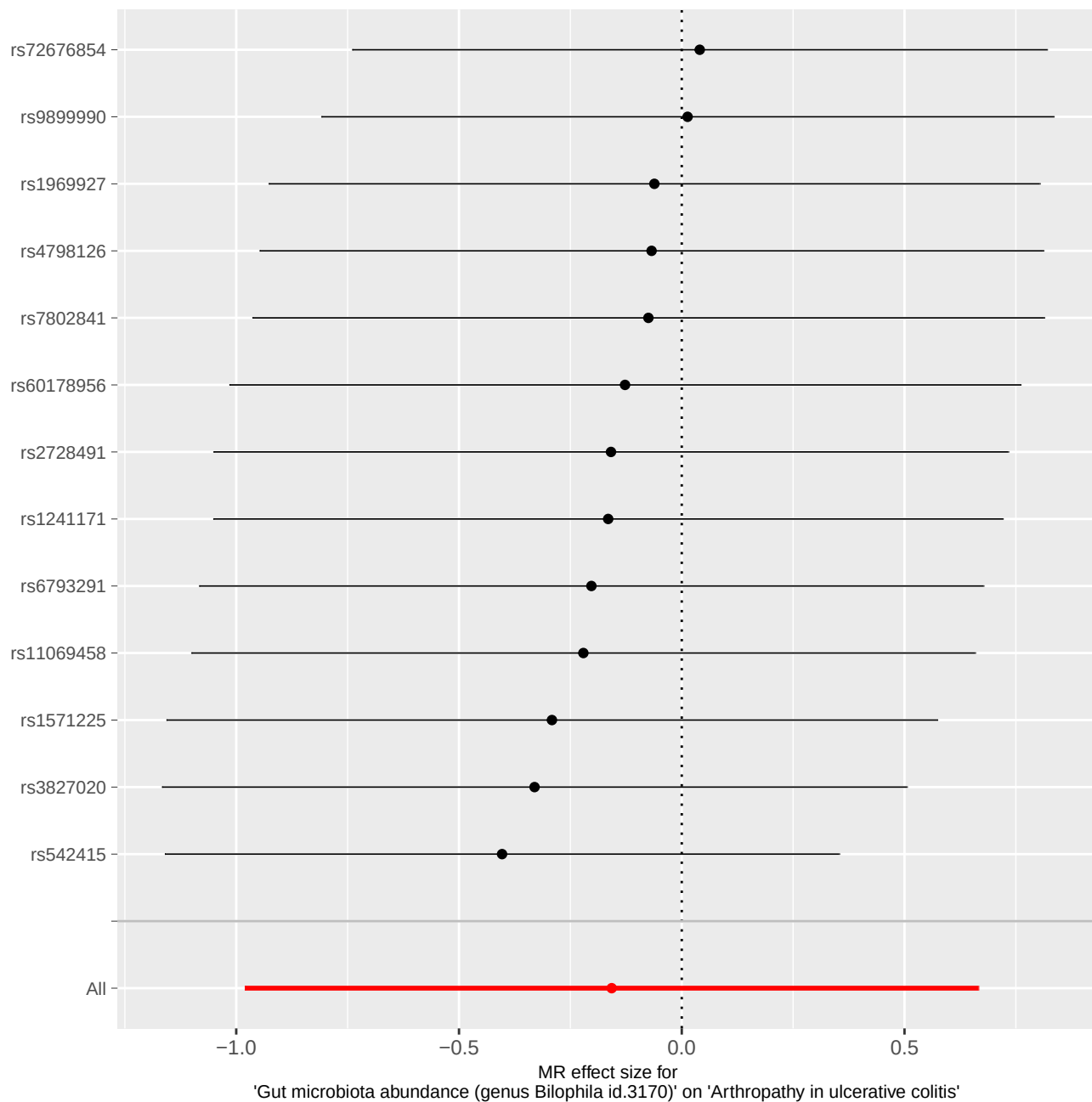


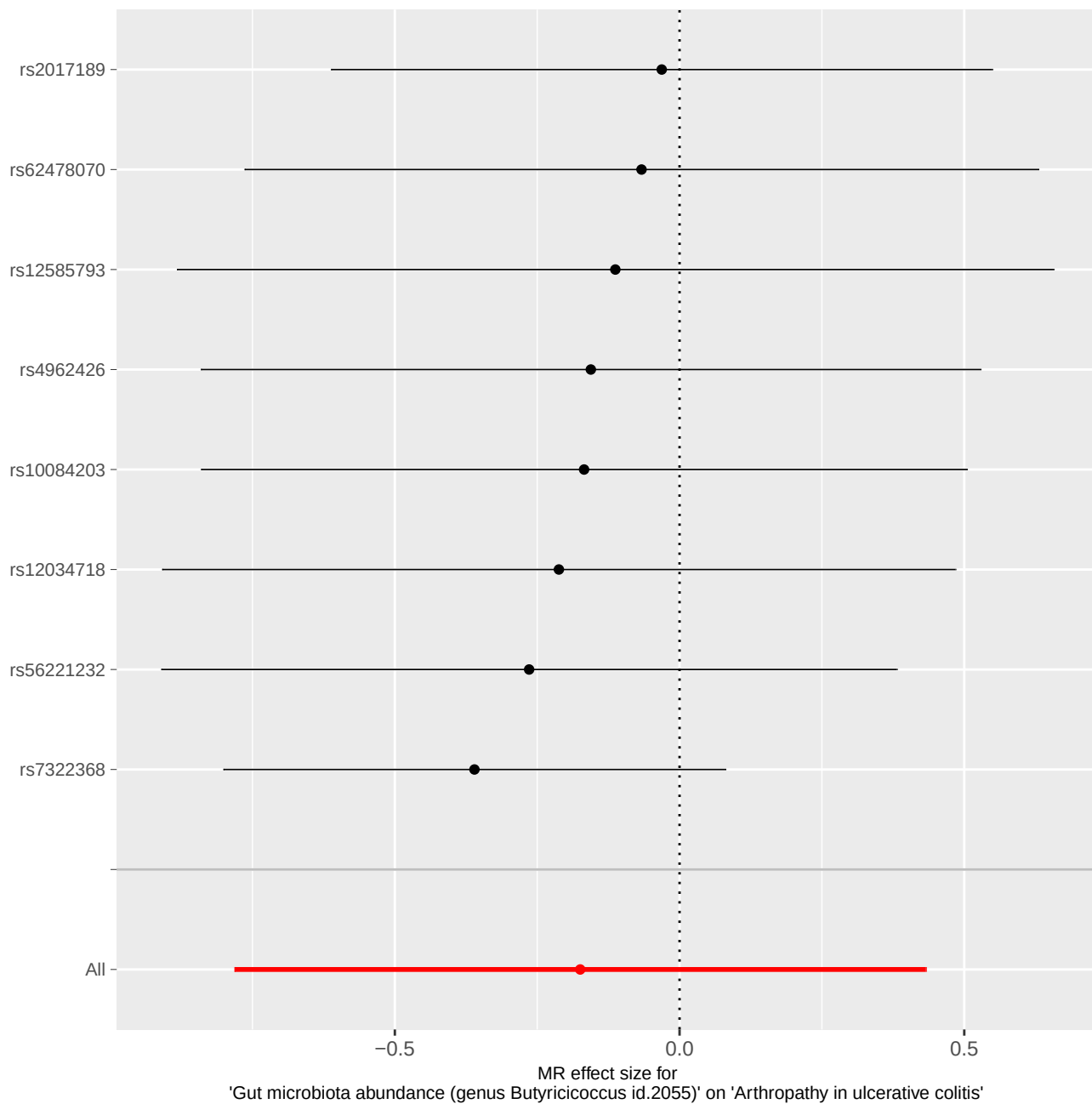


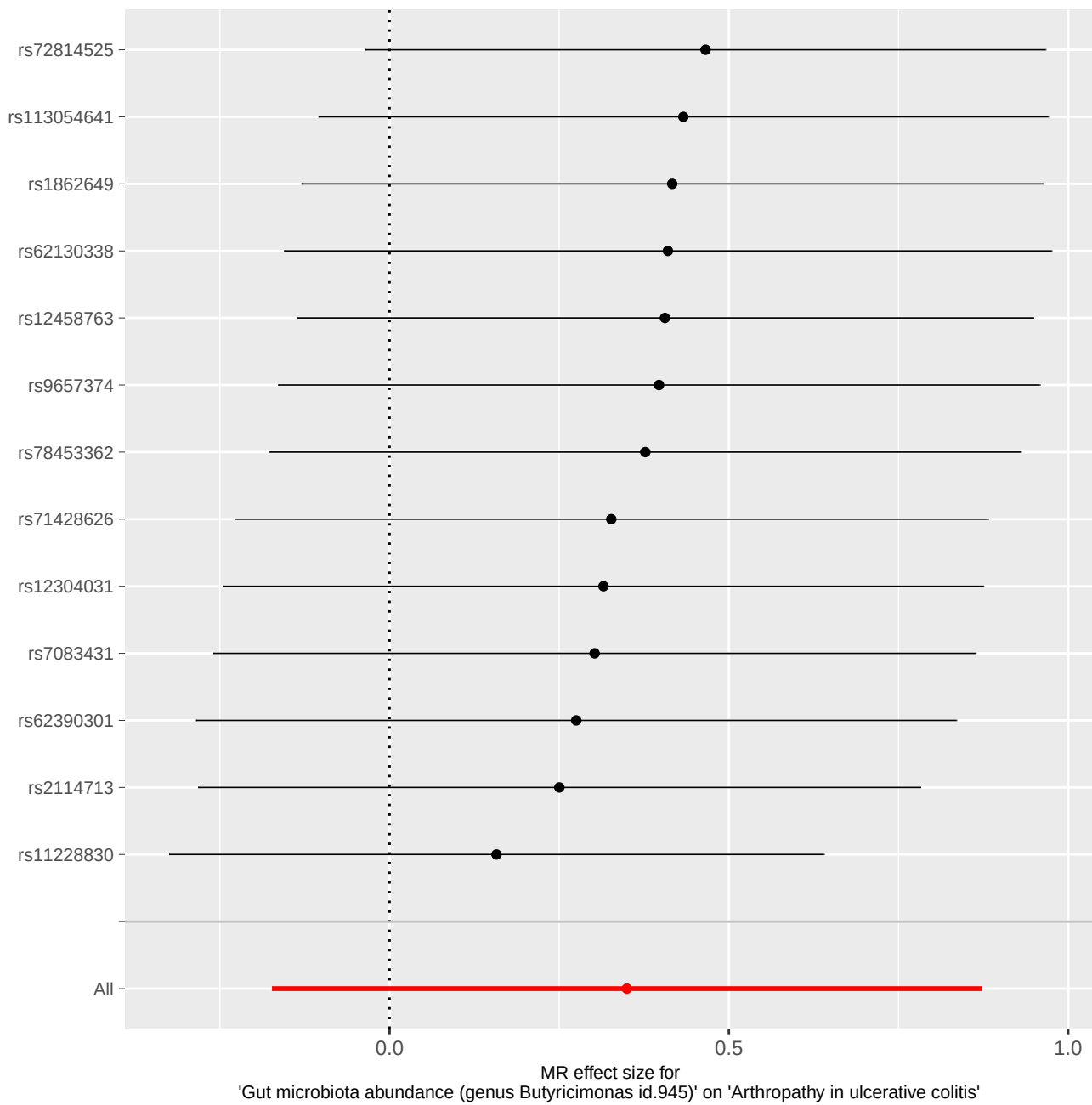


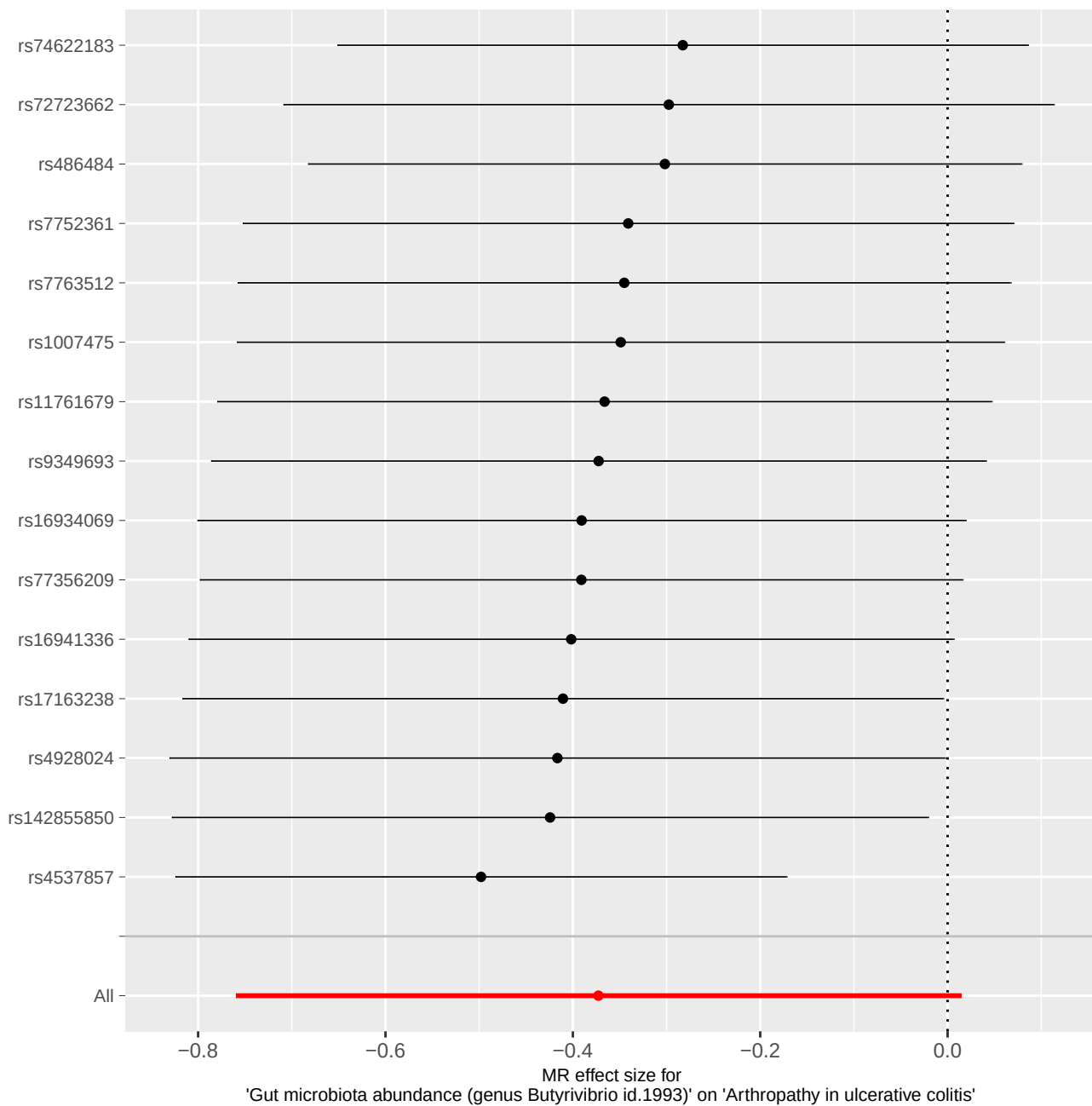


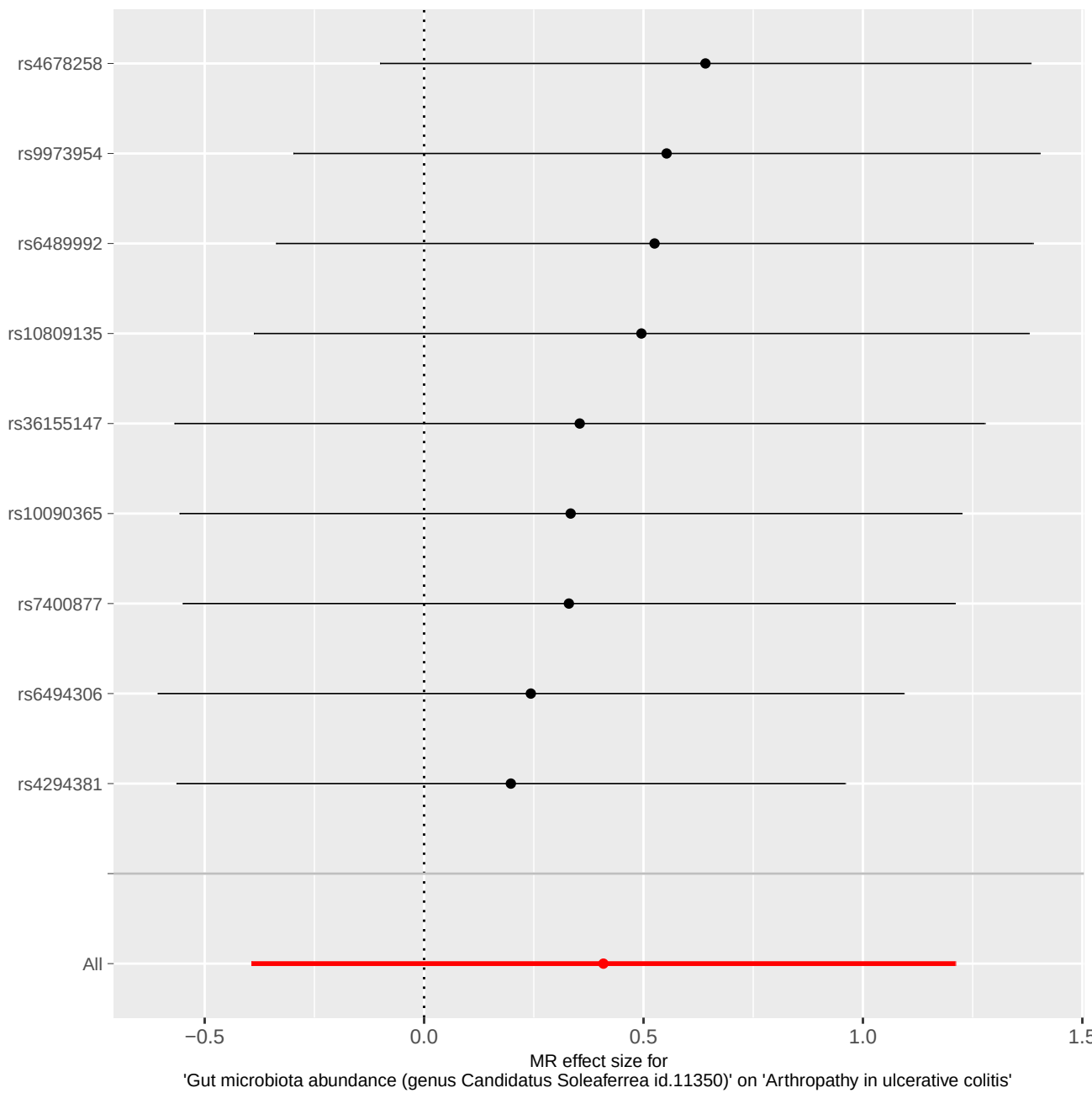
Batch 795 : Gut microbiota abundance (genus Bilophila id.3170) on Arthropathy in ulcerative colitis

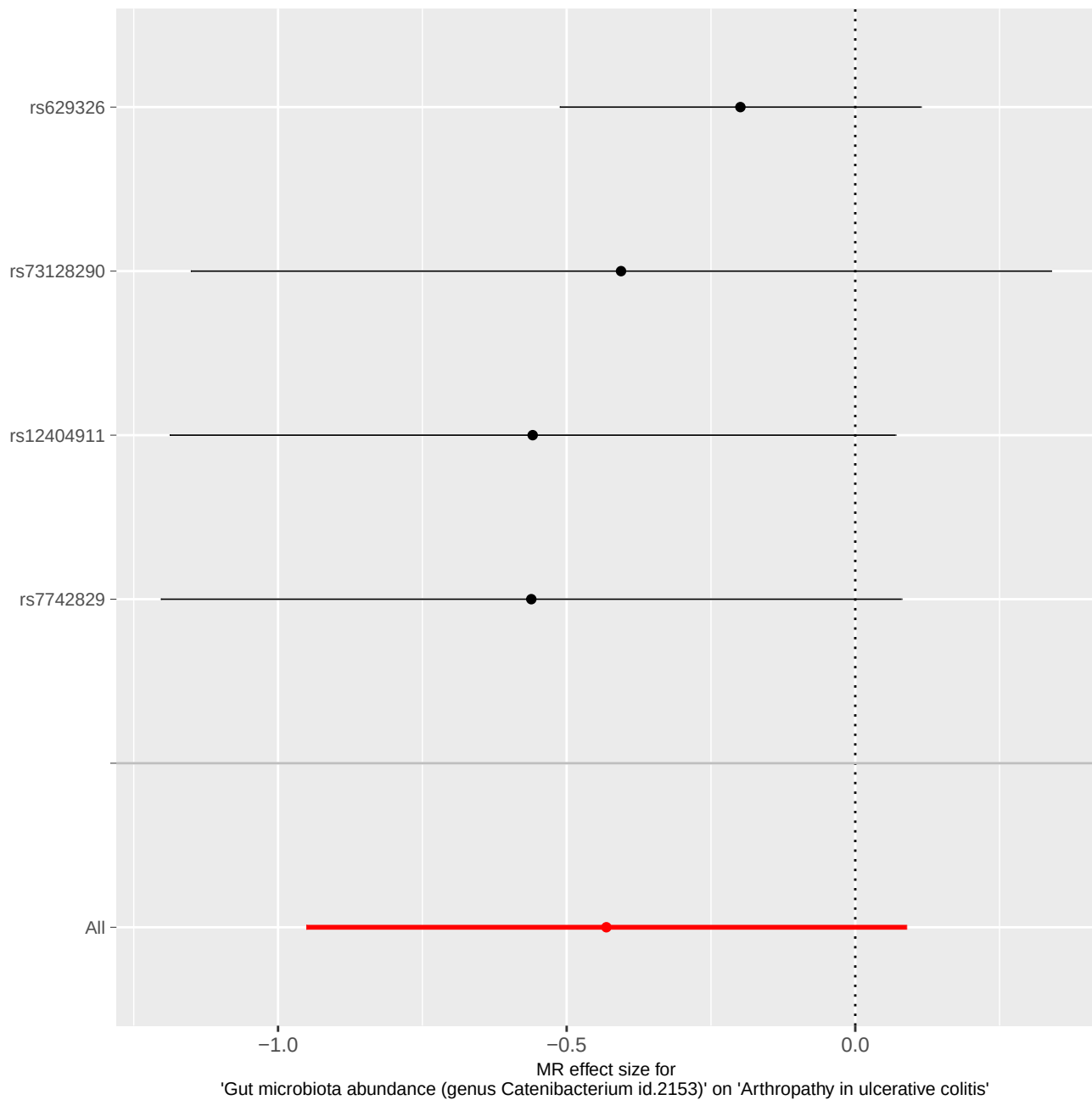


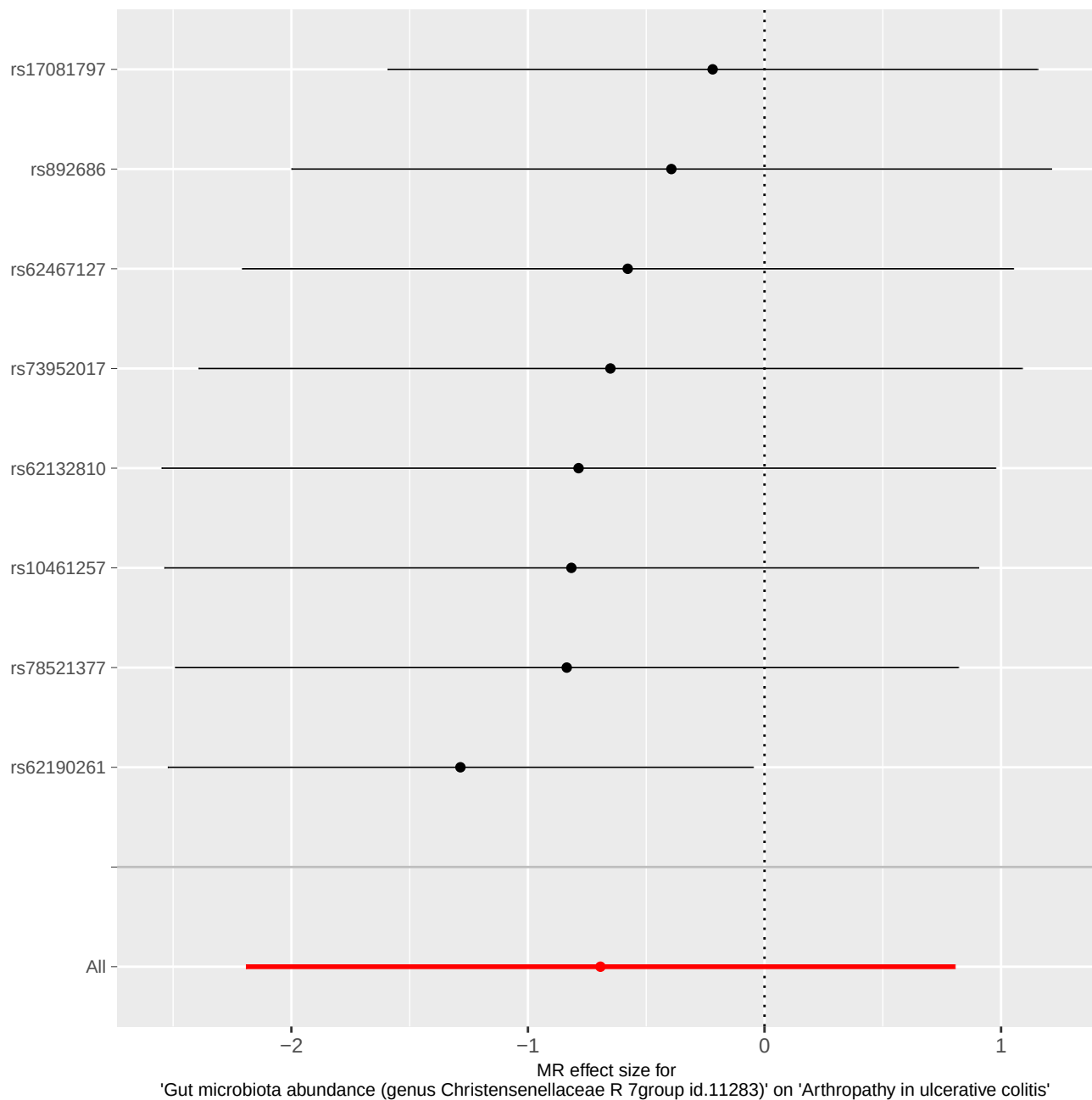


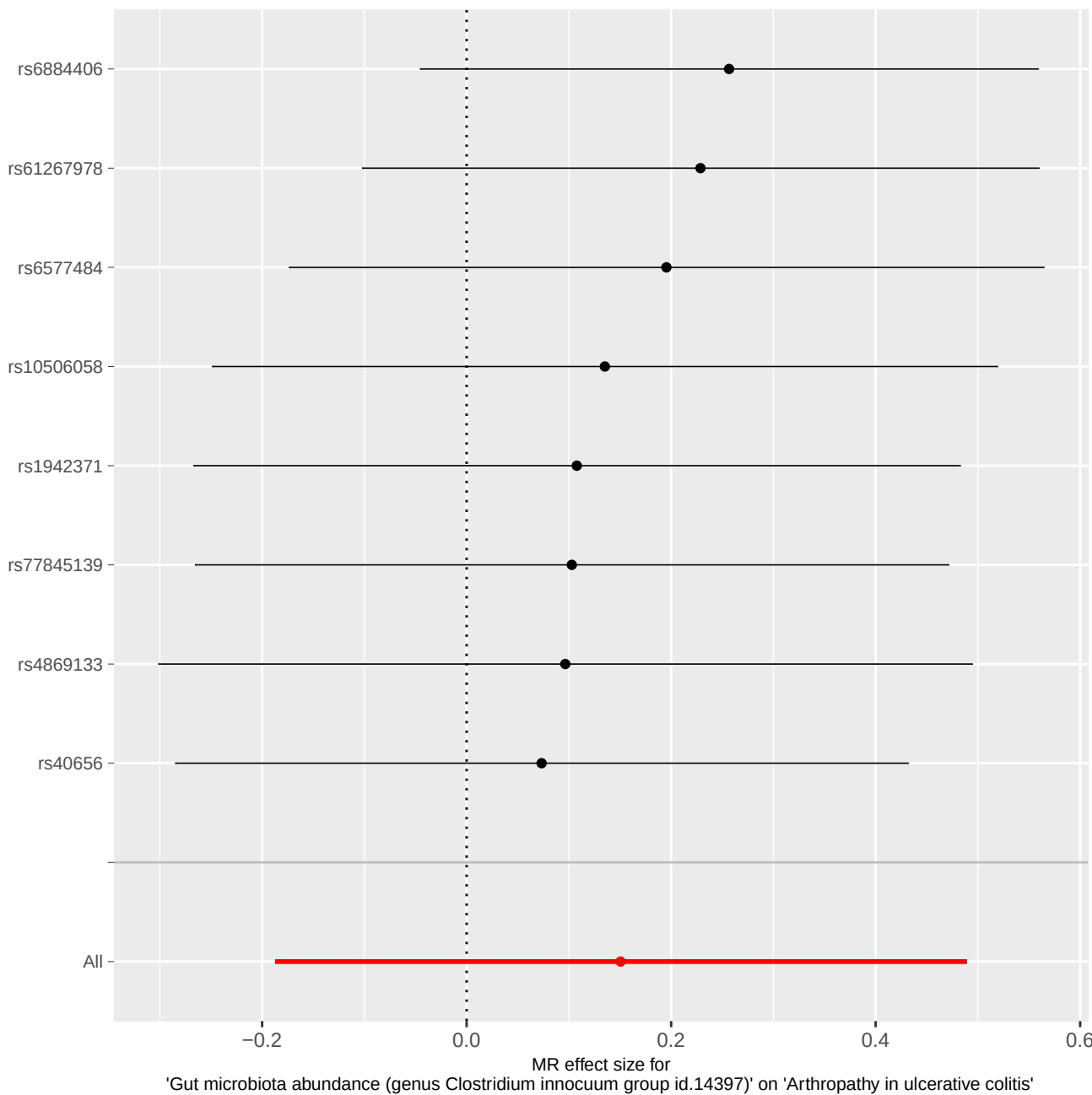


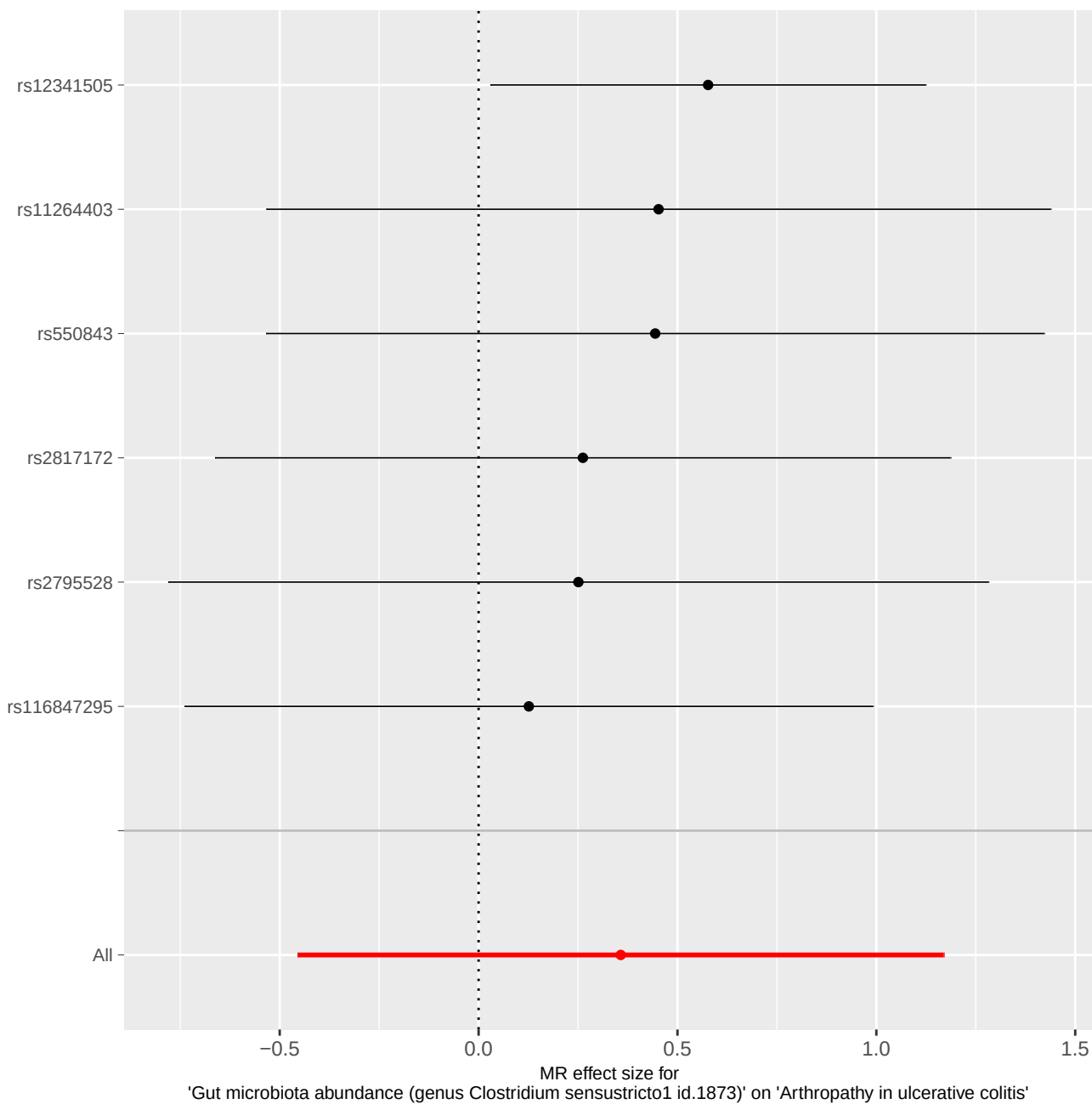


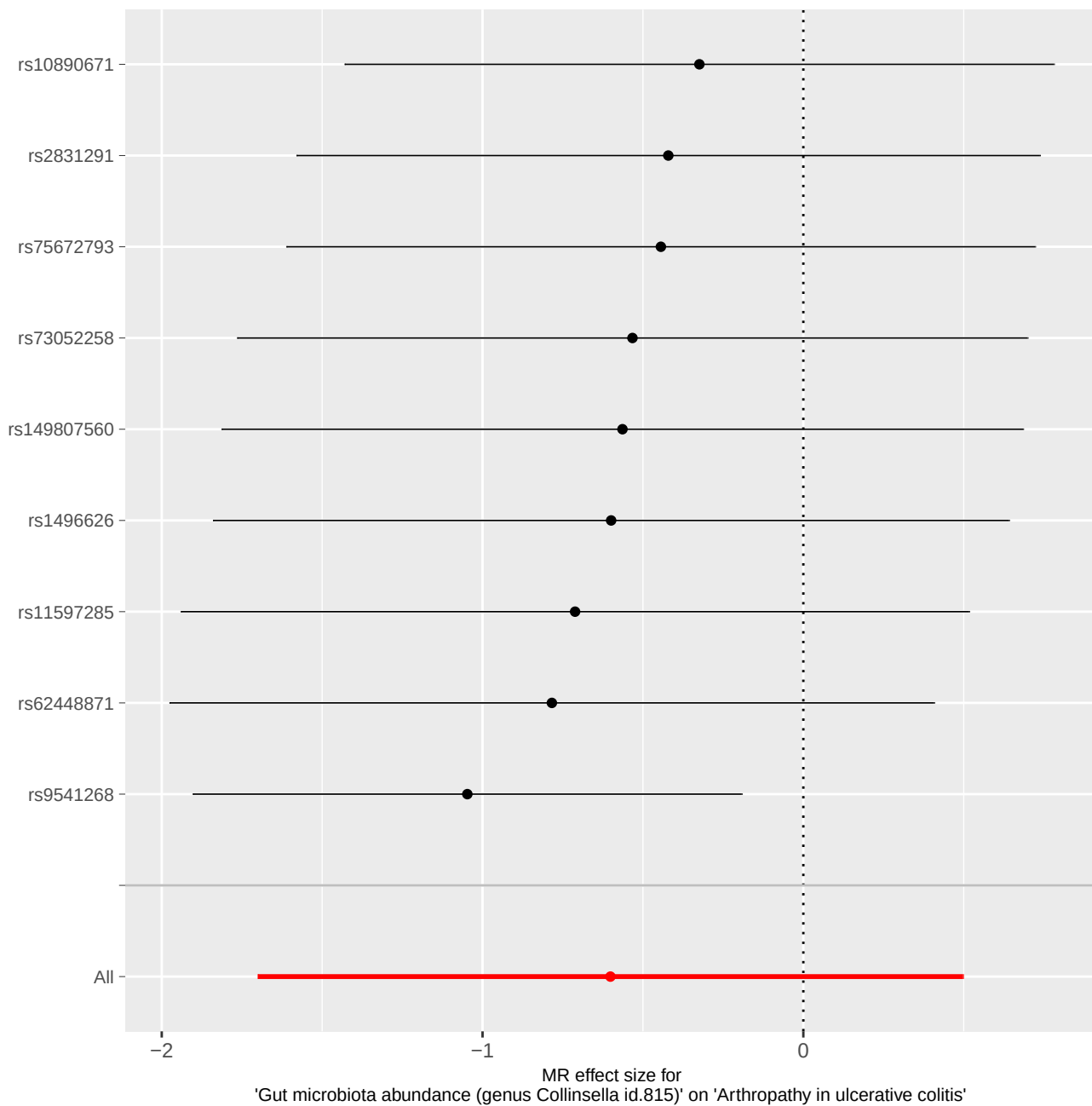


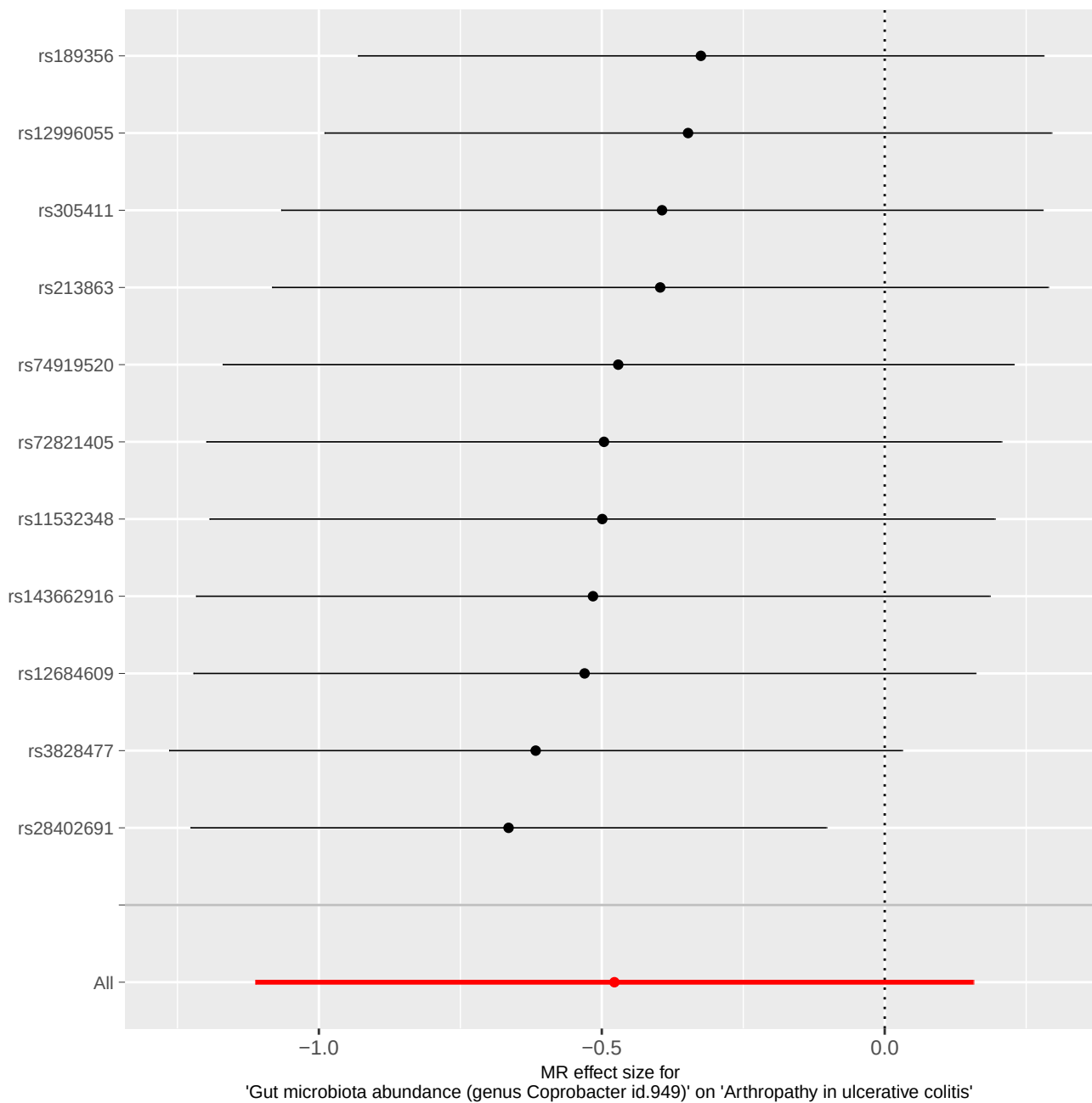


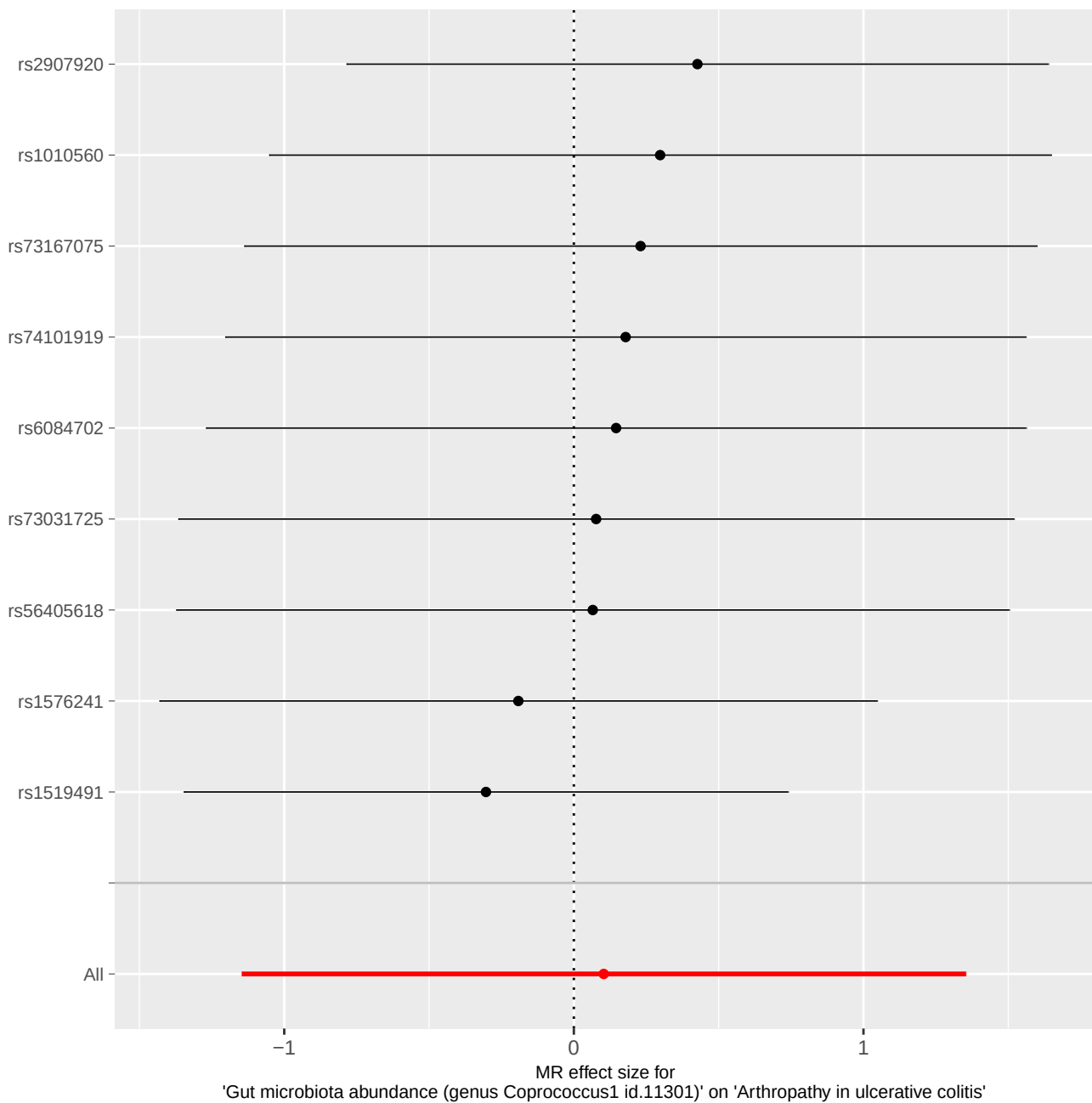


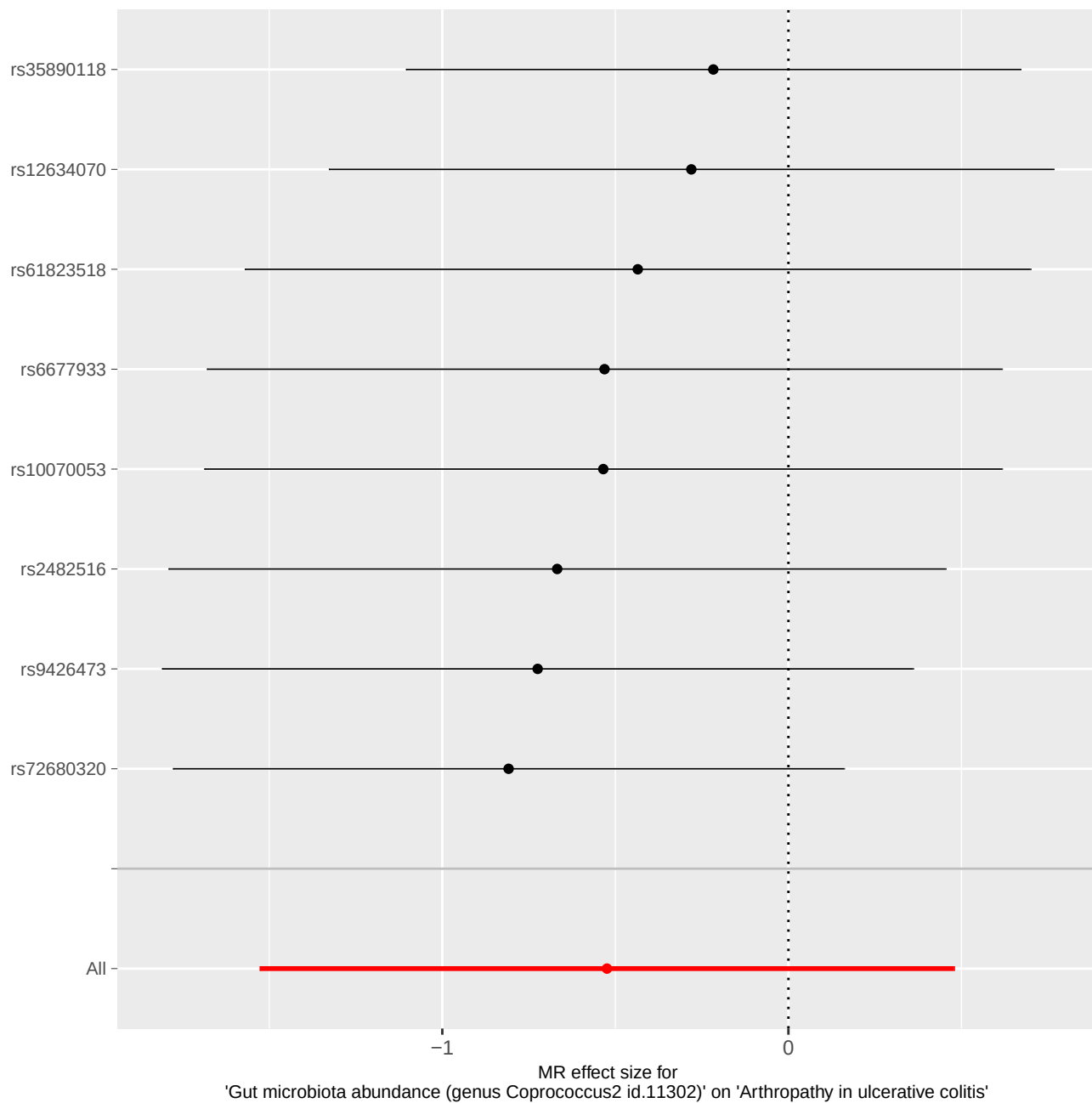


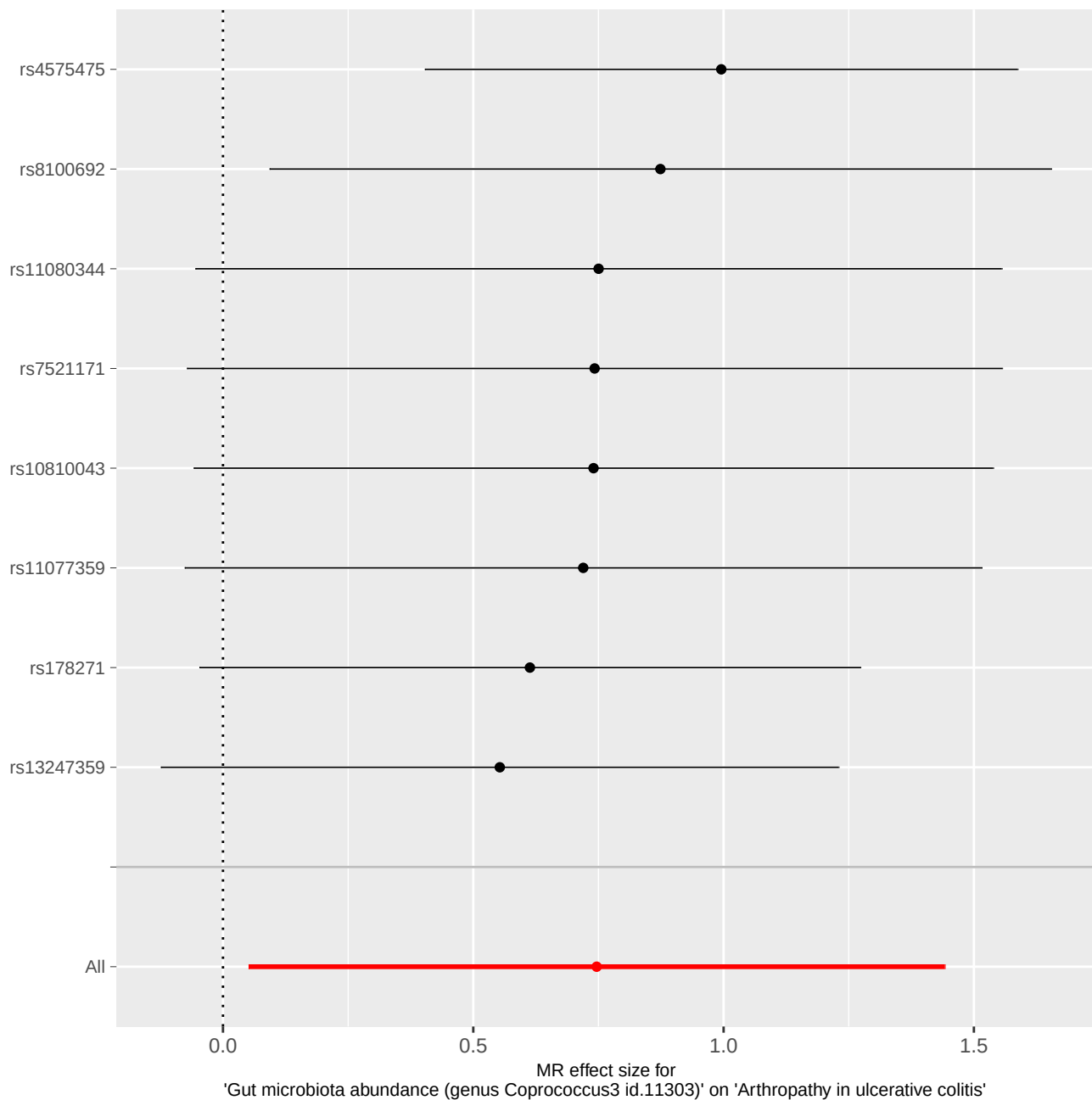


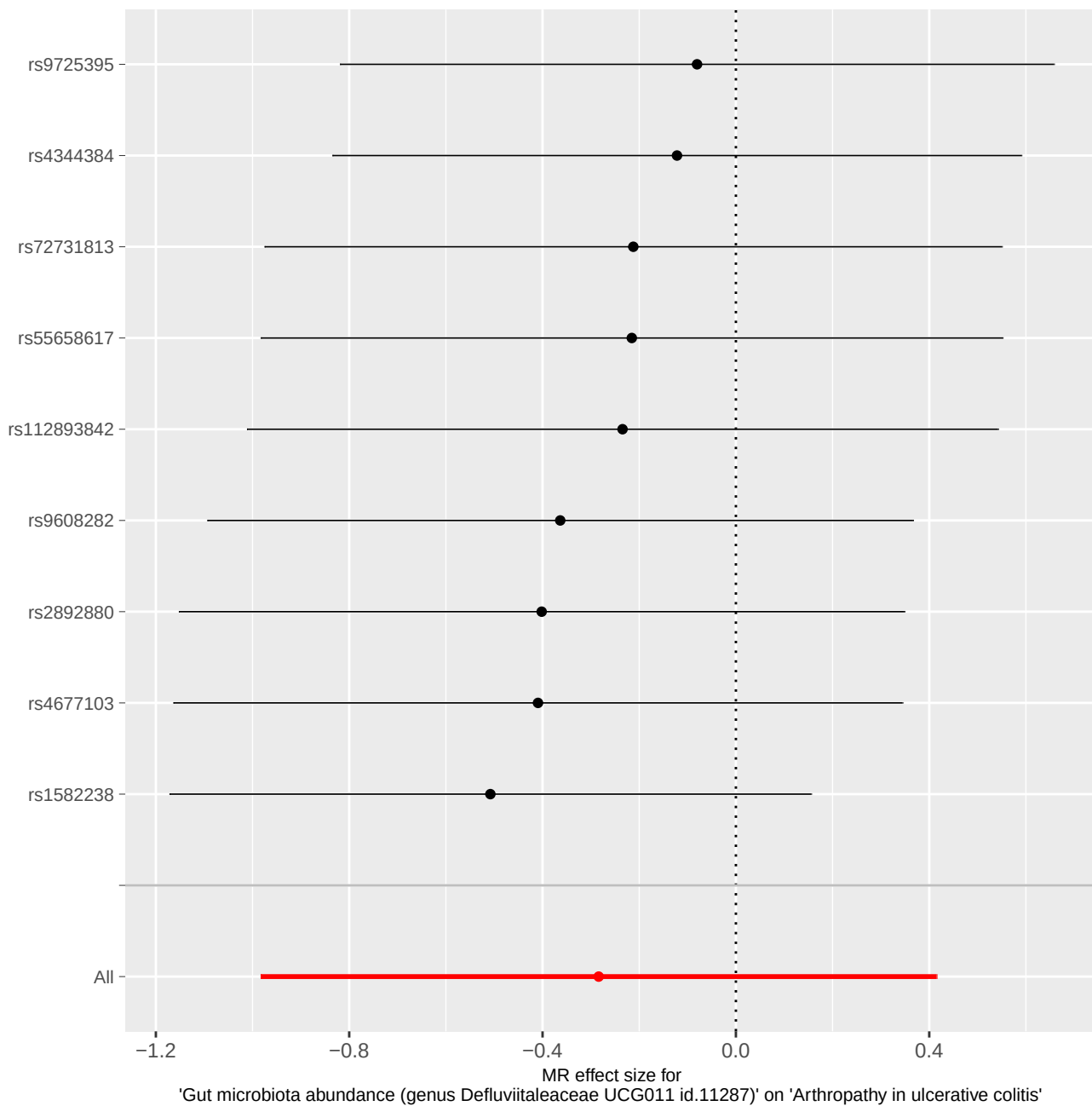






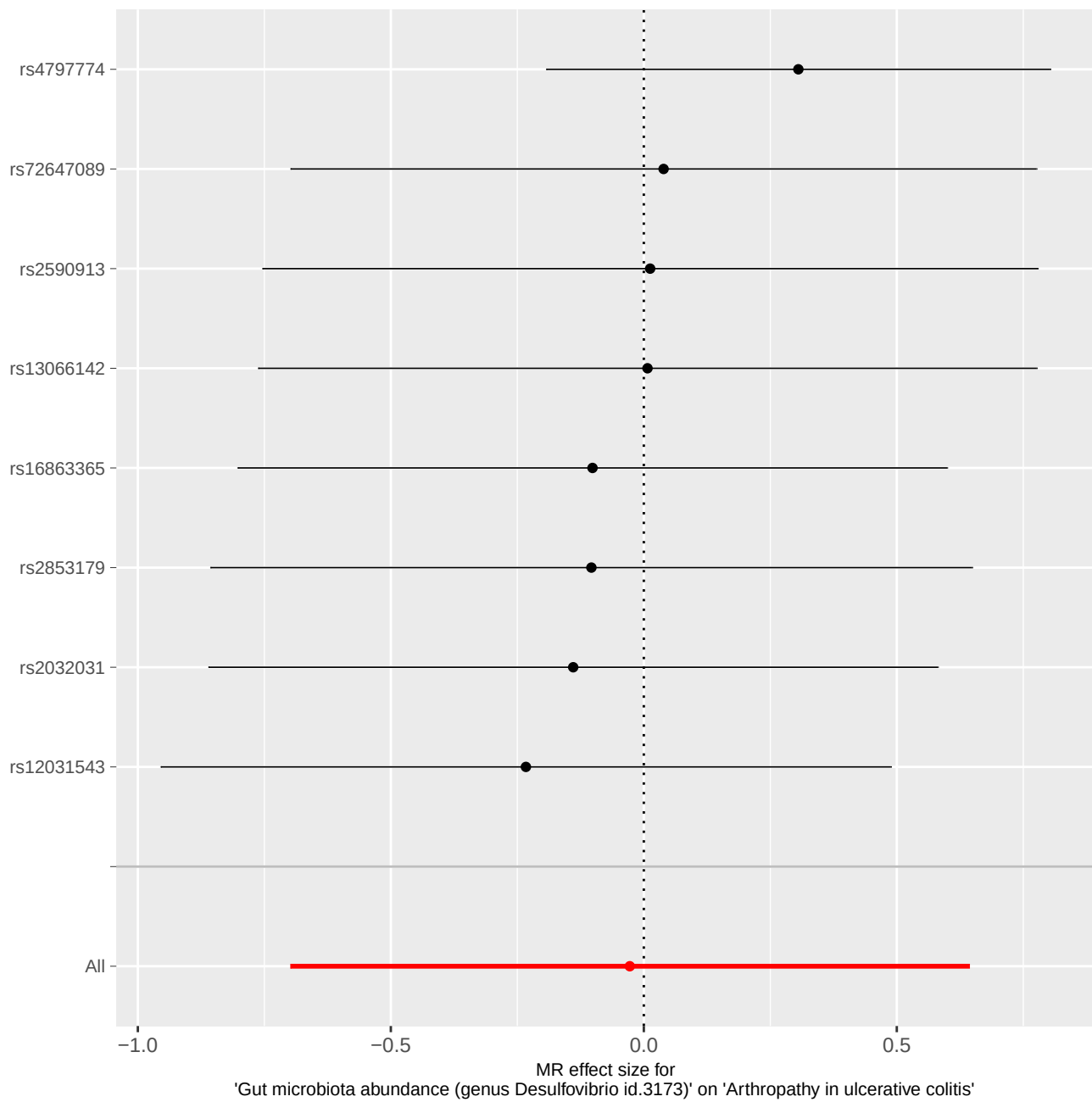


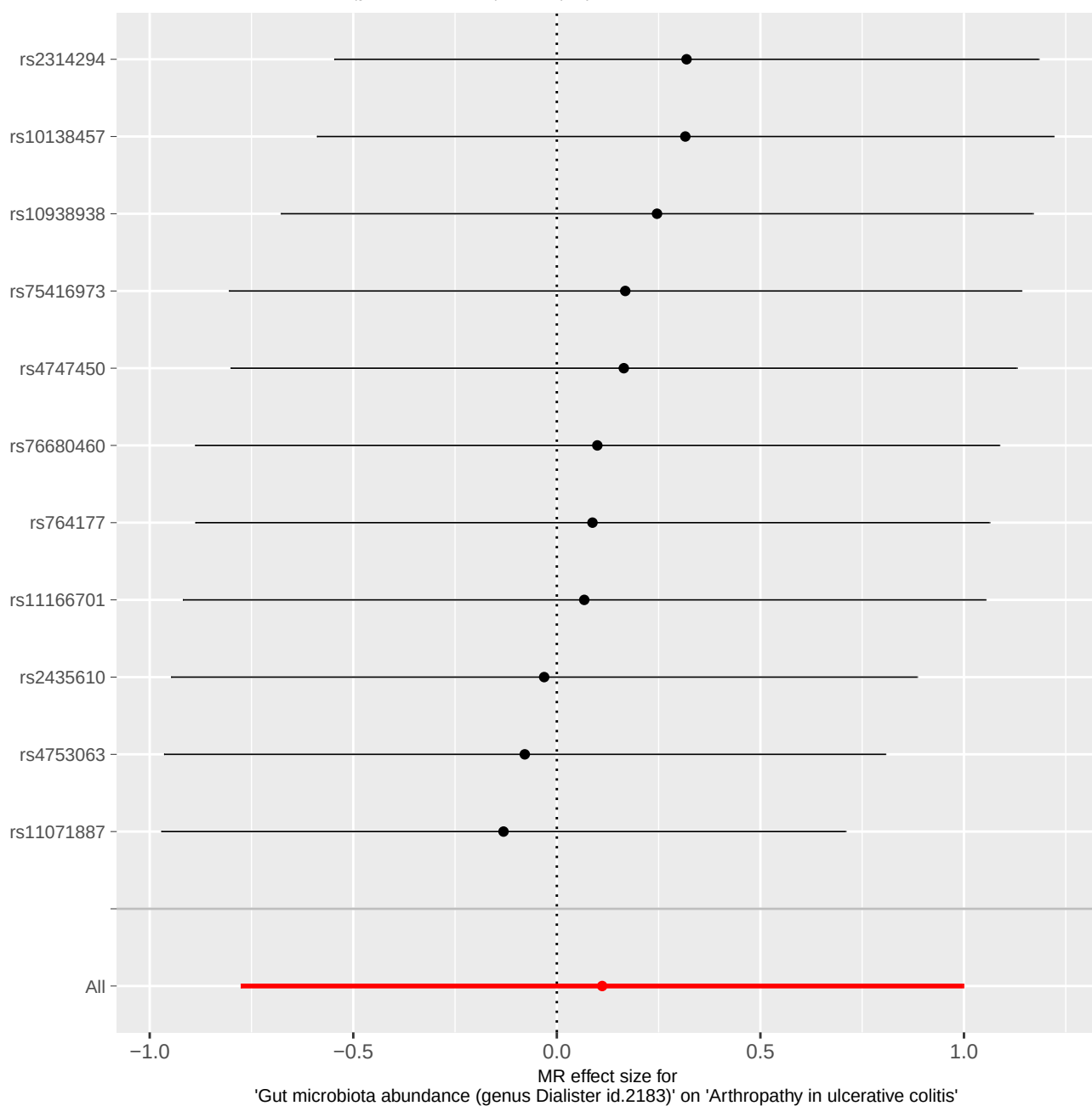




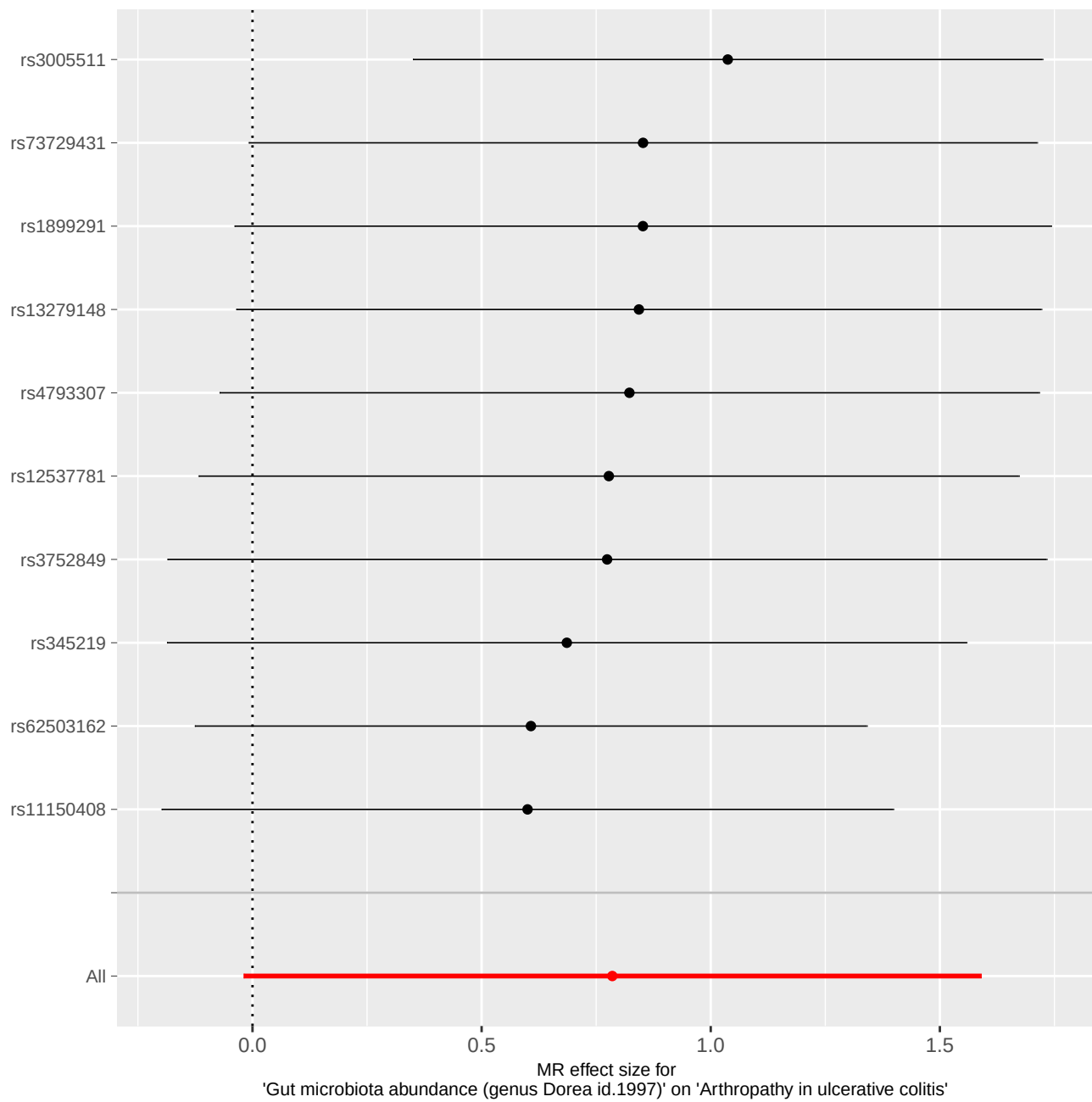
MR effect size for
'Gut microbiota abundance (genus Defluviitaleaceae UCG011 id.11287)' on 'Arthropathy in ulcerative colitis'

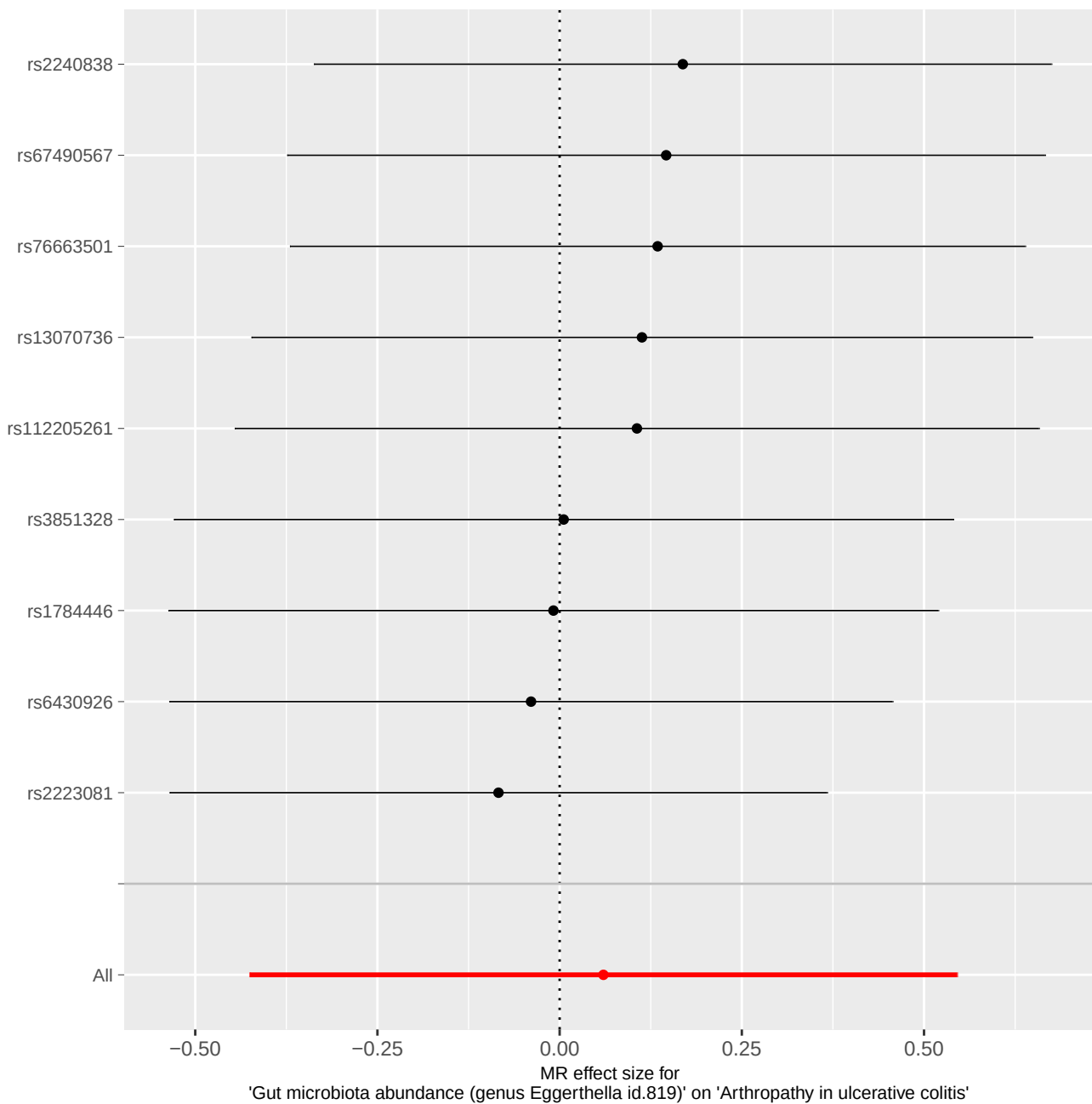
Batch 811 : Gut microbiota abundance (genus Desulfovibrio id.3173) on Arthropathy in ulcerative colitis

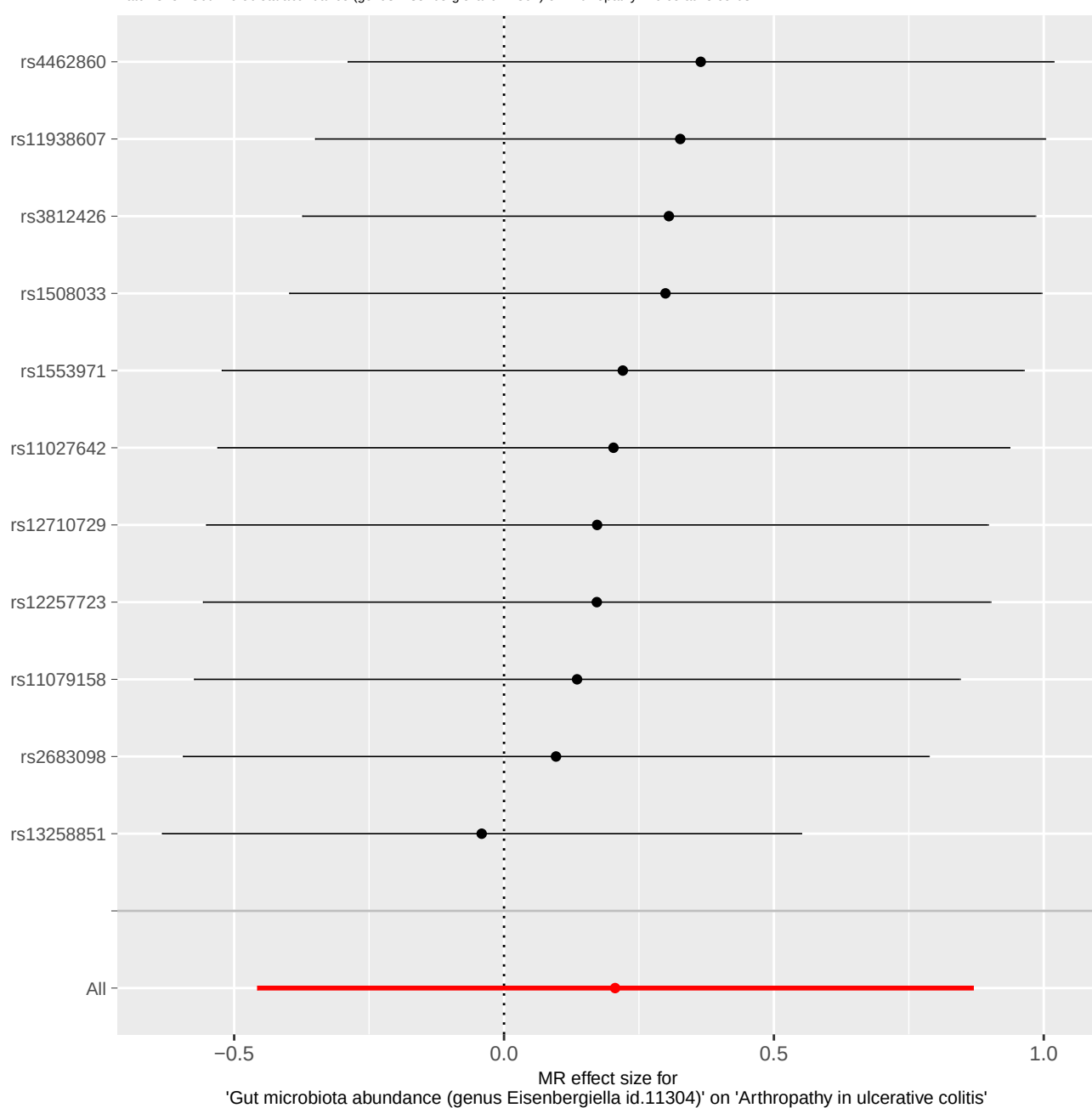


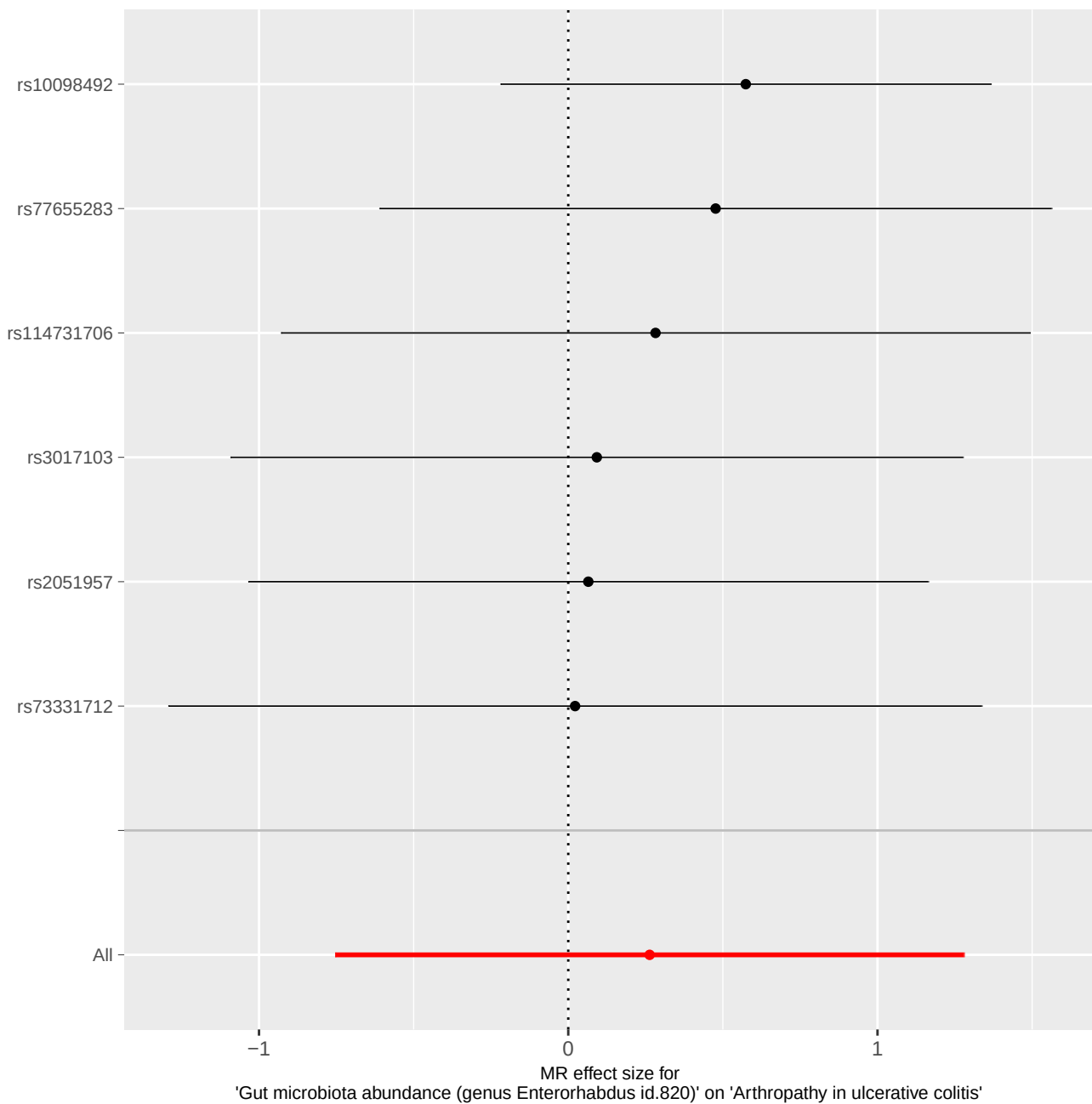


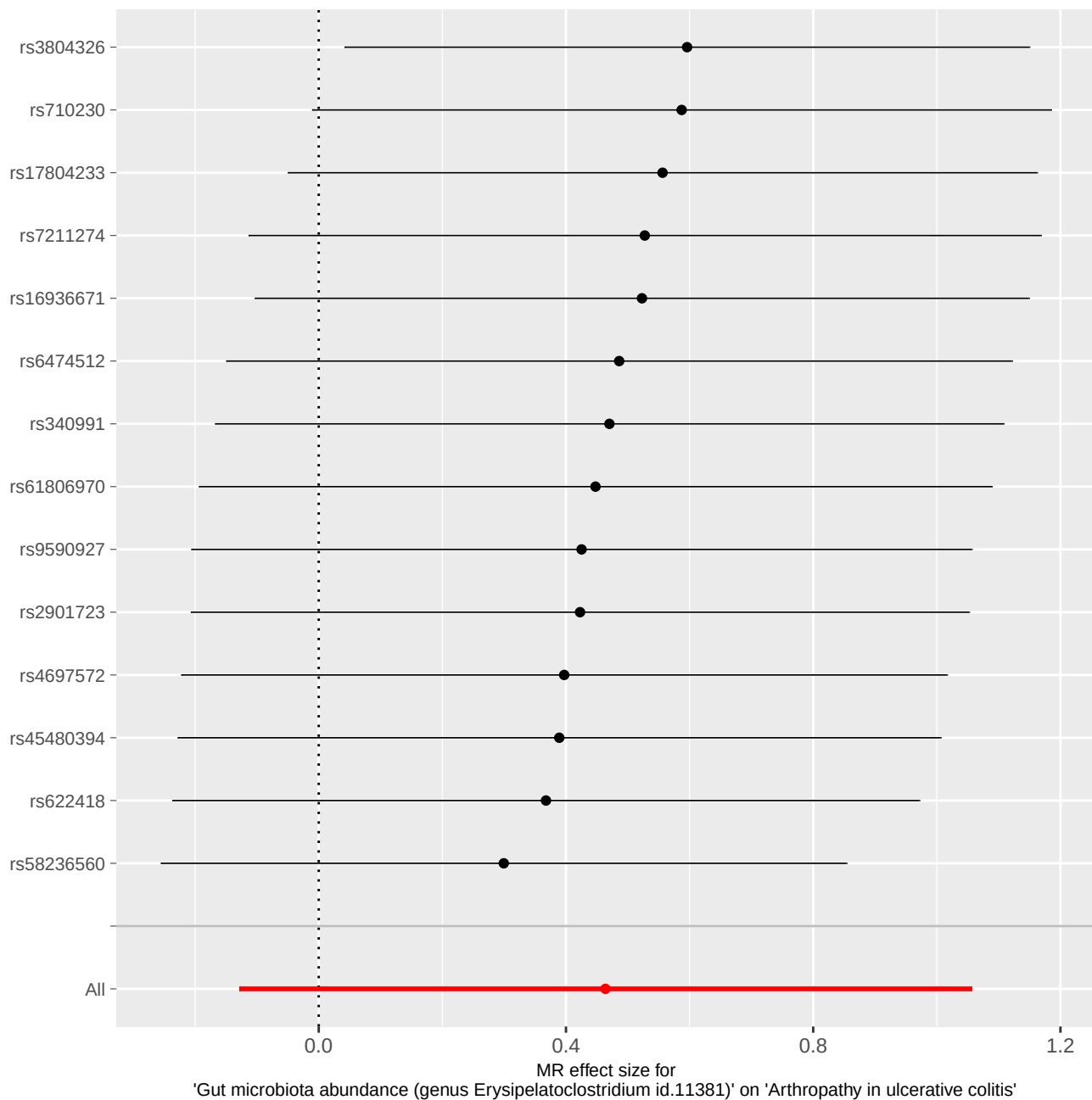
Batch 813 : Gut microbiota abundance (genus Dorea id.1997) on Arthropathy in ulcerative colitis

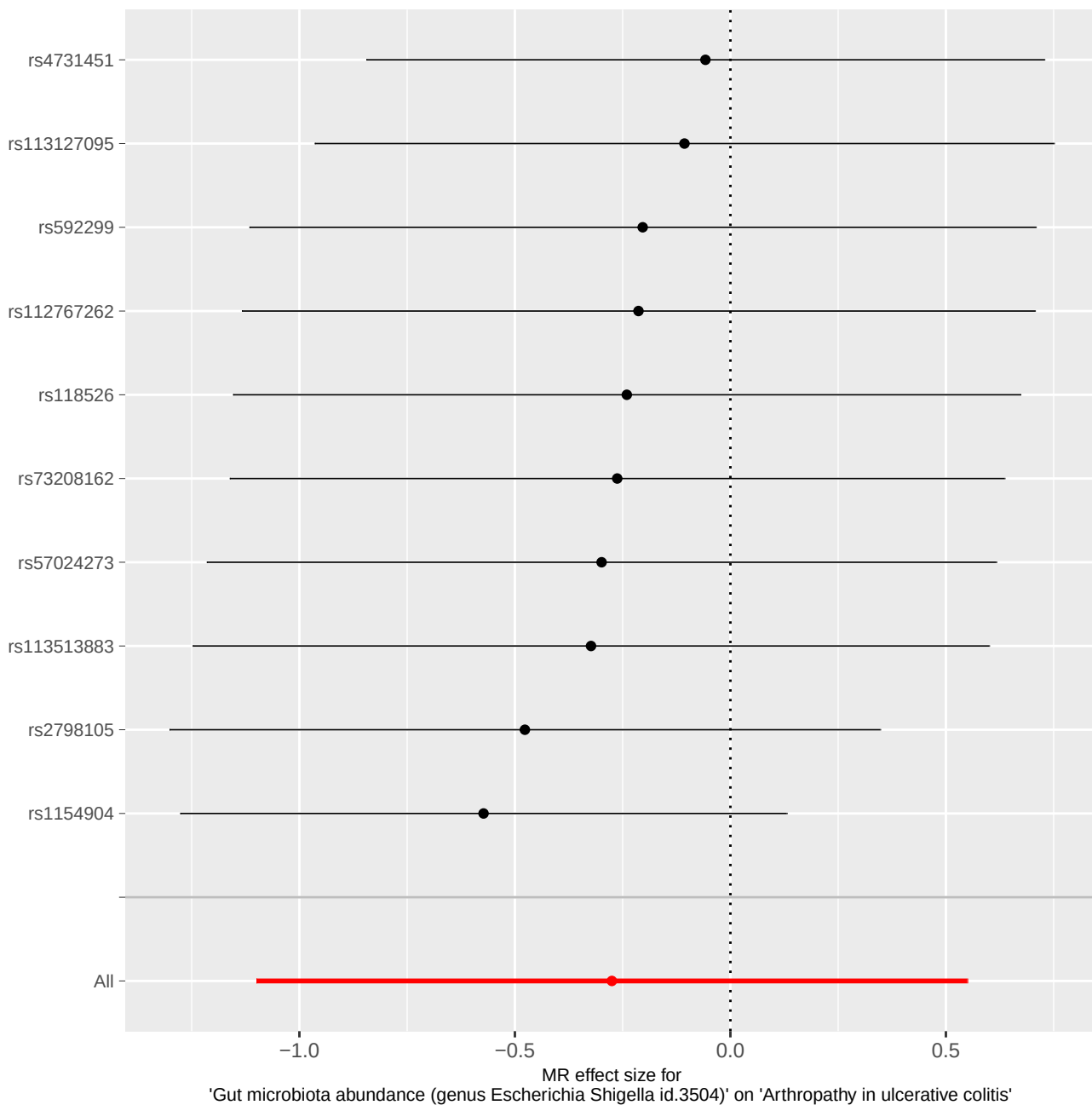


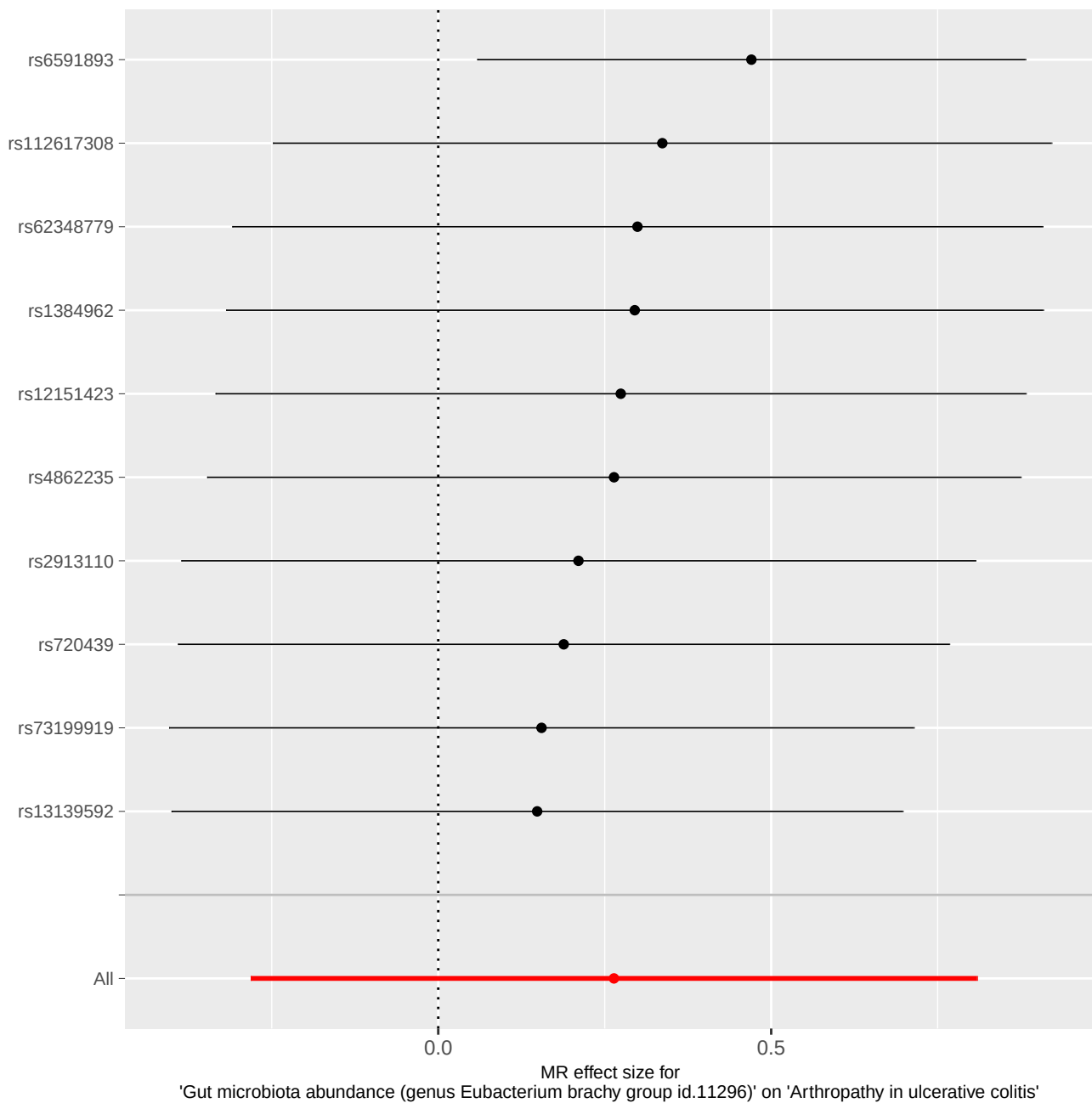




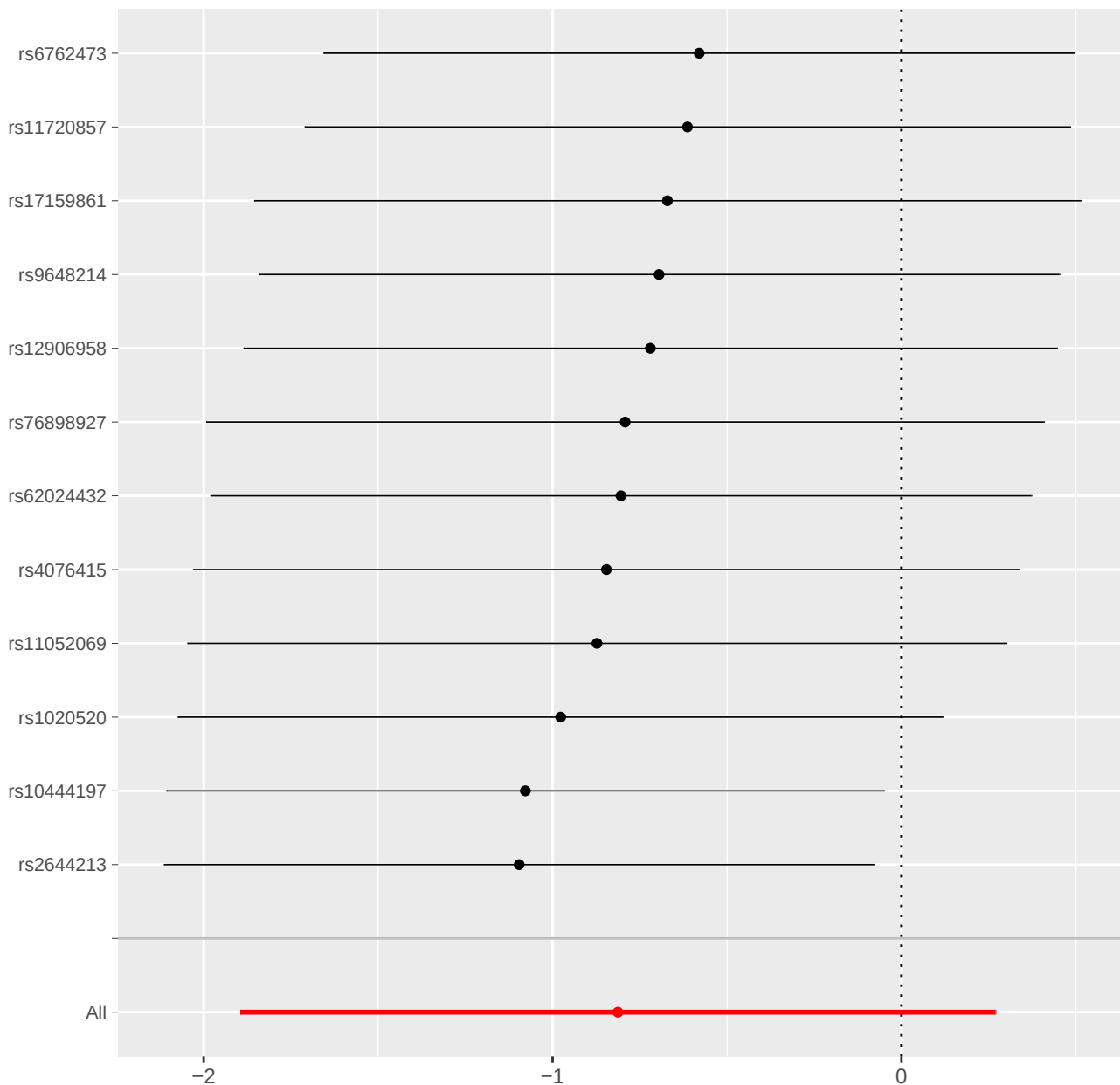




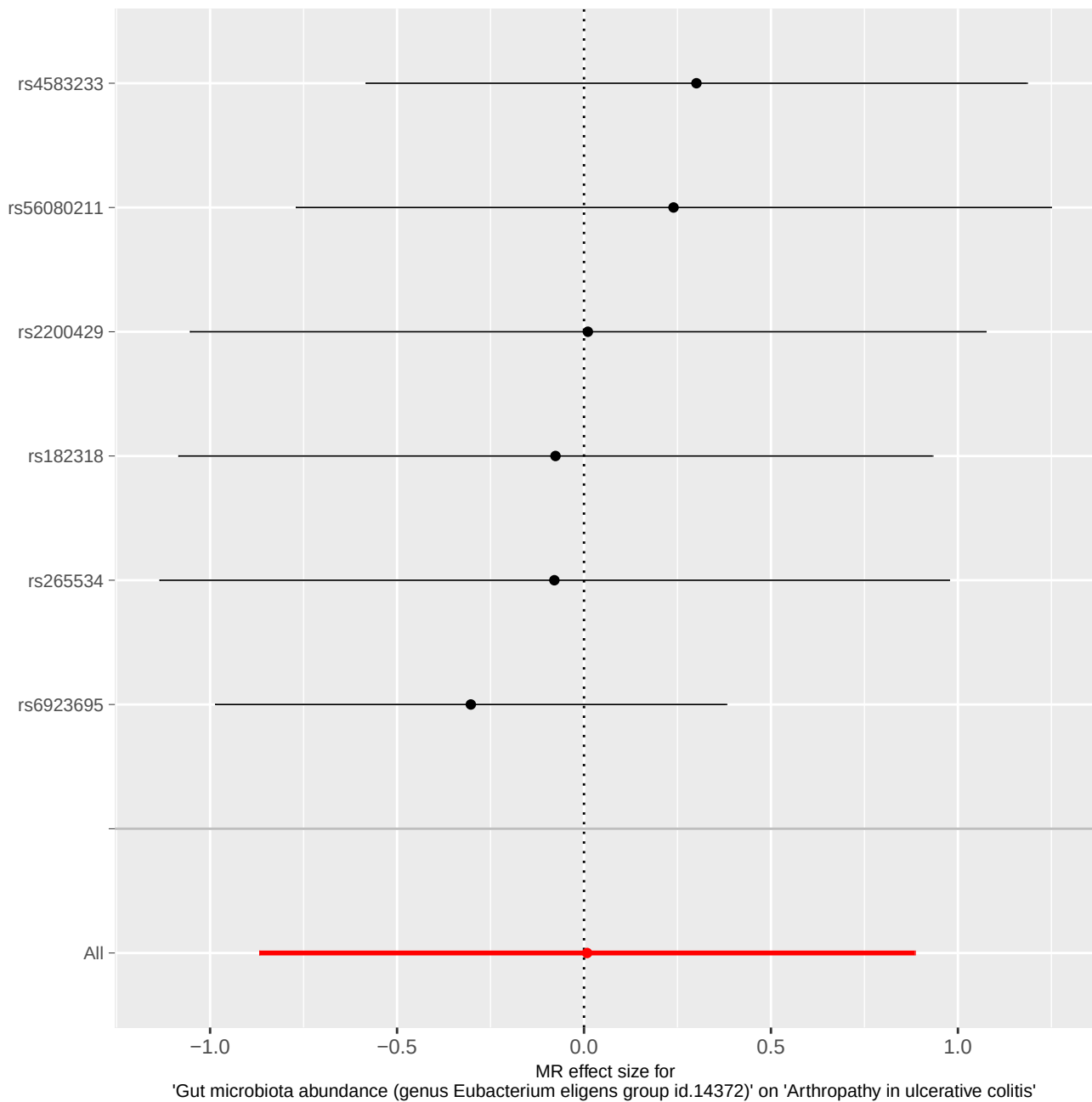


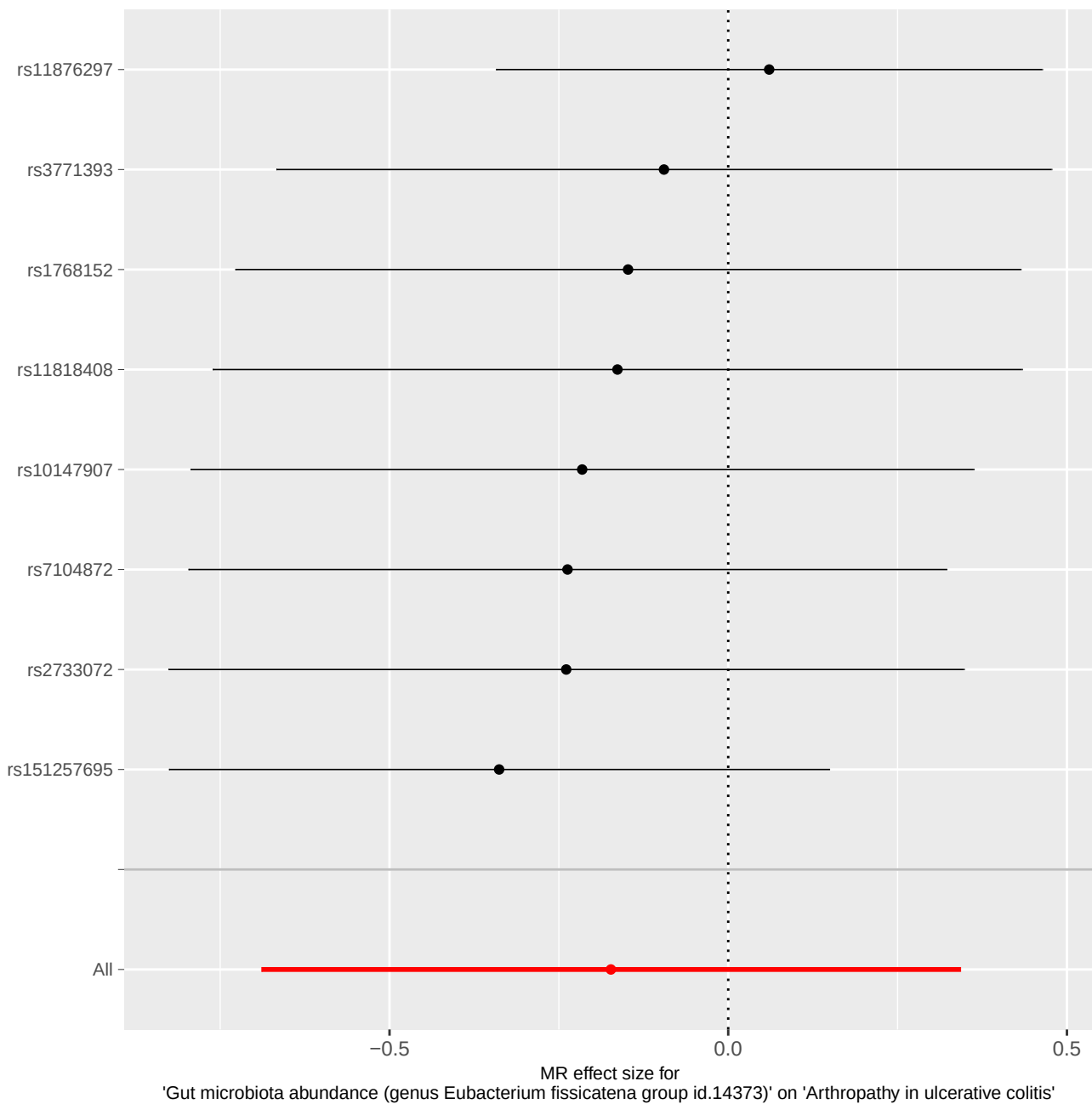


MR effect size for
'Gut microbiota abundance (genus Eubacterium brachy group id.11296)' on 'Arthropathy in ulcerative colitis'

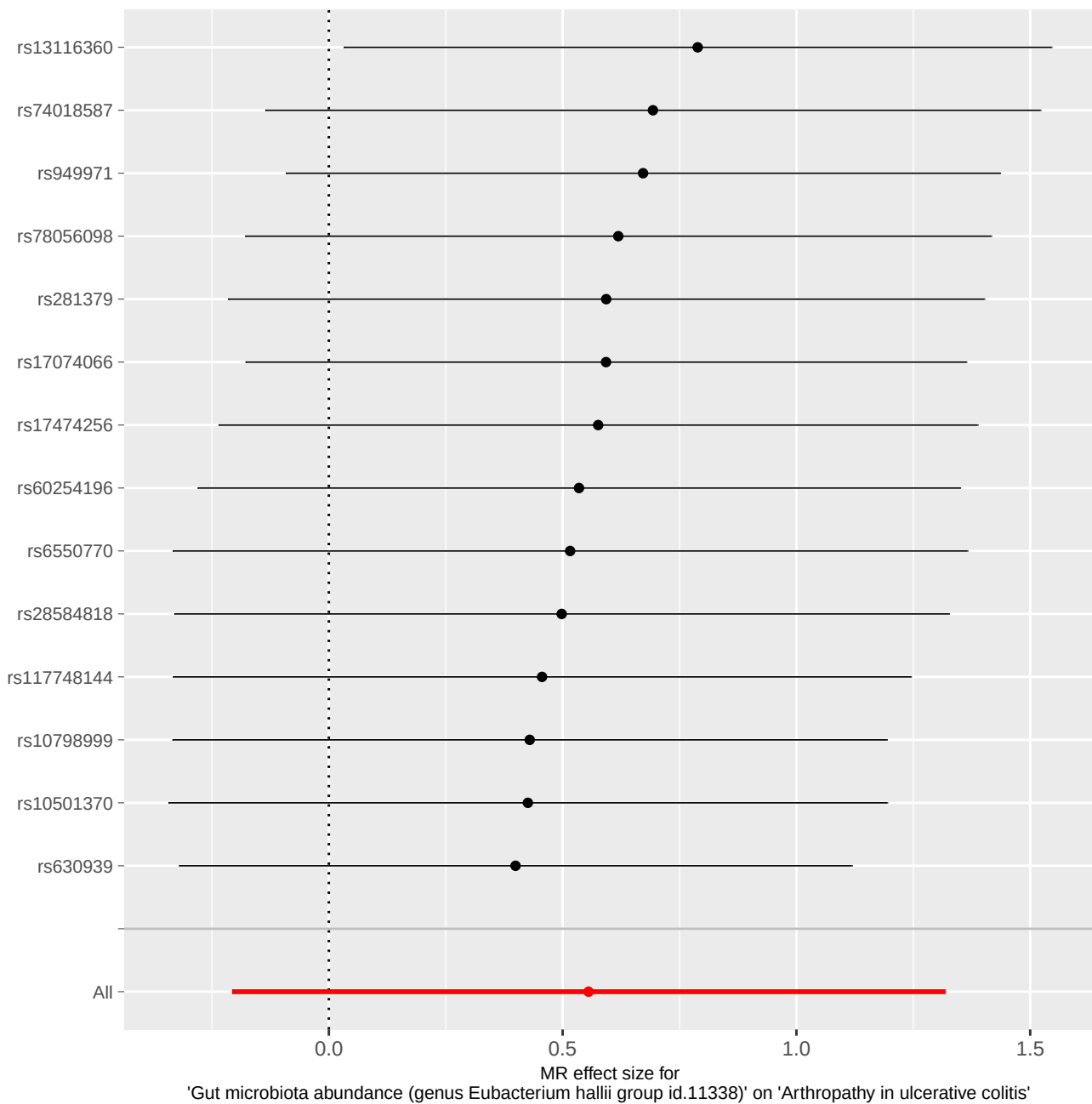


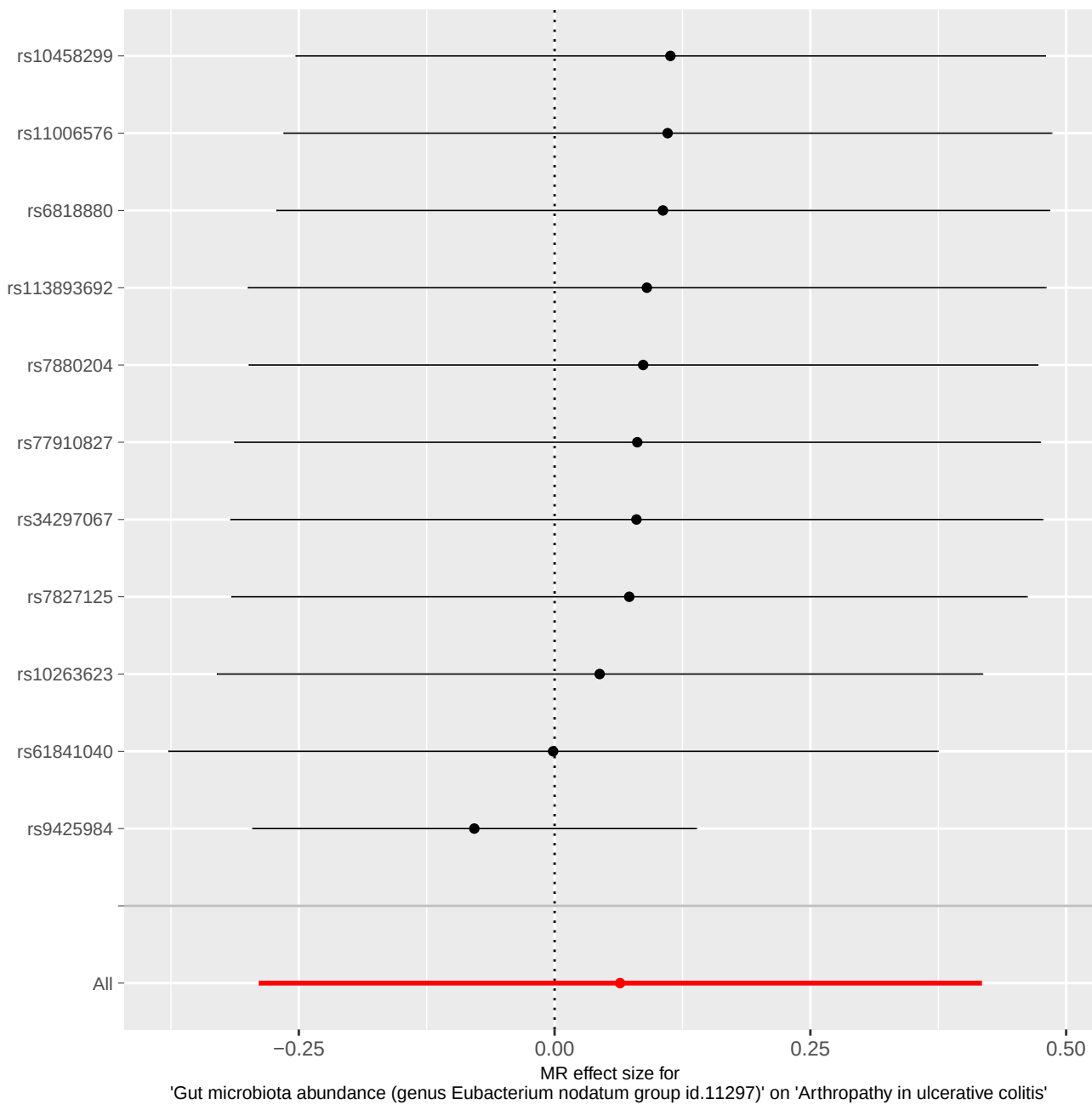
MR effect size for
'Gut microbiota abundance (genus Eubacterium coprostanoligenes group id.11375)' on 'Arthropathy in ulcerative colitis'

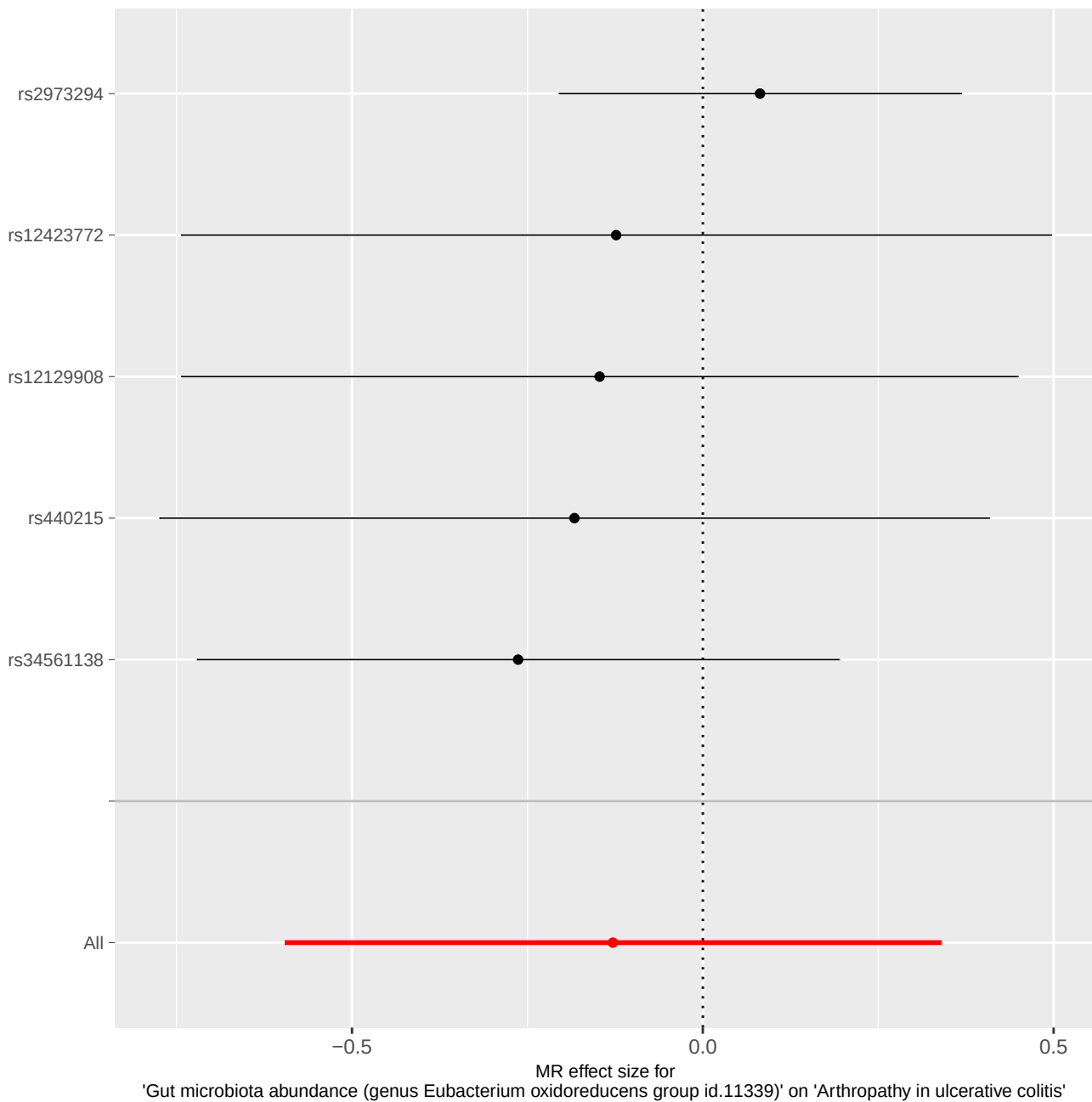


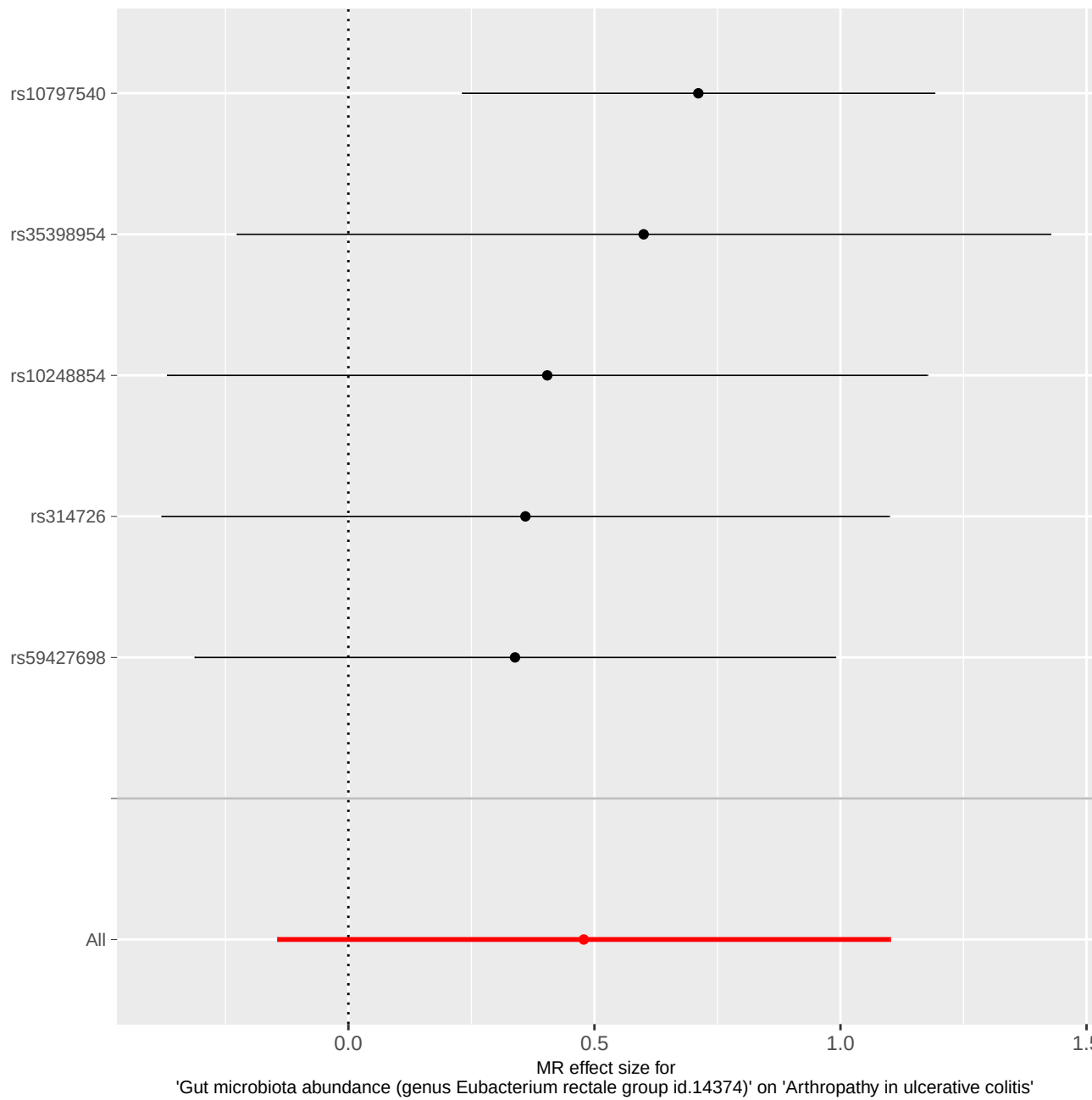


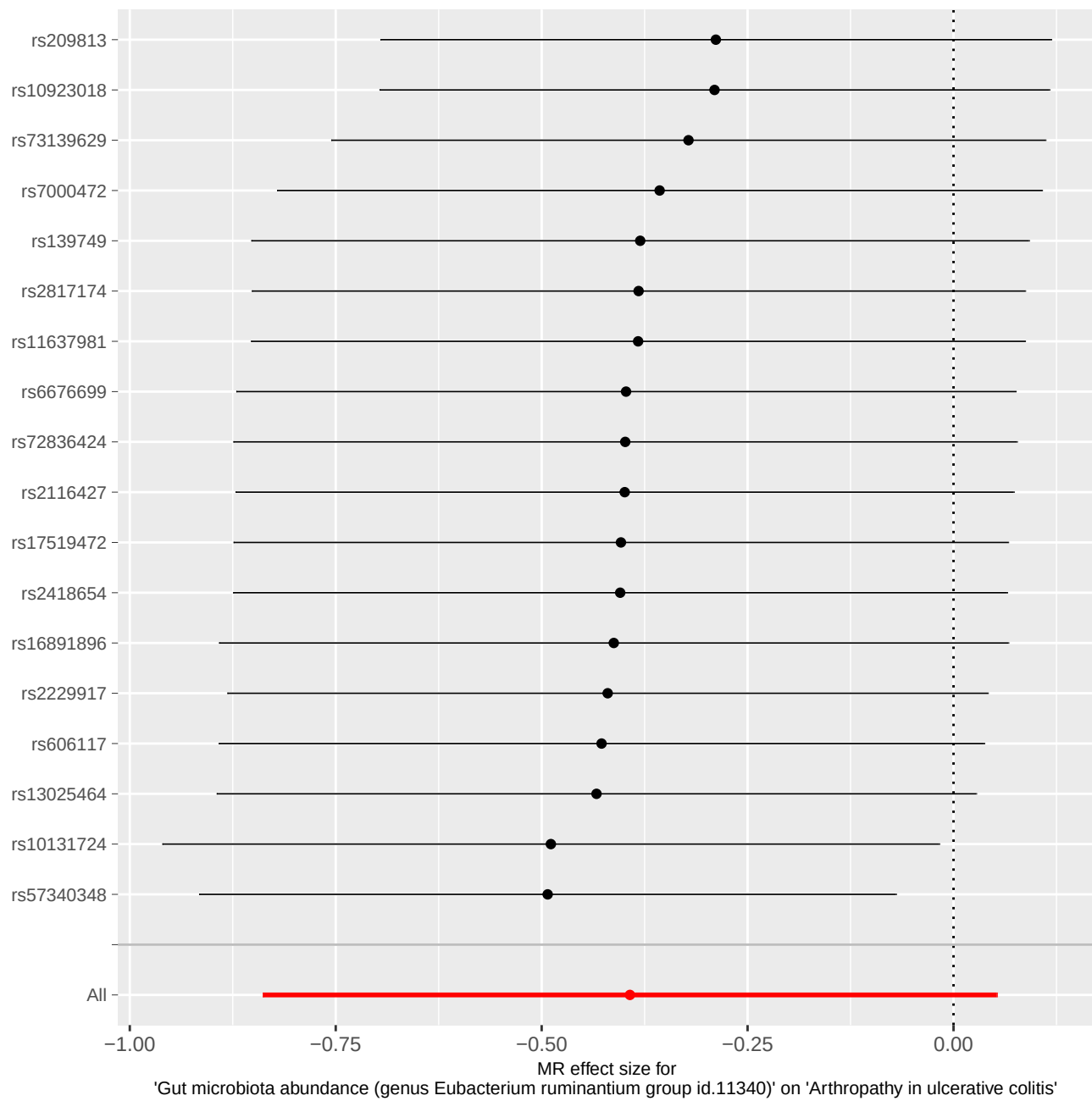
Batch 824 : Gut microbiota abundance (genus Eubacterium hallii group id.11338) on Arthropathy in ulcerative colitis

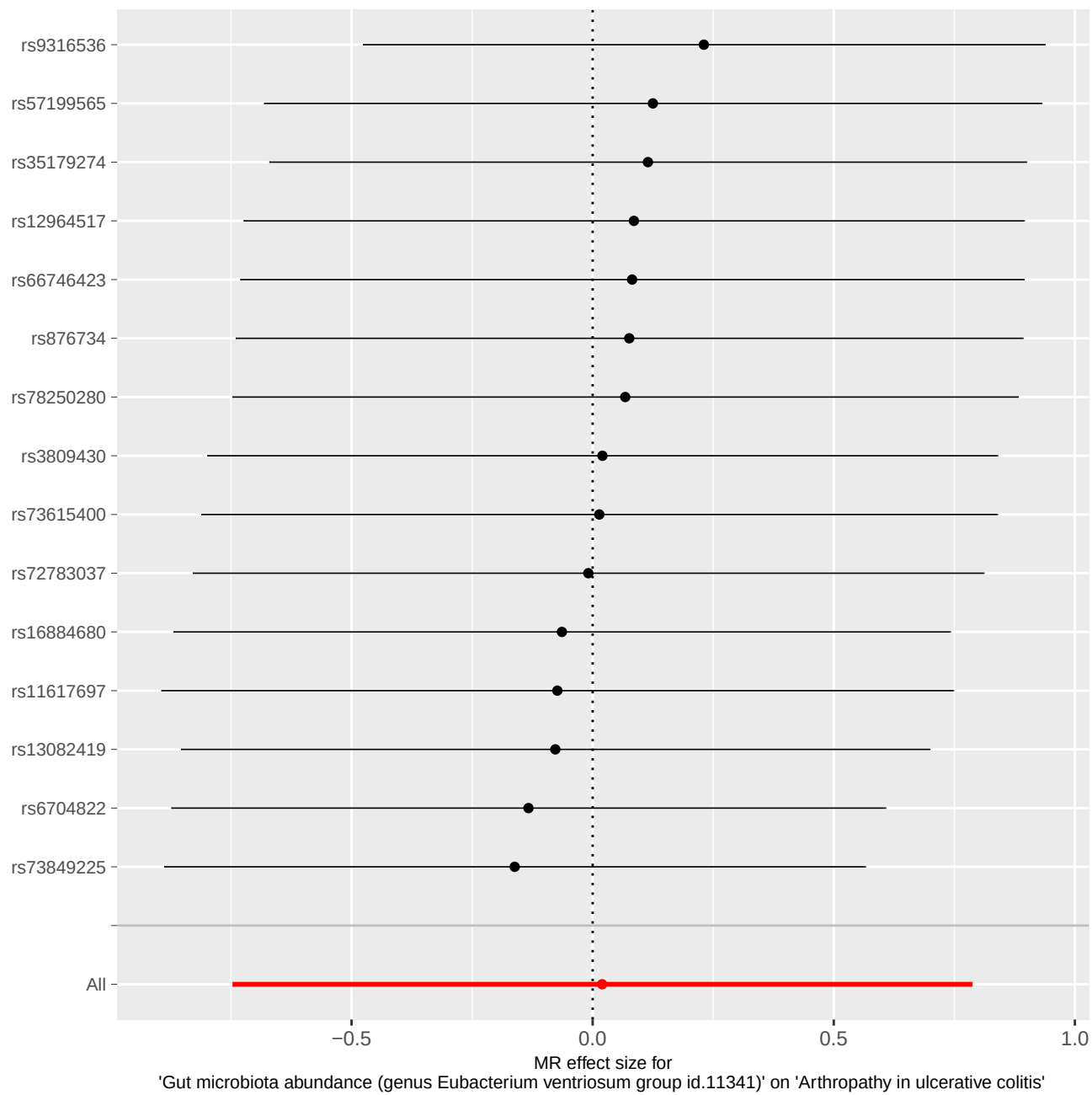


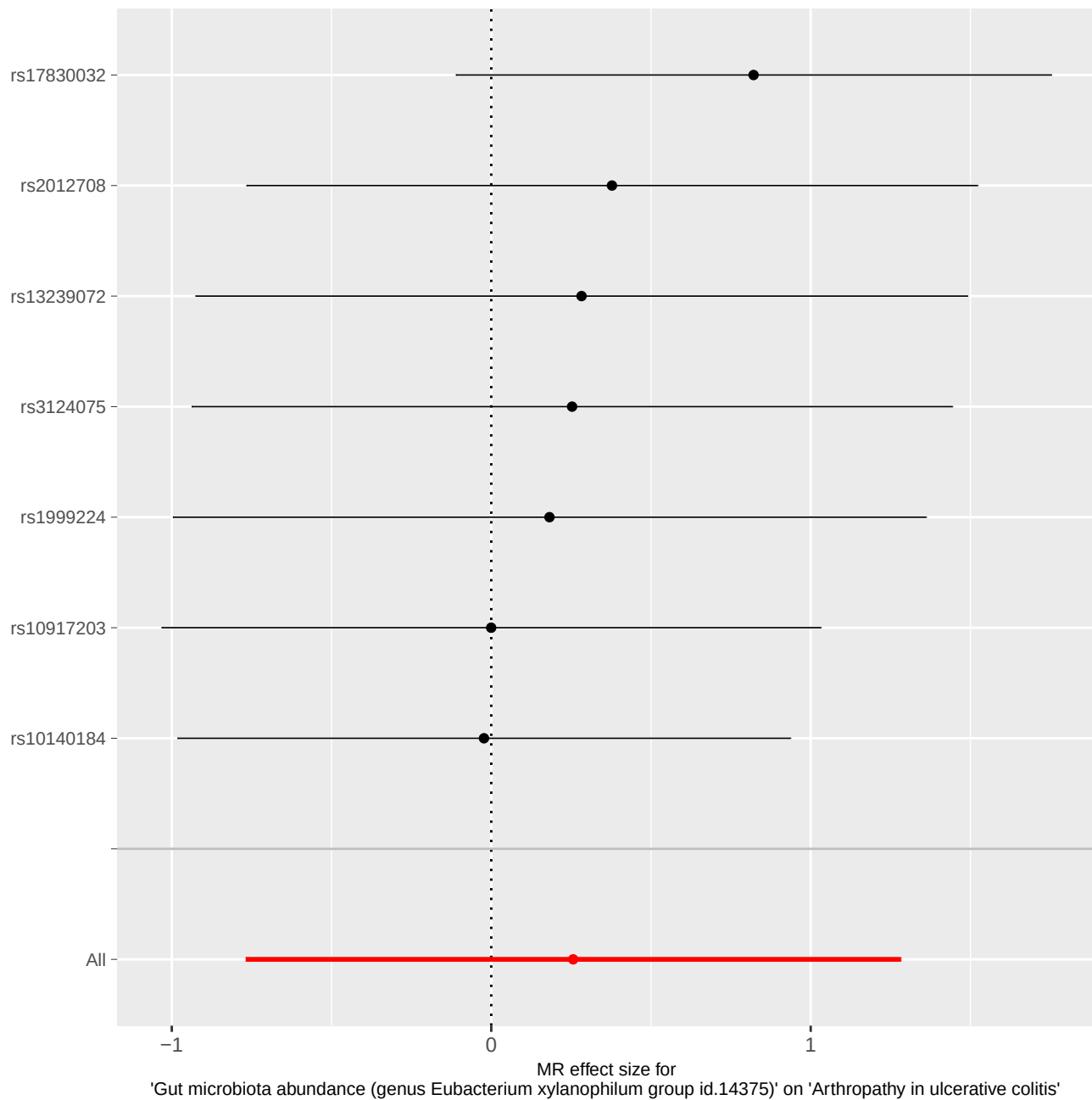


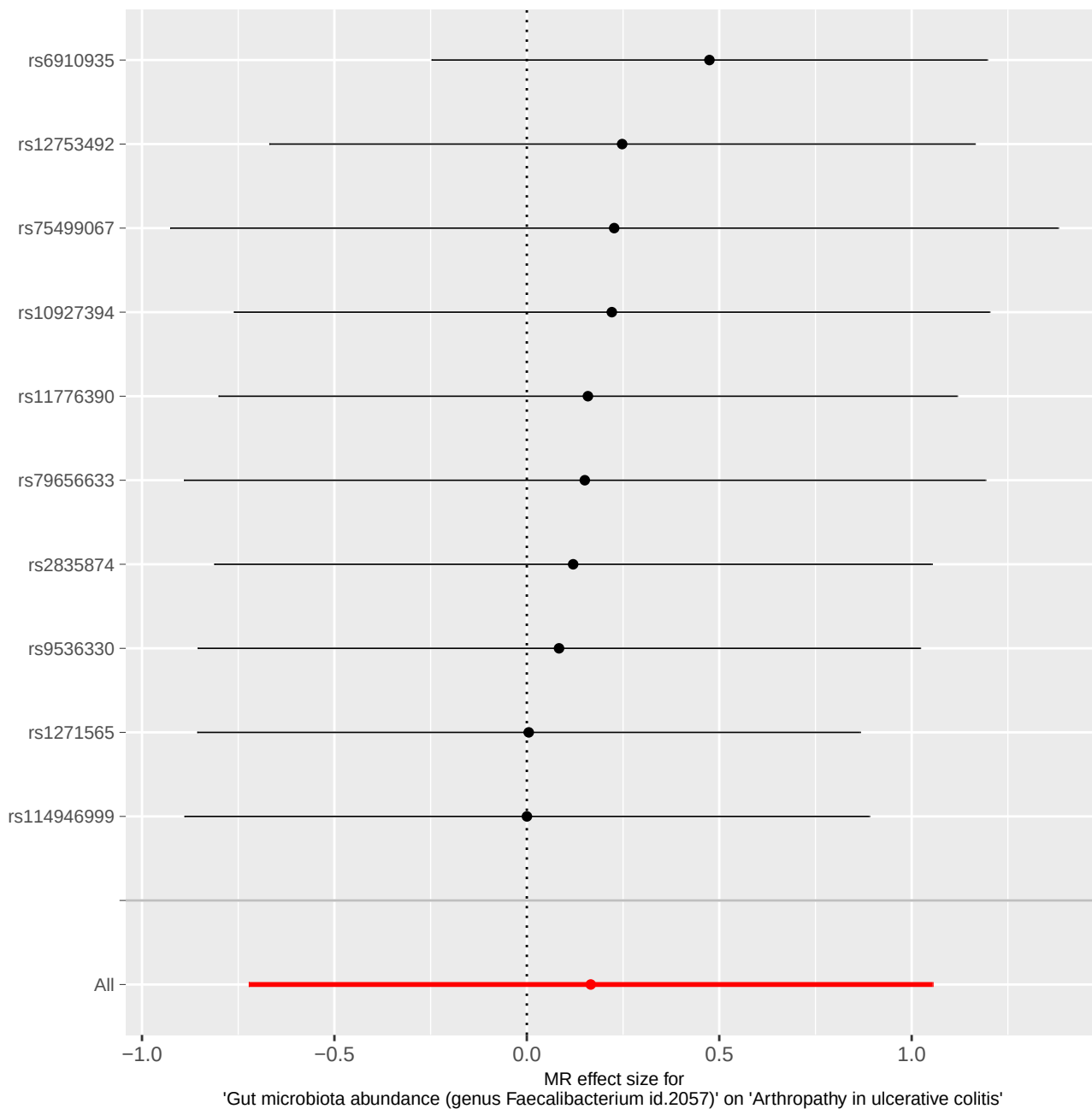


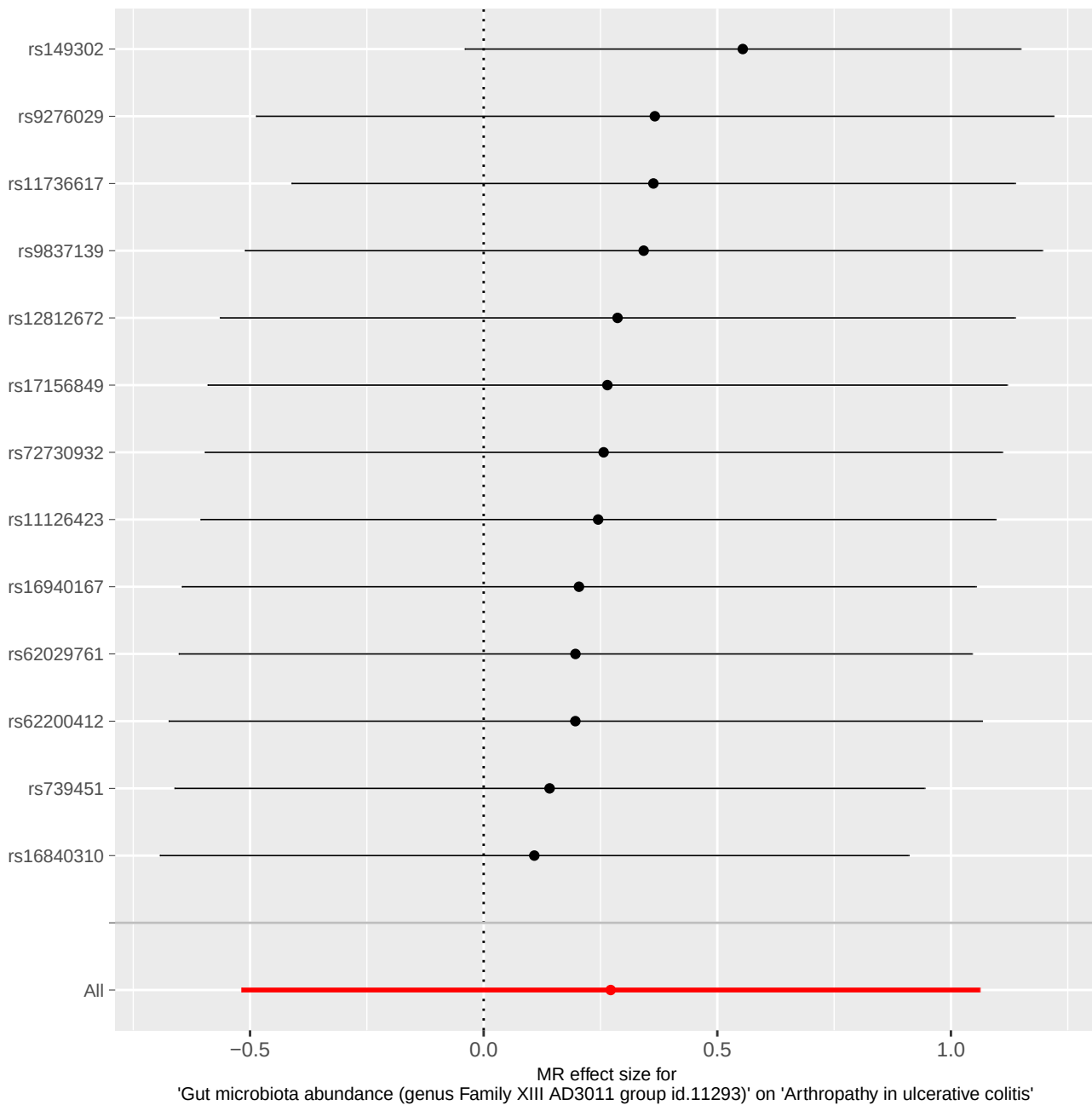


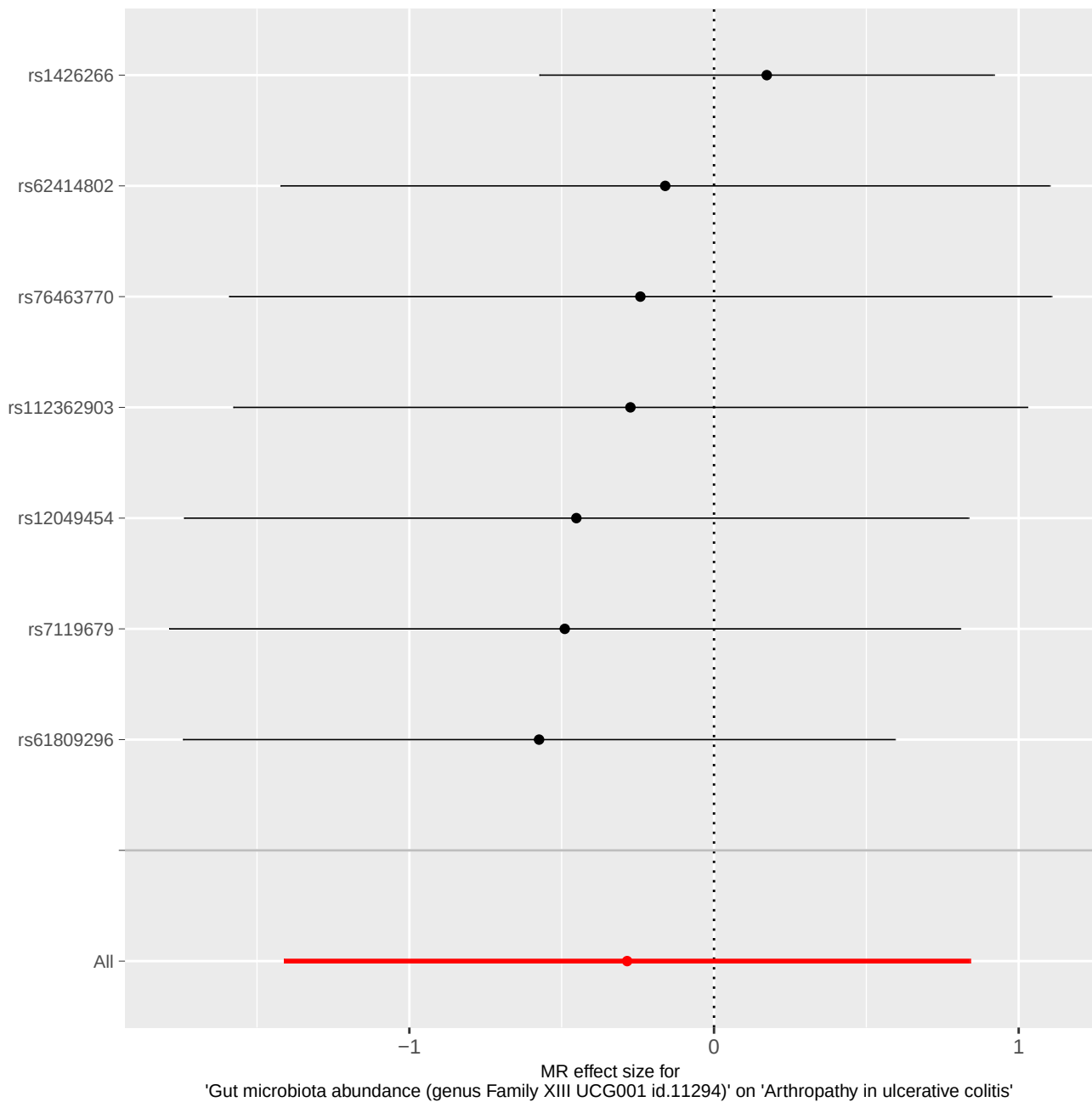


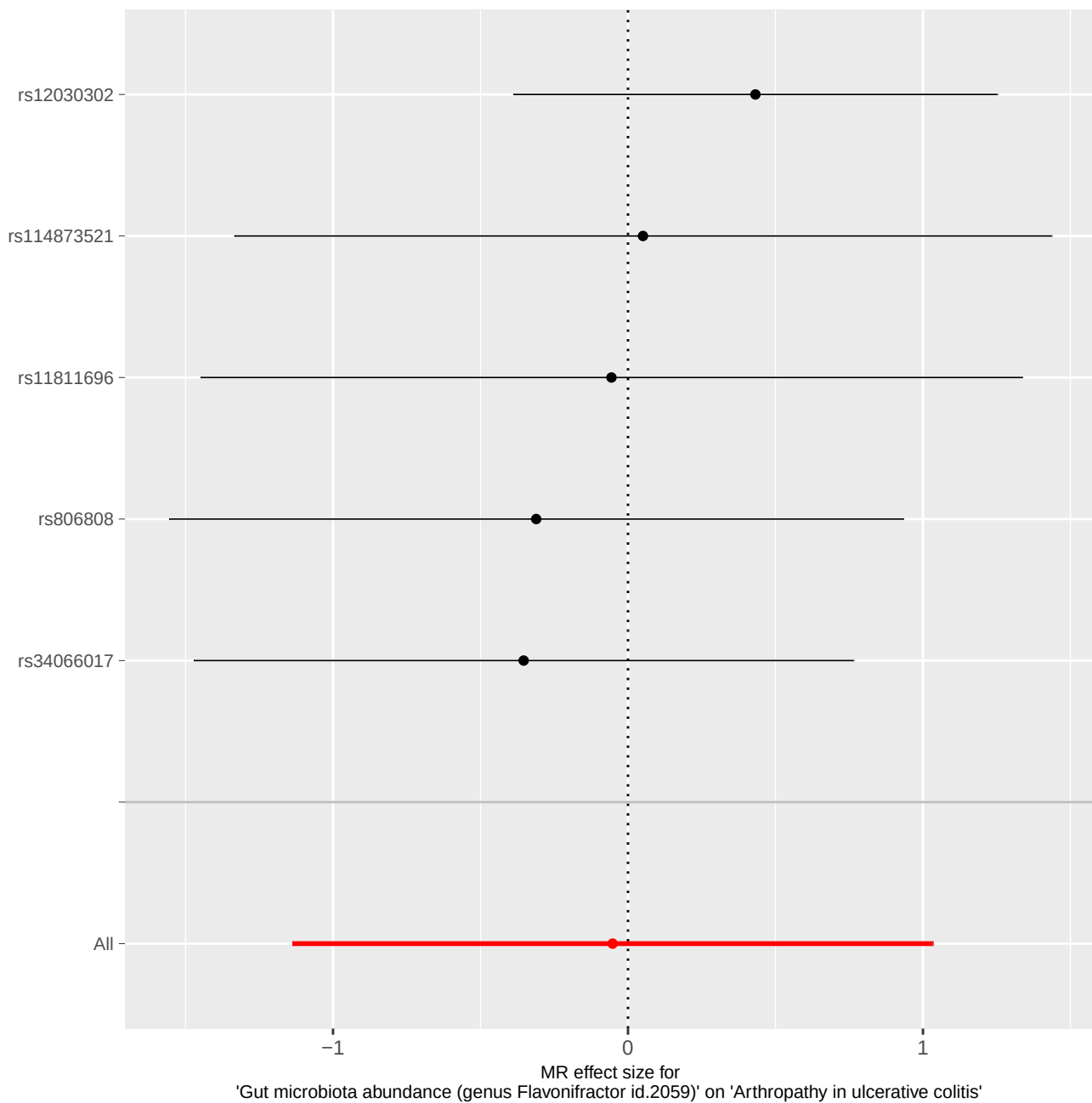


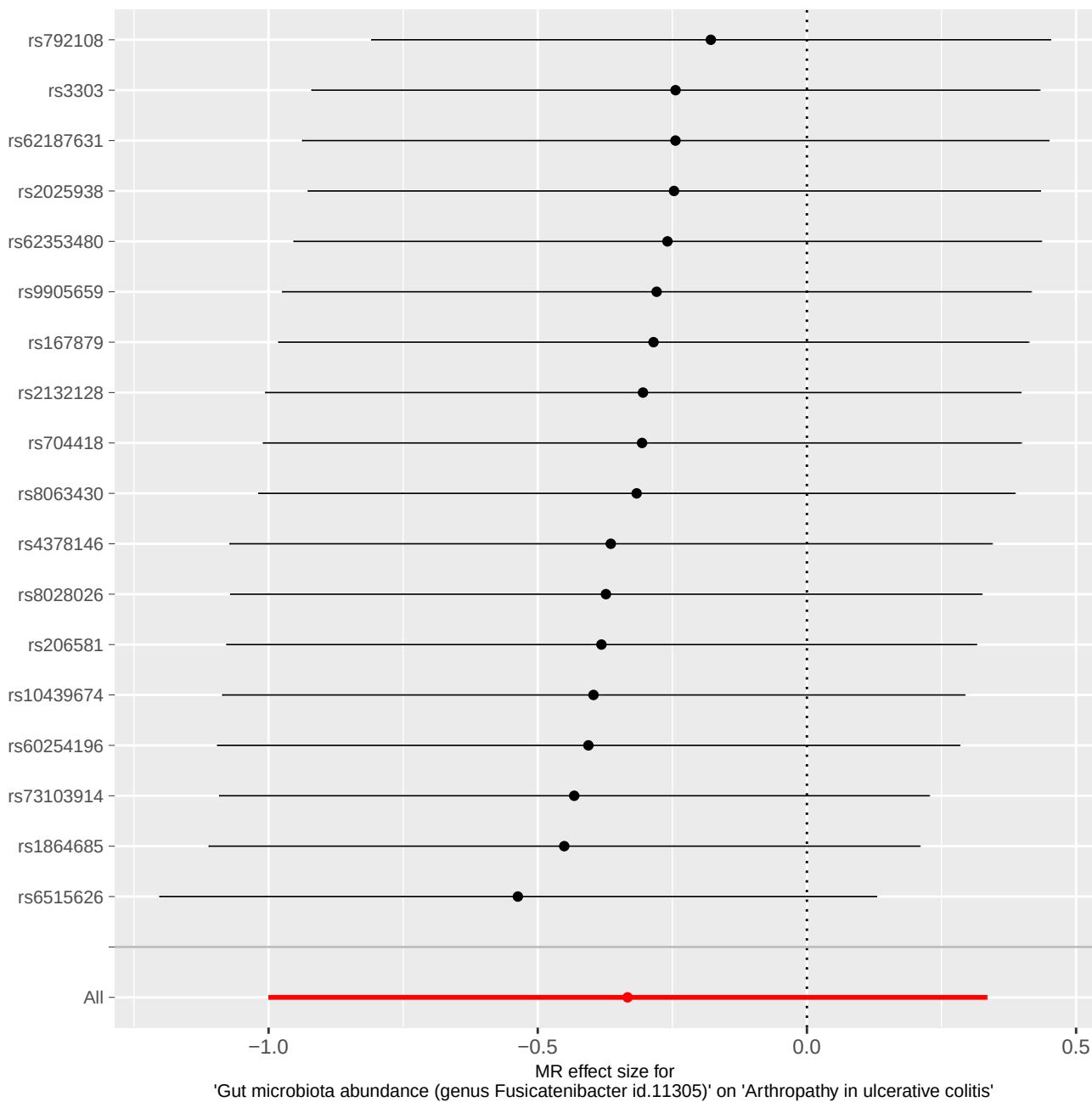


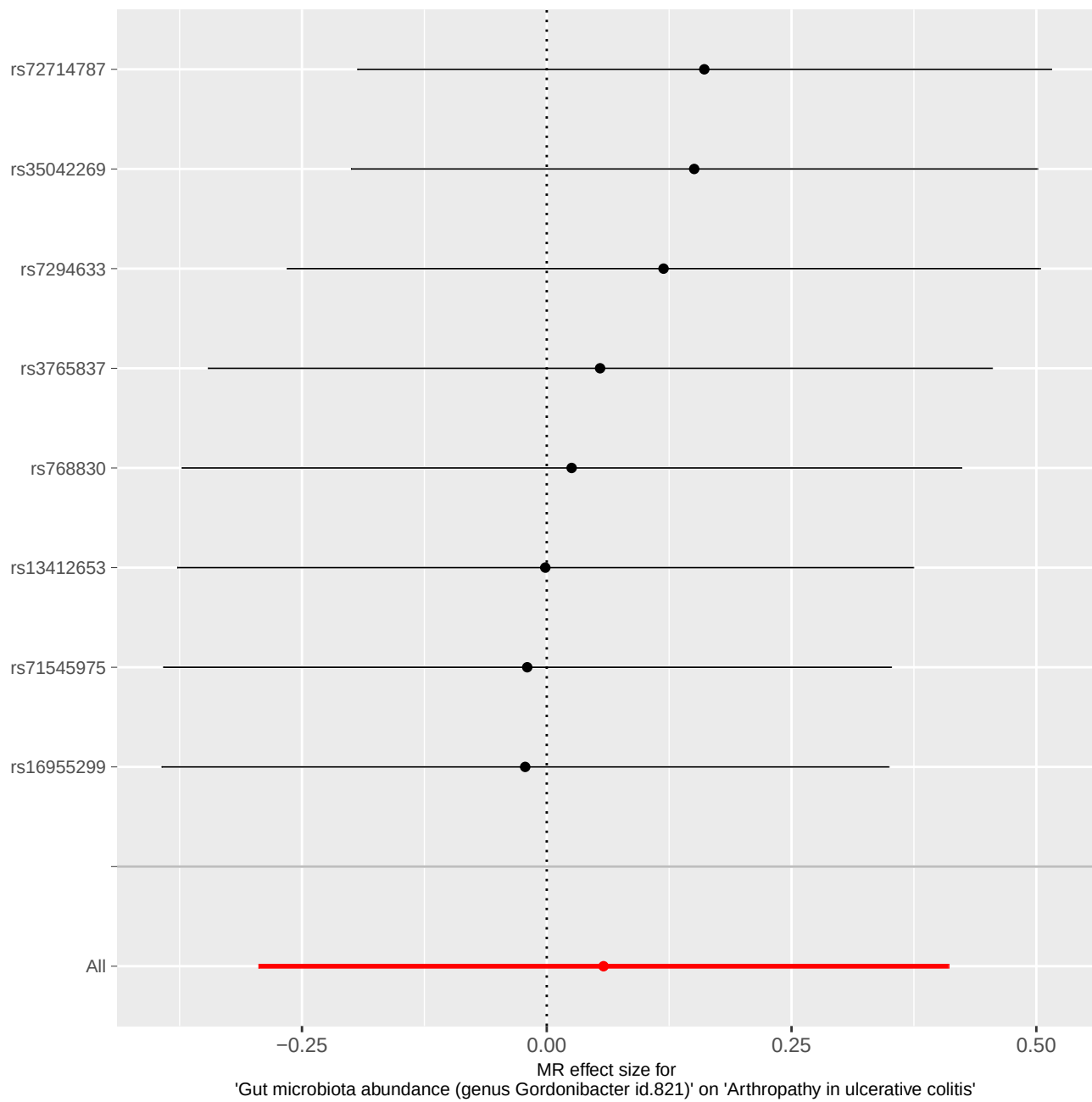


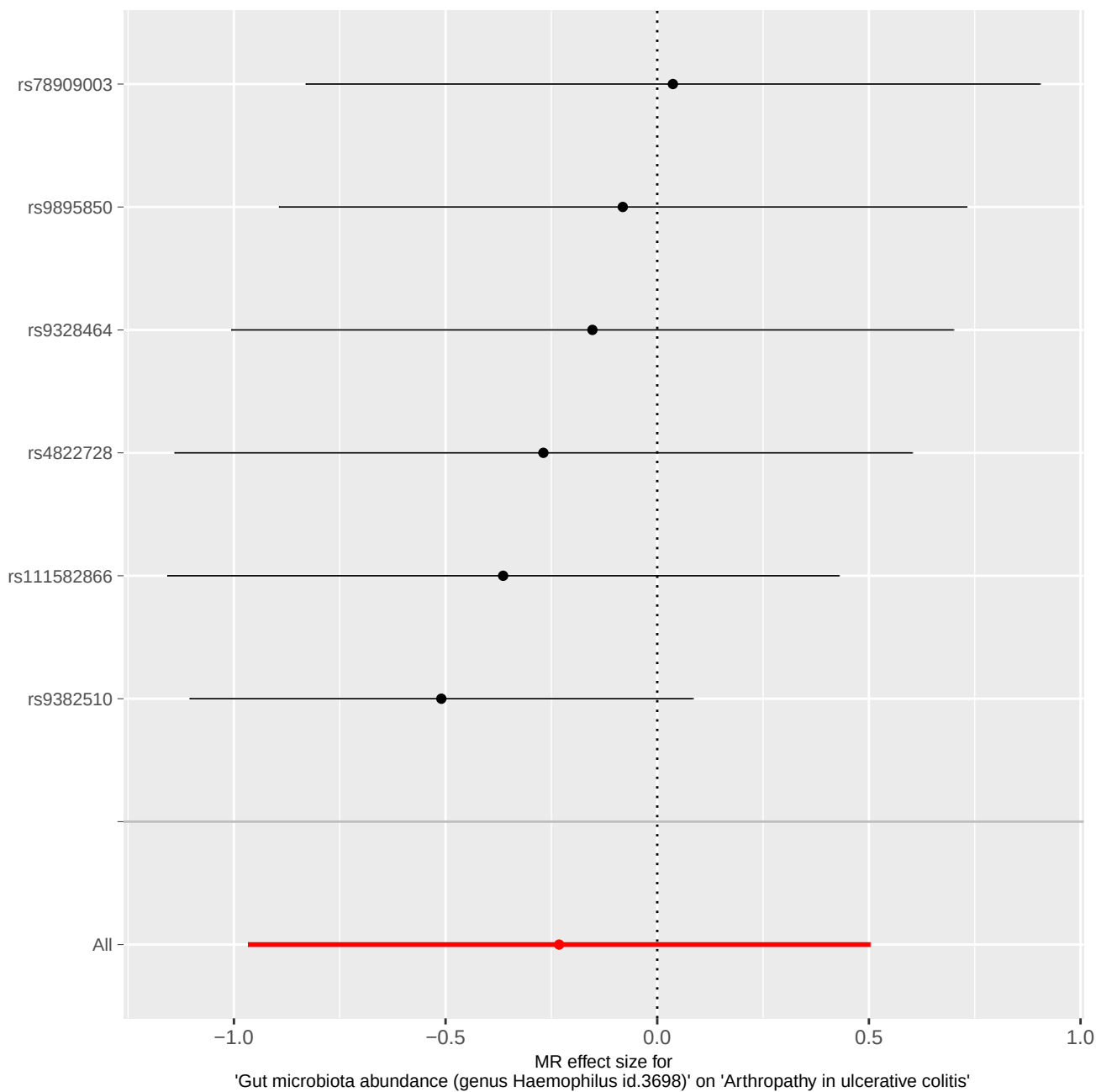


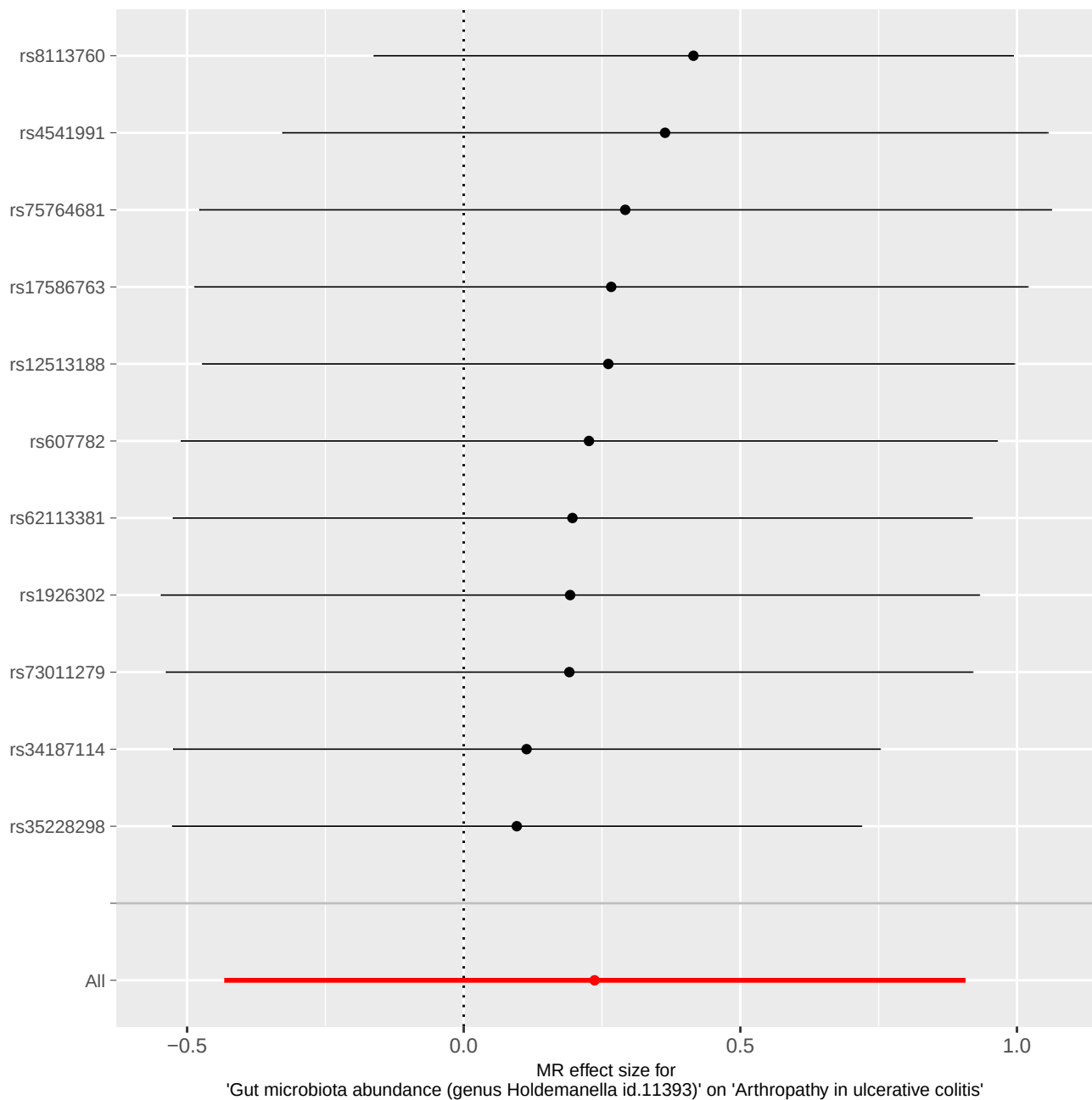


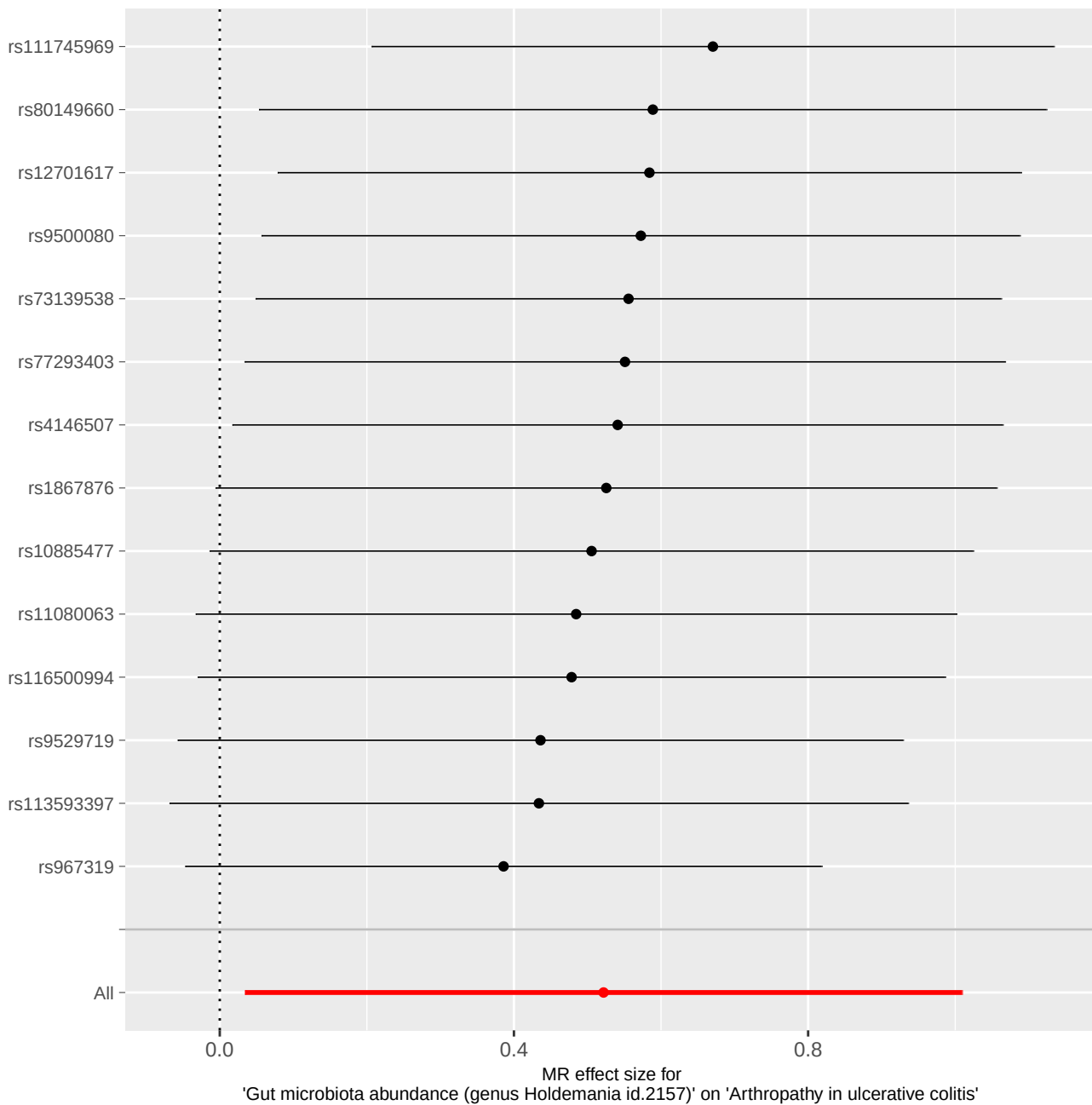


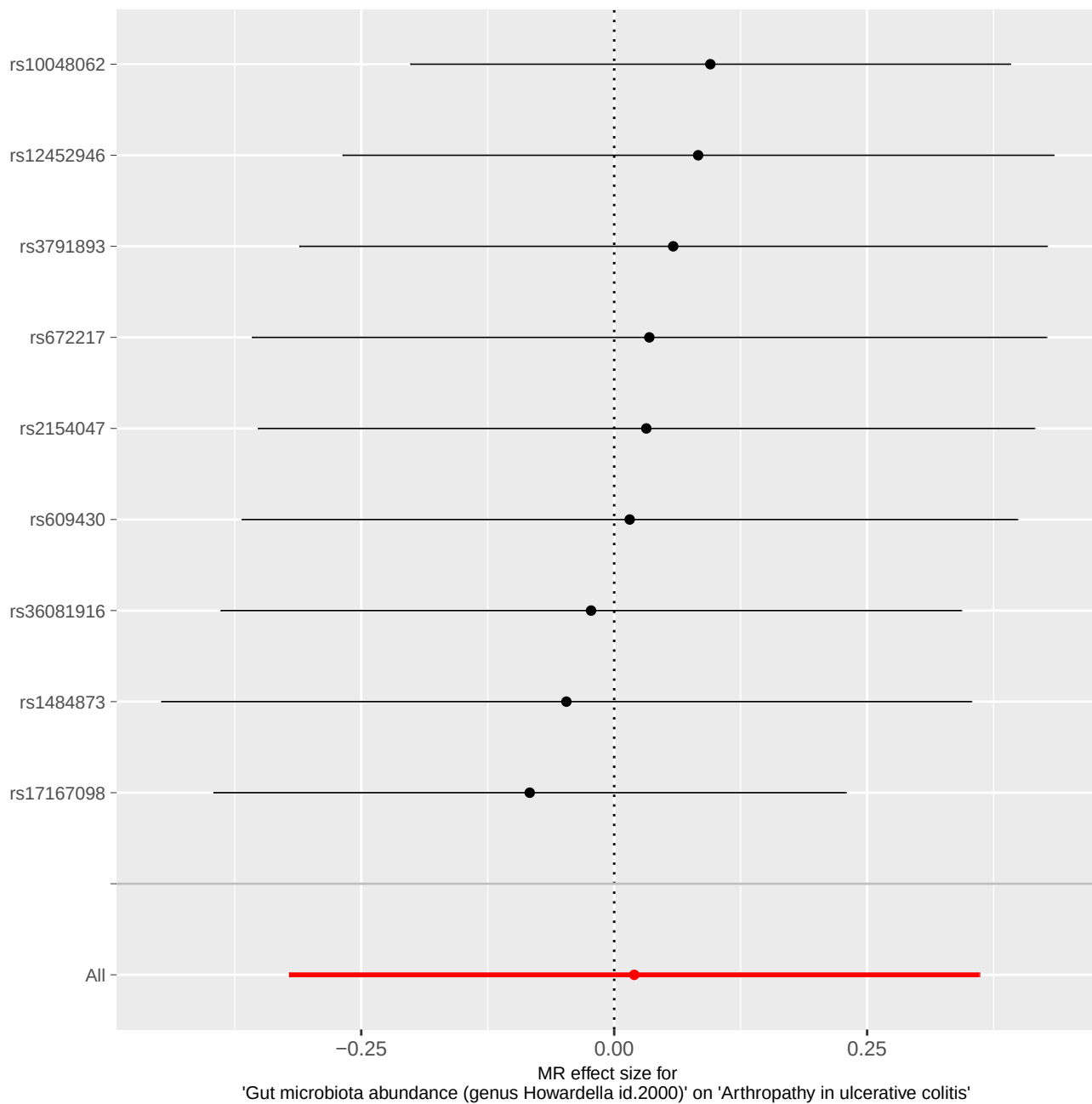


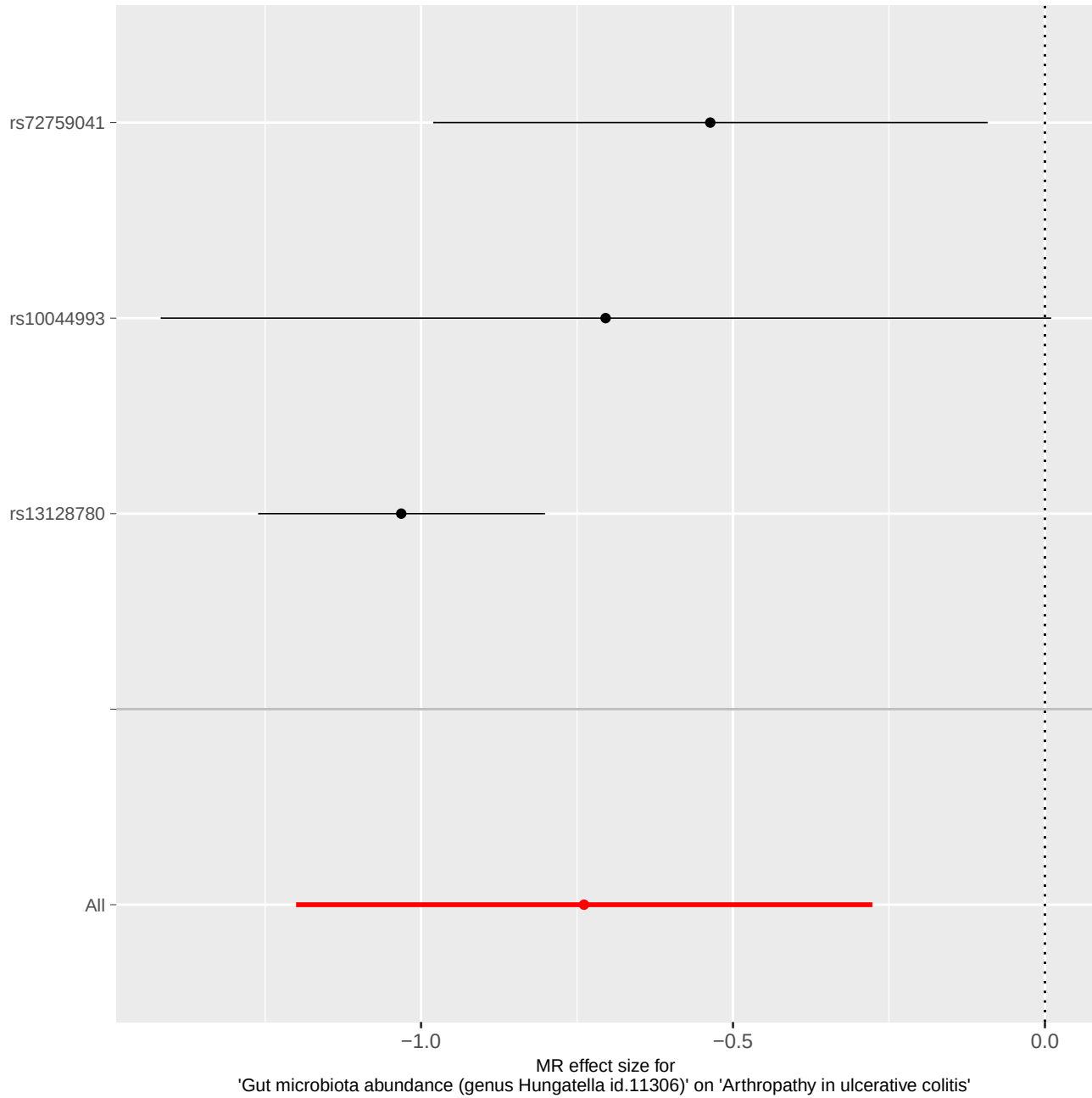


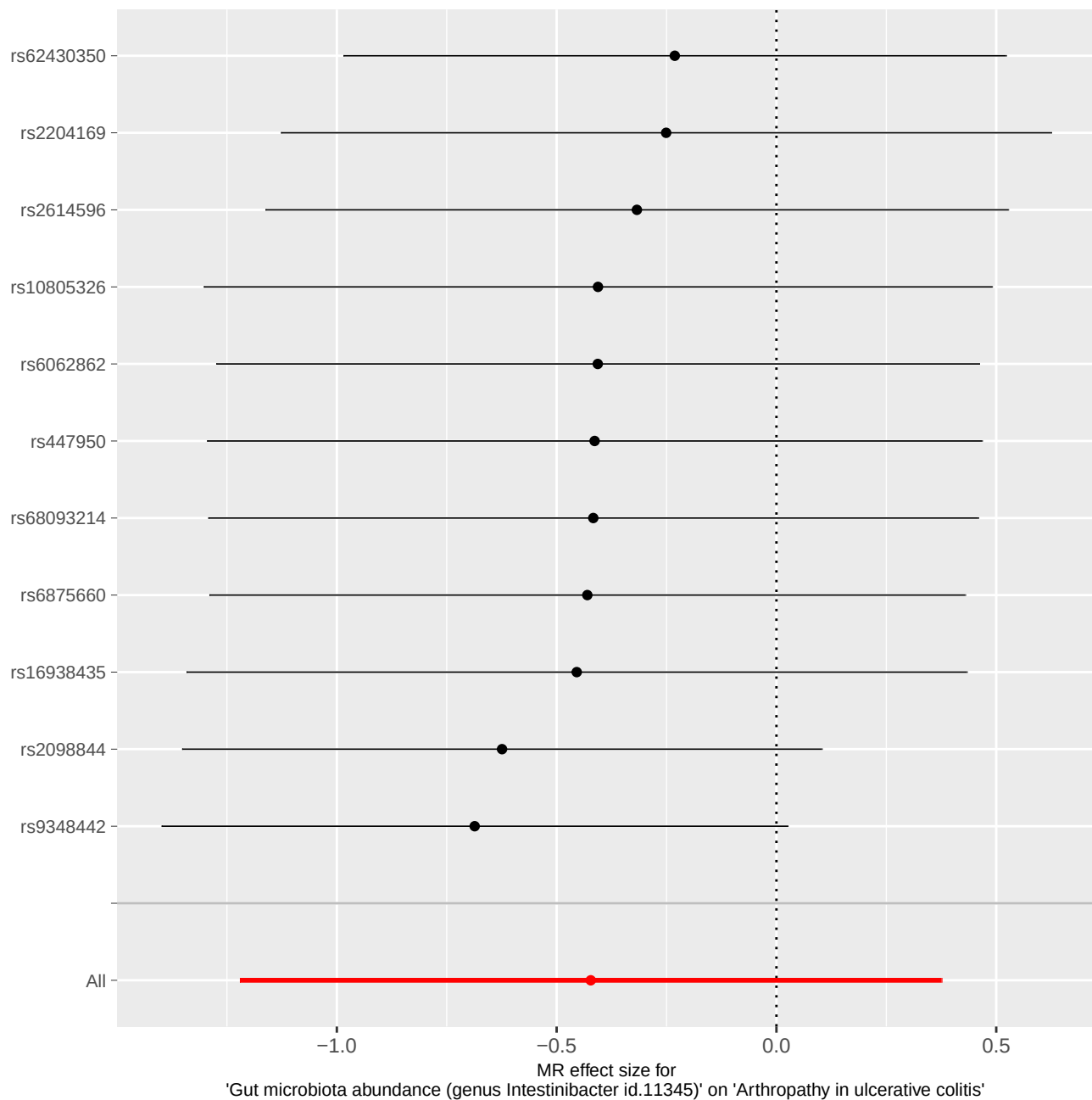


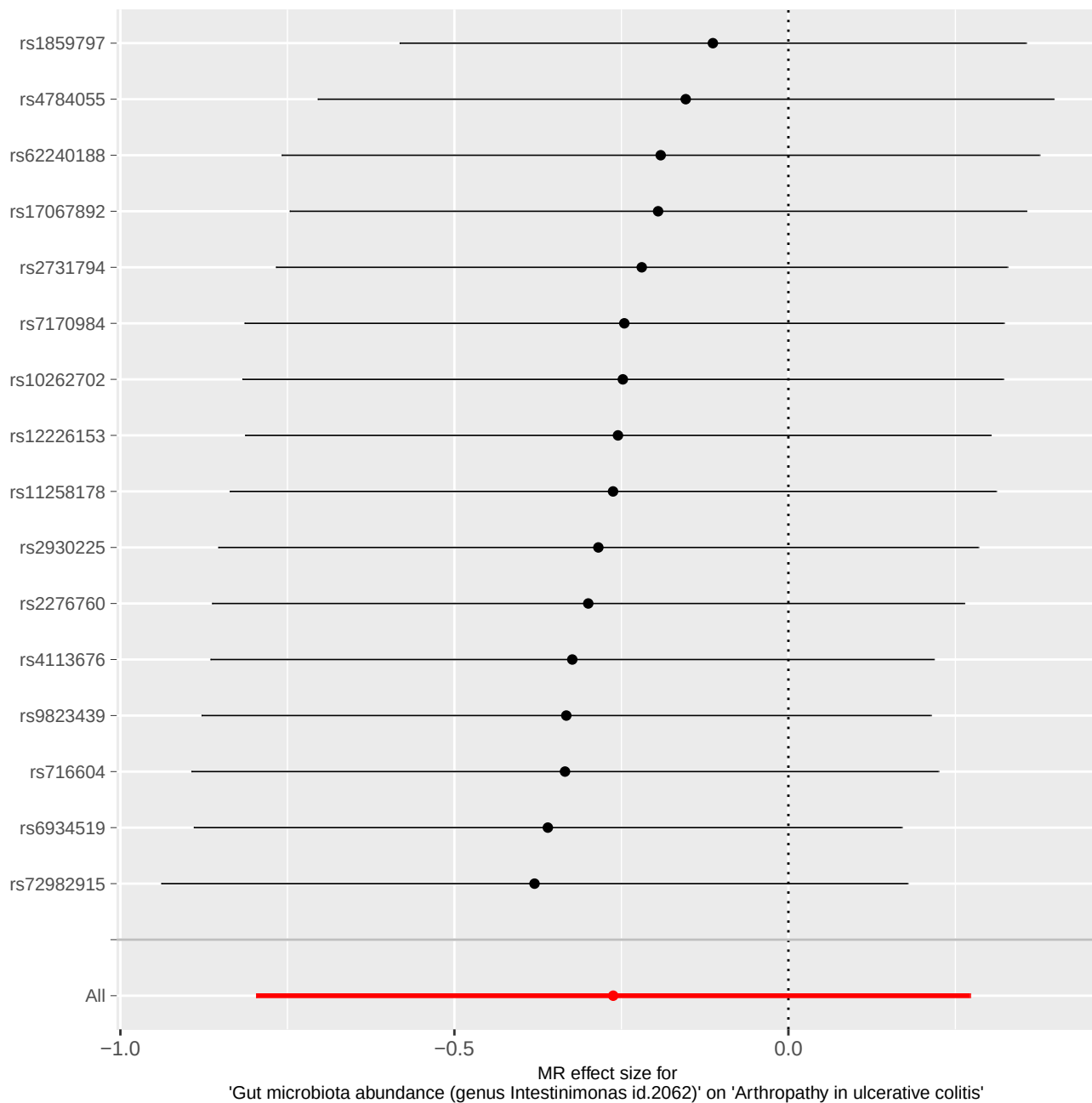


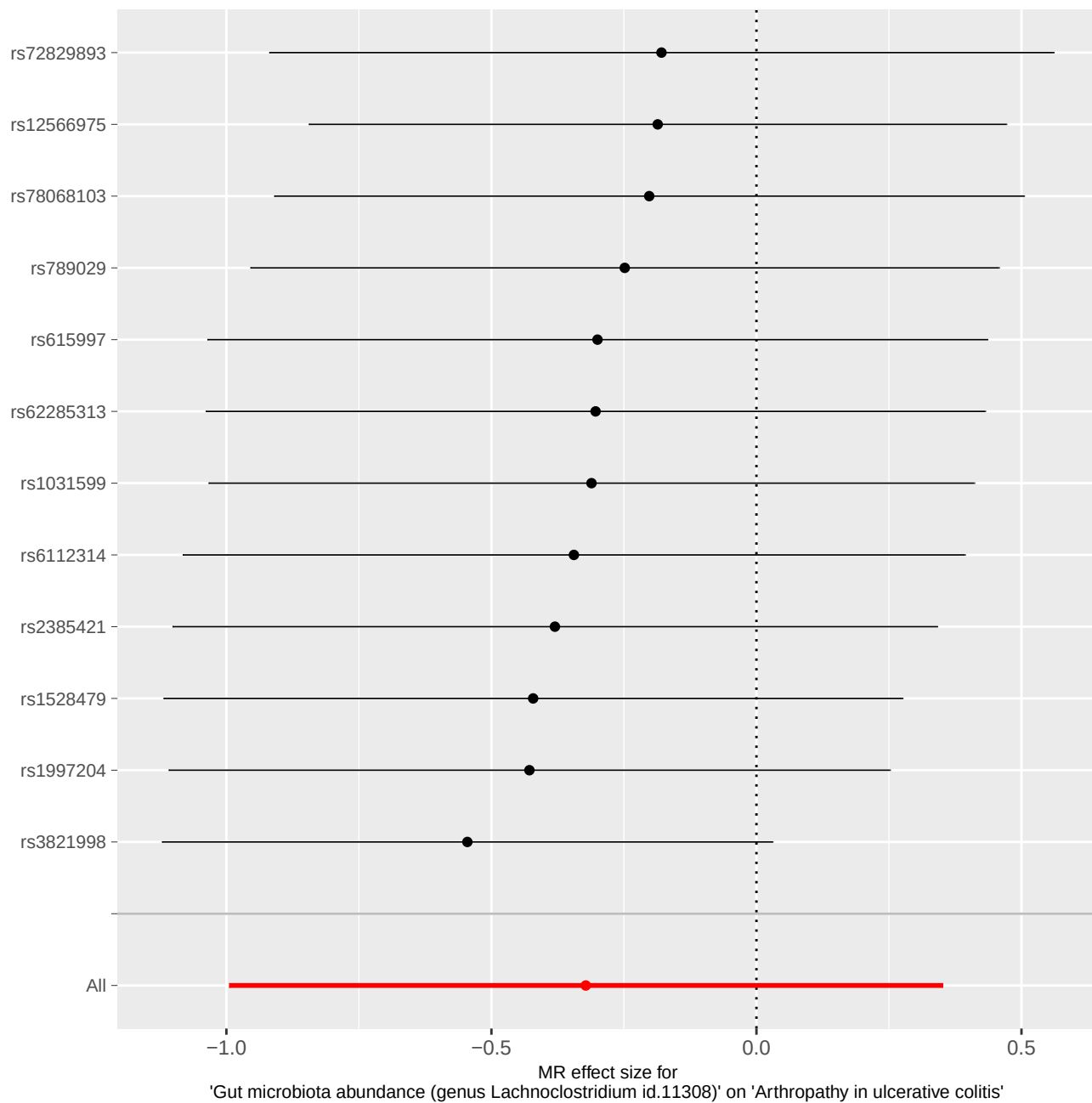


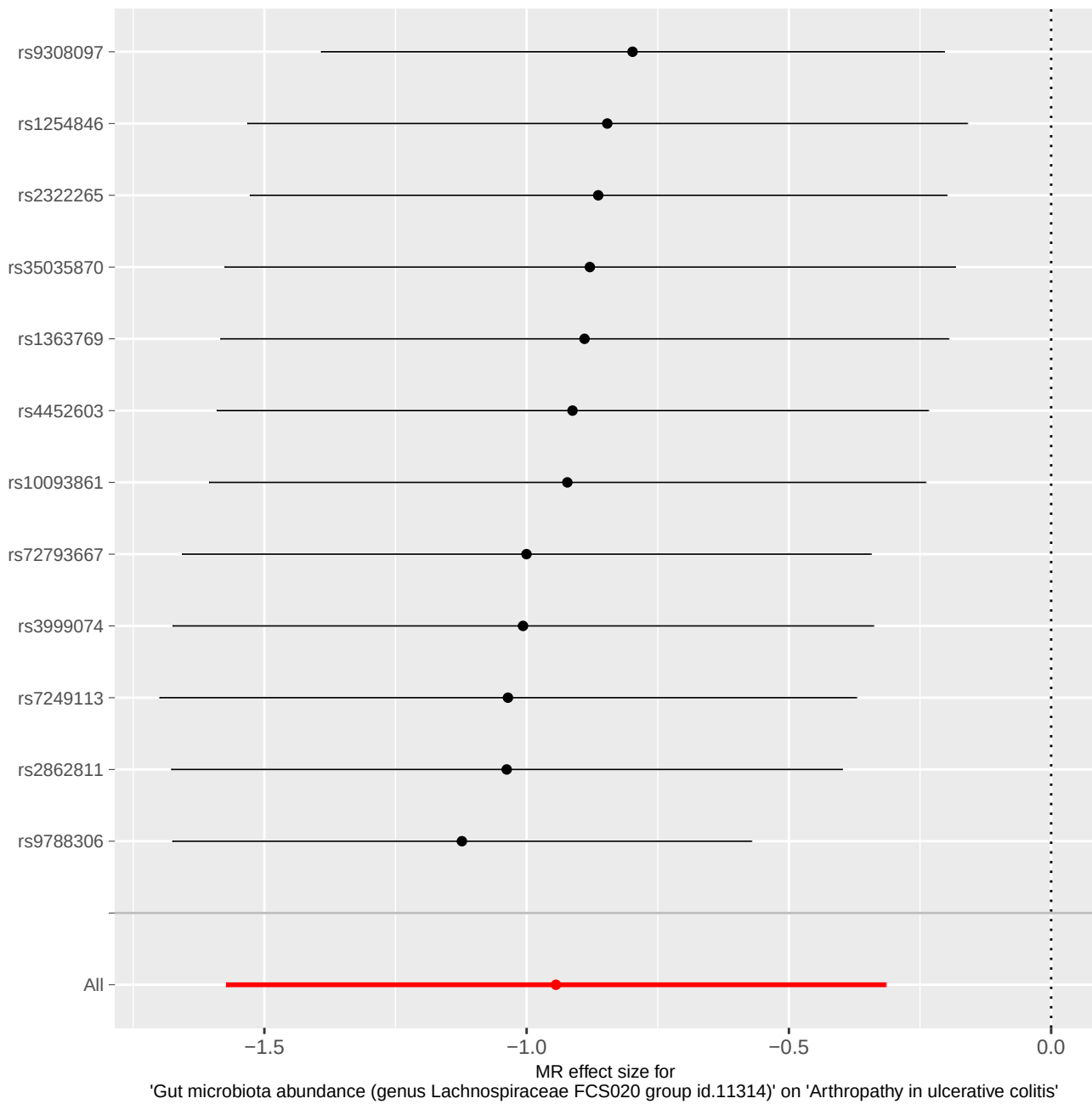


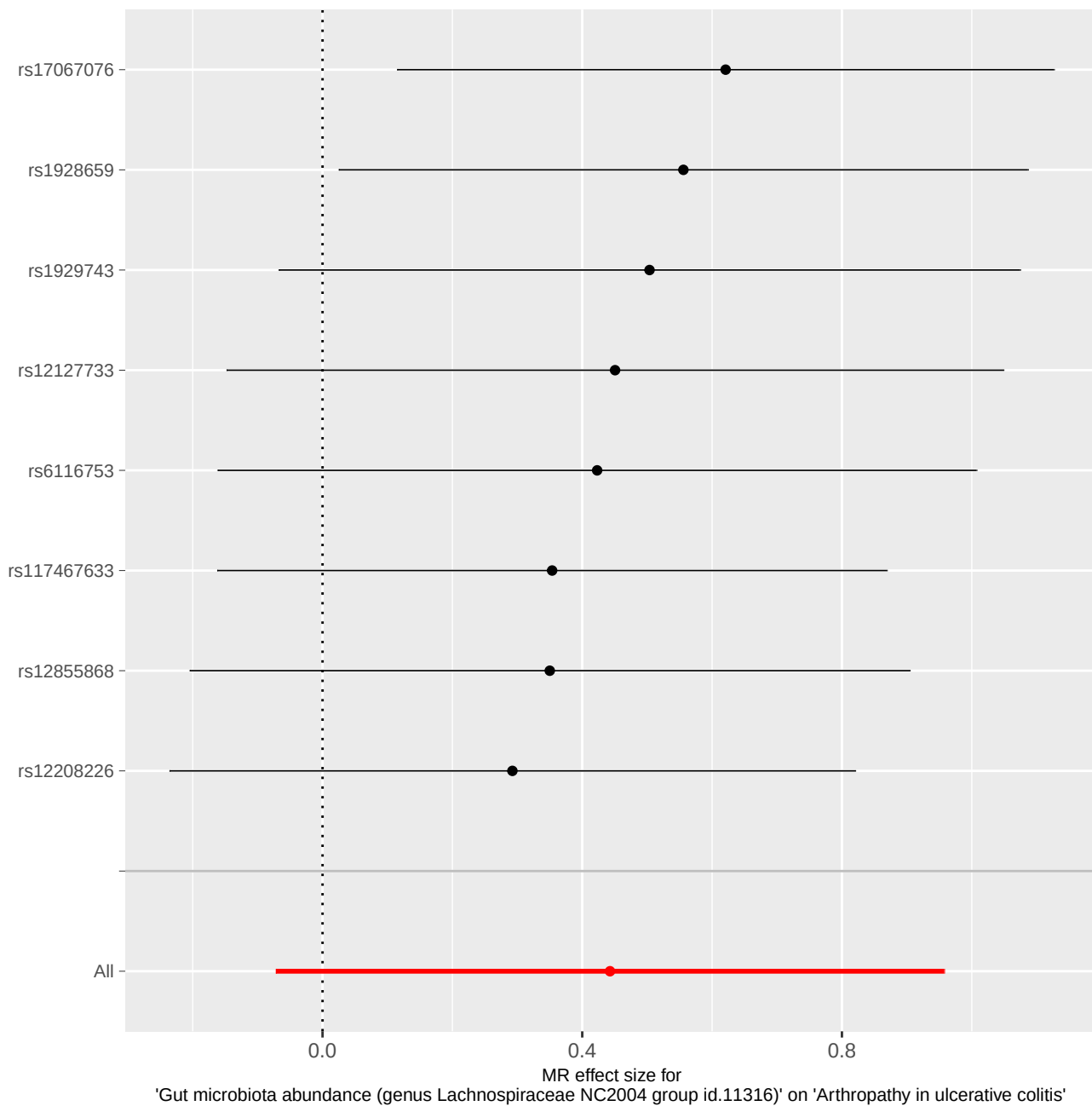


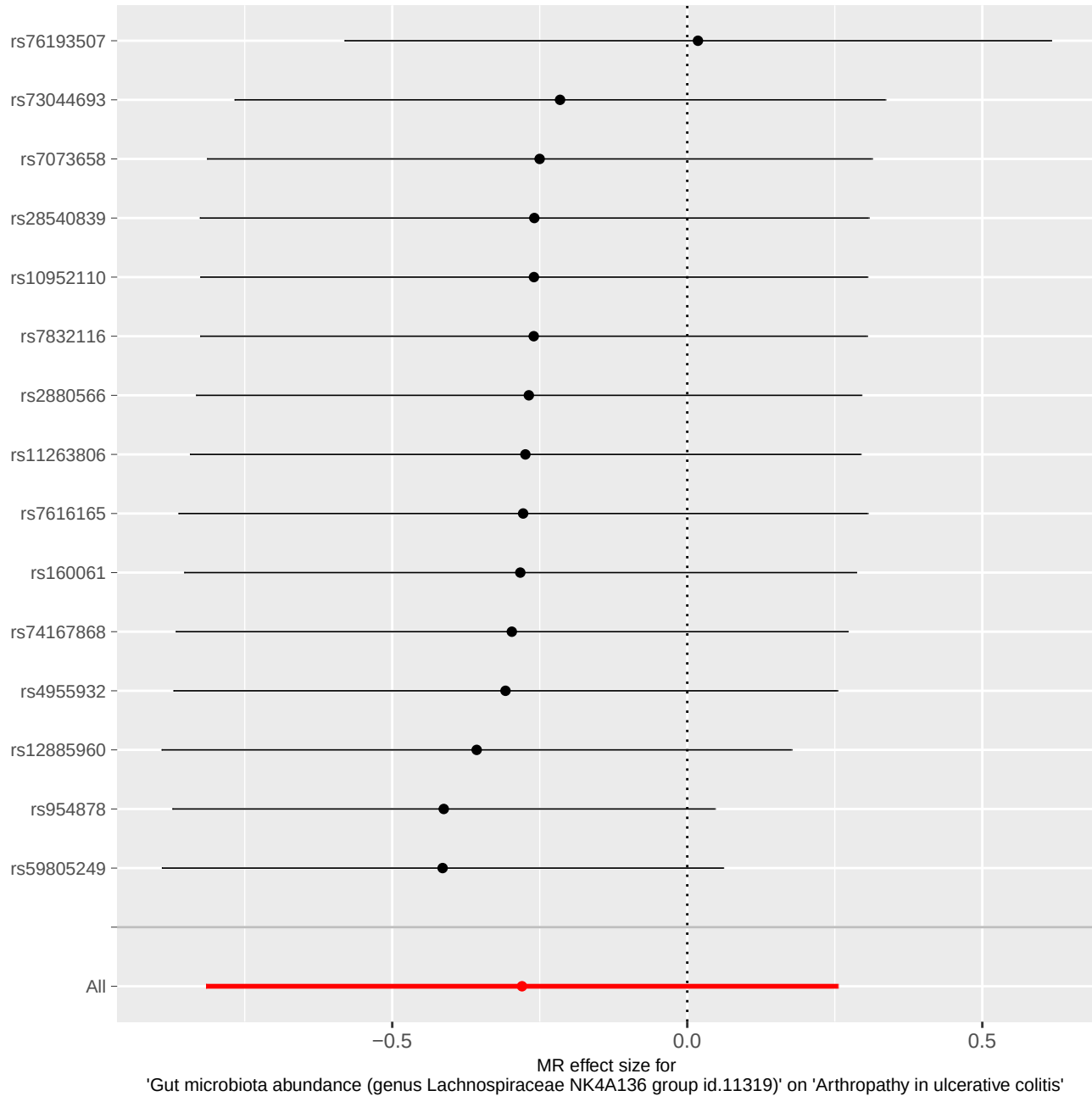


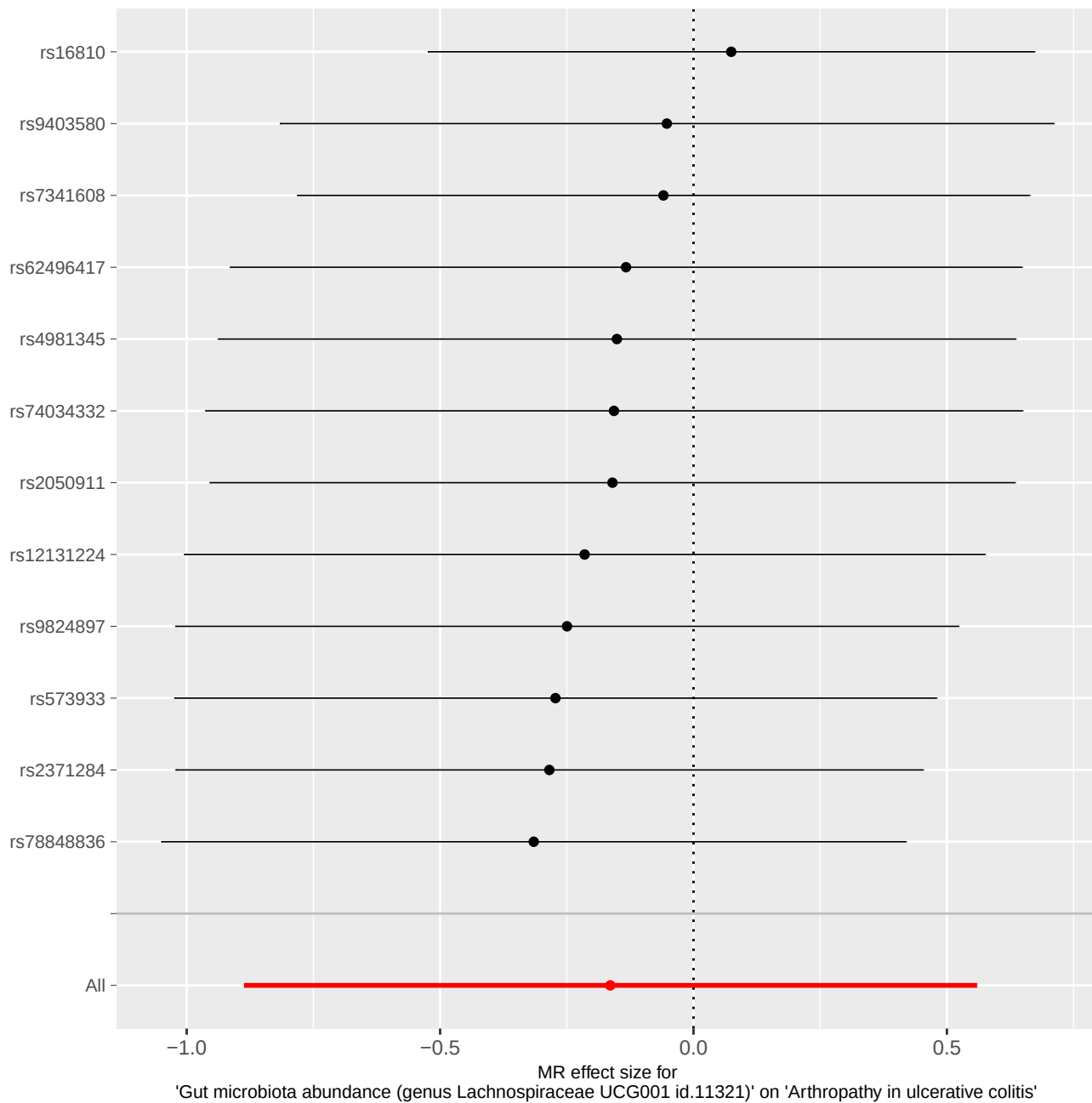


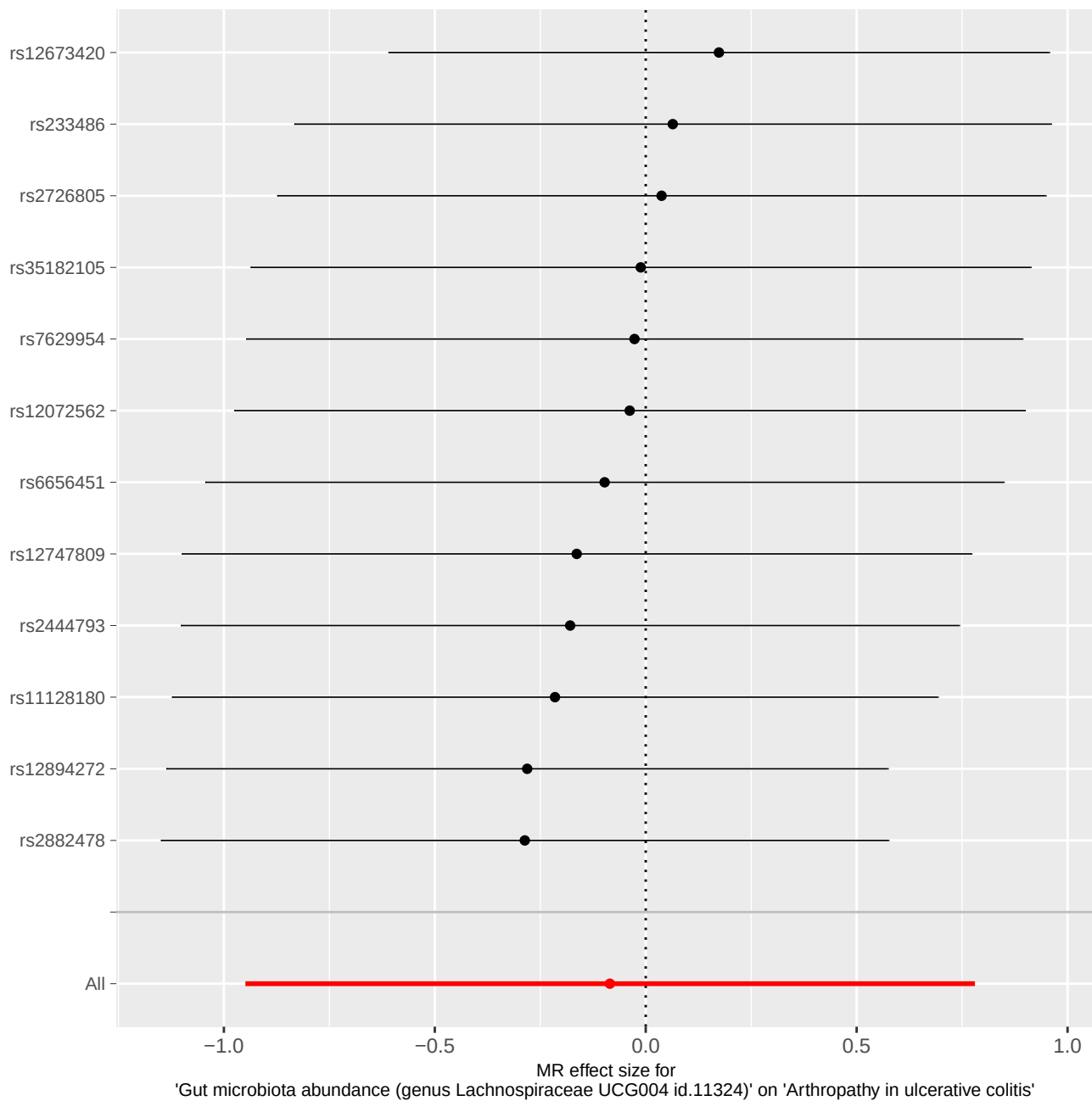


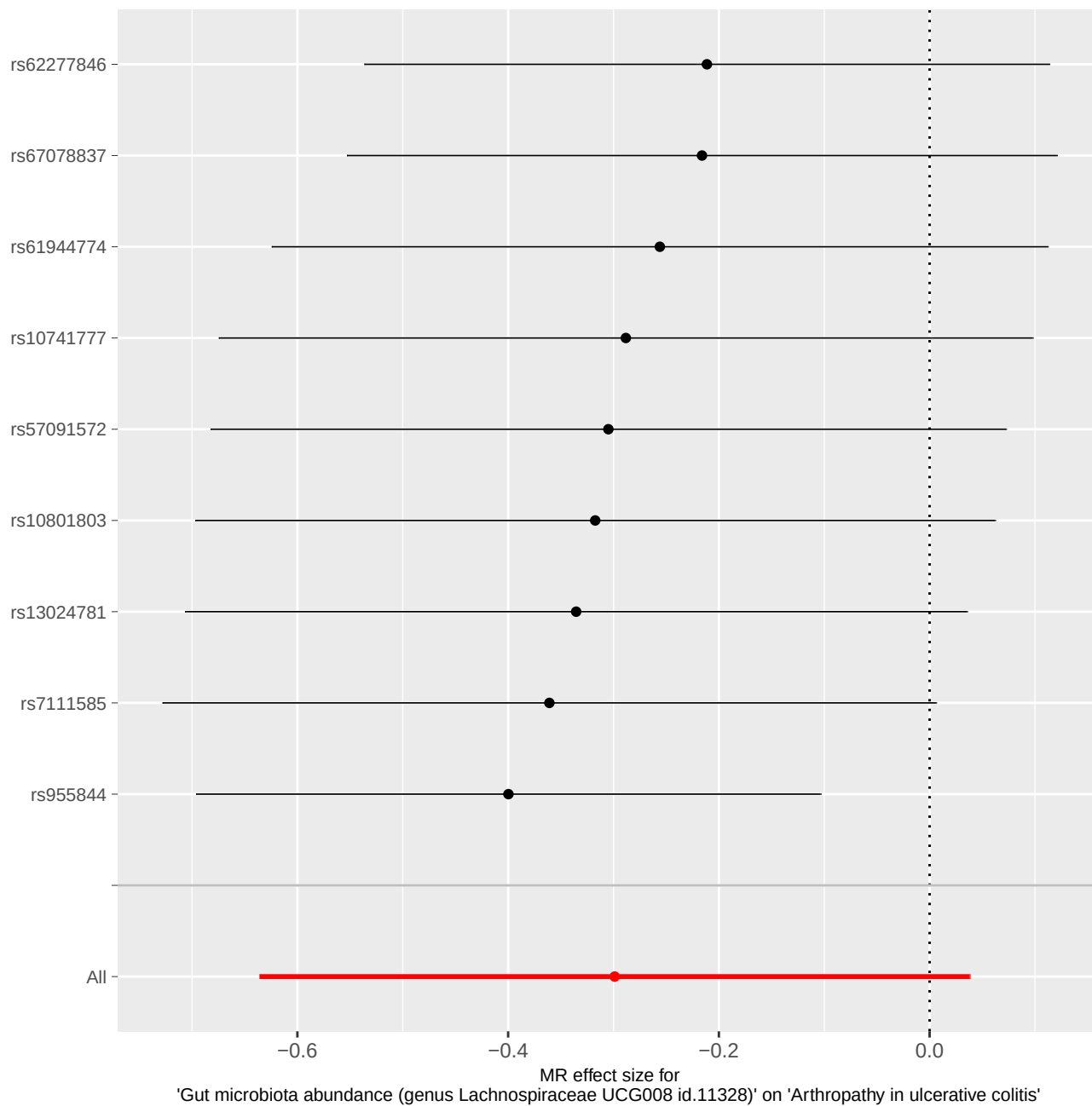




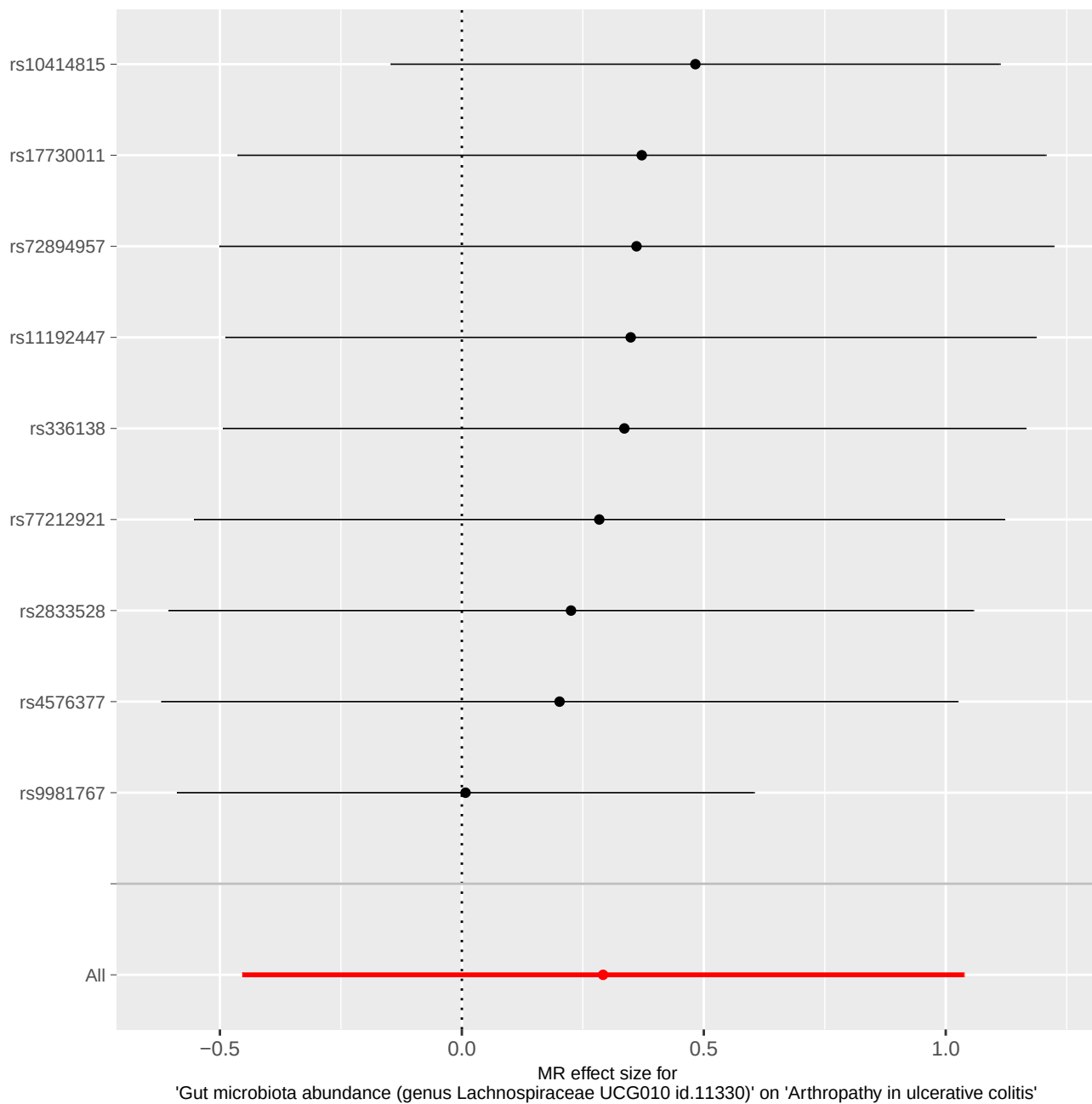




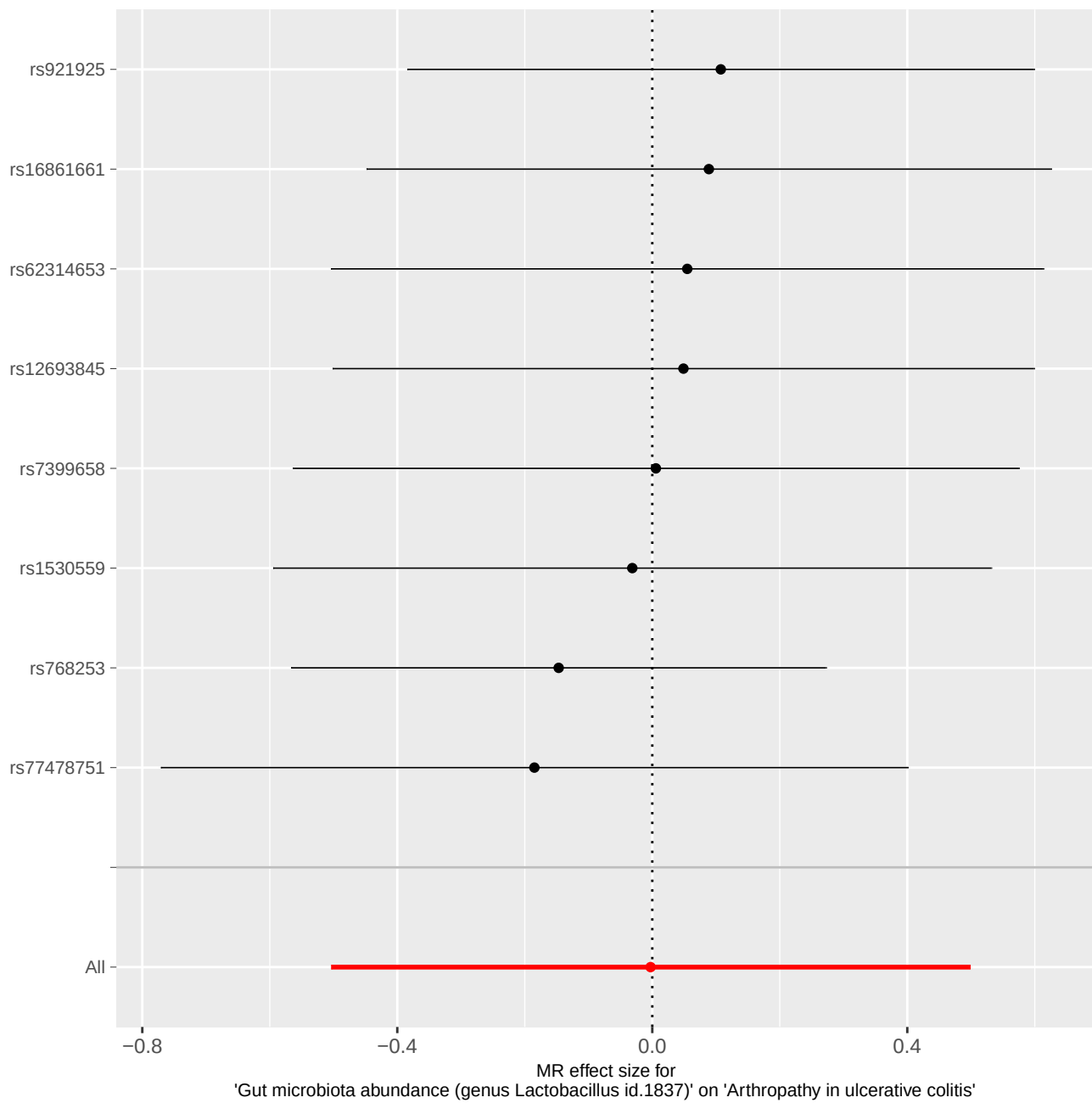


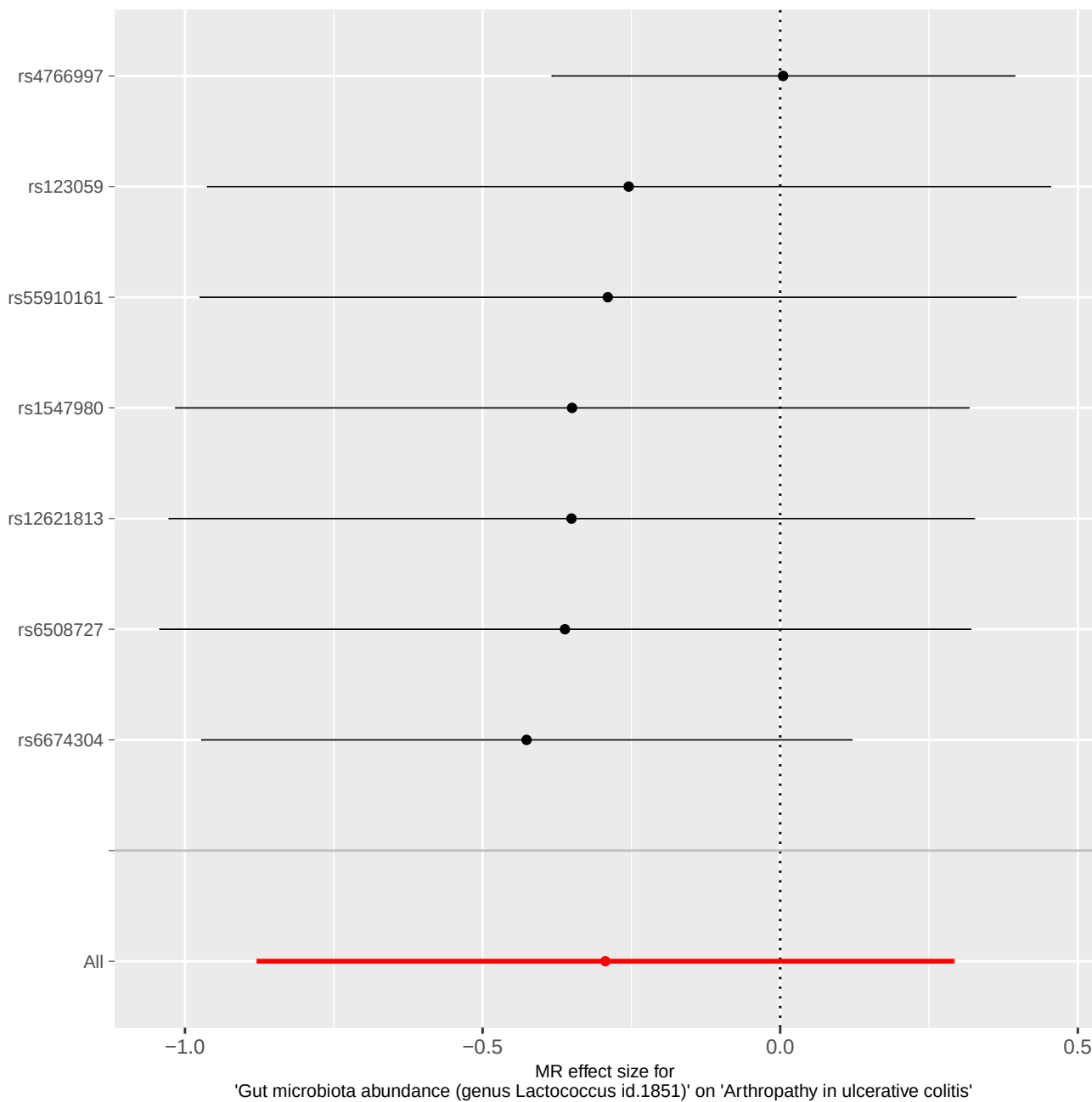


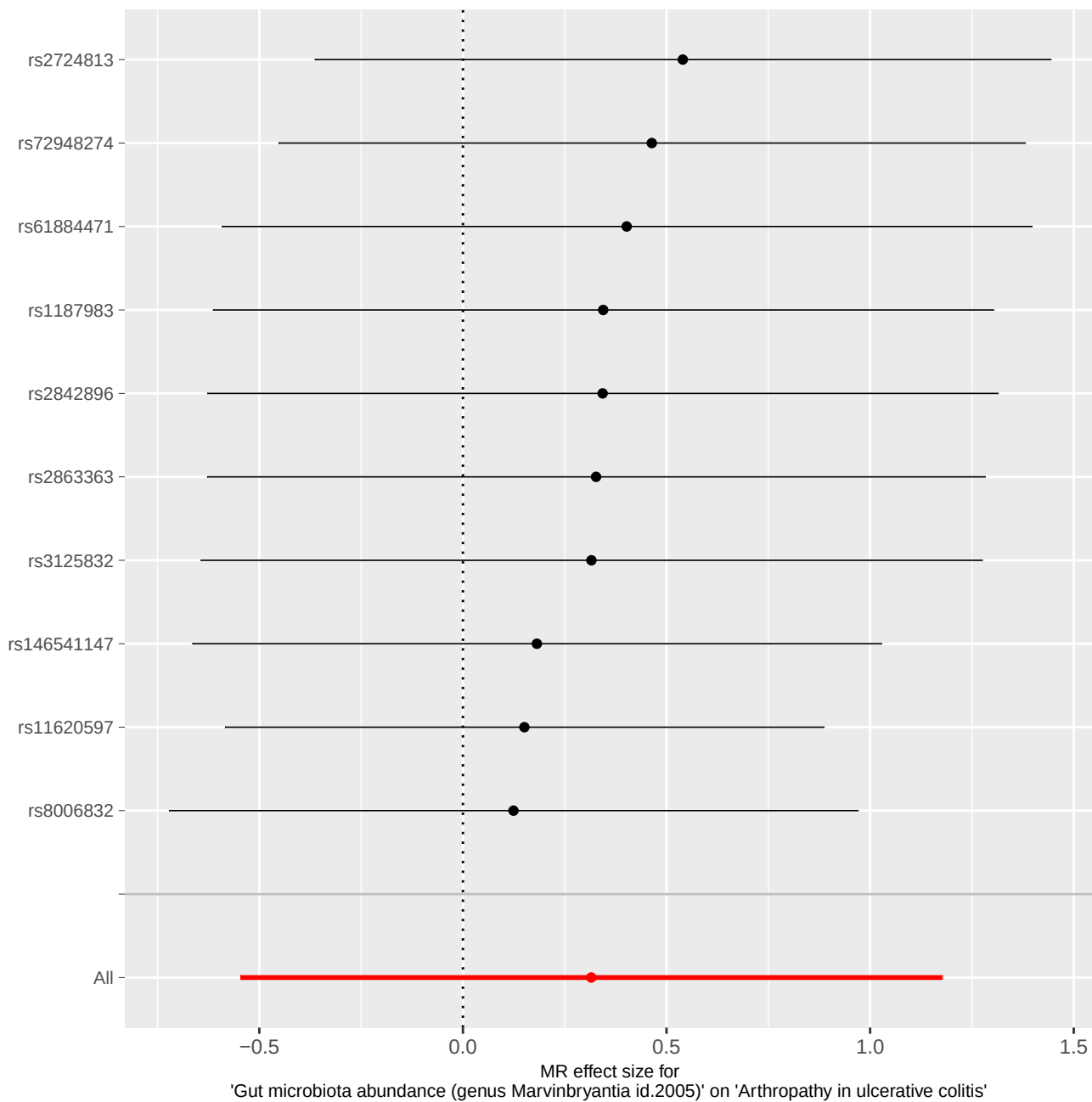
MR effect size for
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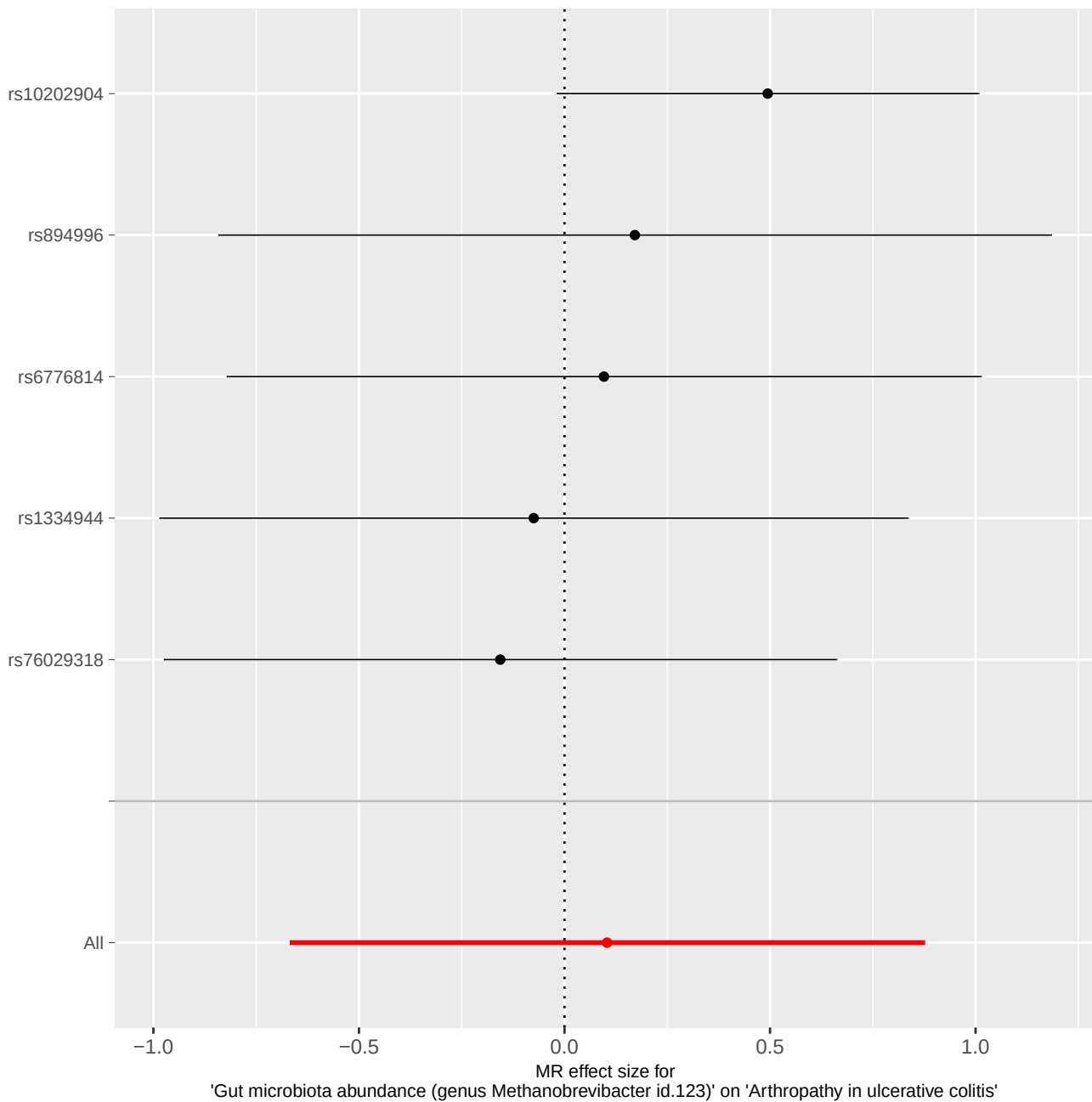


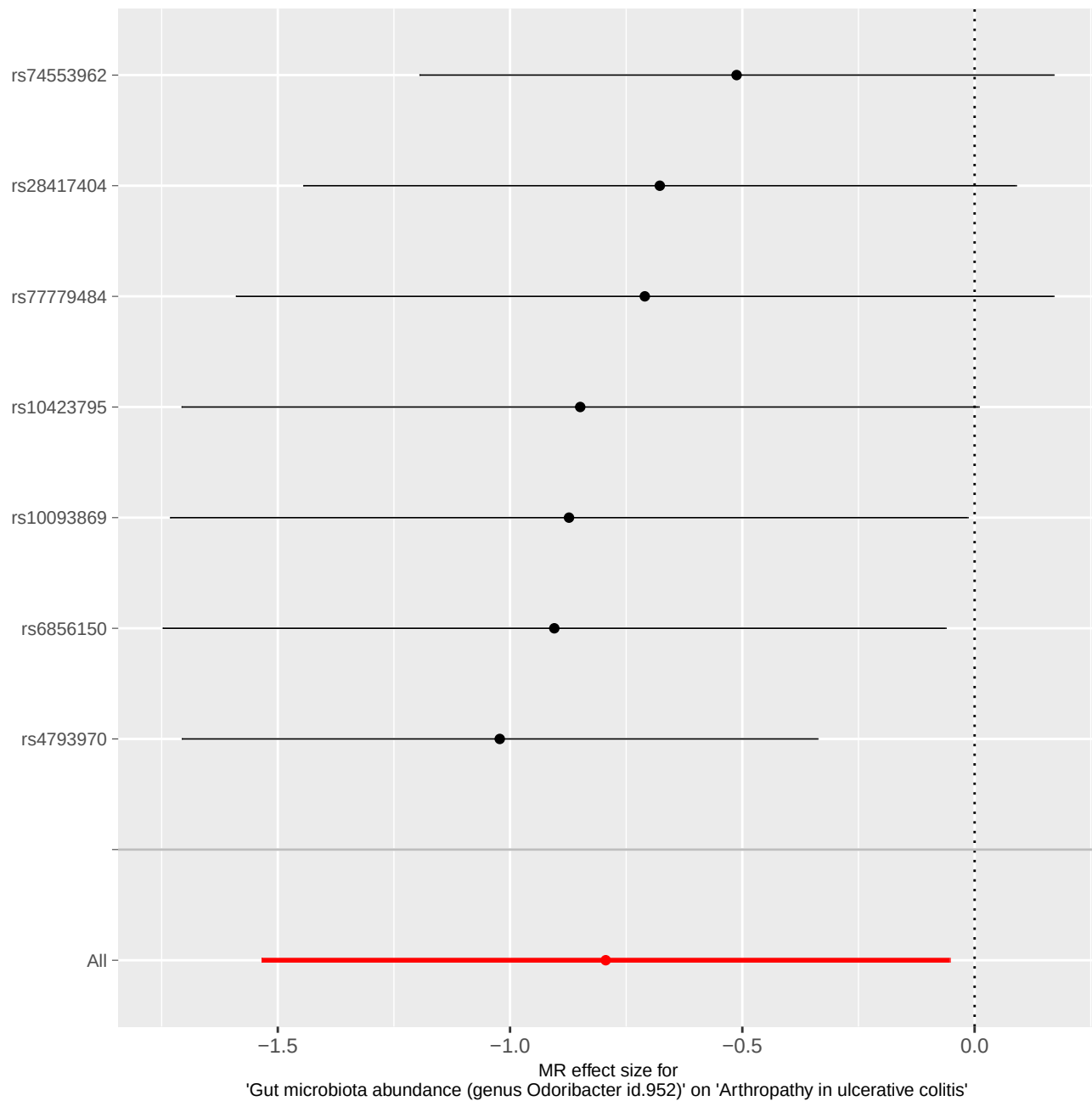
MR effect size for
'Gut microbiota abundance (genus Lachnospiraceae UCG010 id.11330)' on 'Arthropathy in ulcerative colitis'

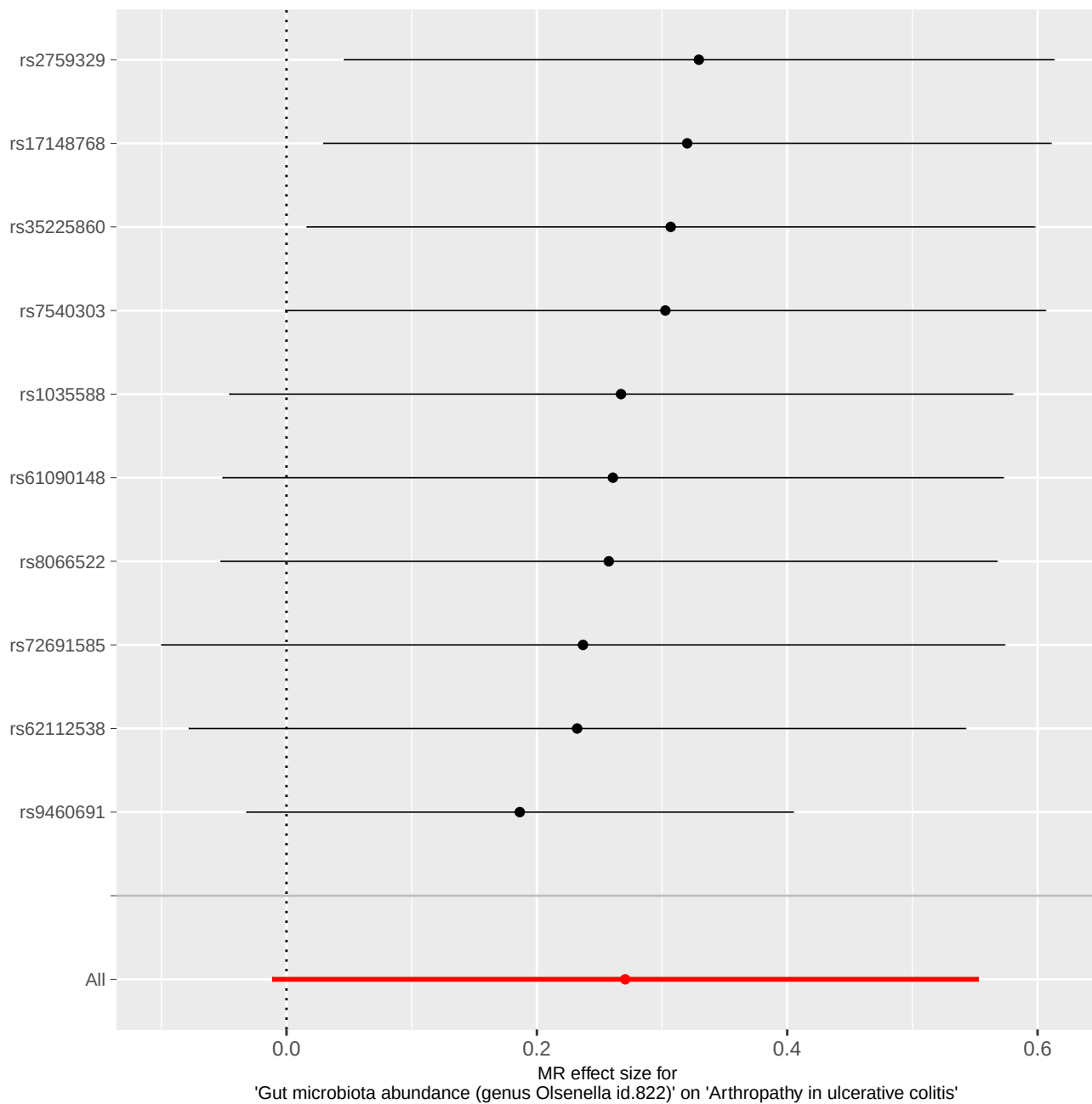


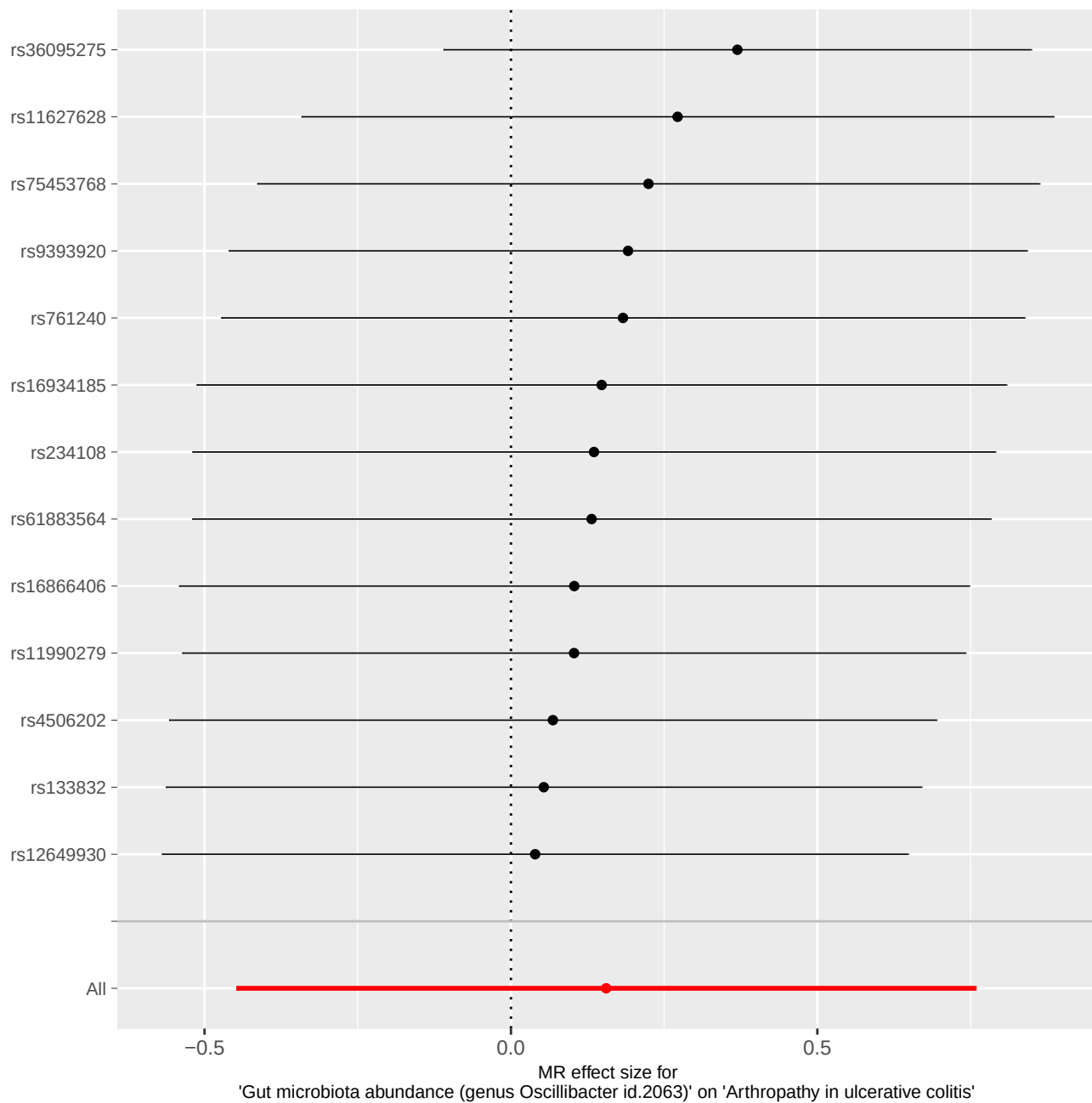


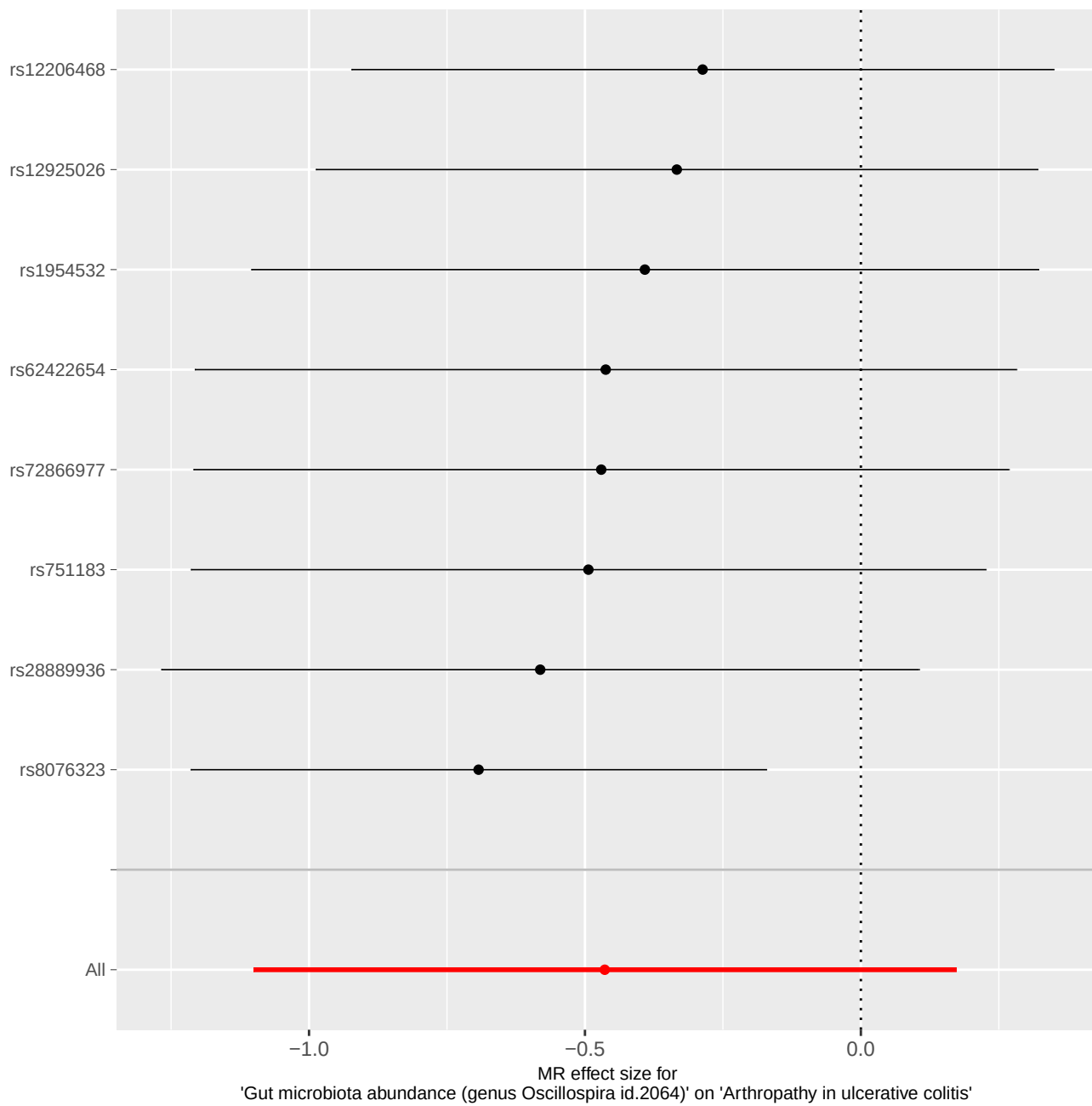


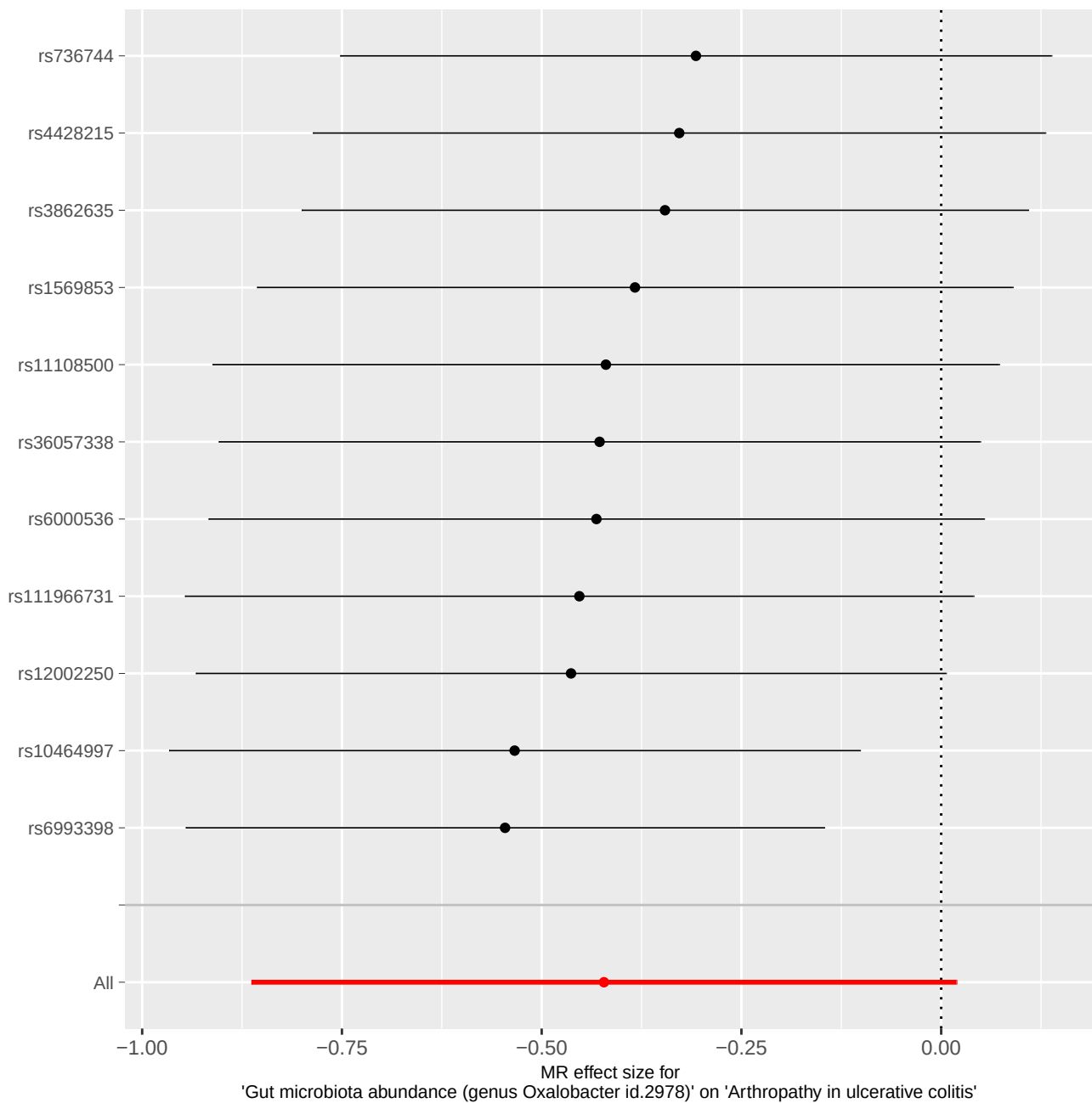


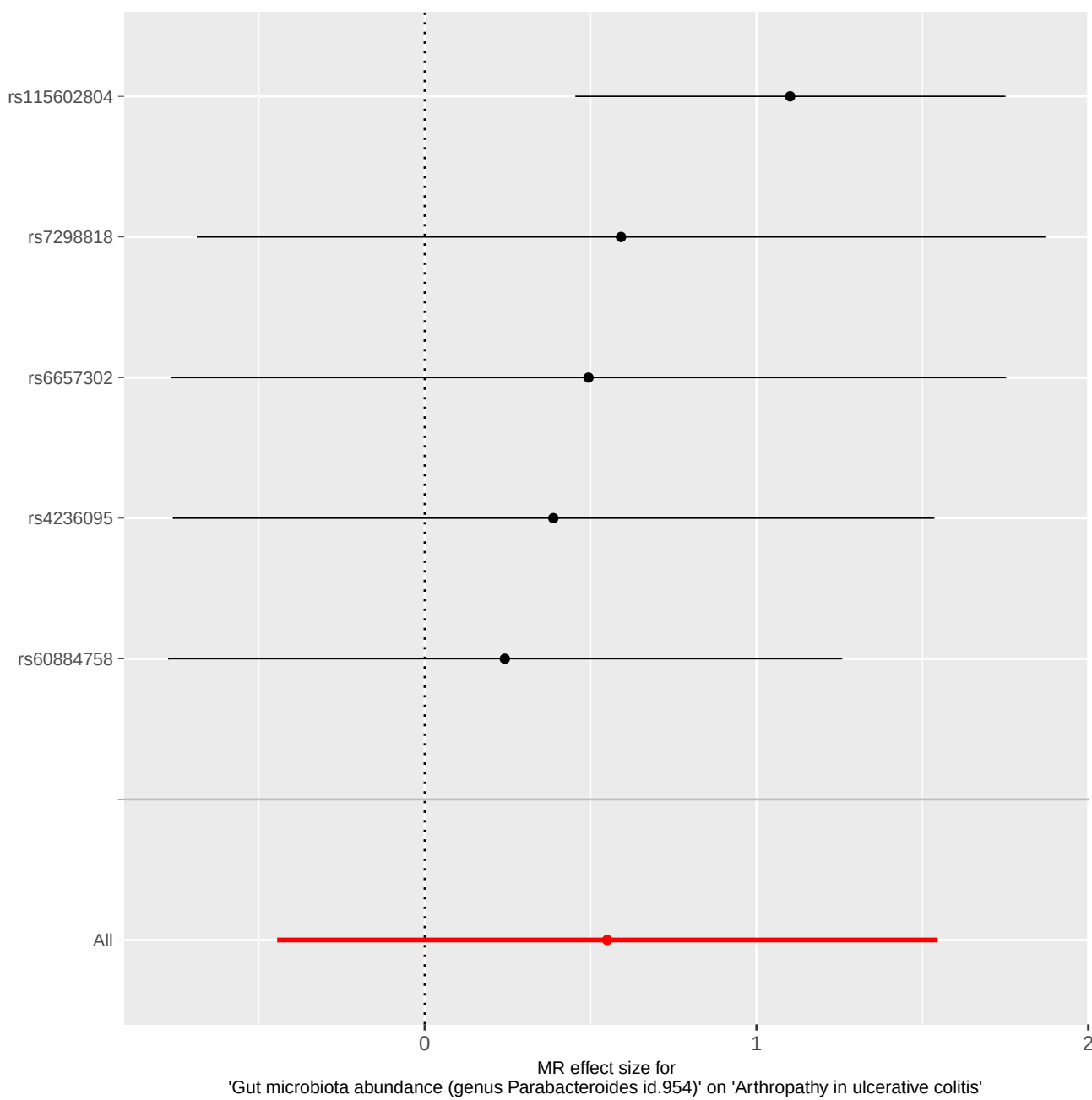


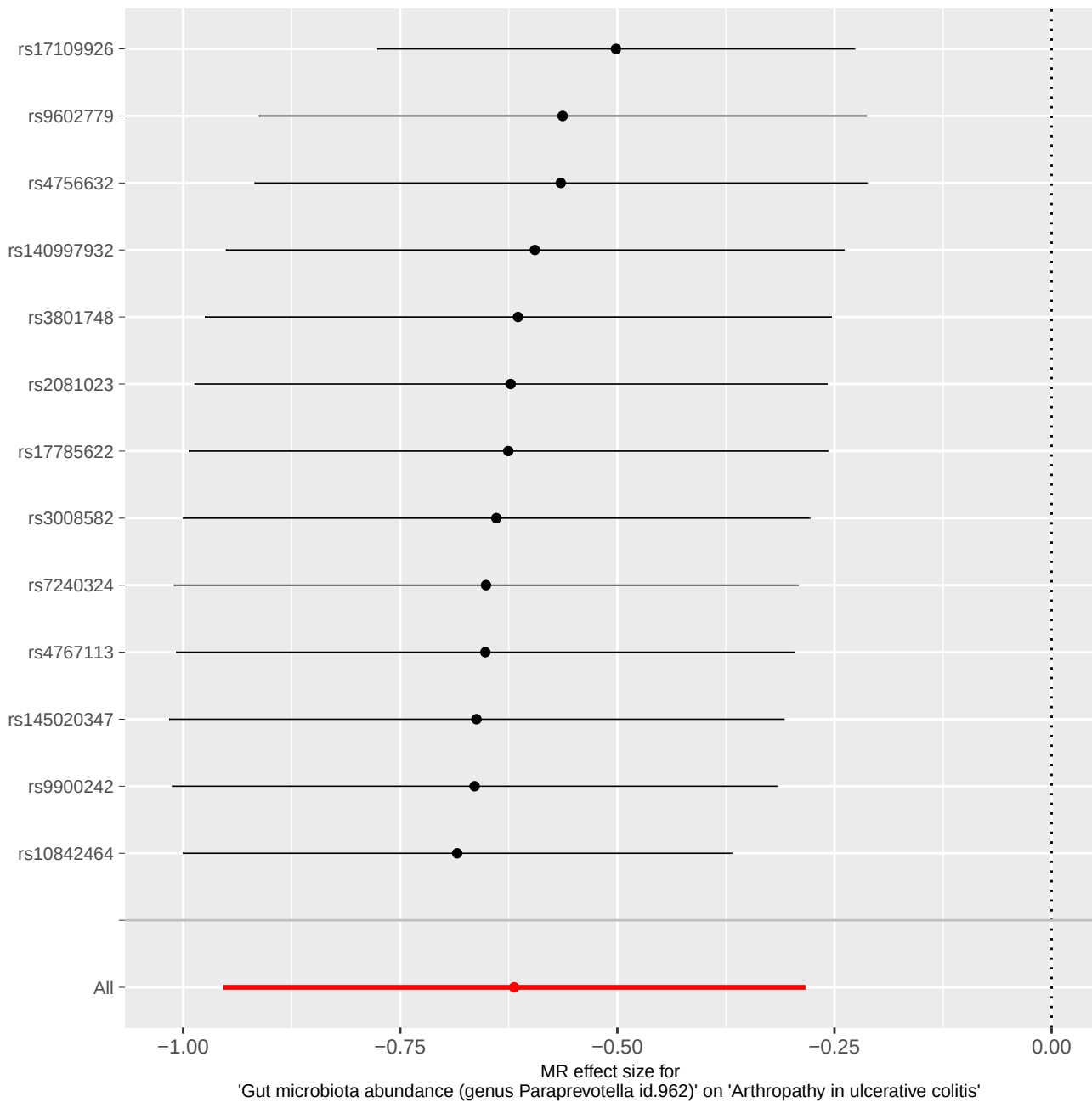


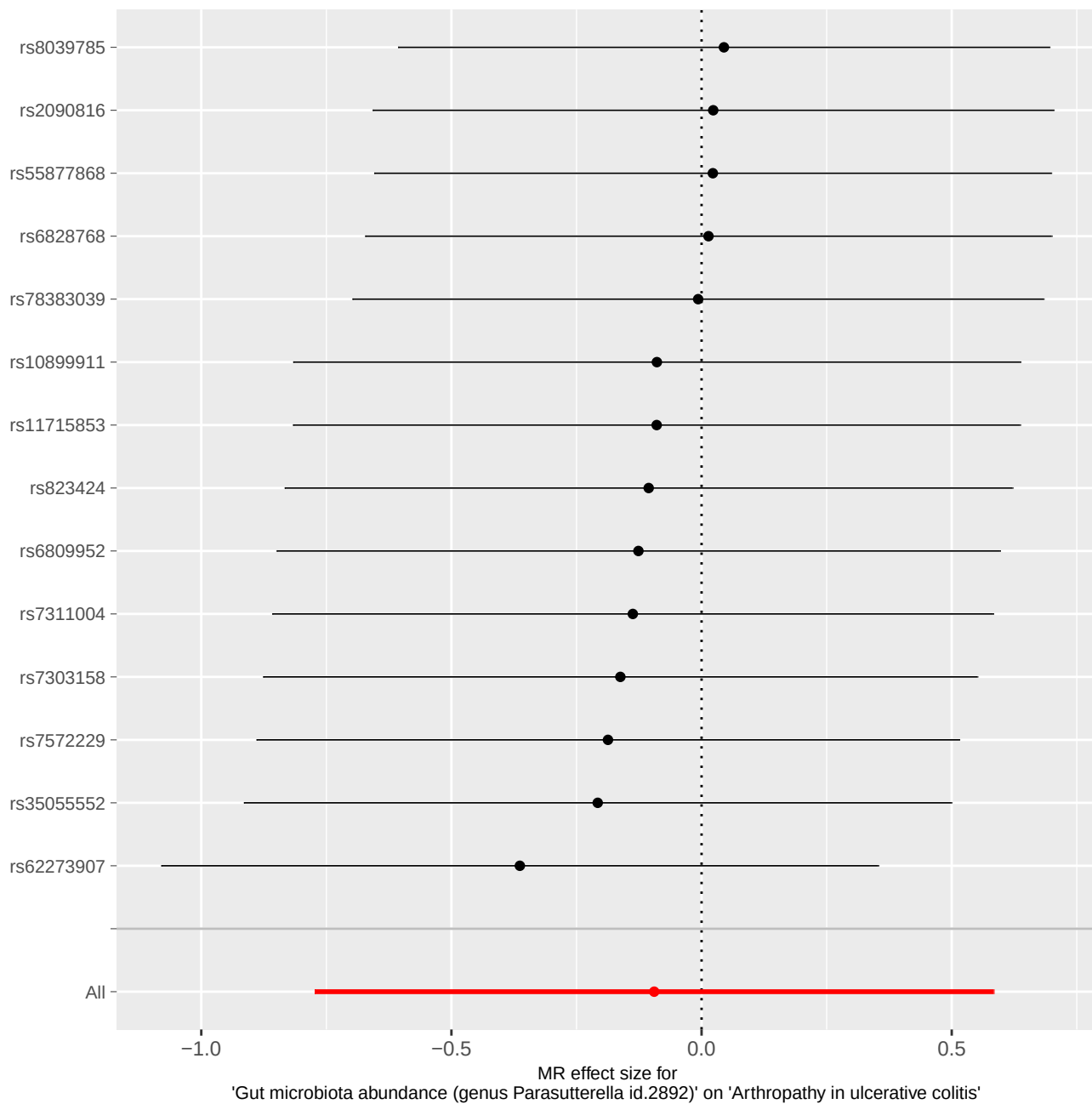


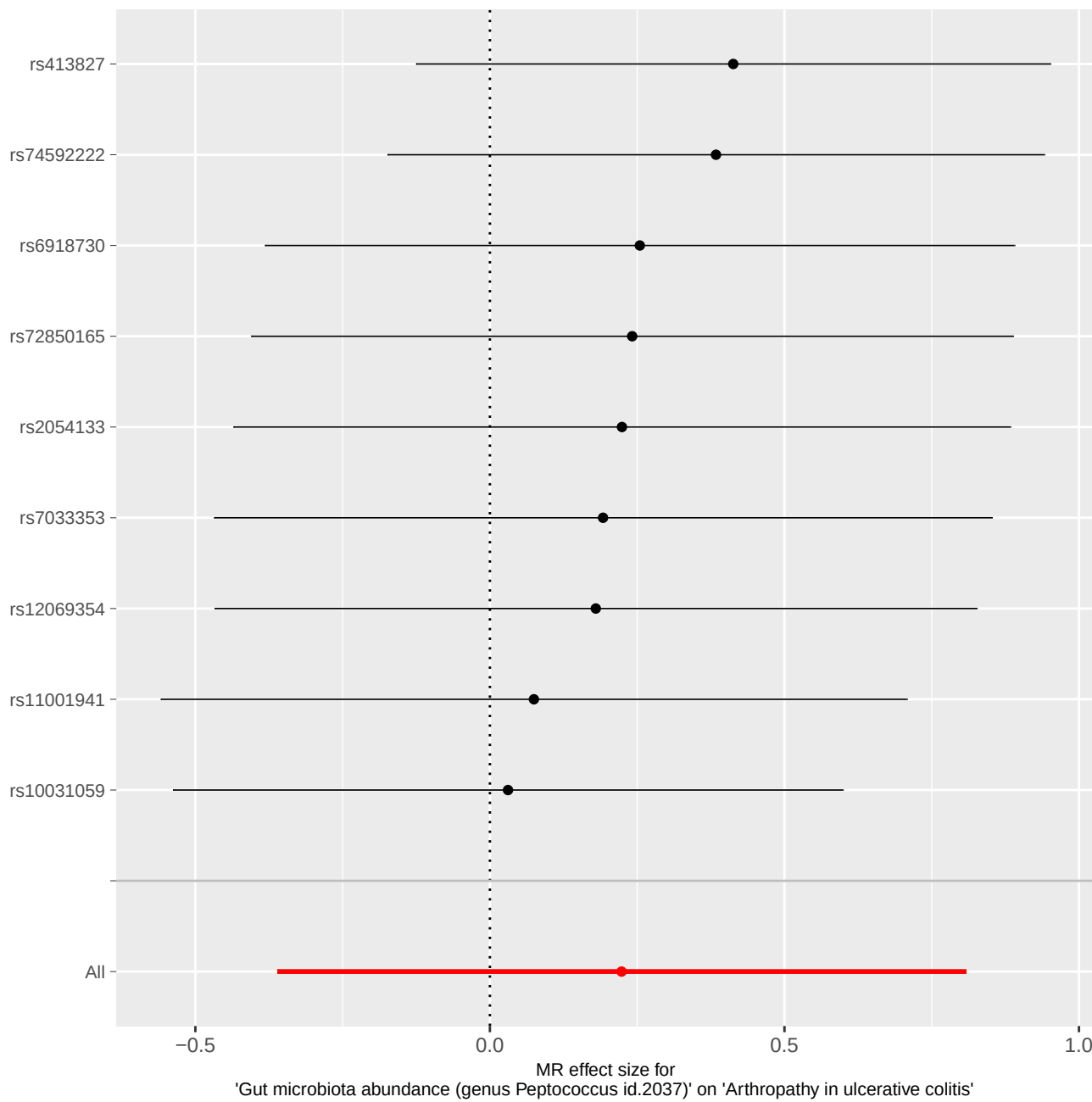


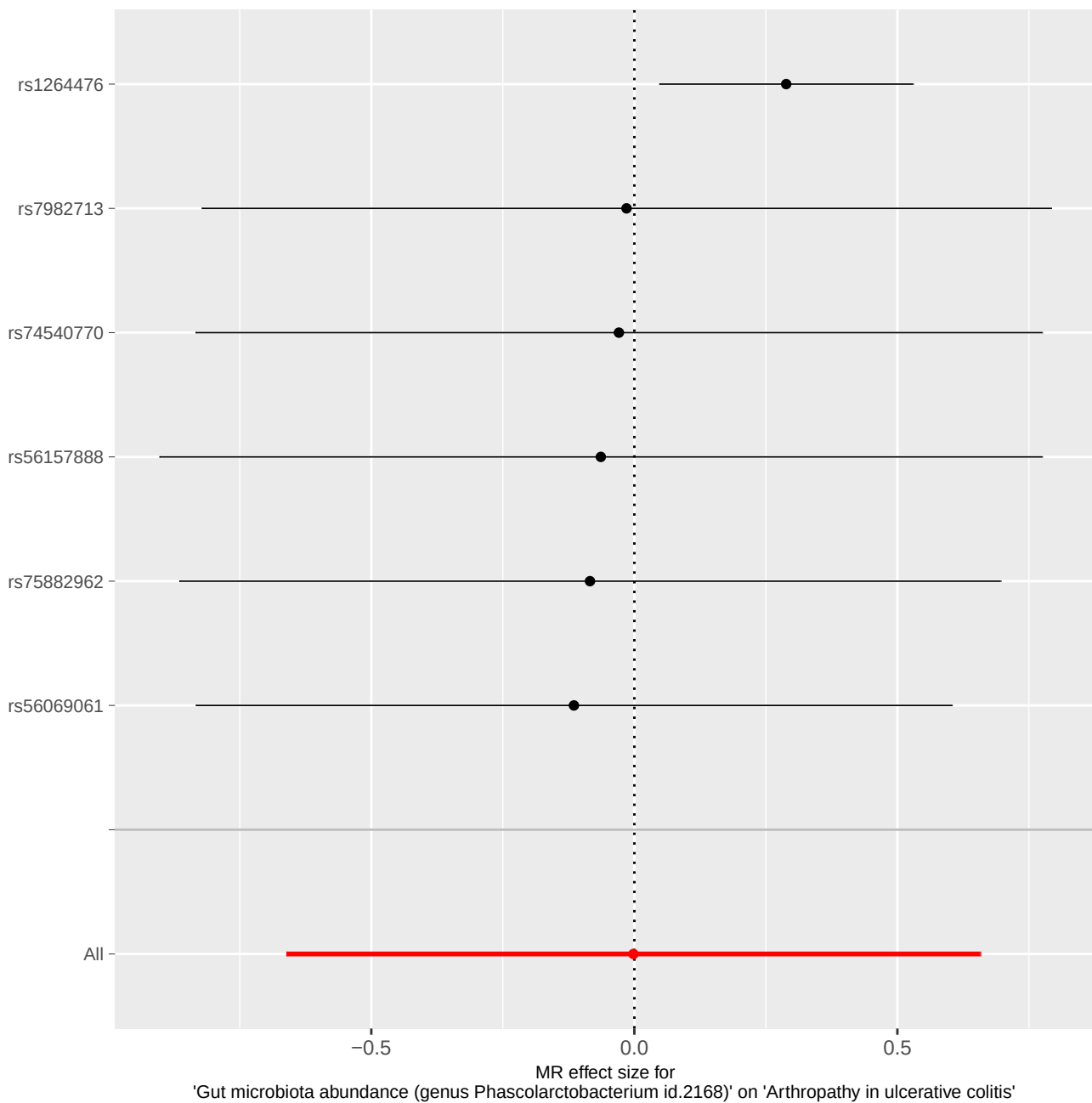


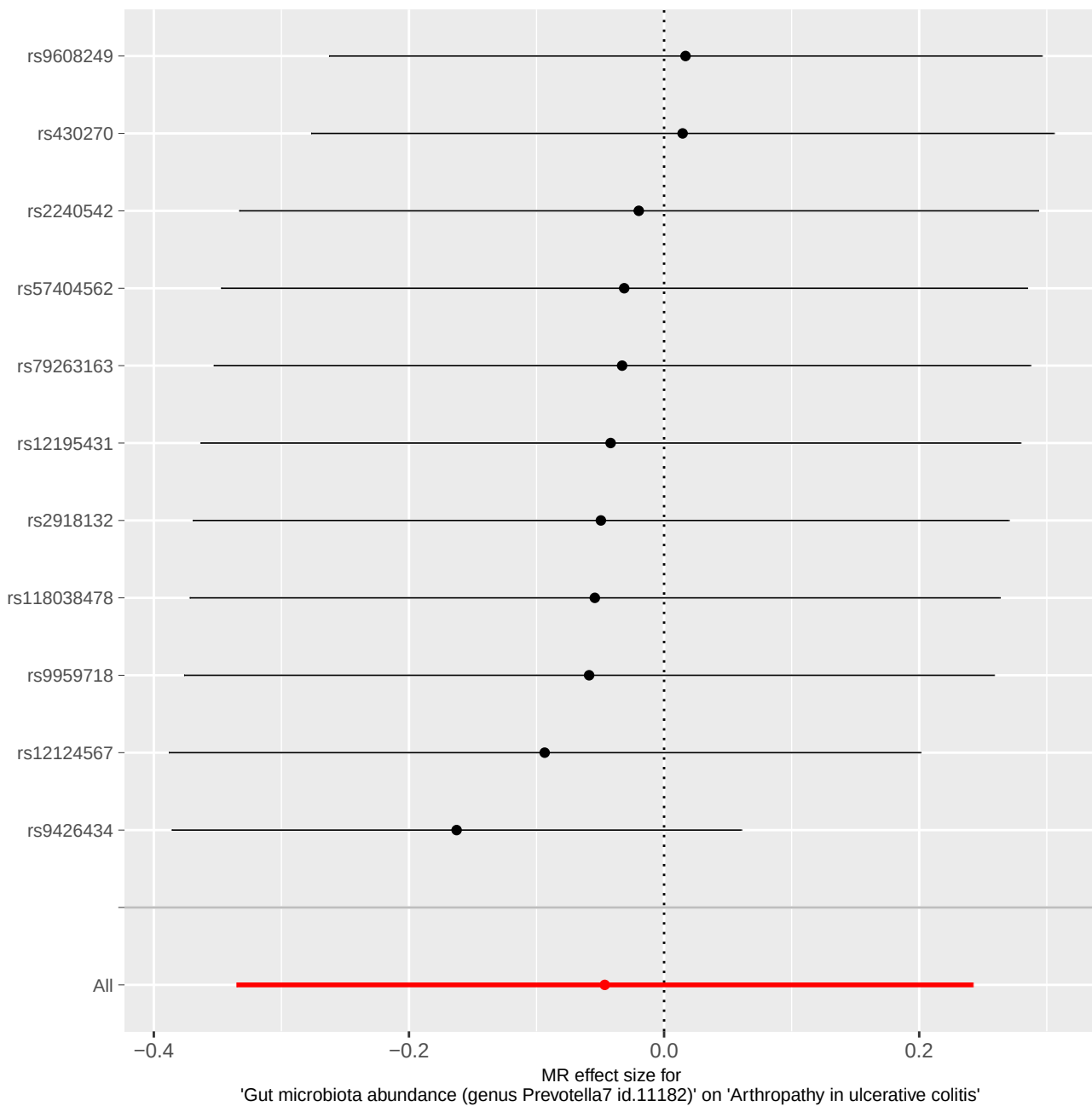


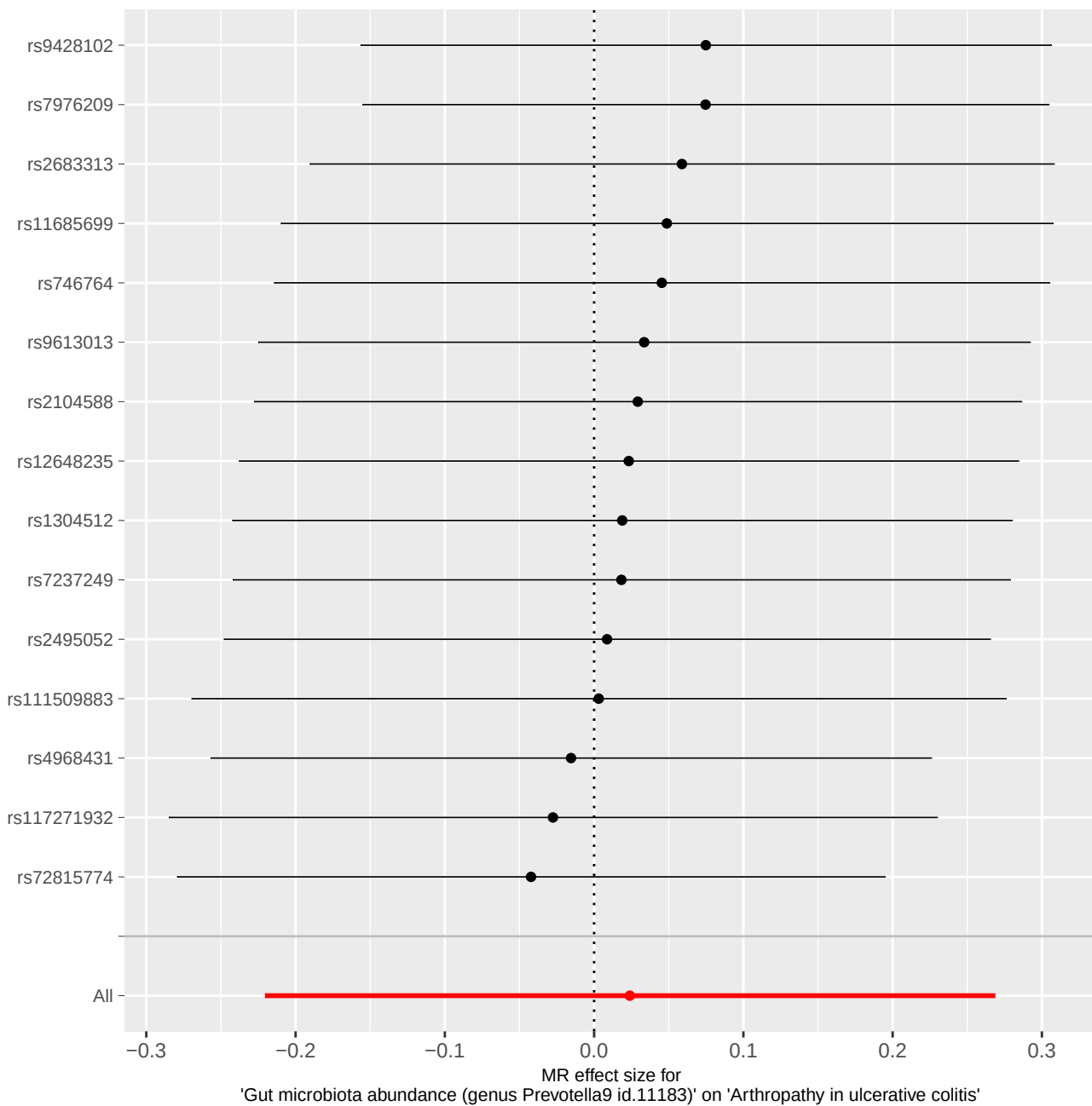


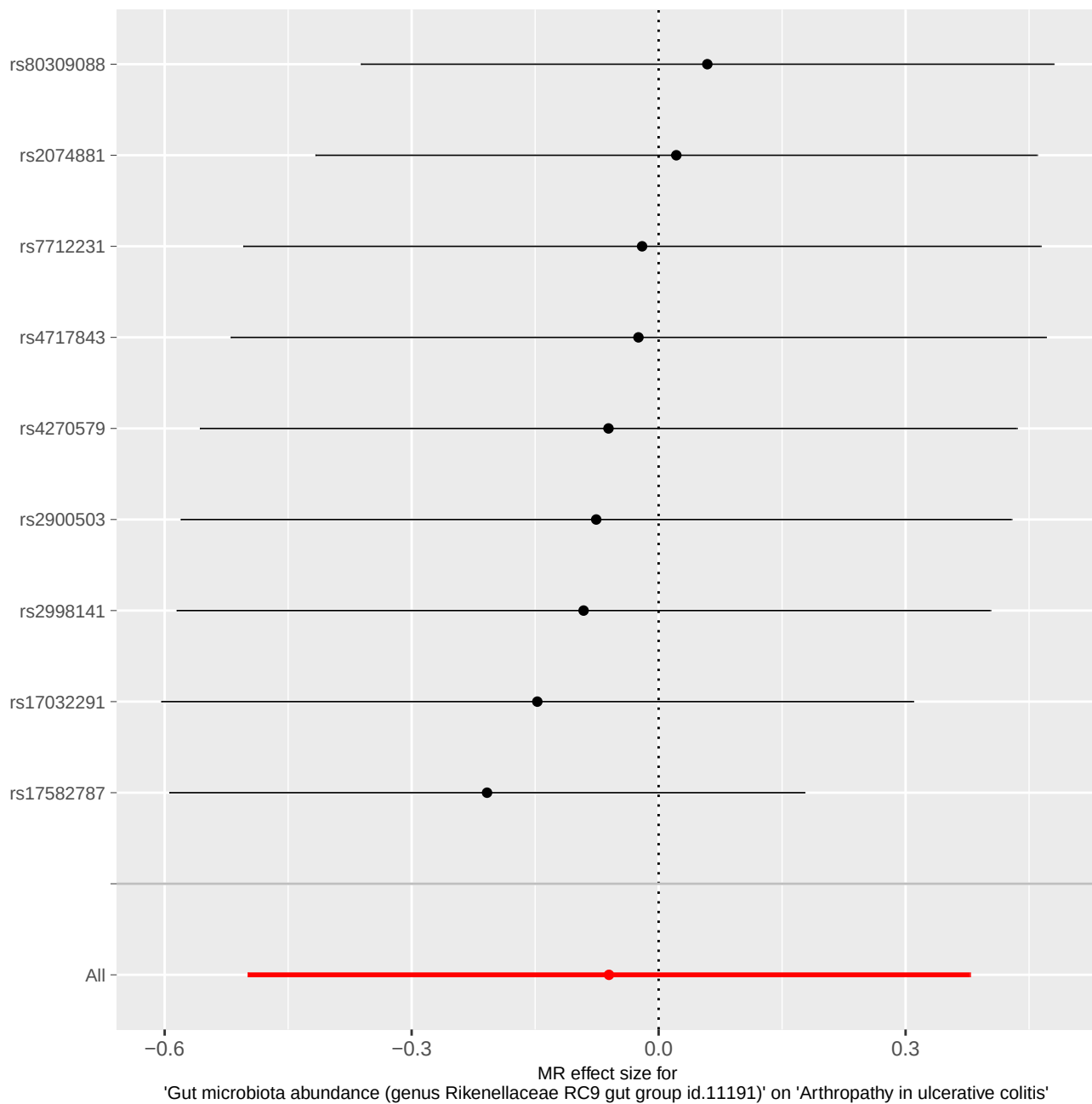




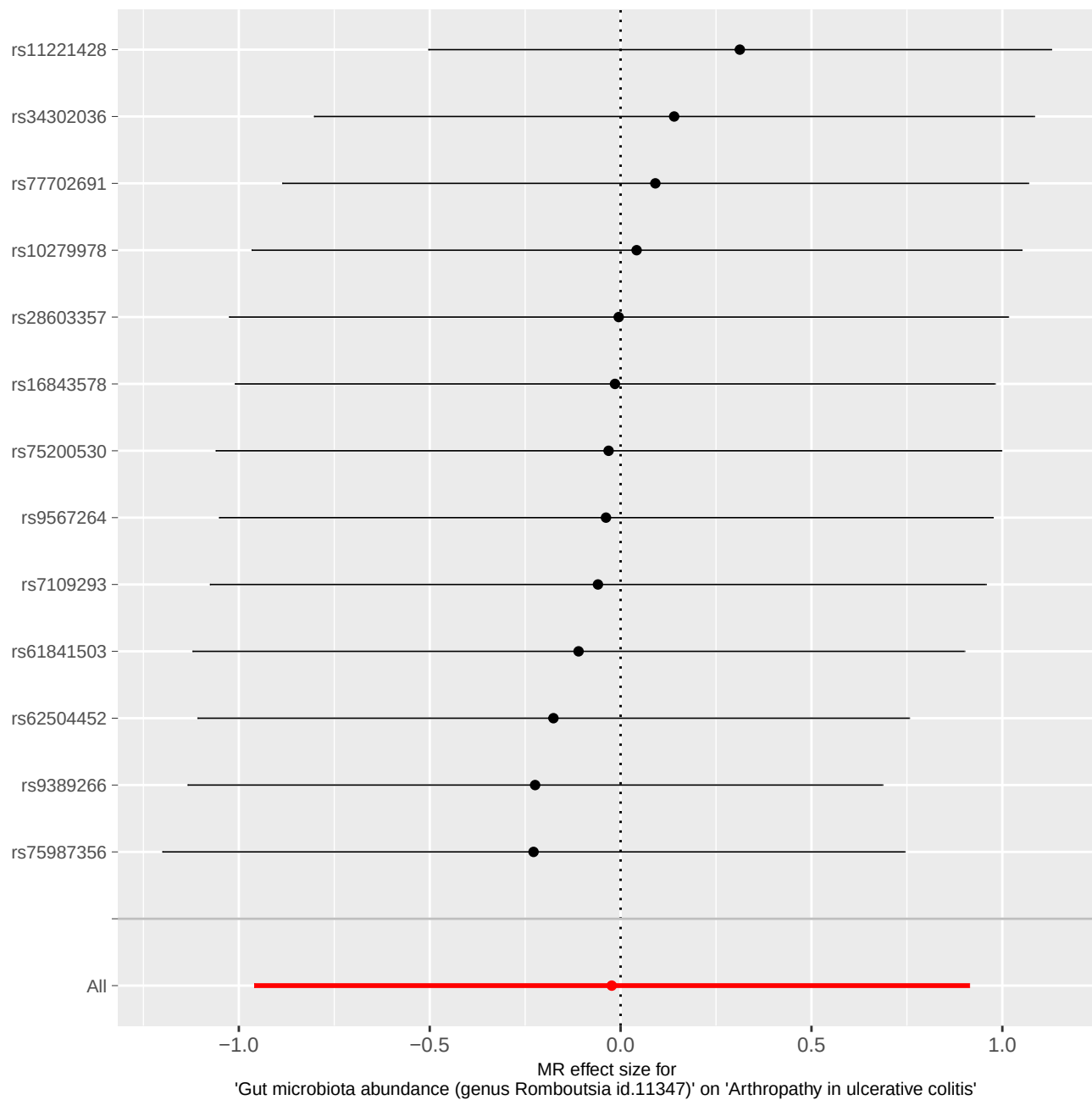


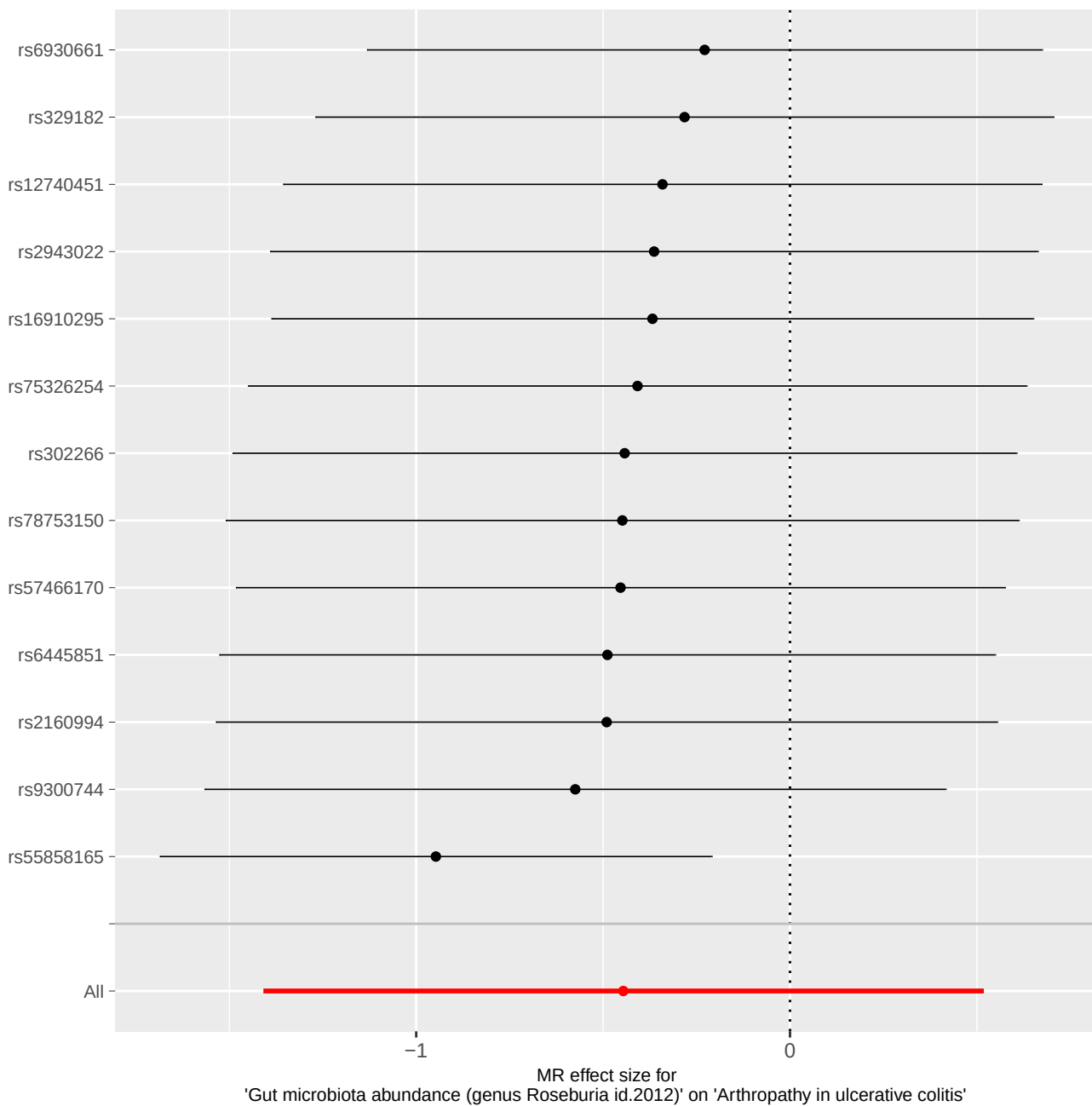


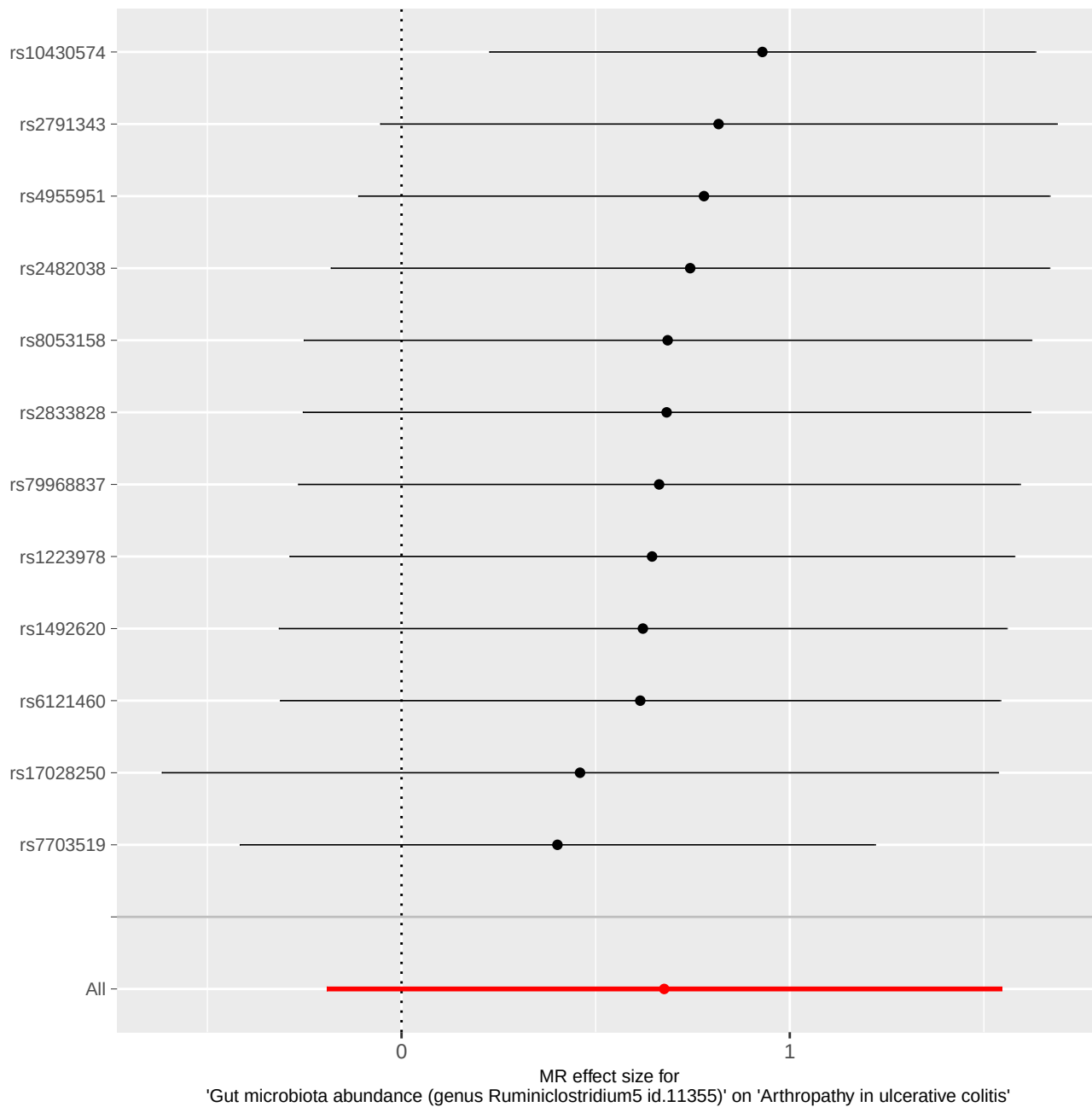


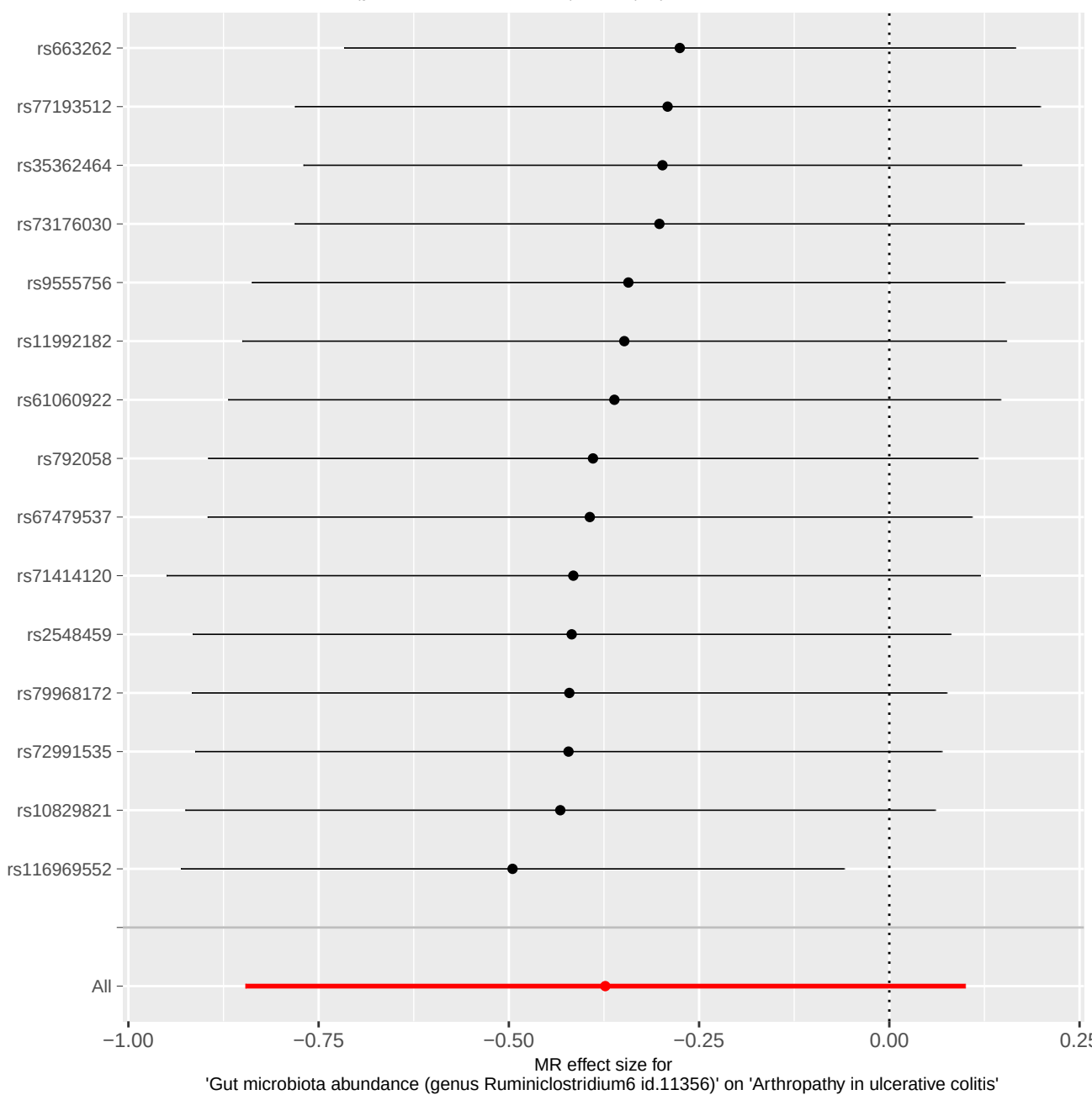


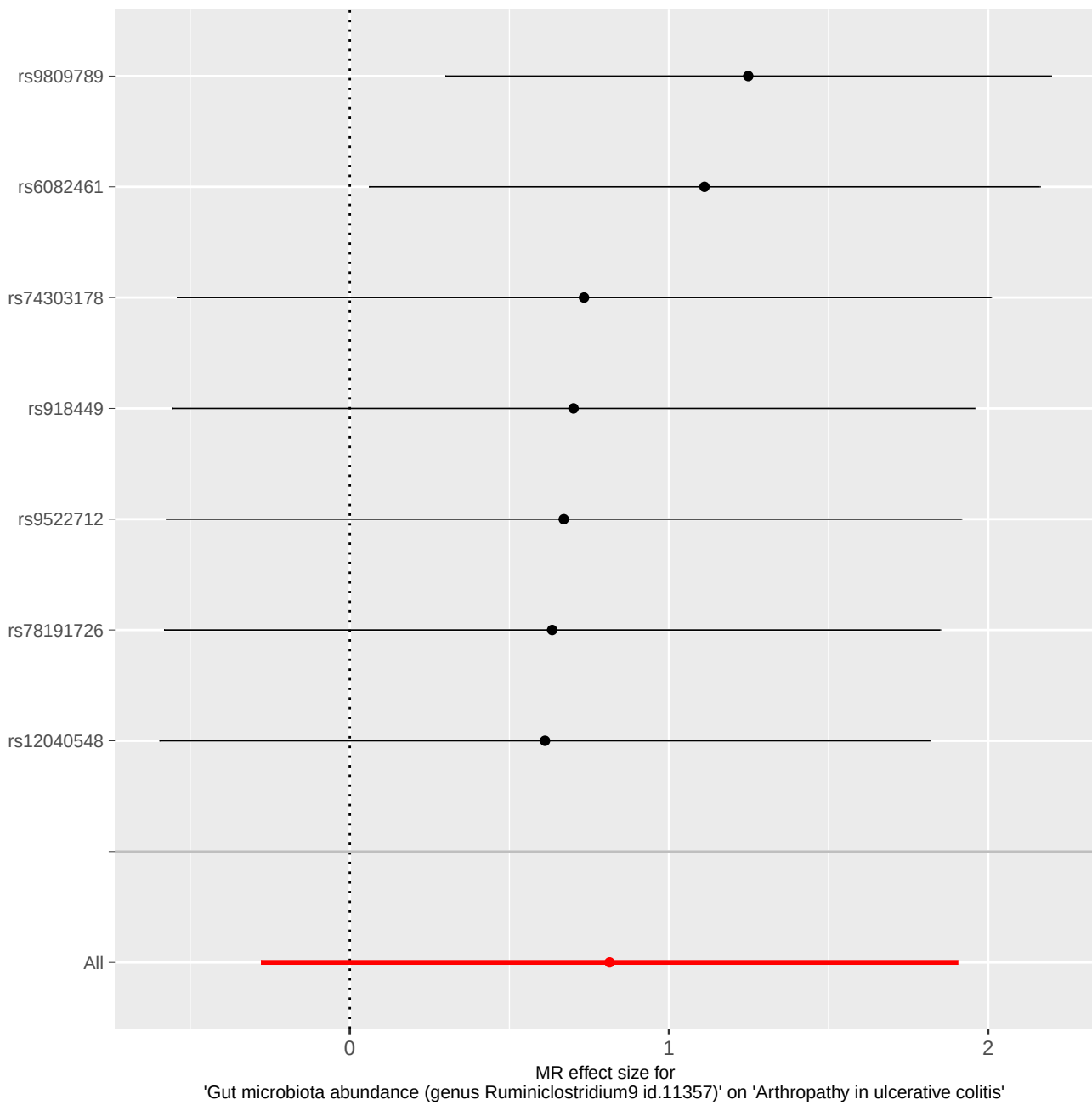
MR effect size for
'Gut microbiota abundance (genus Rikenellaceae RC9 gut group id.11191)' on 'Arthropathy in ulcerative colitis'

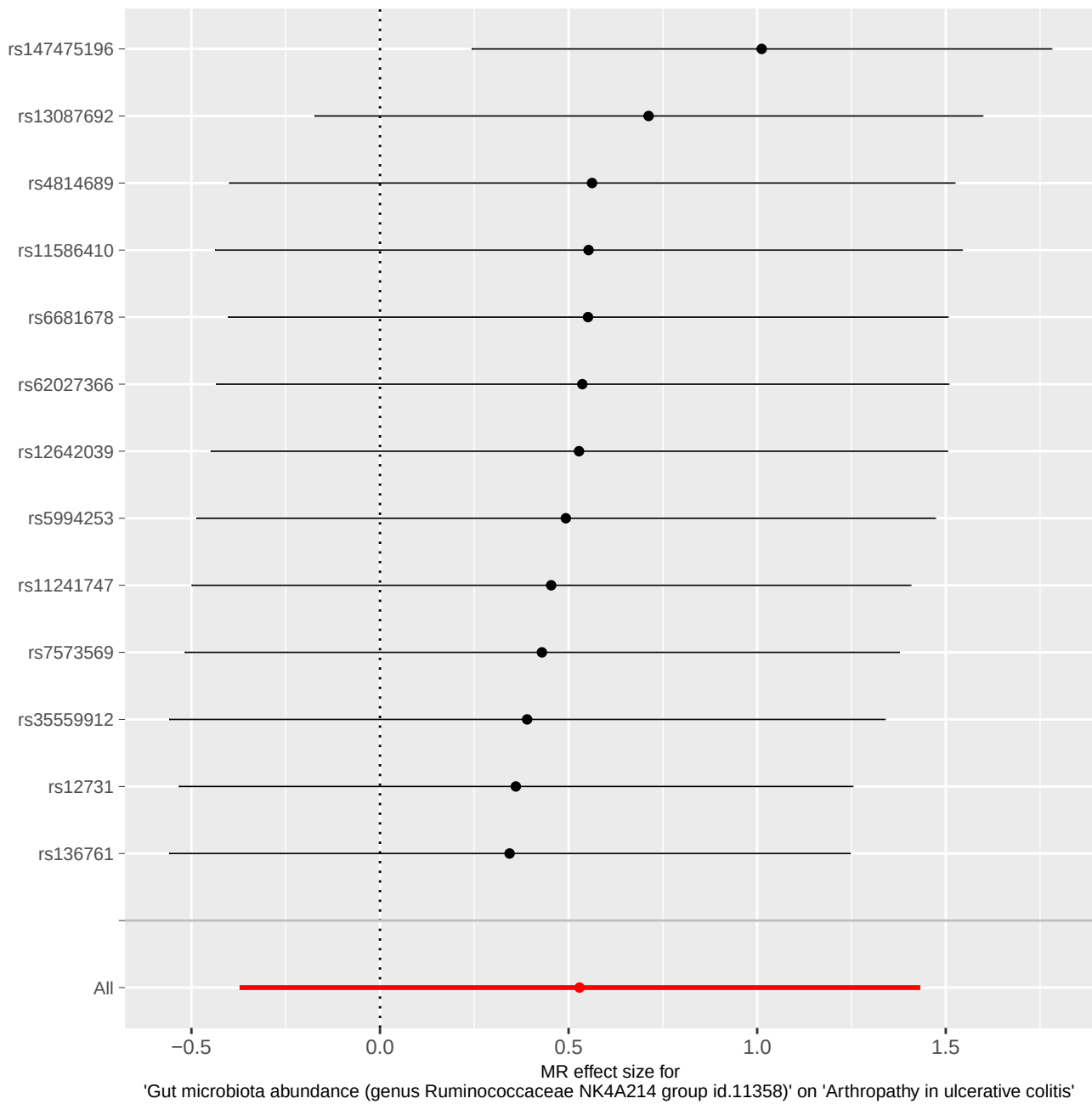


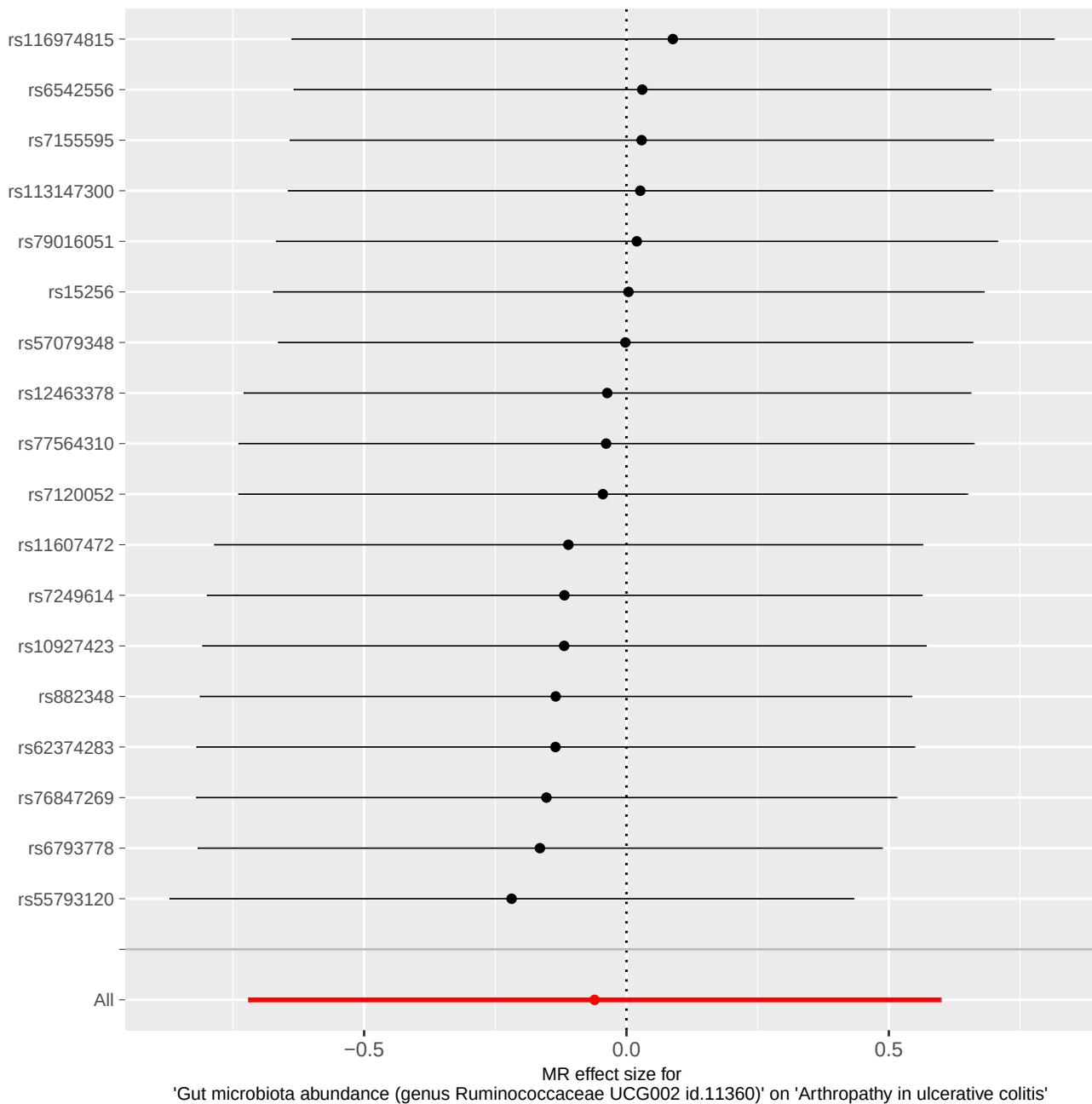




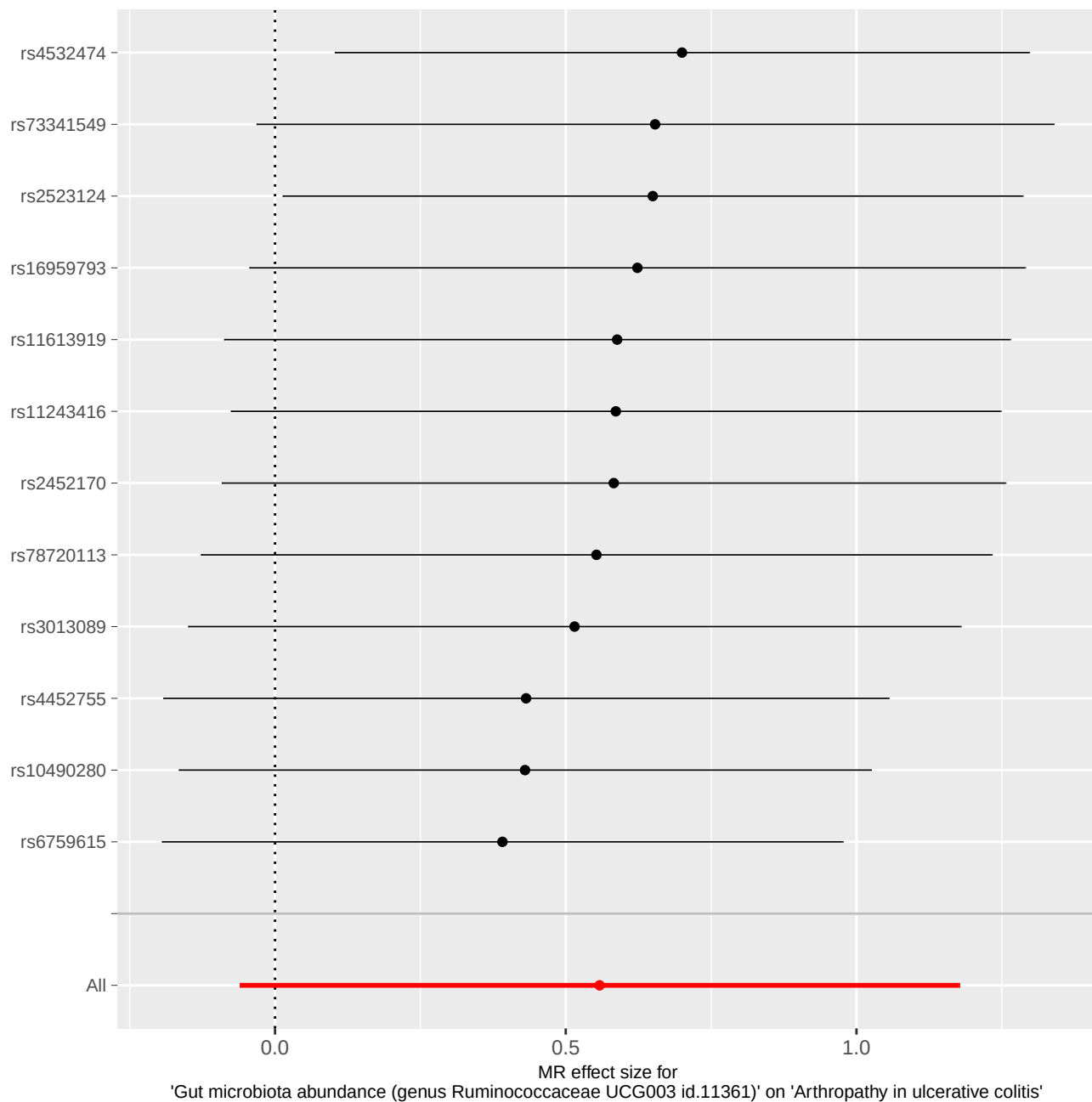


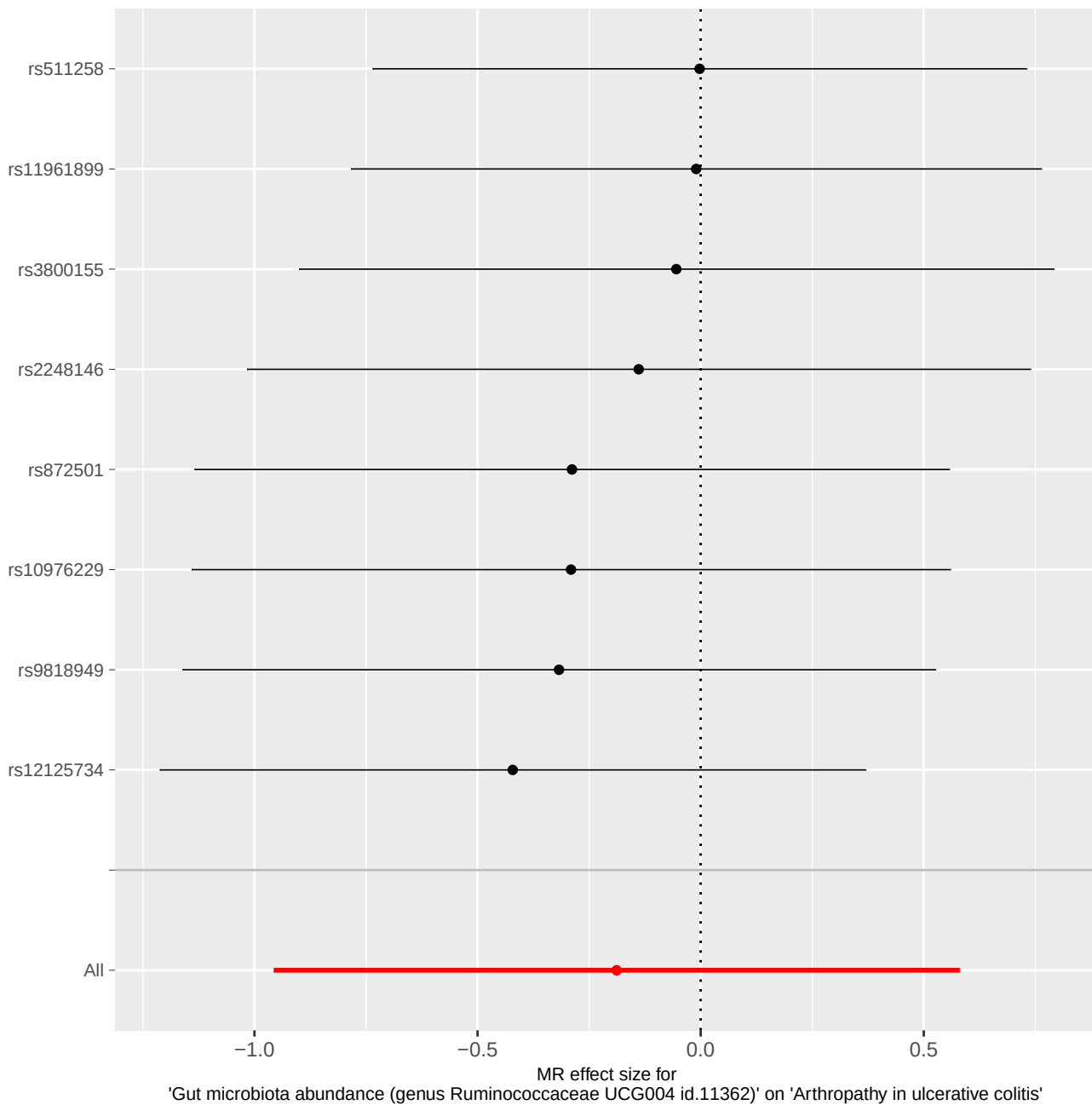


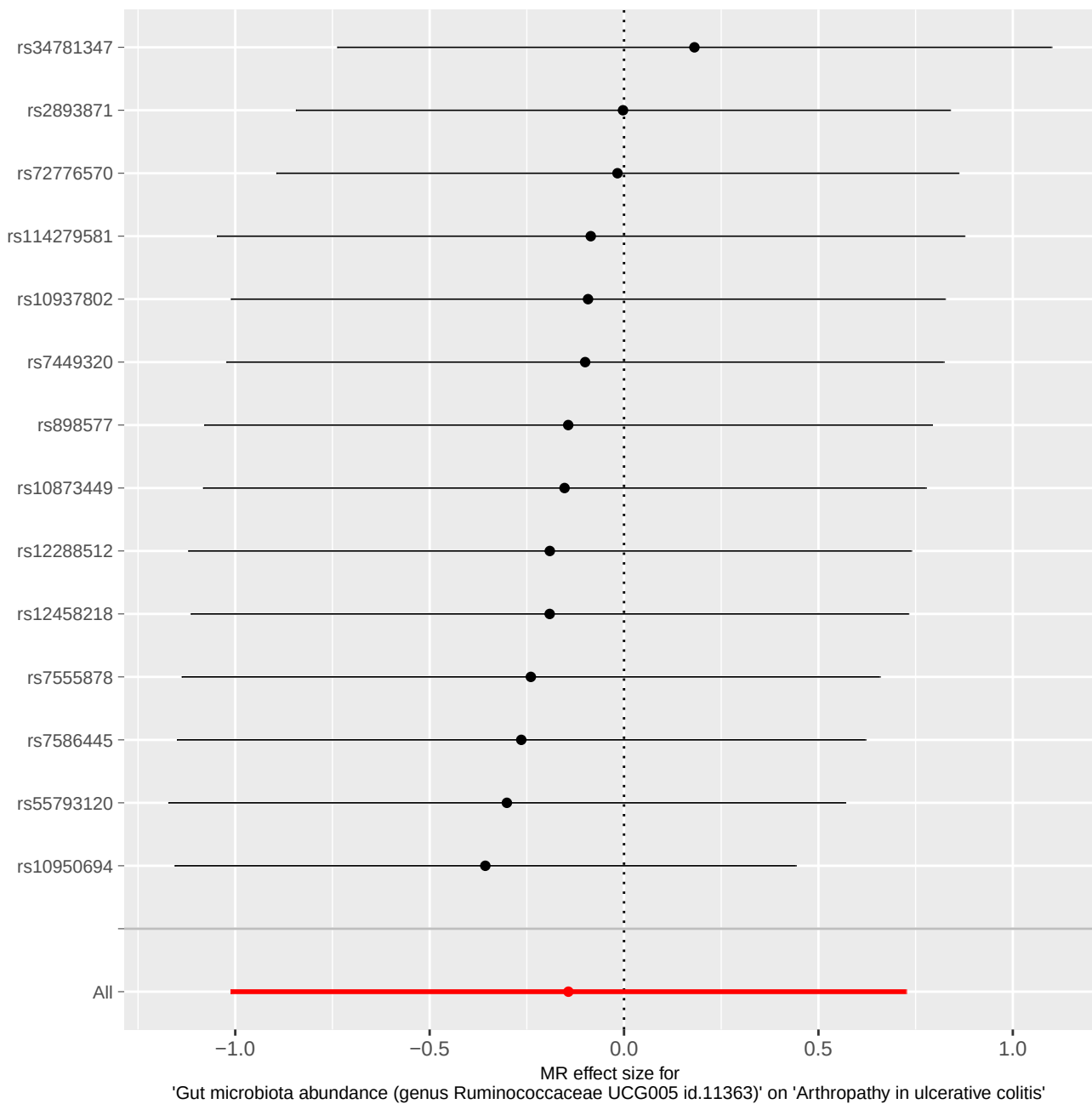


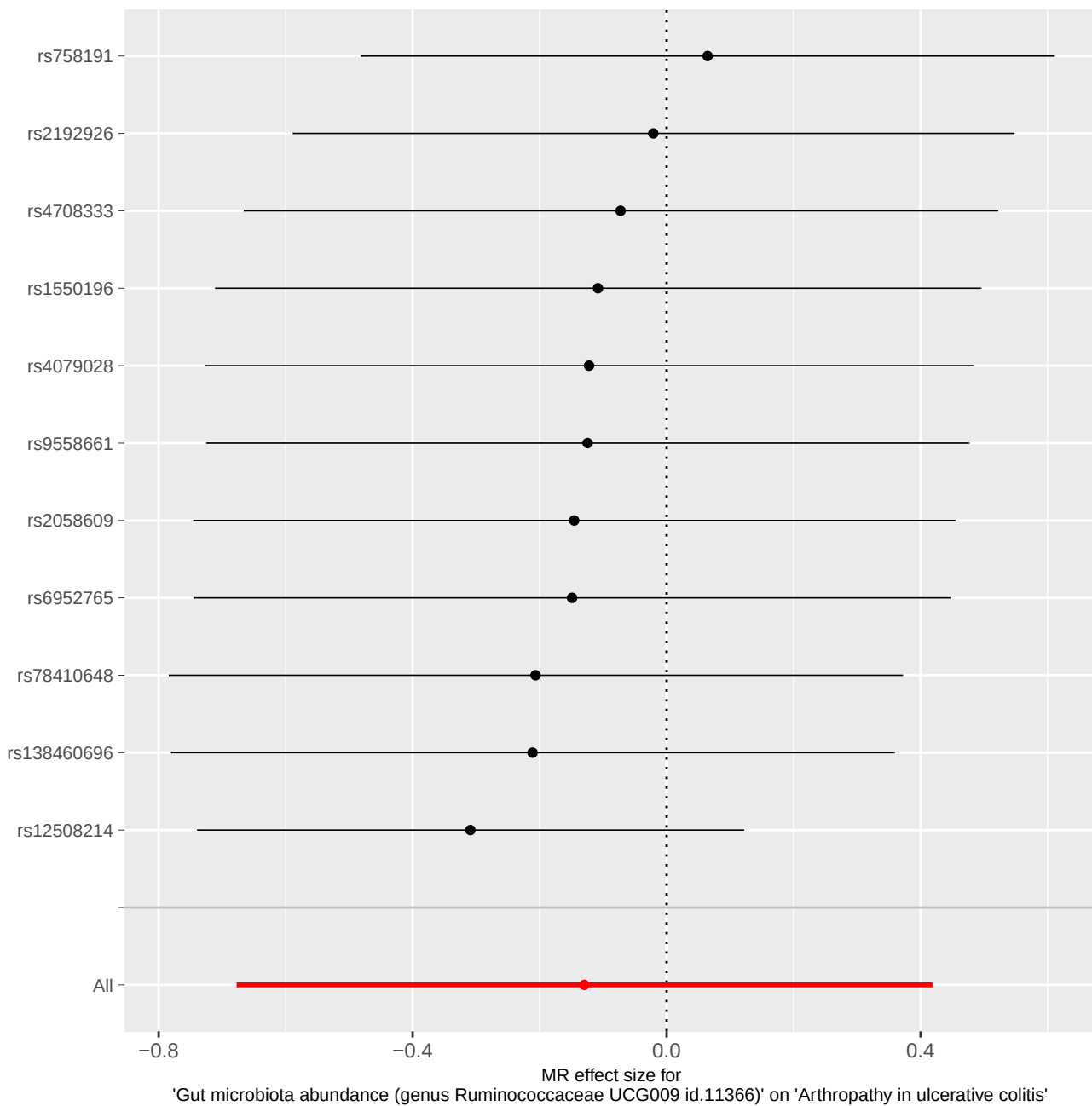


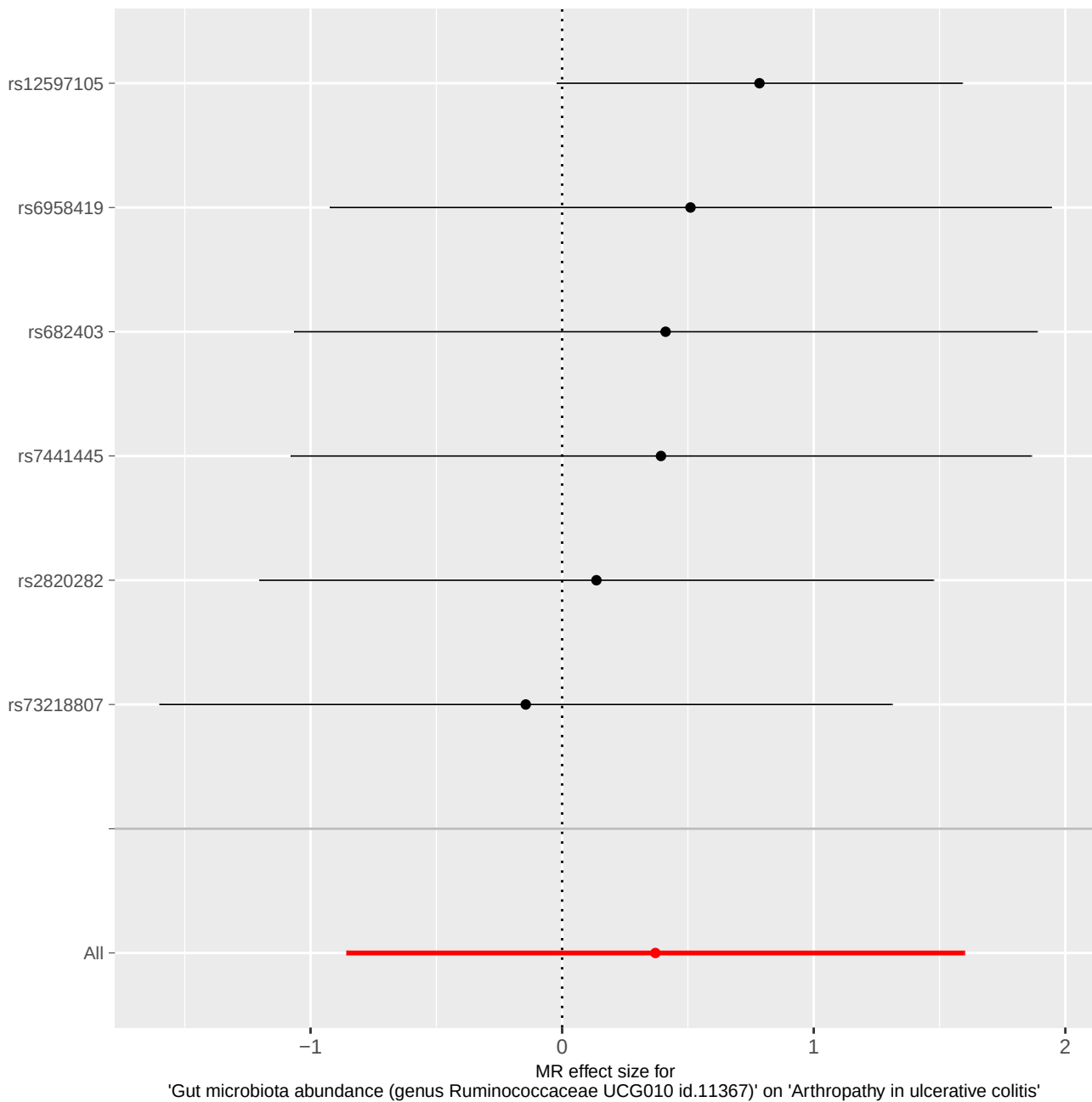
MR effect size for
'Gut microbiota abundance (genus Ruminococcaceae UCG002 id.11360)' on 'Arthropathy in ulcerative colitis'

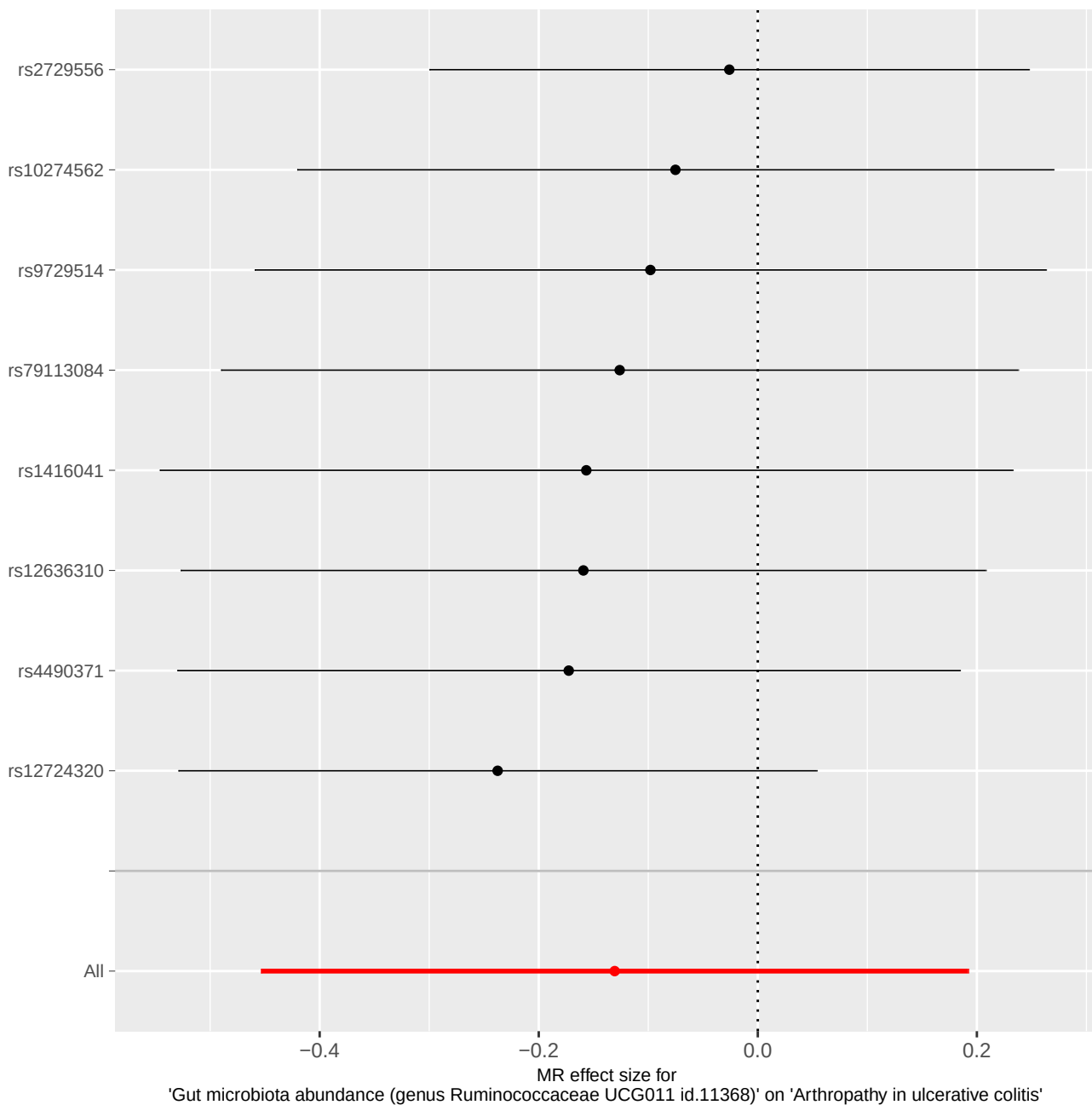


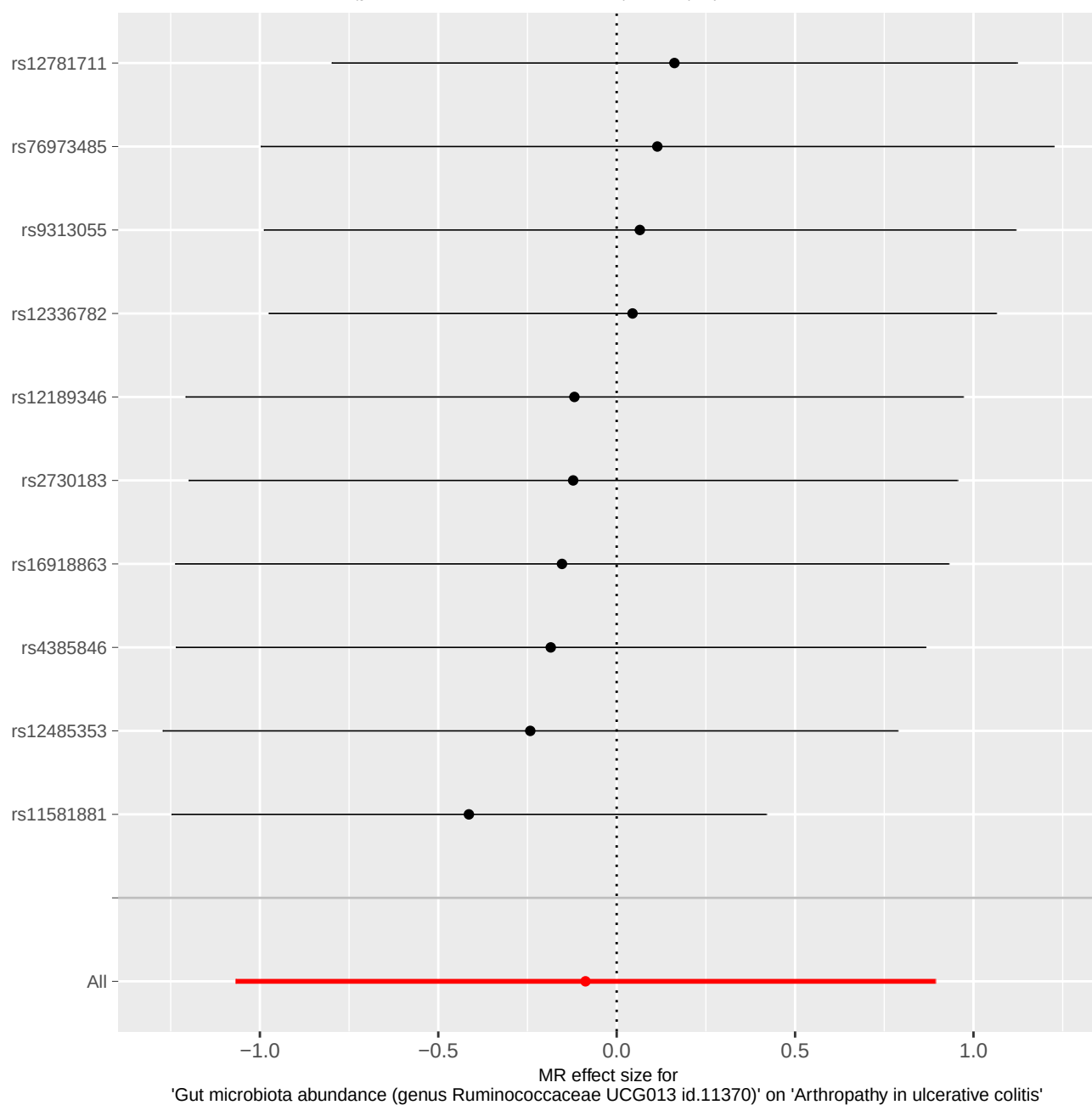


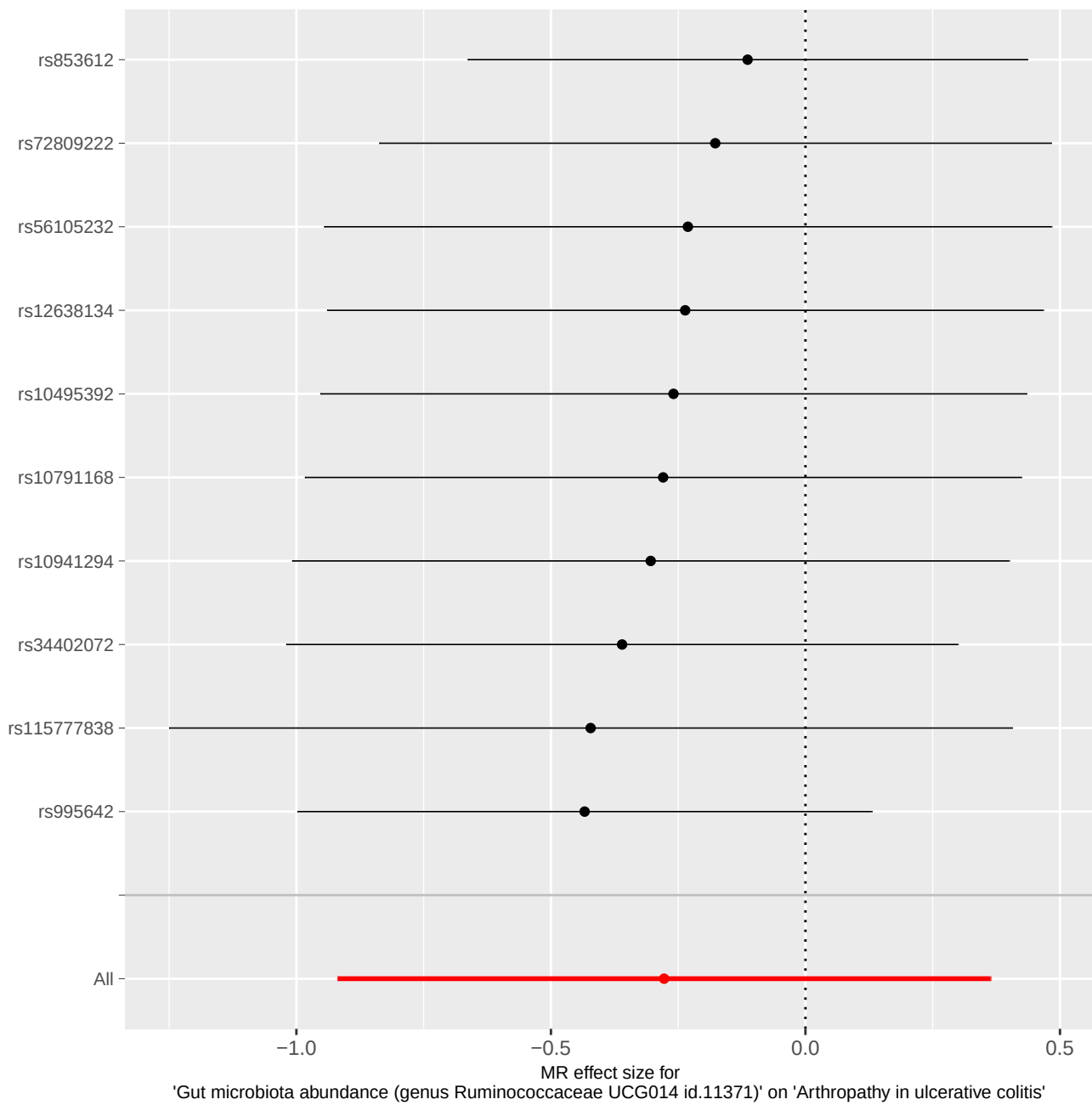


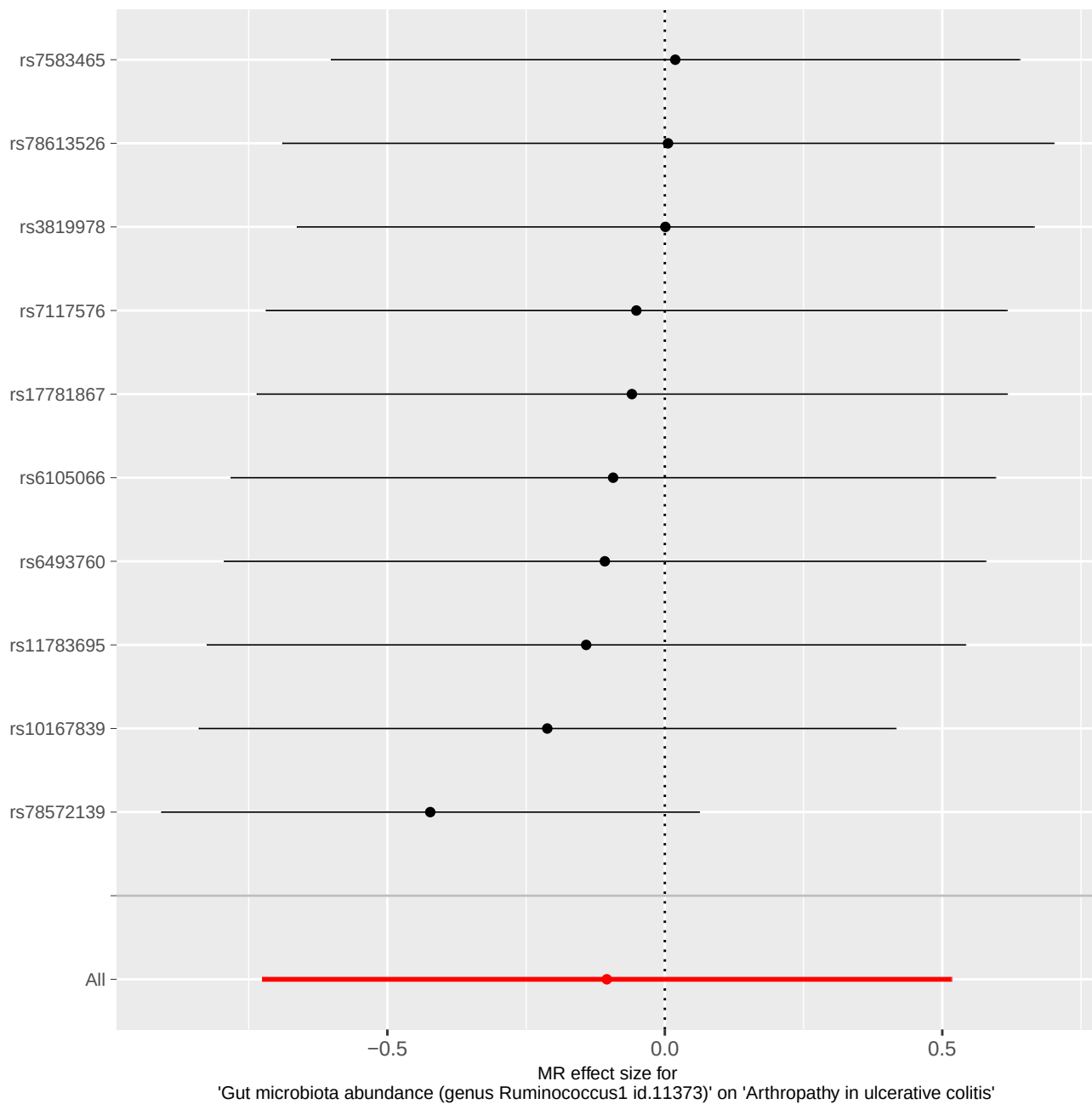


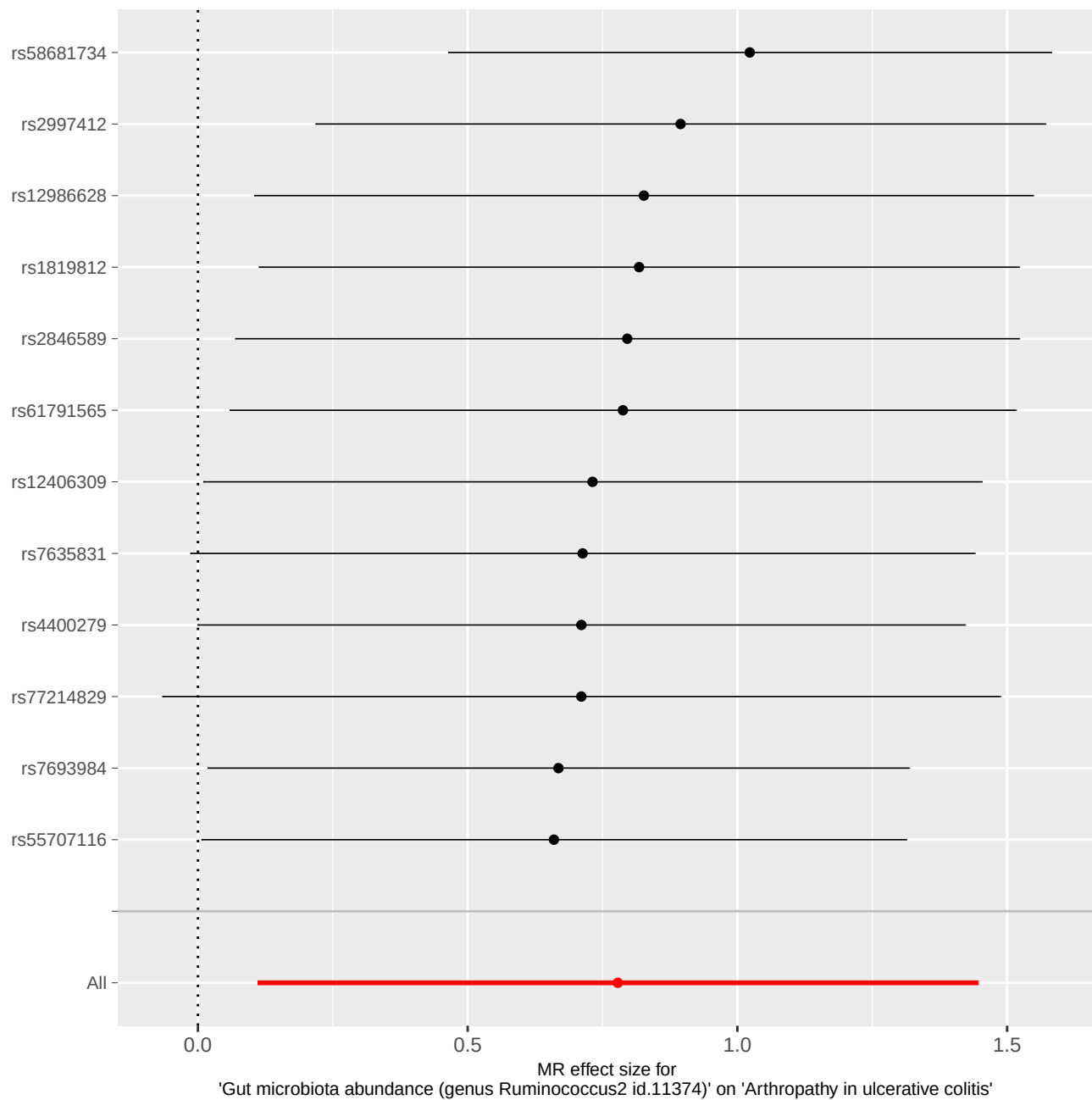


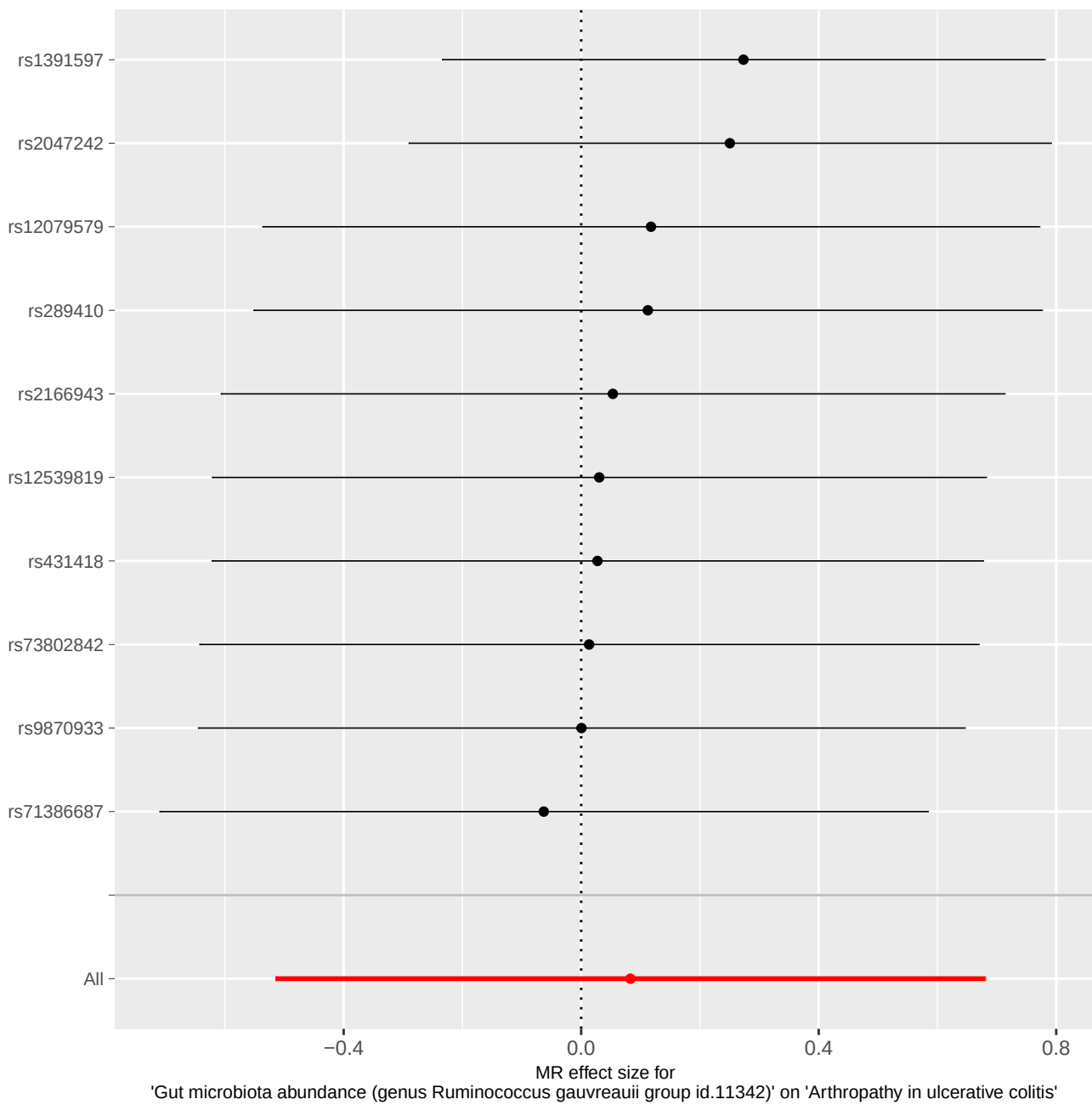


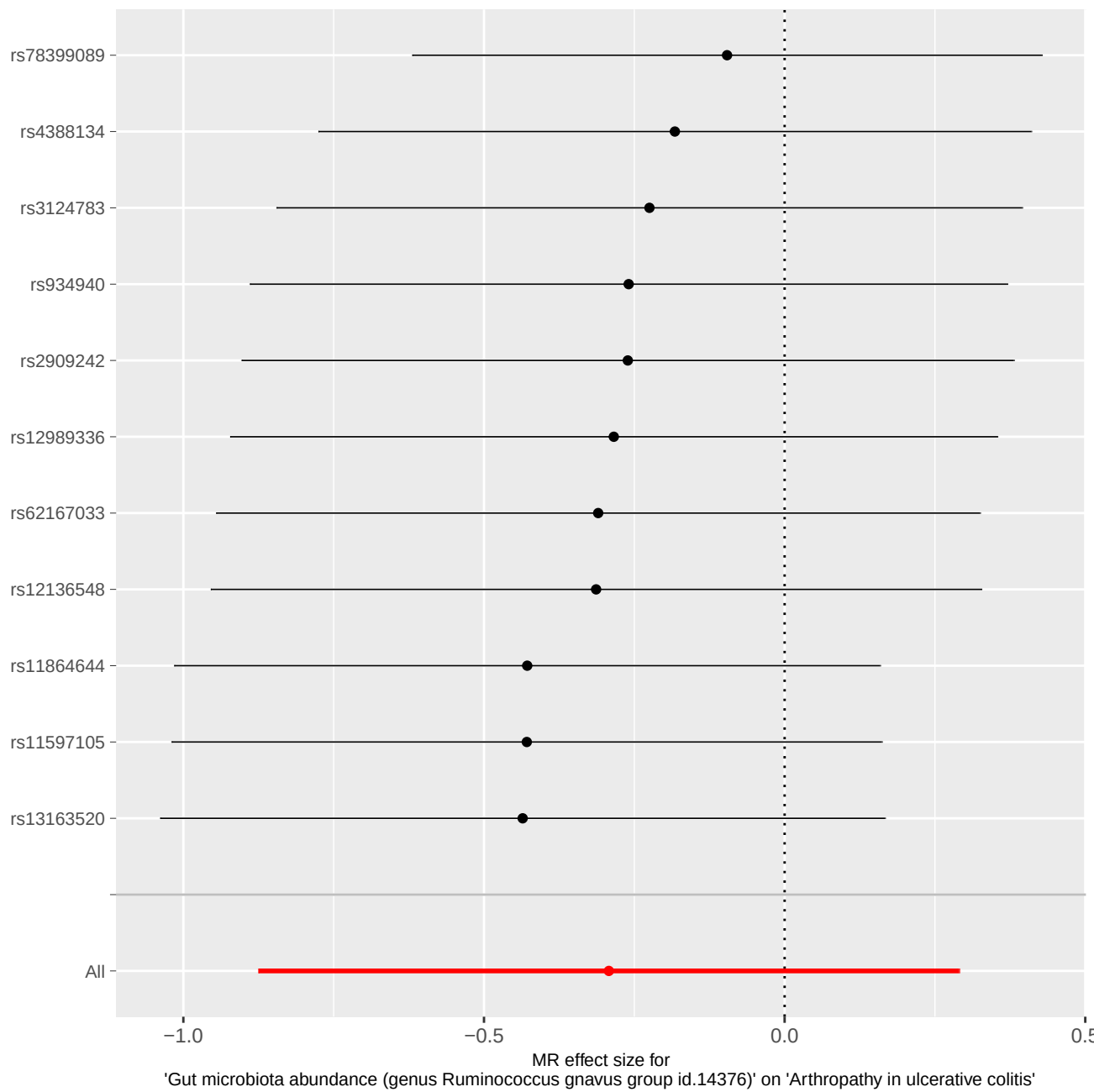


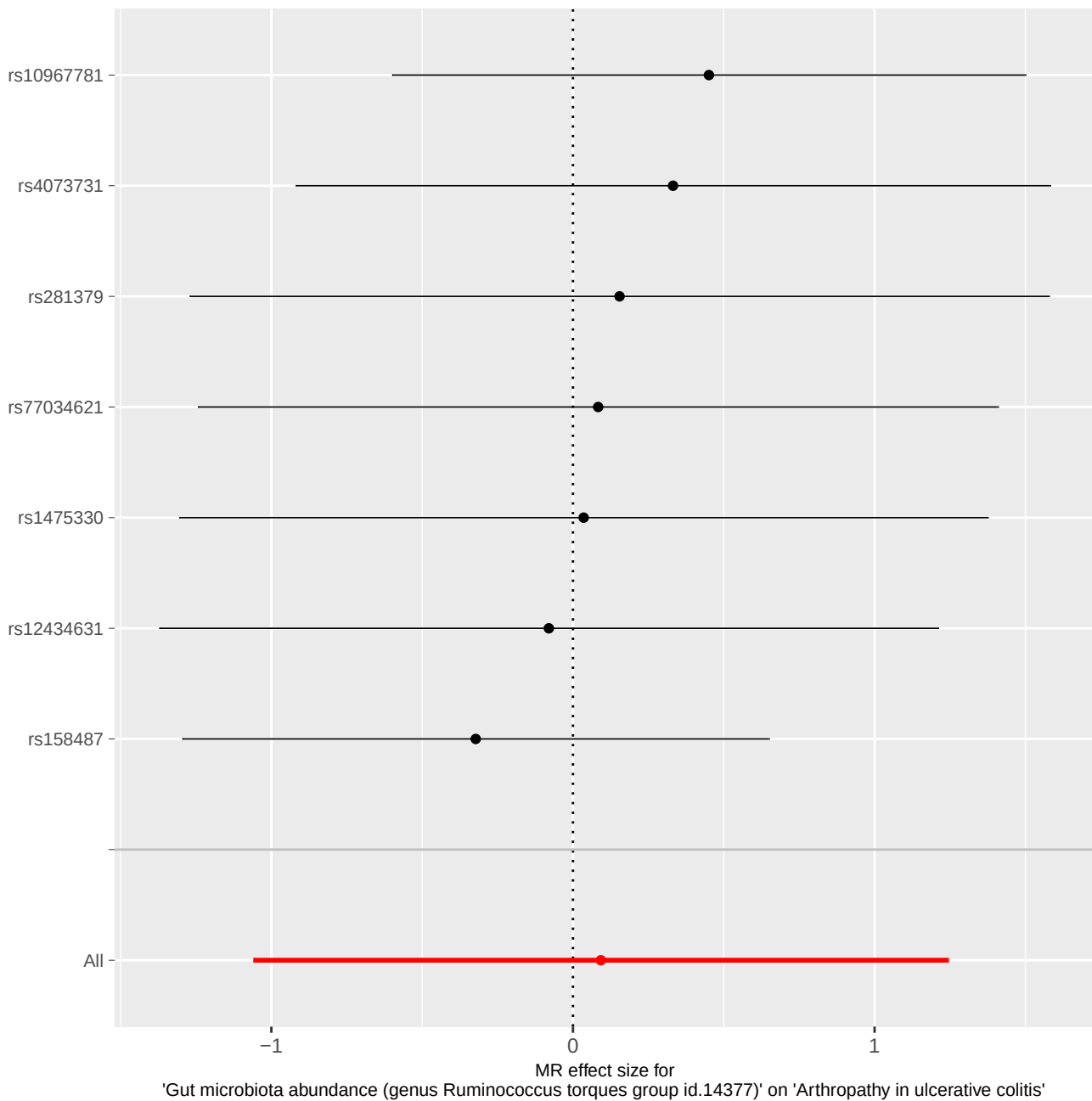


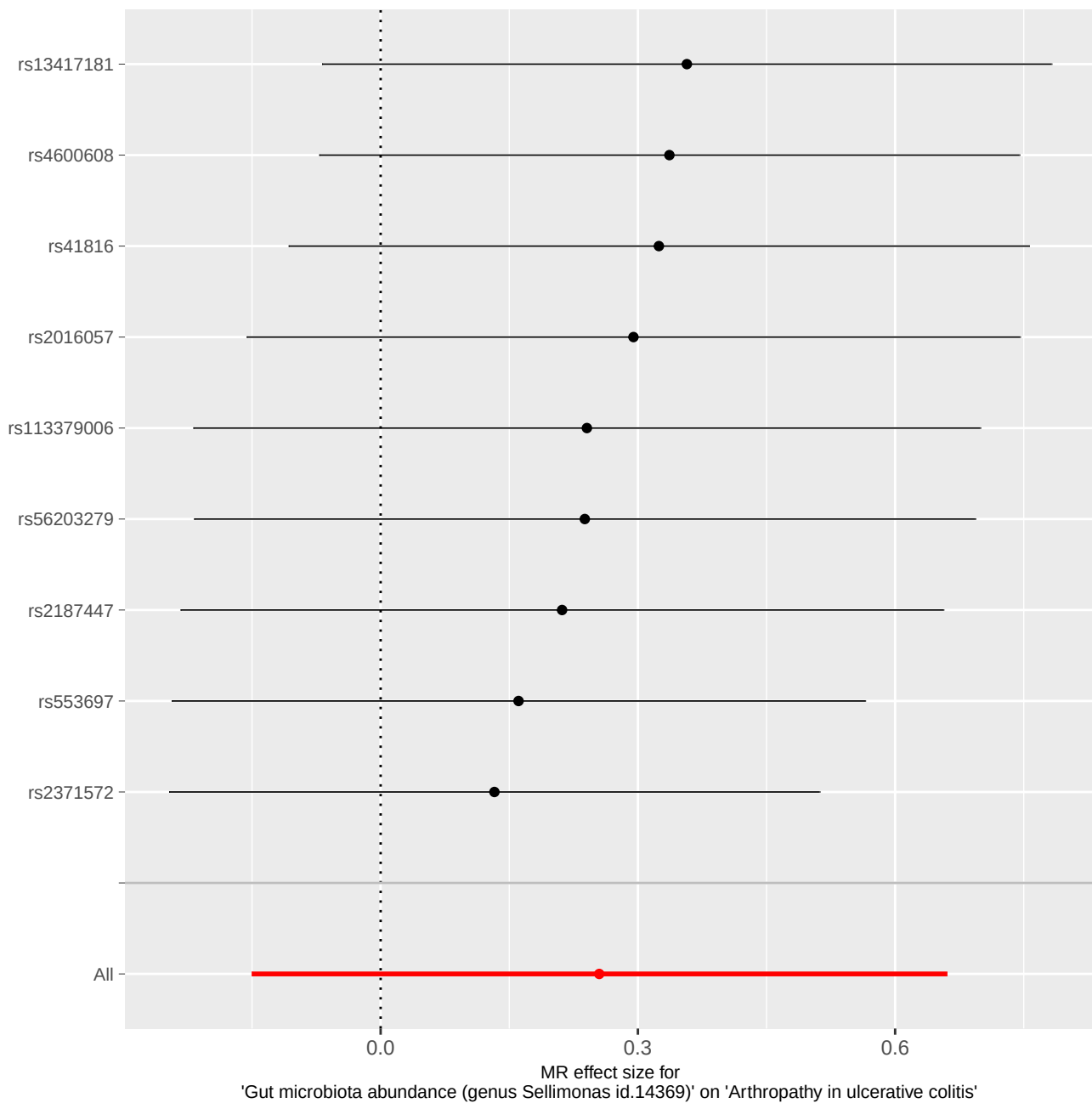


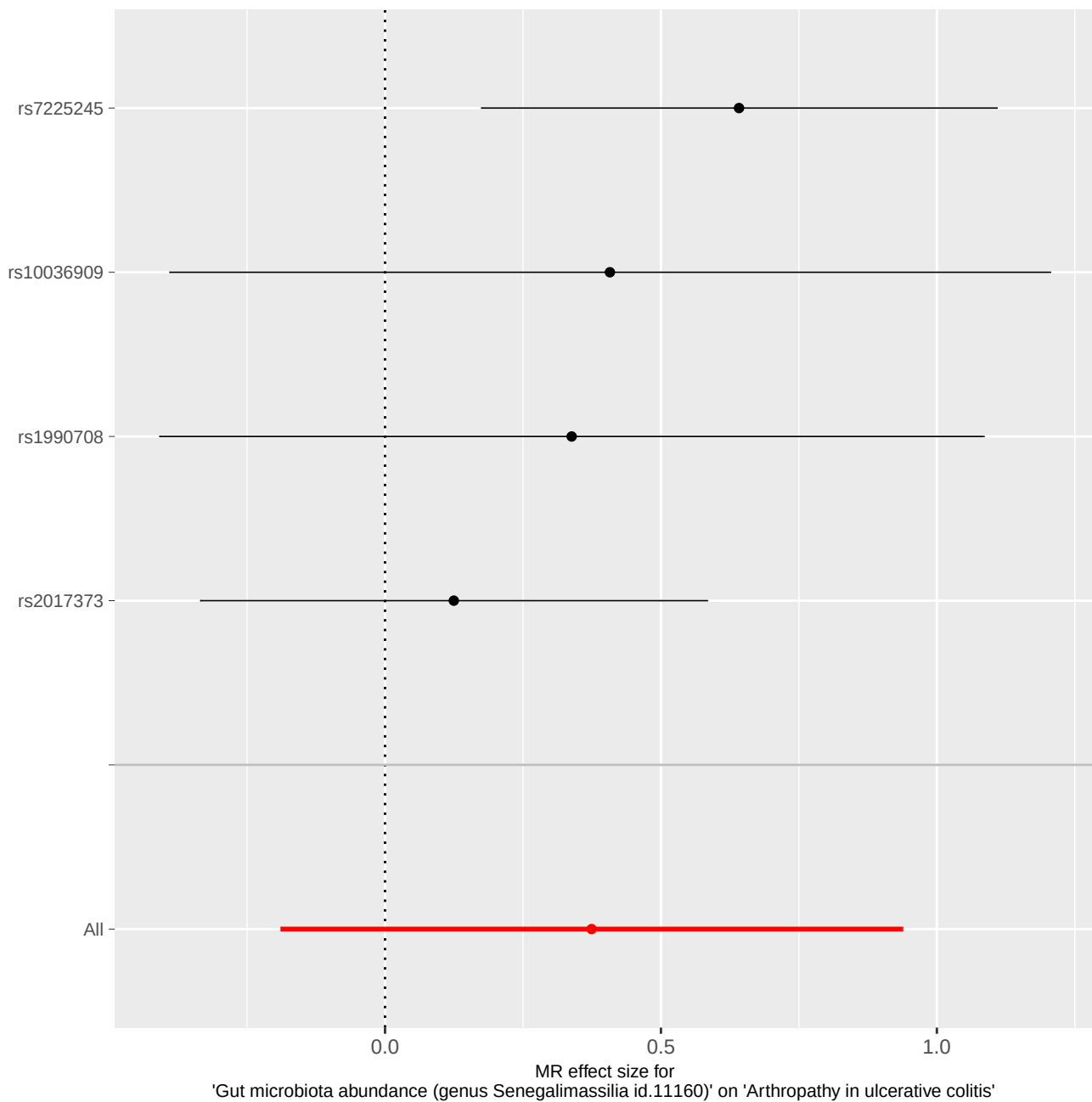


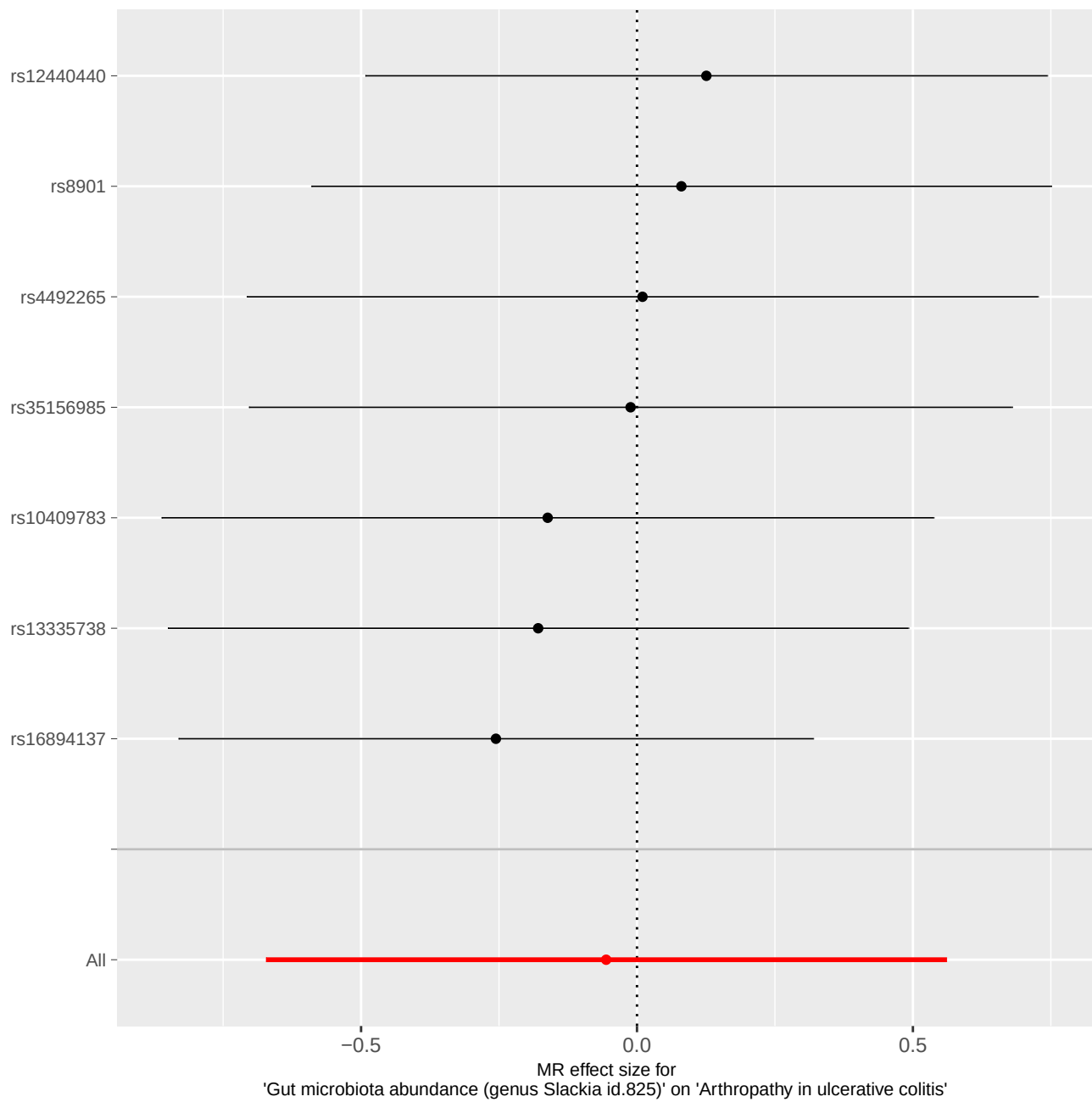


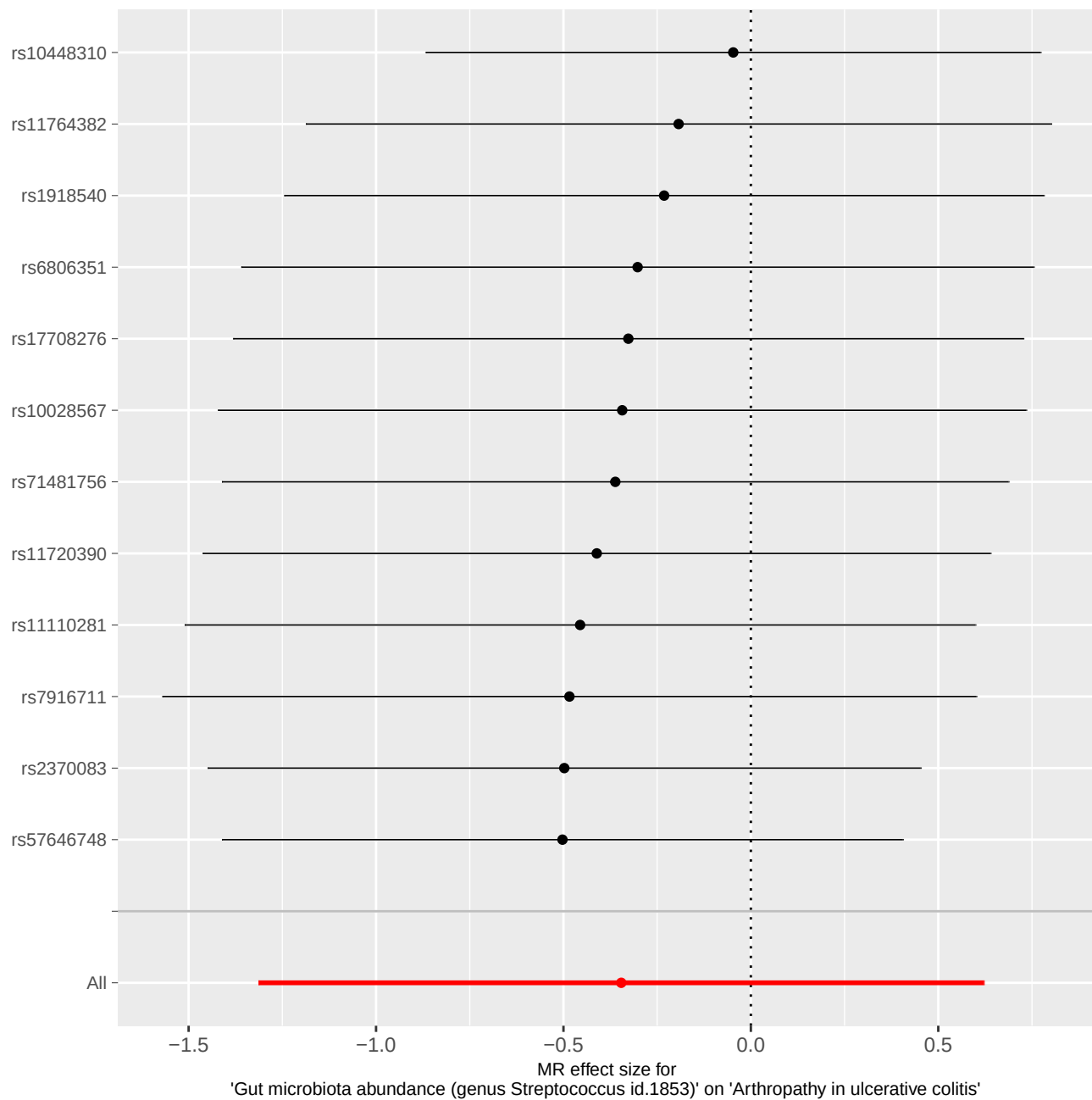


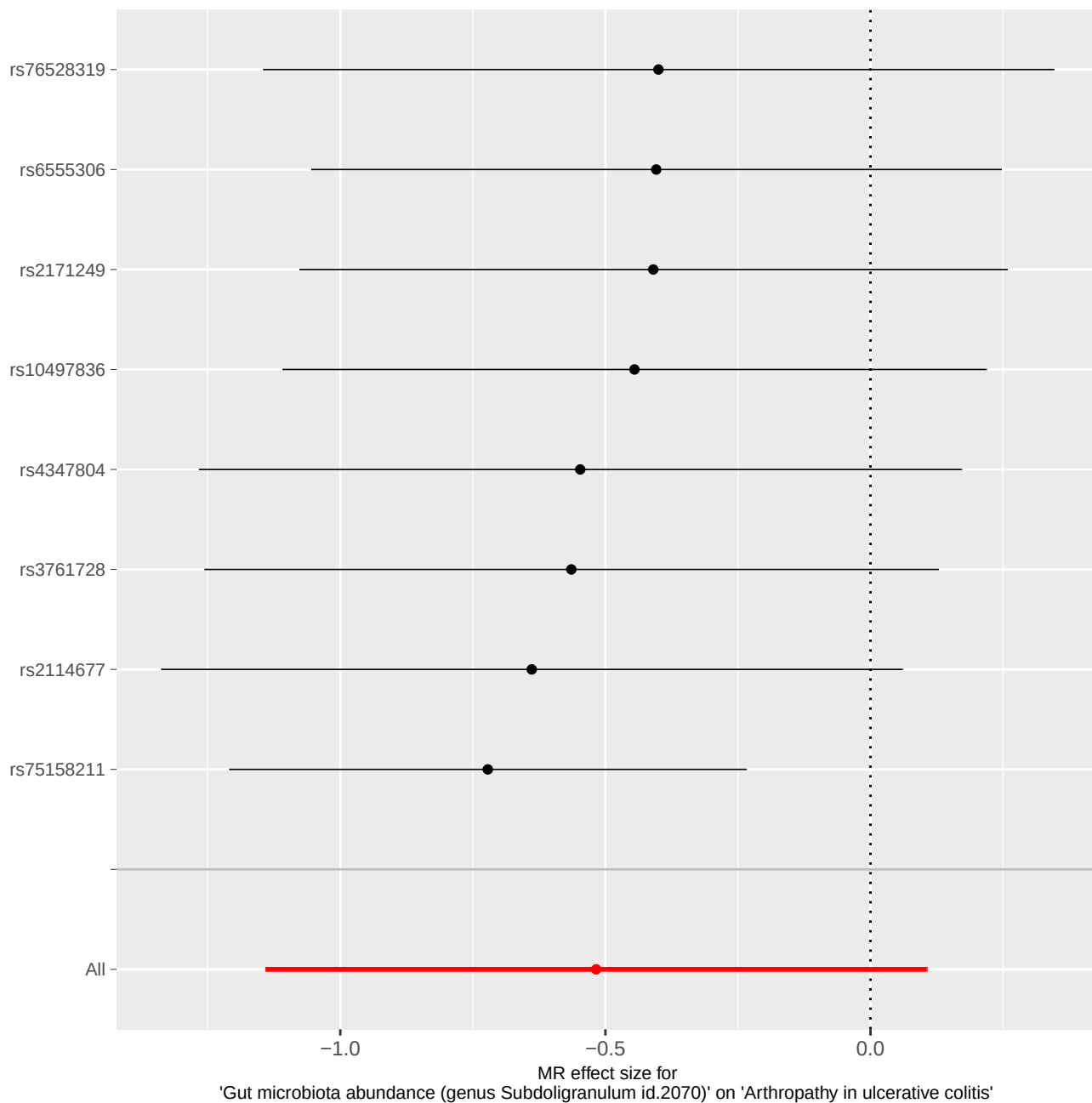


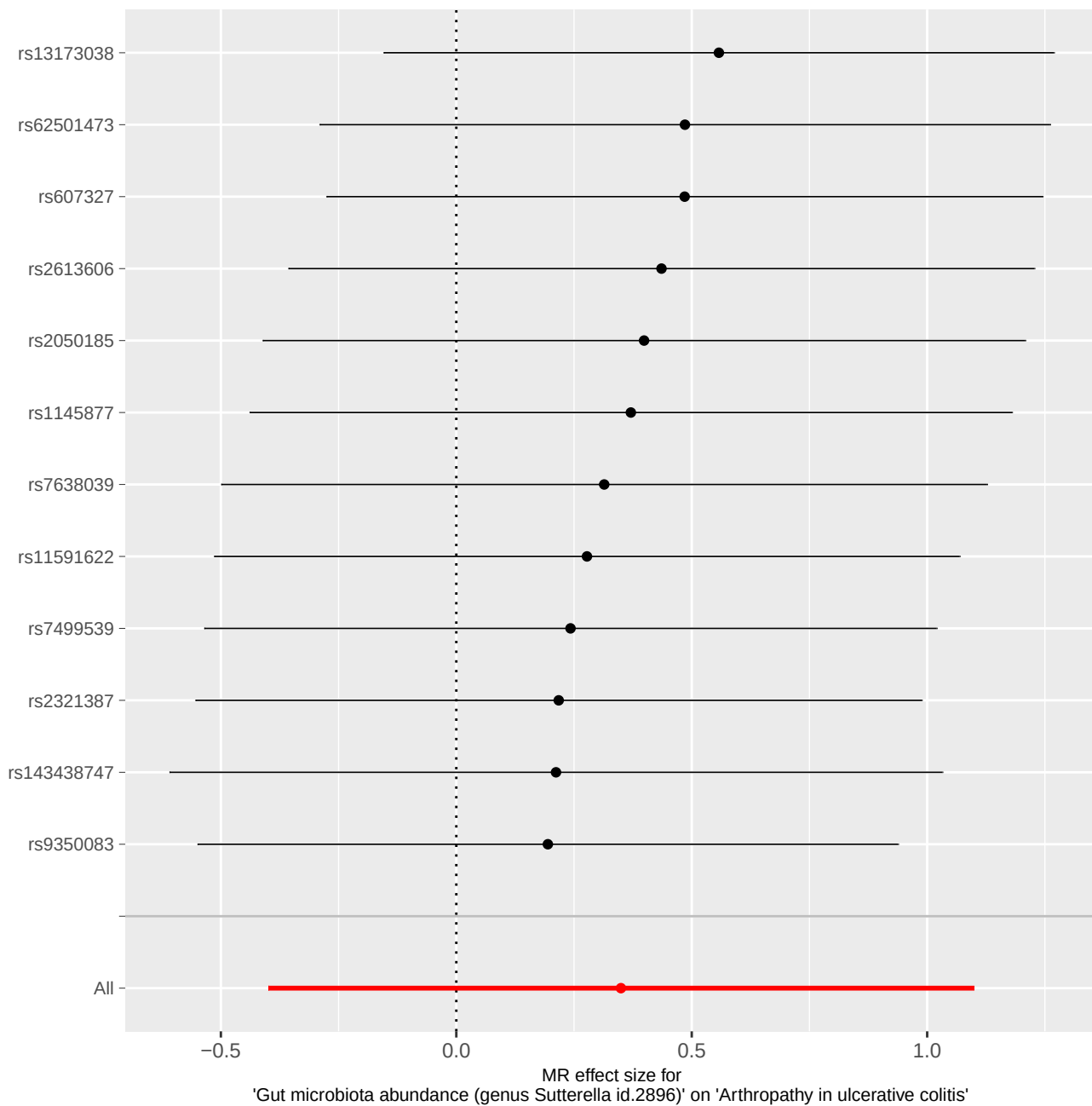


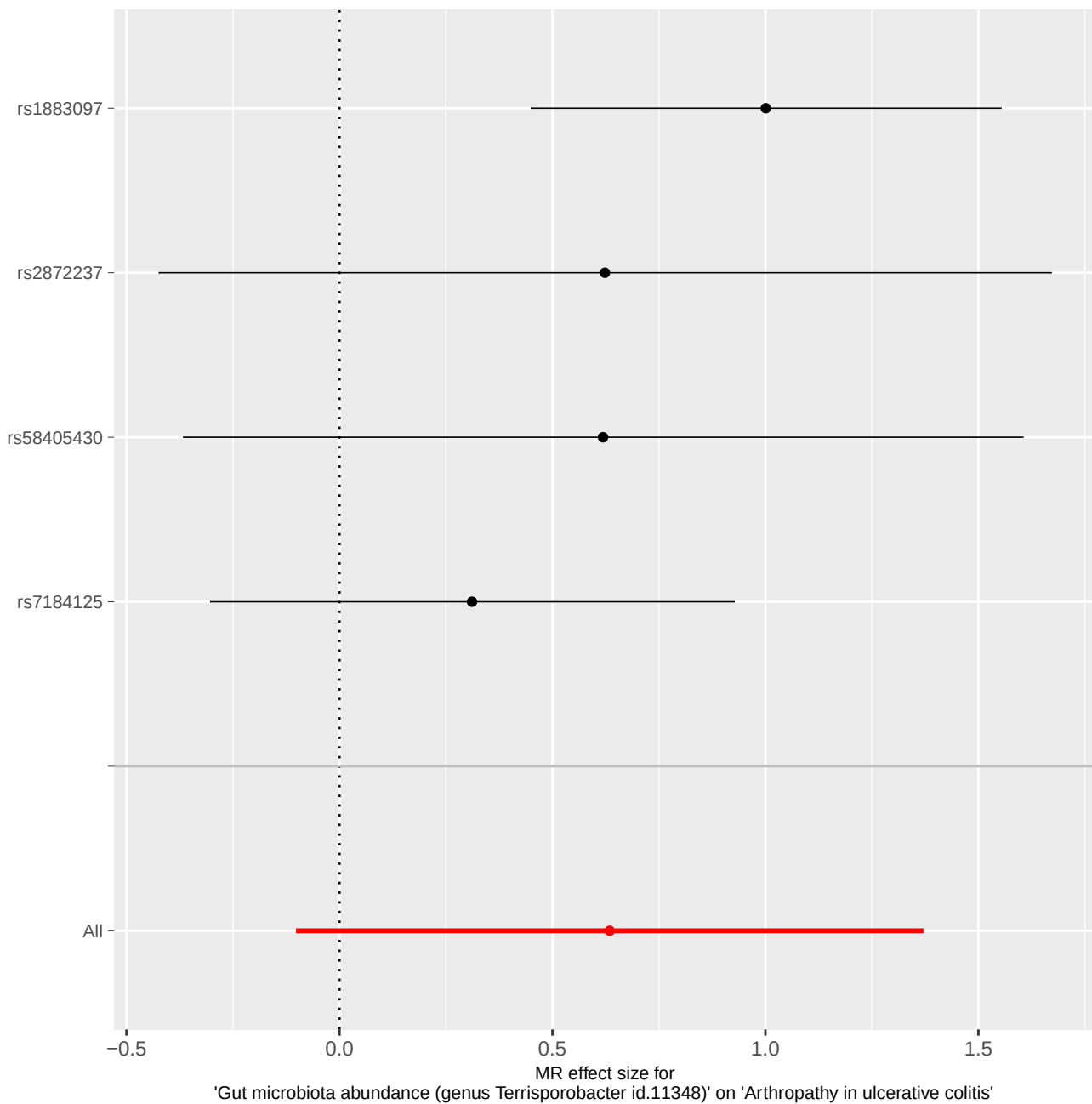


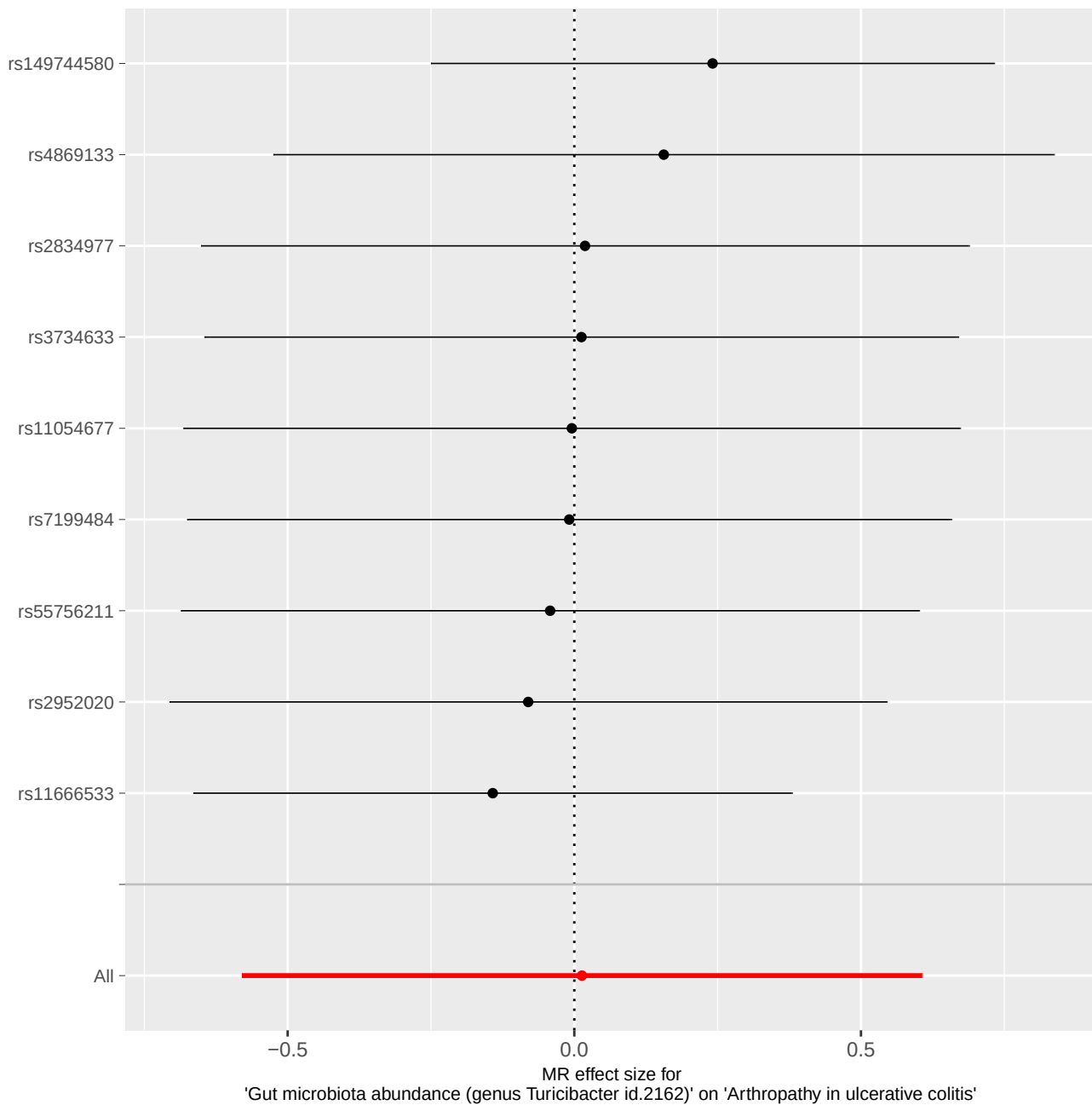


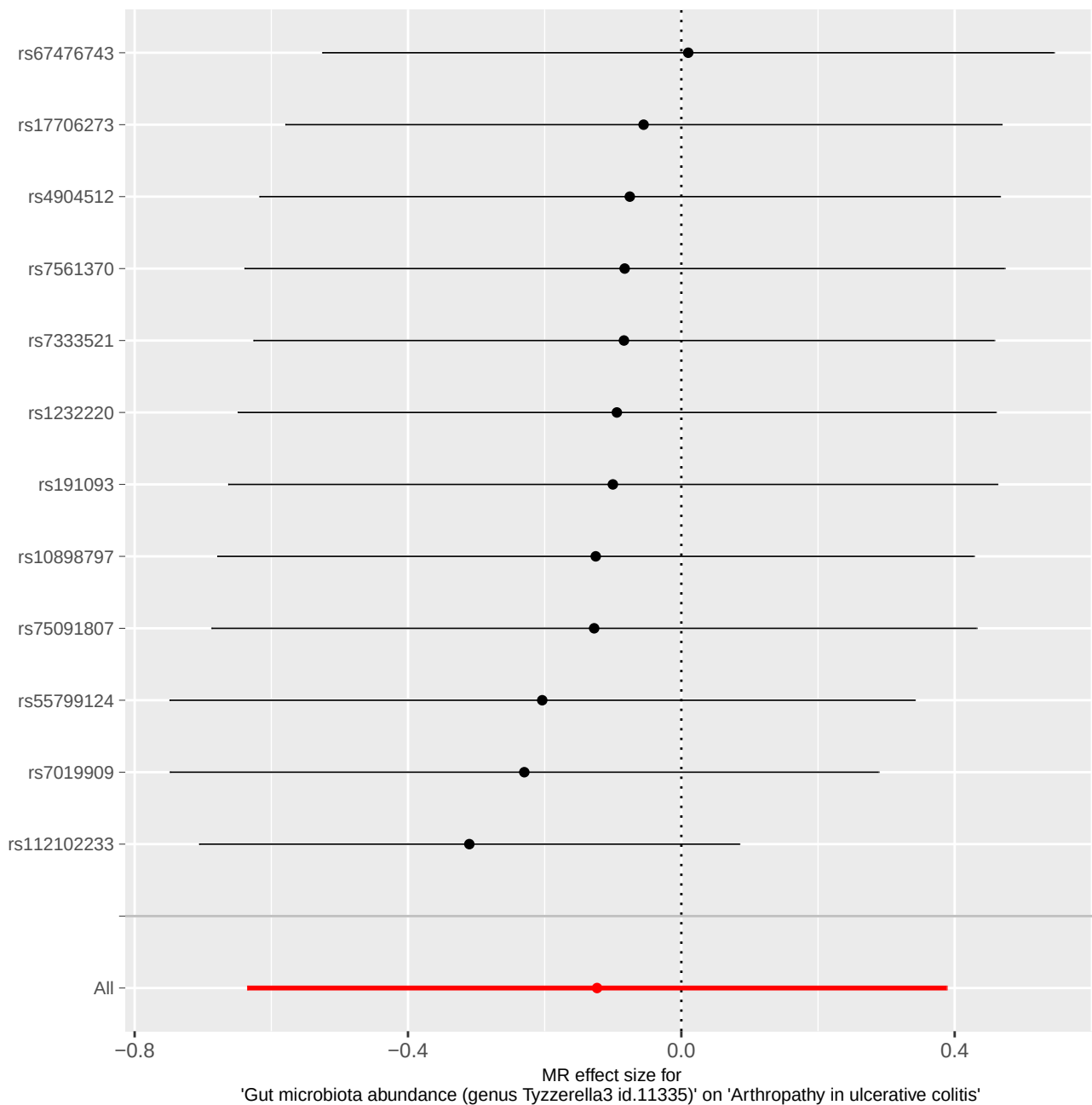


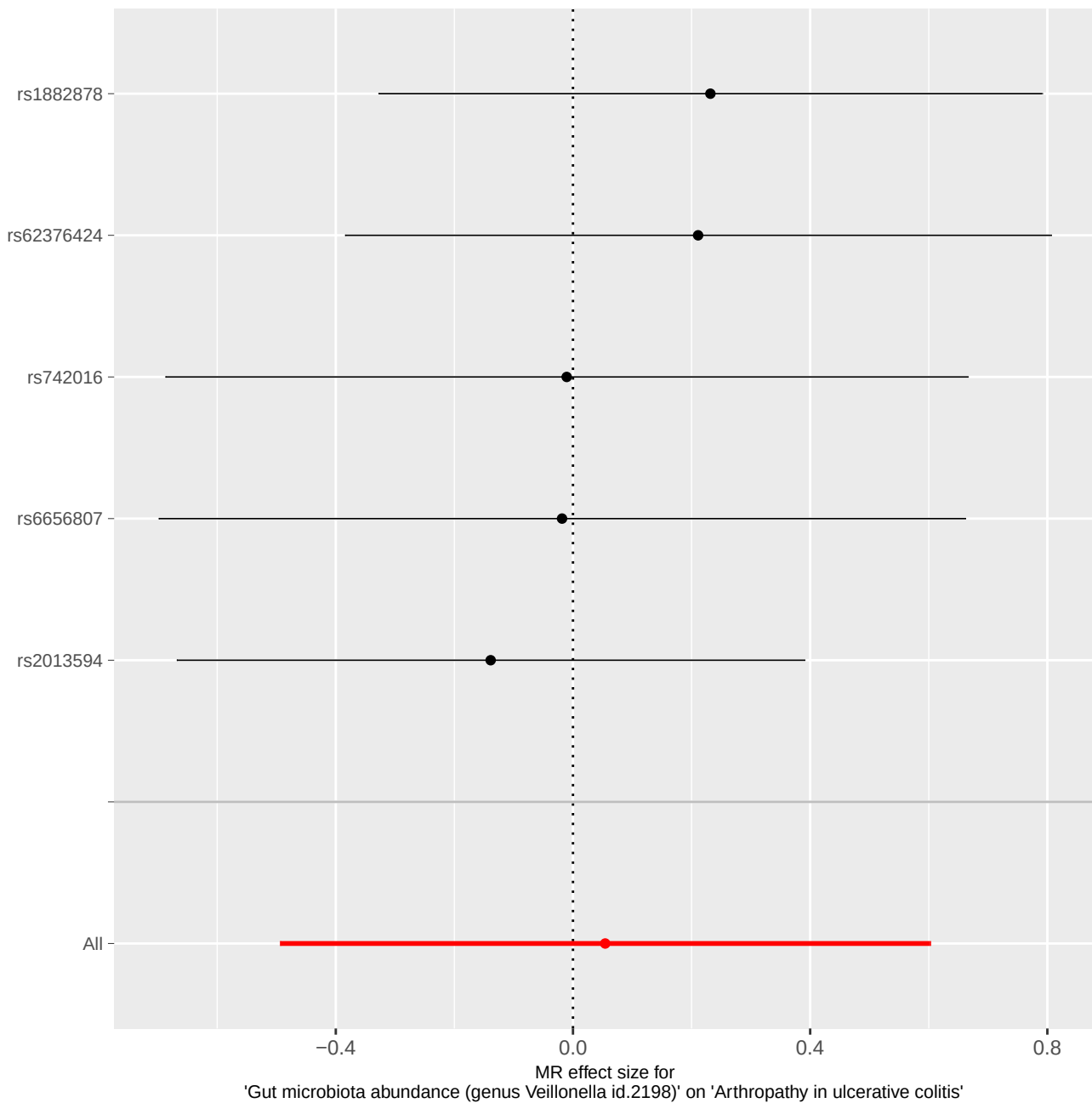


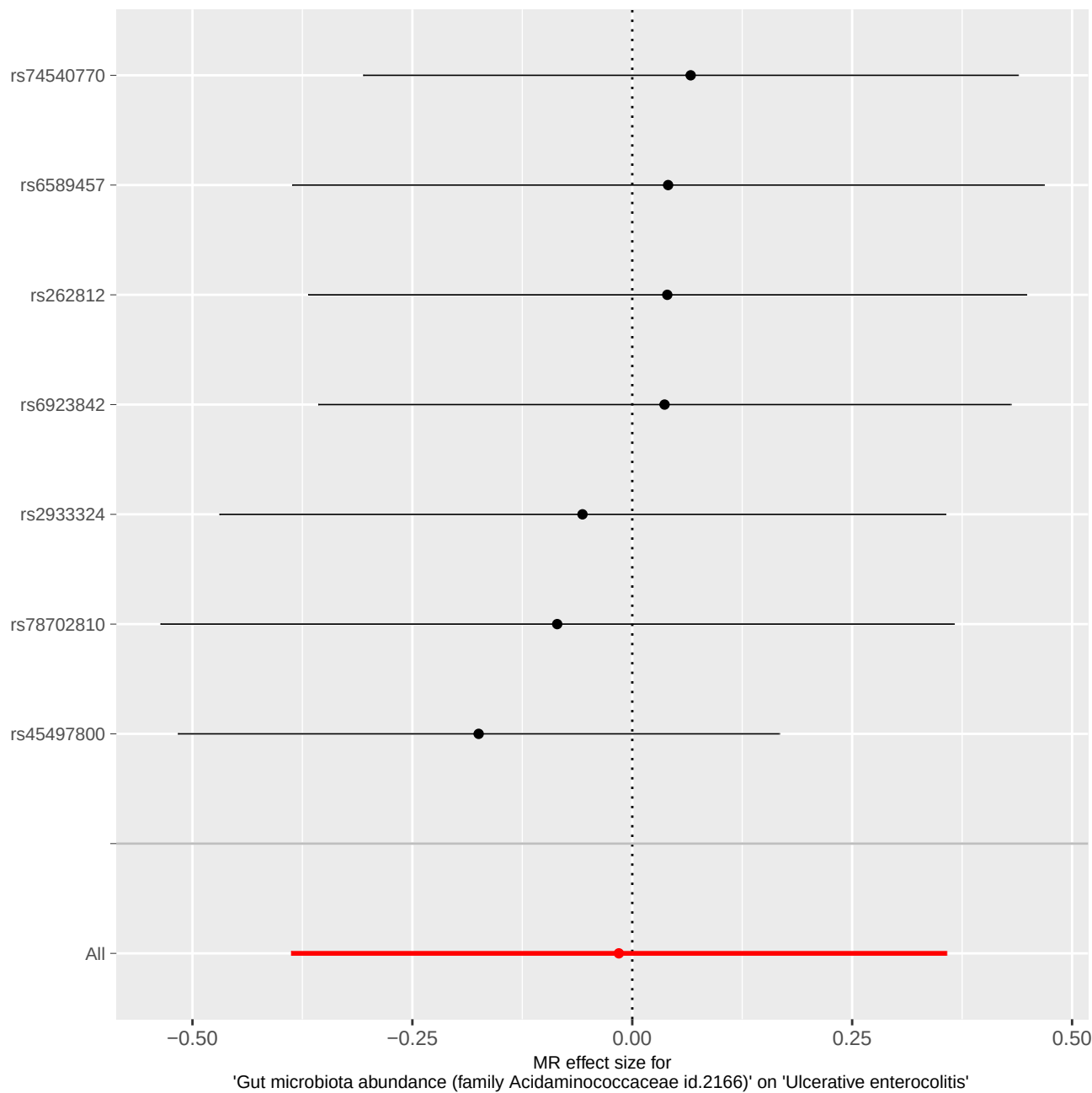


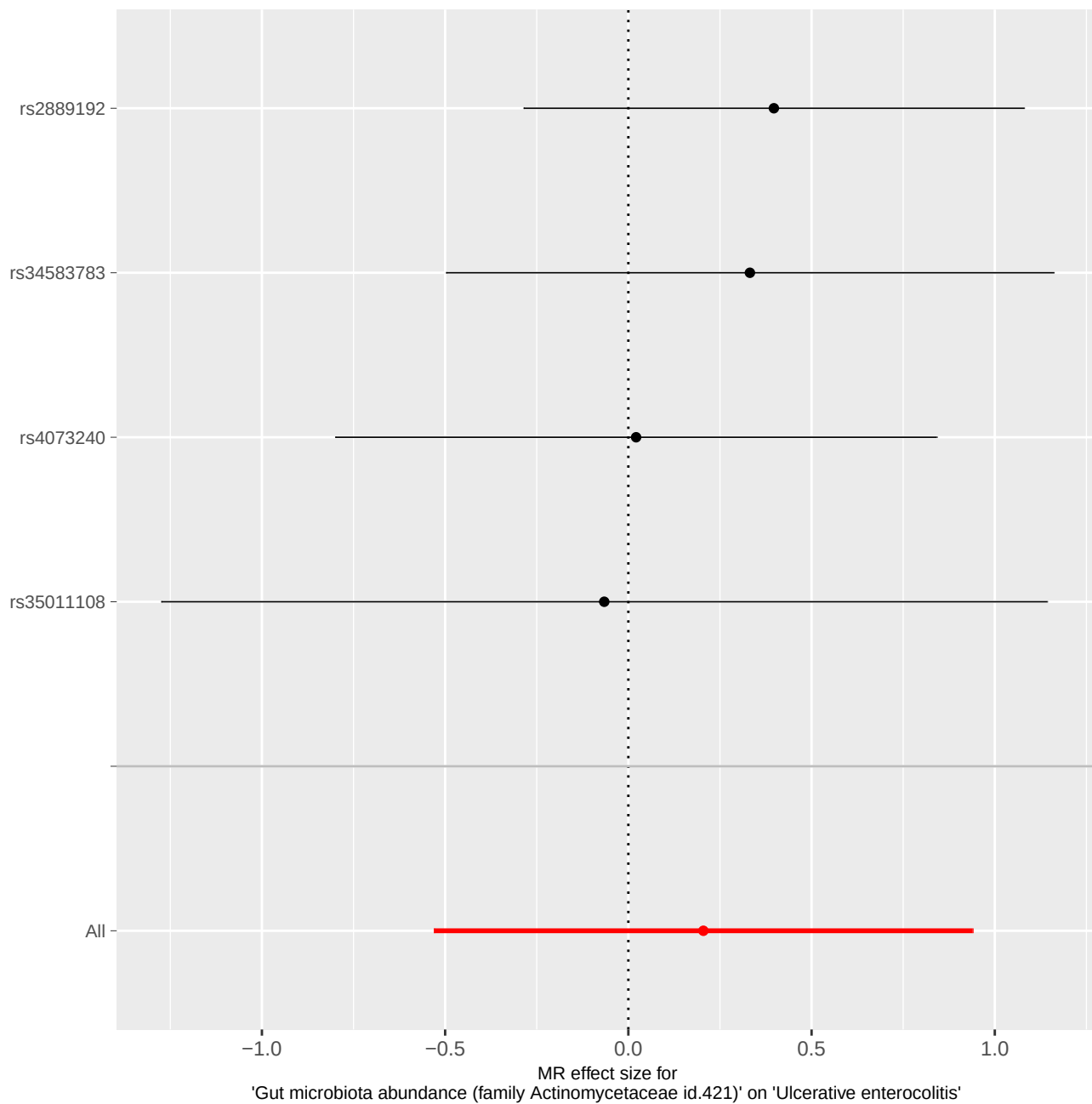


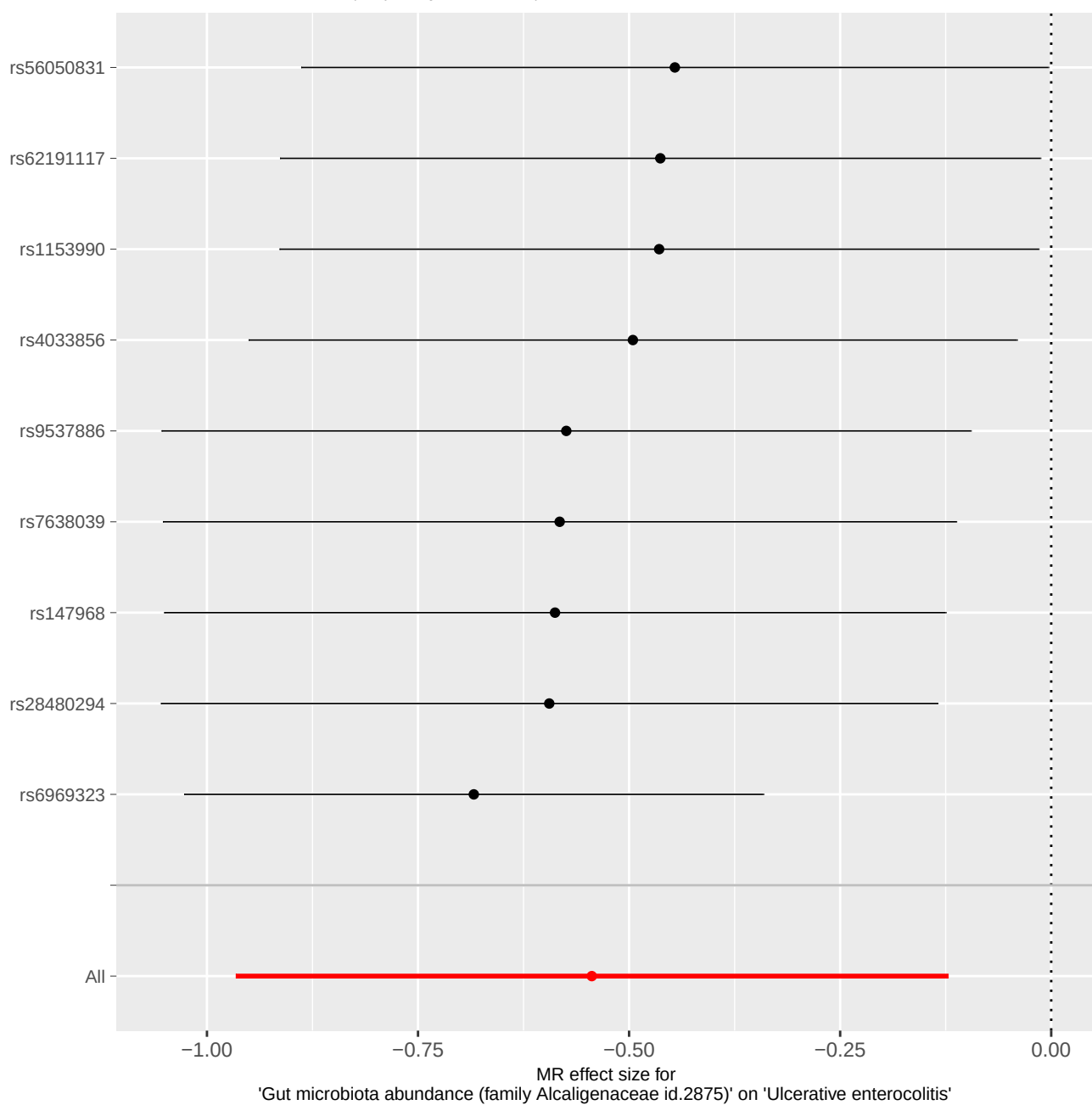


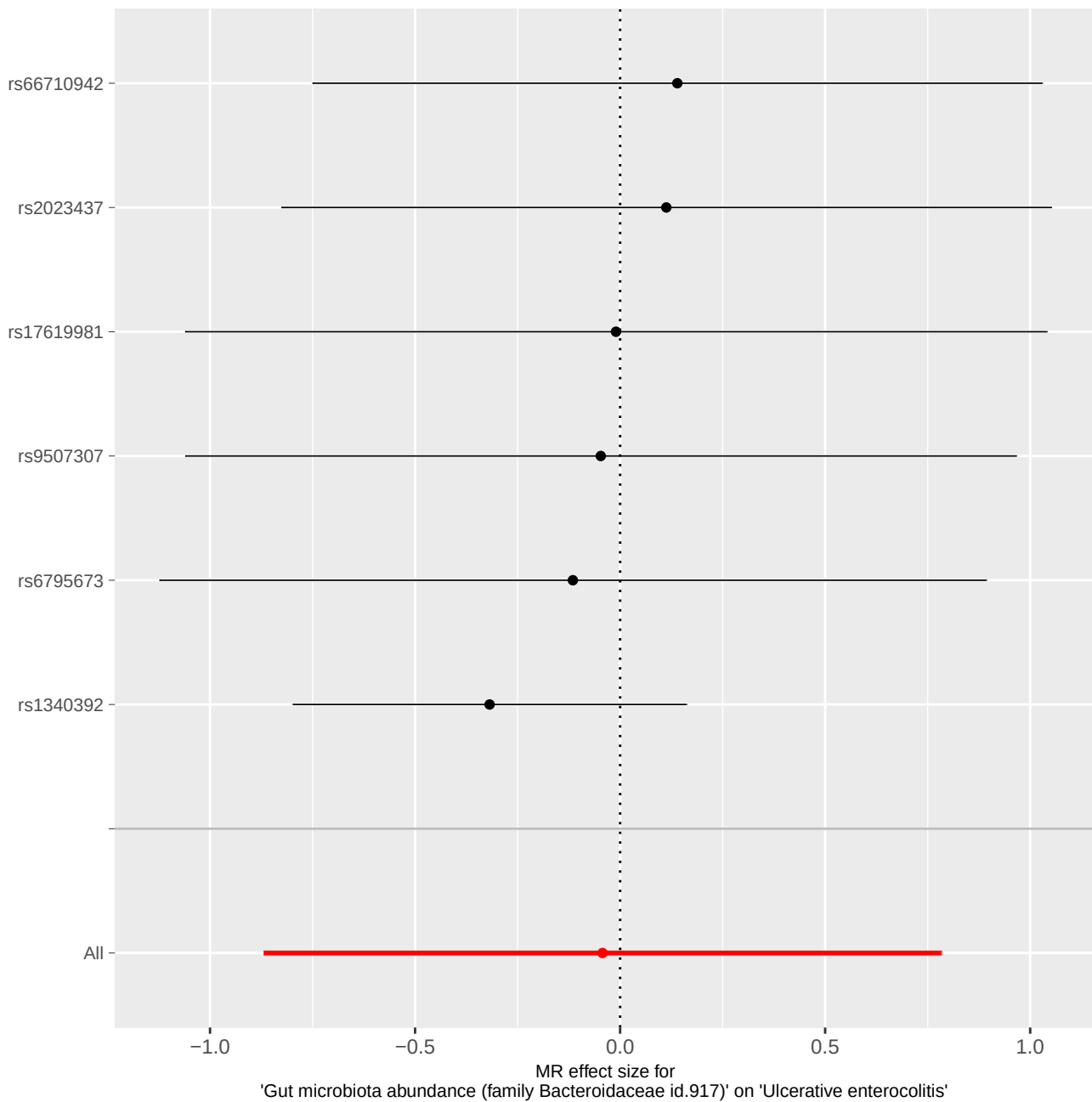


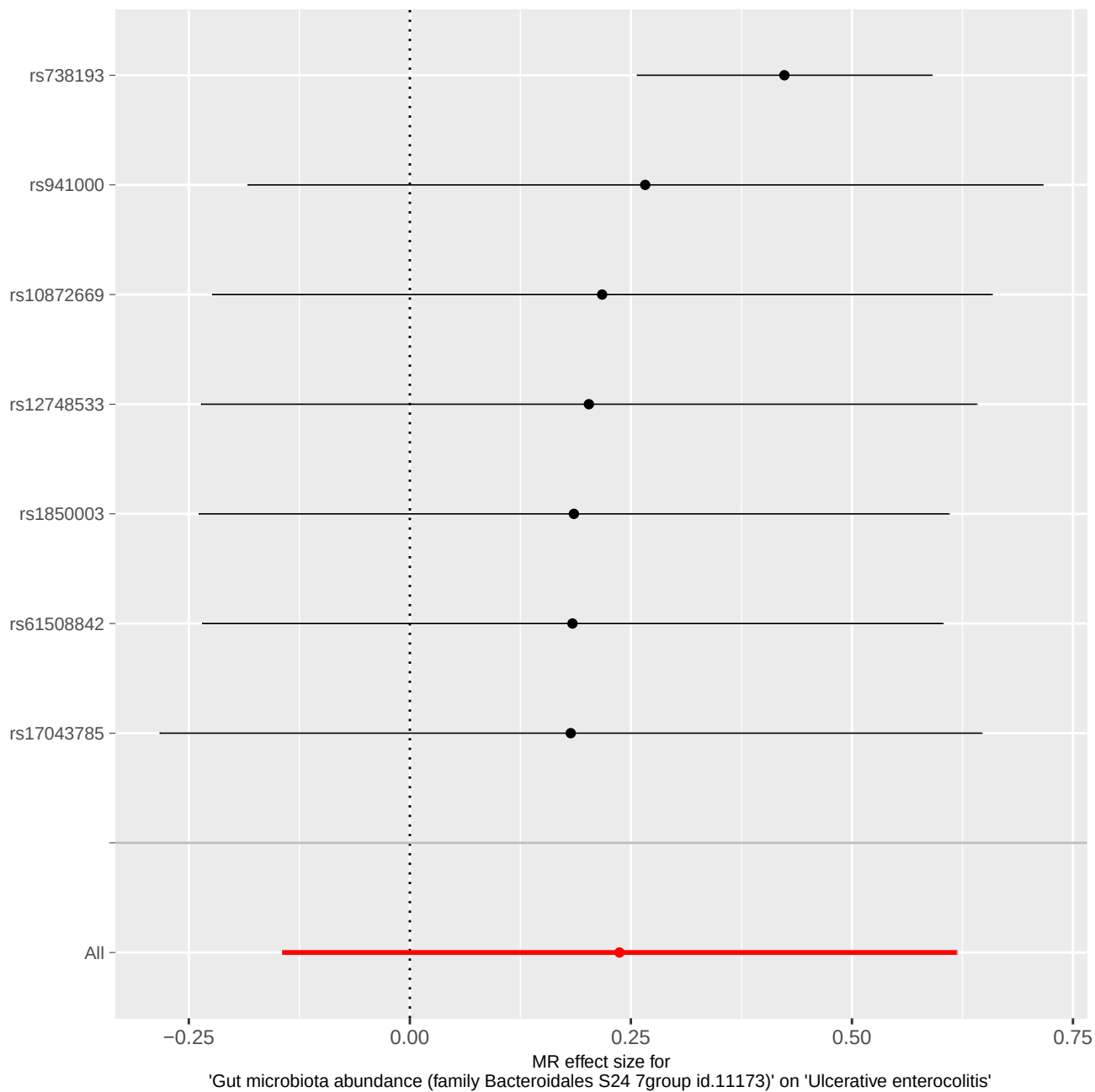


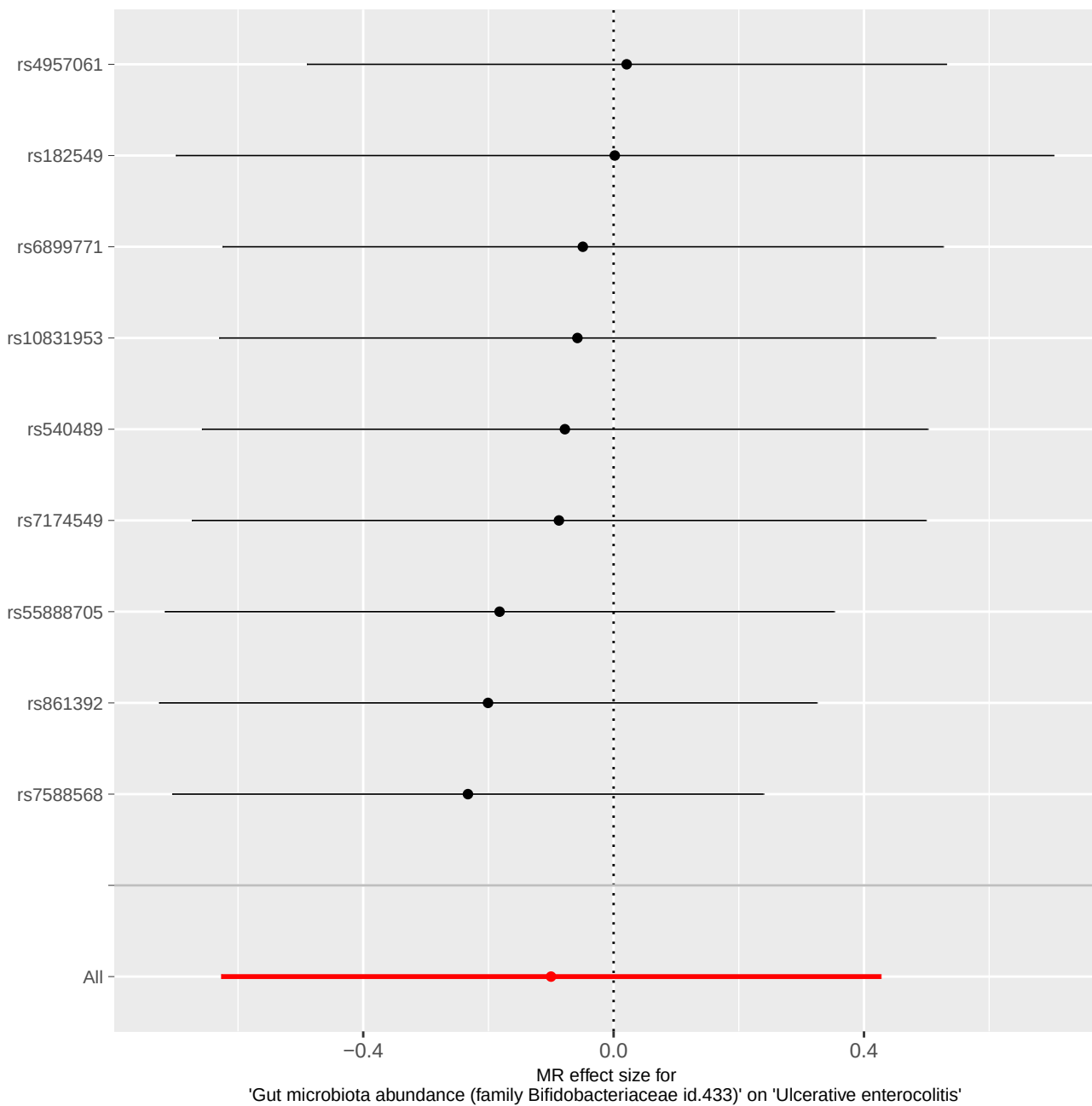


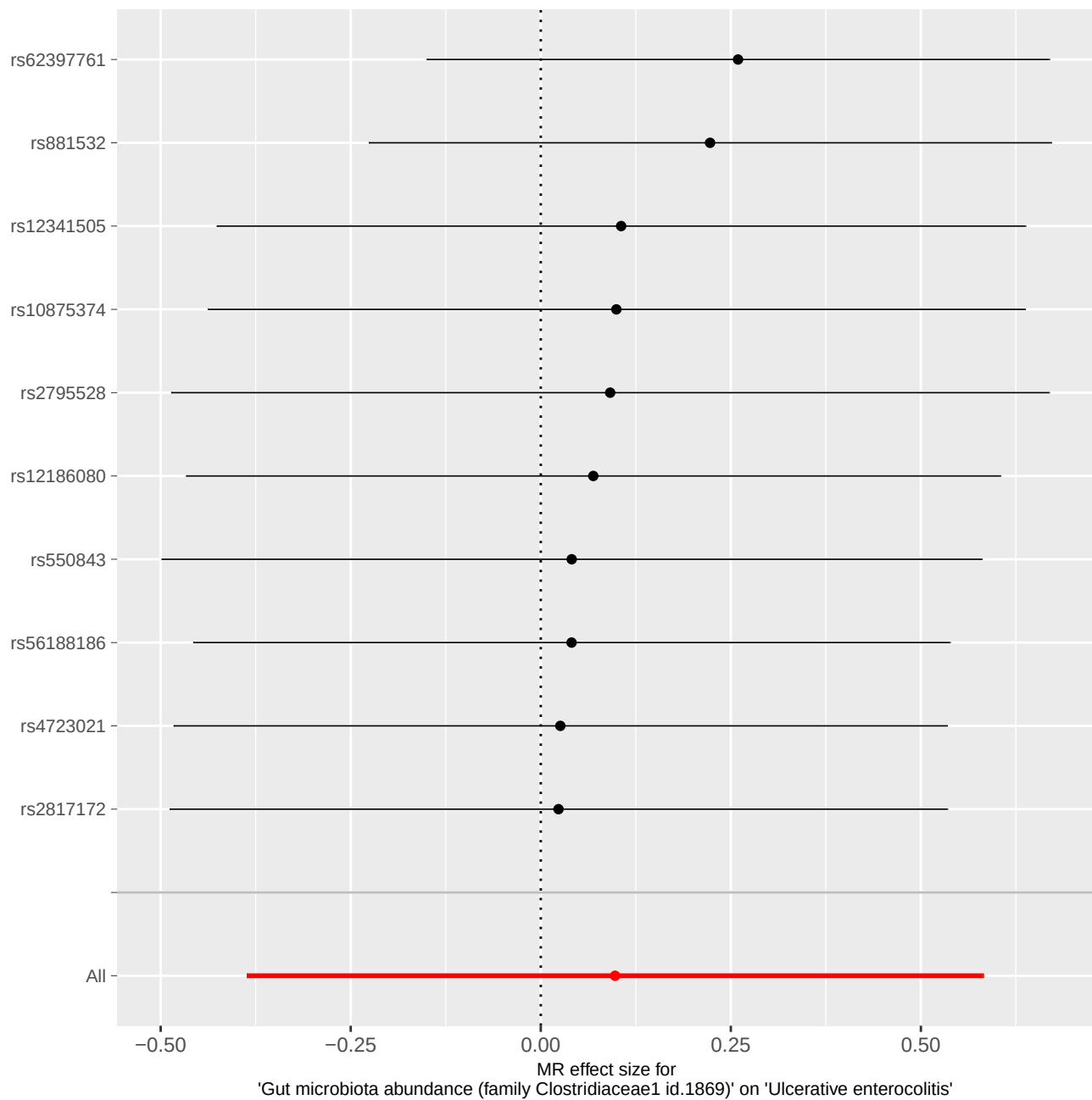


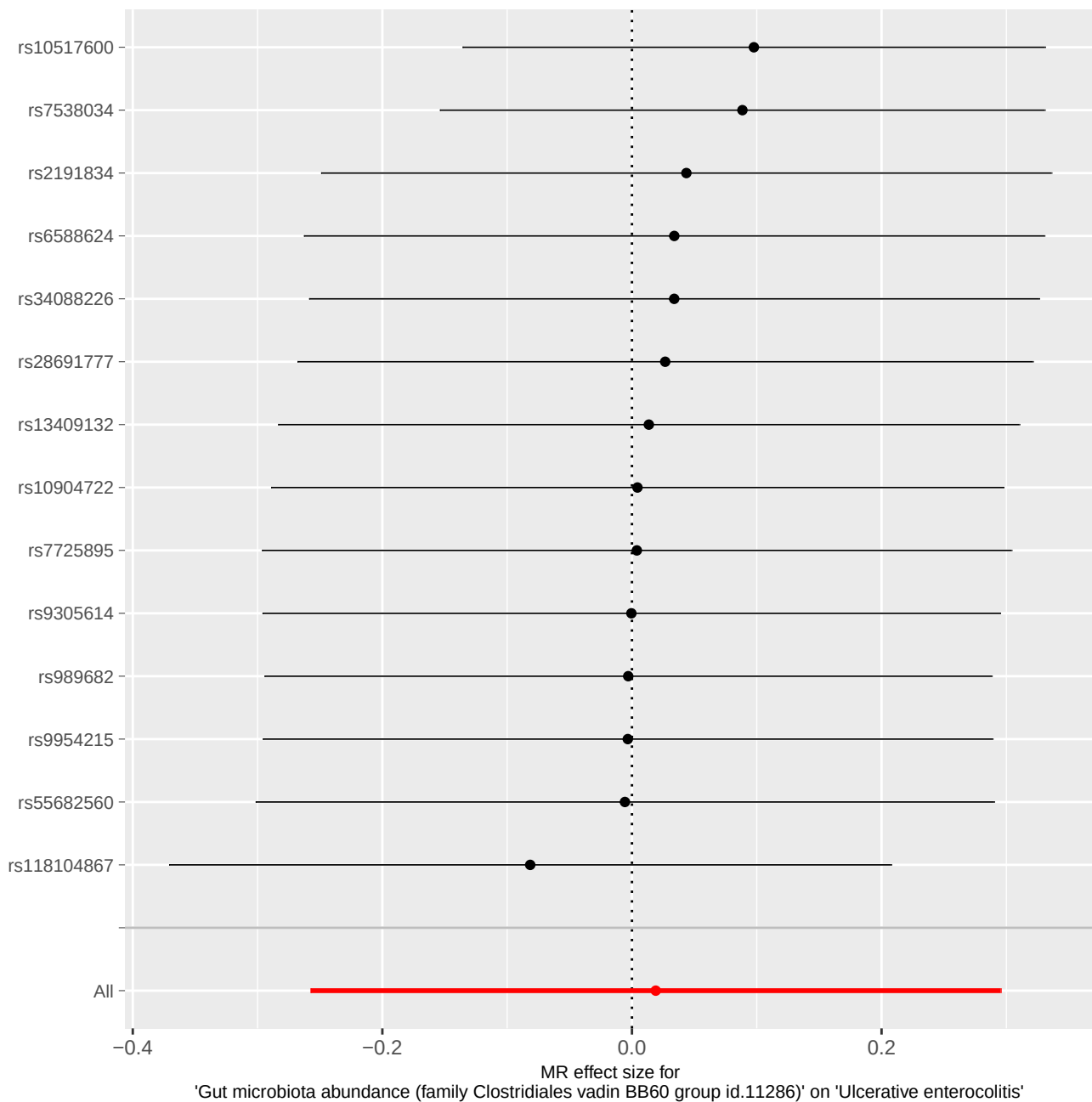


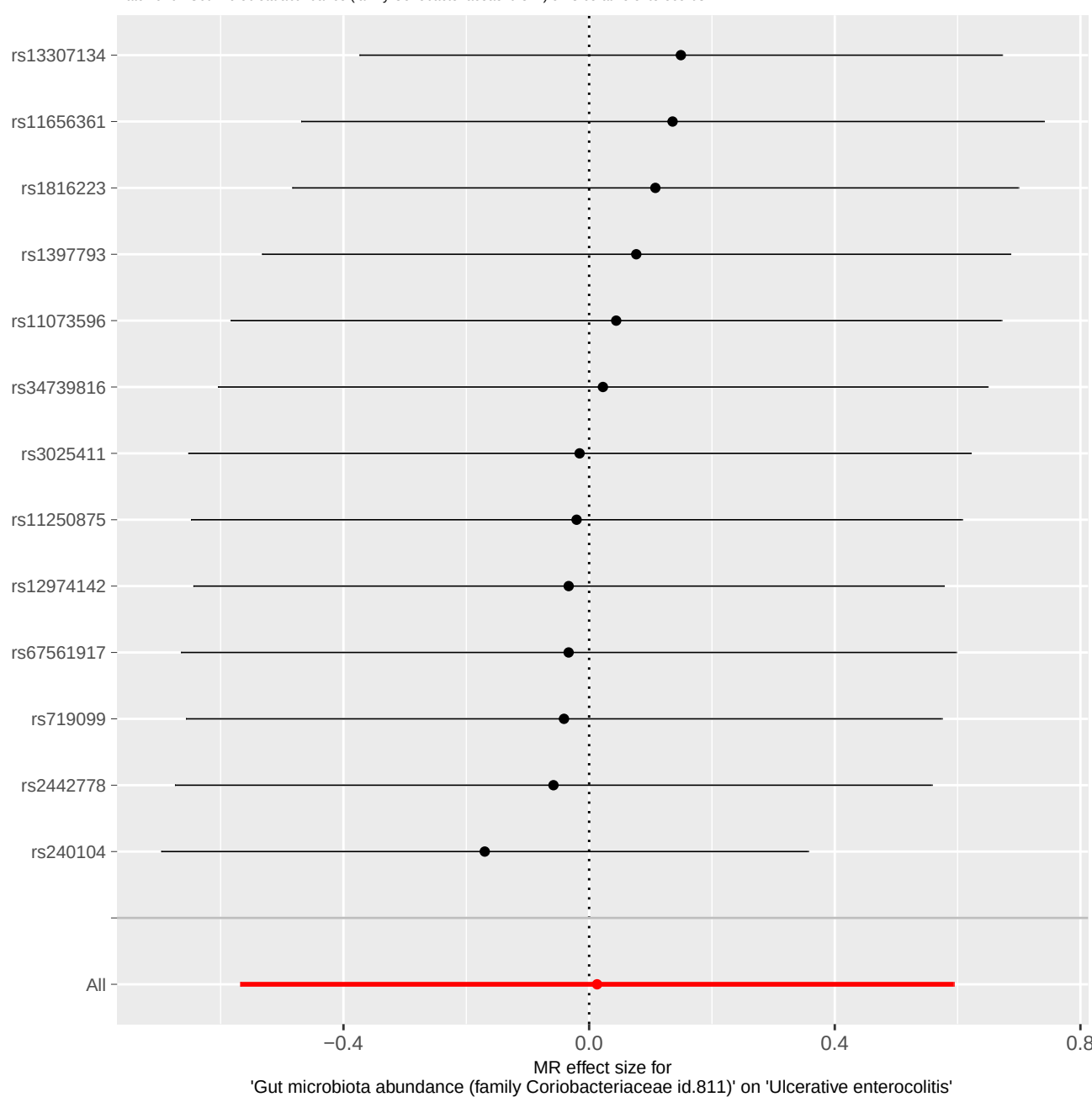


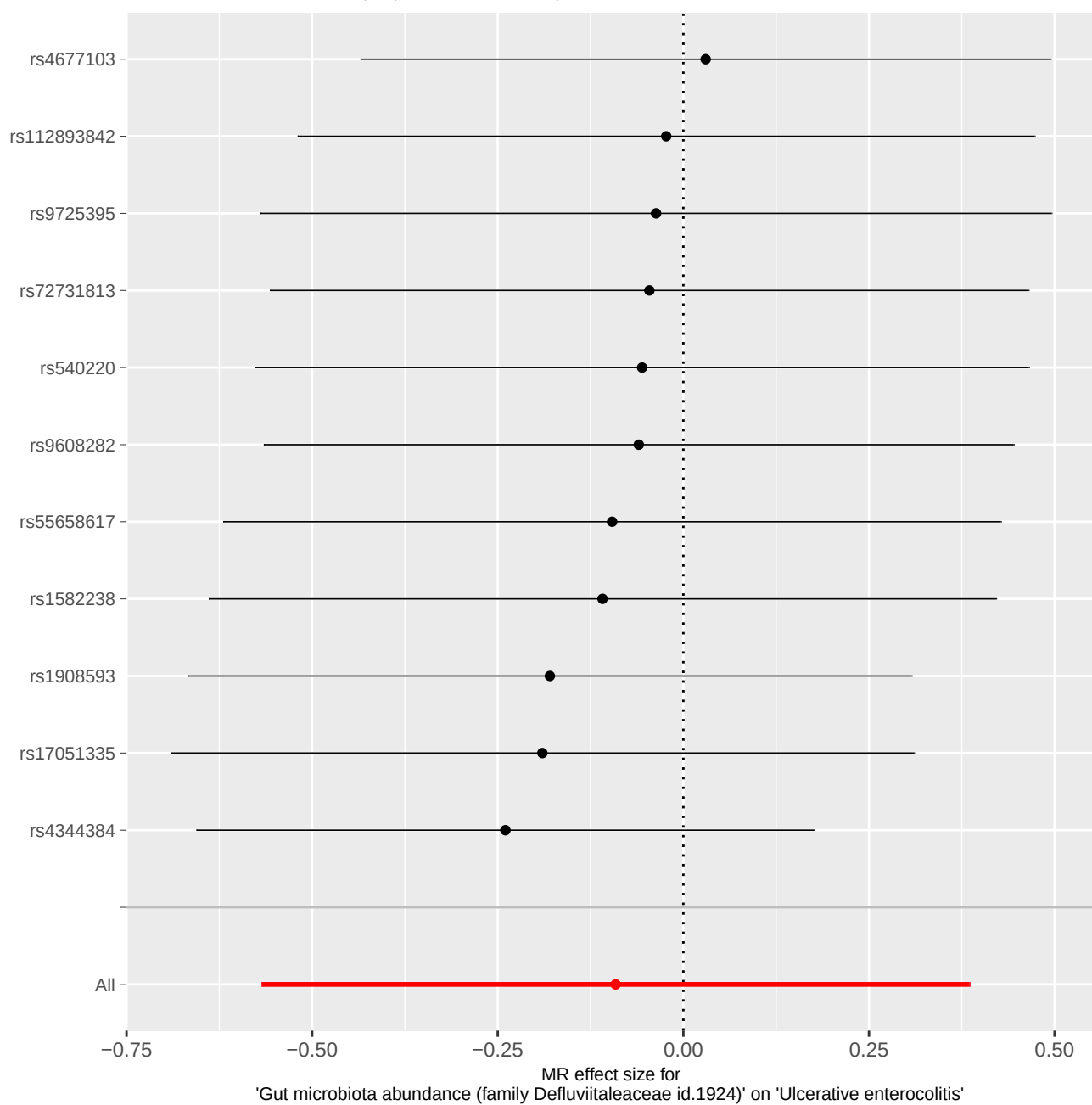


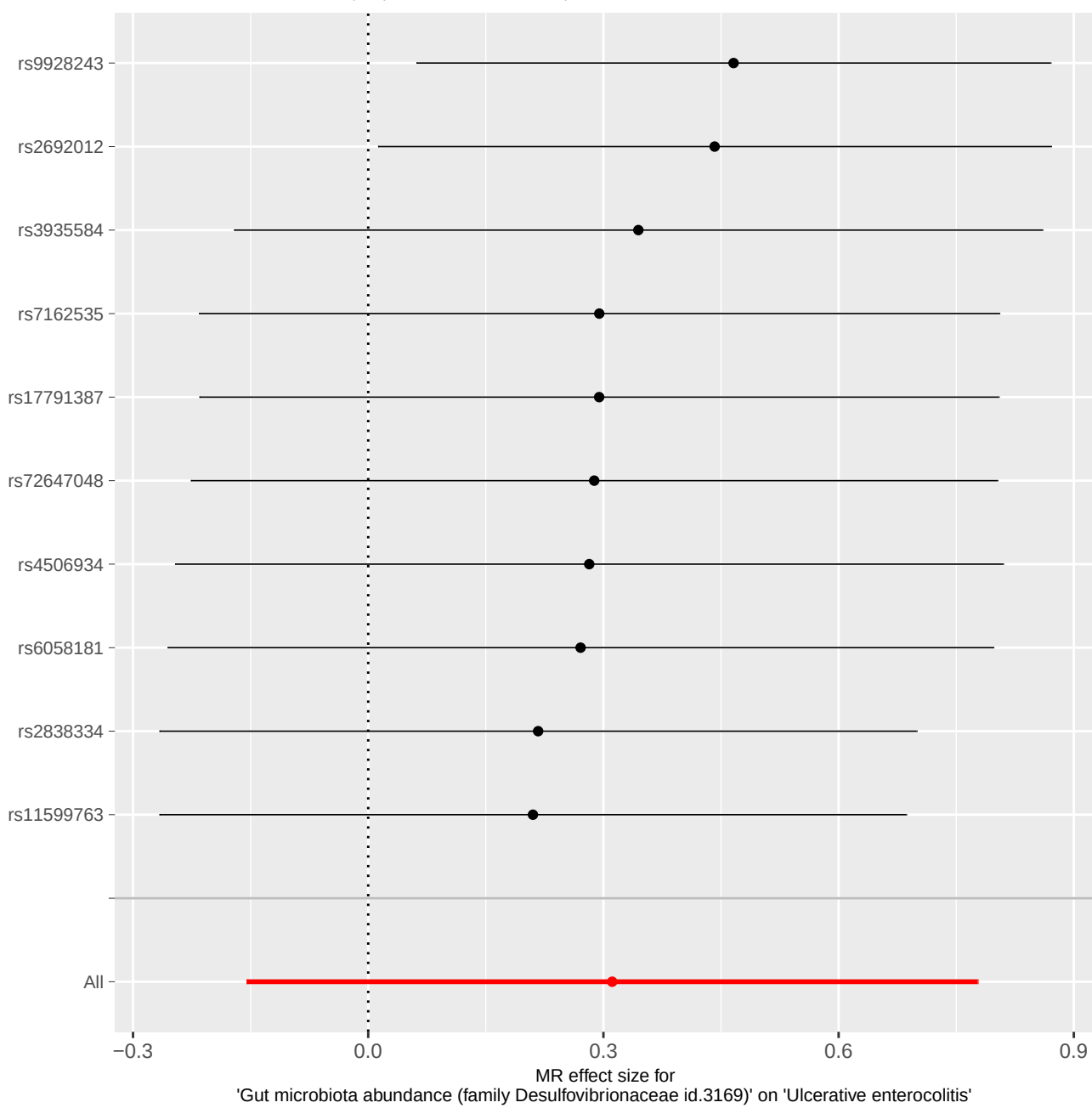


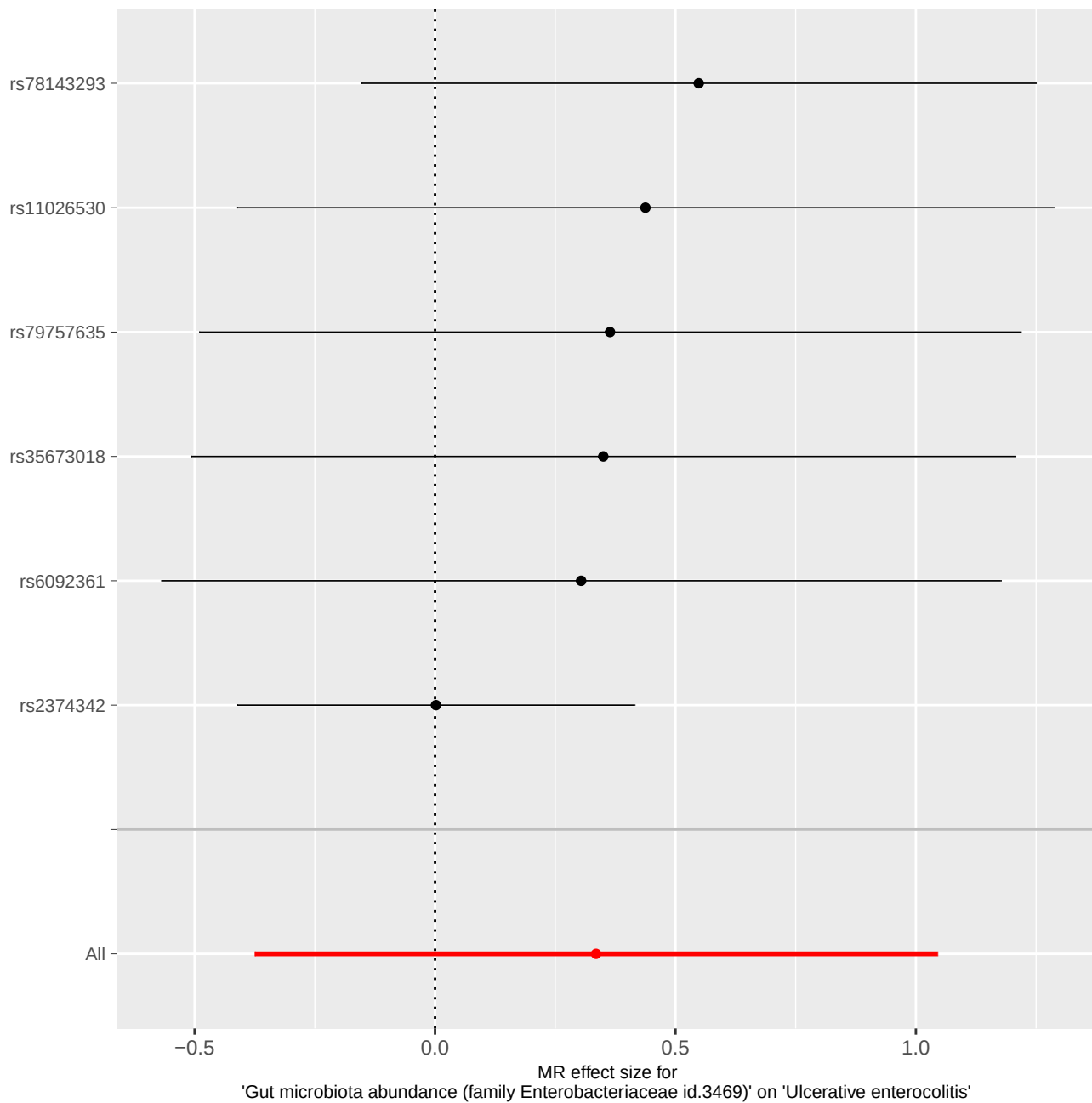


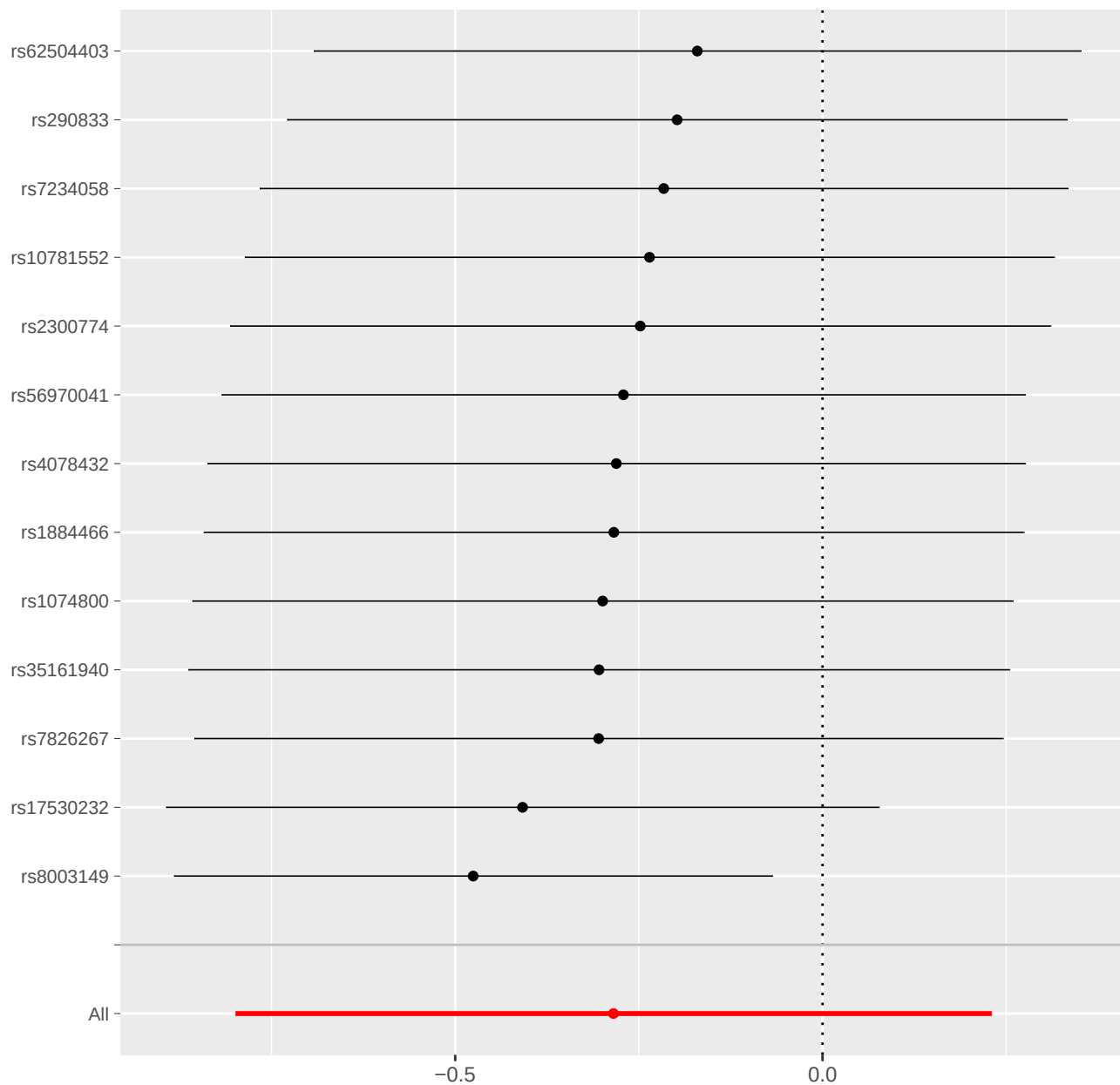






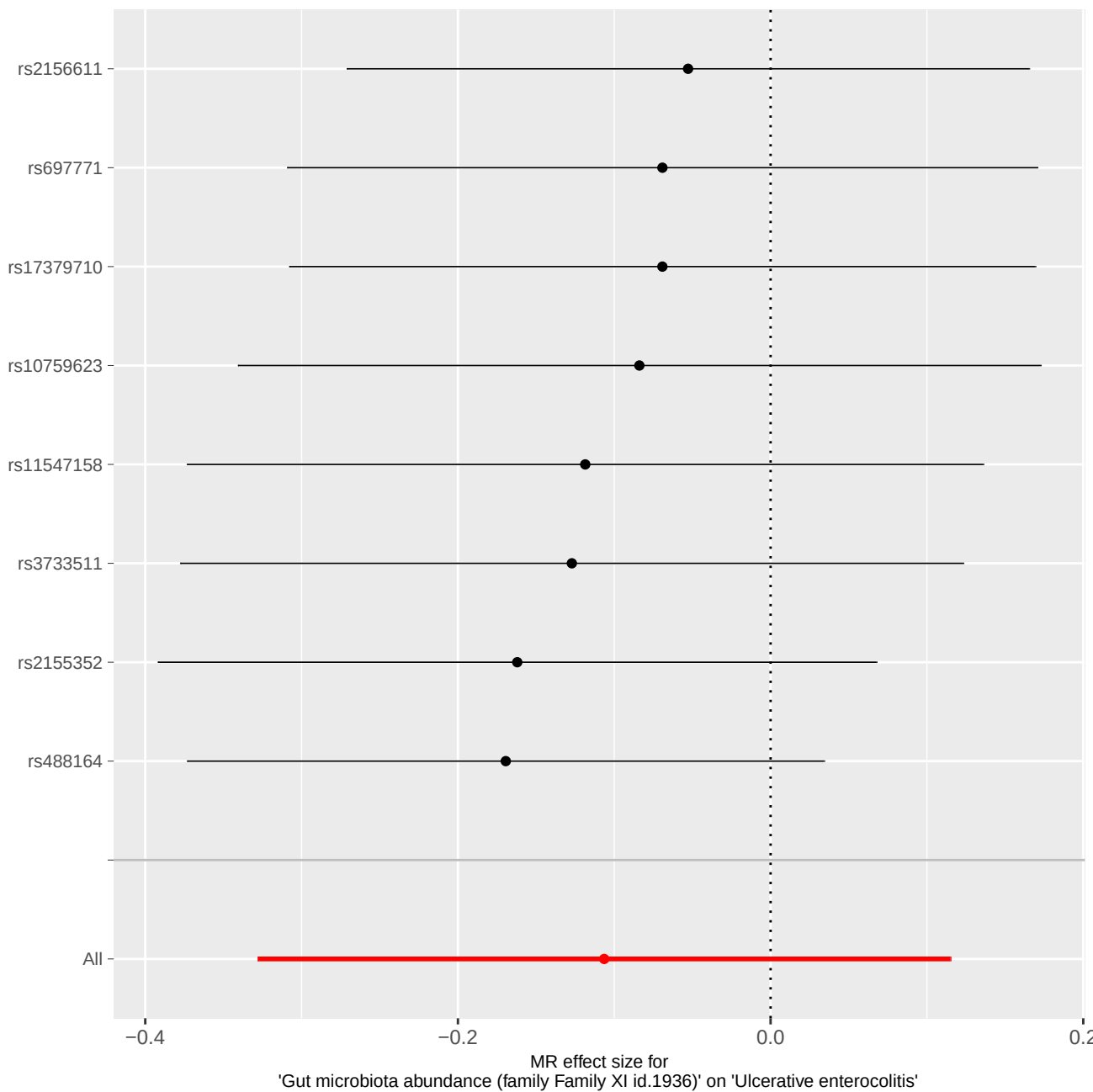


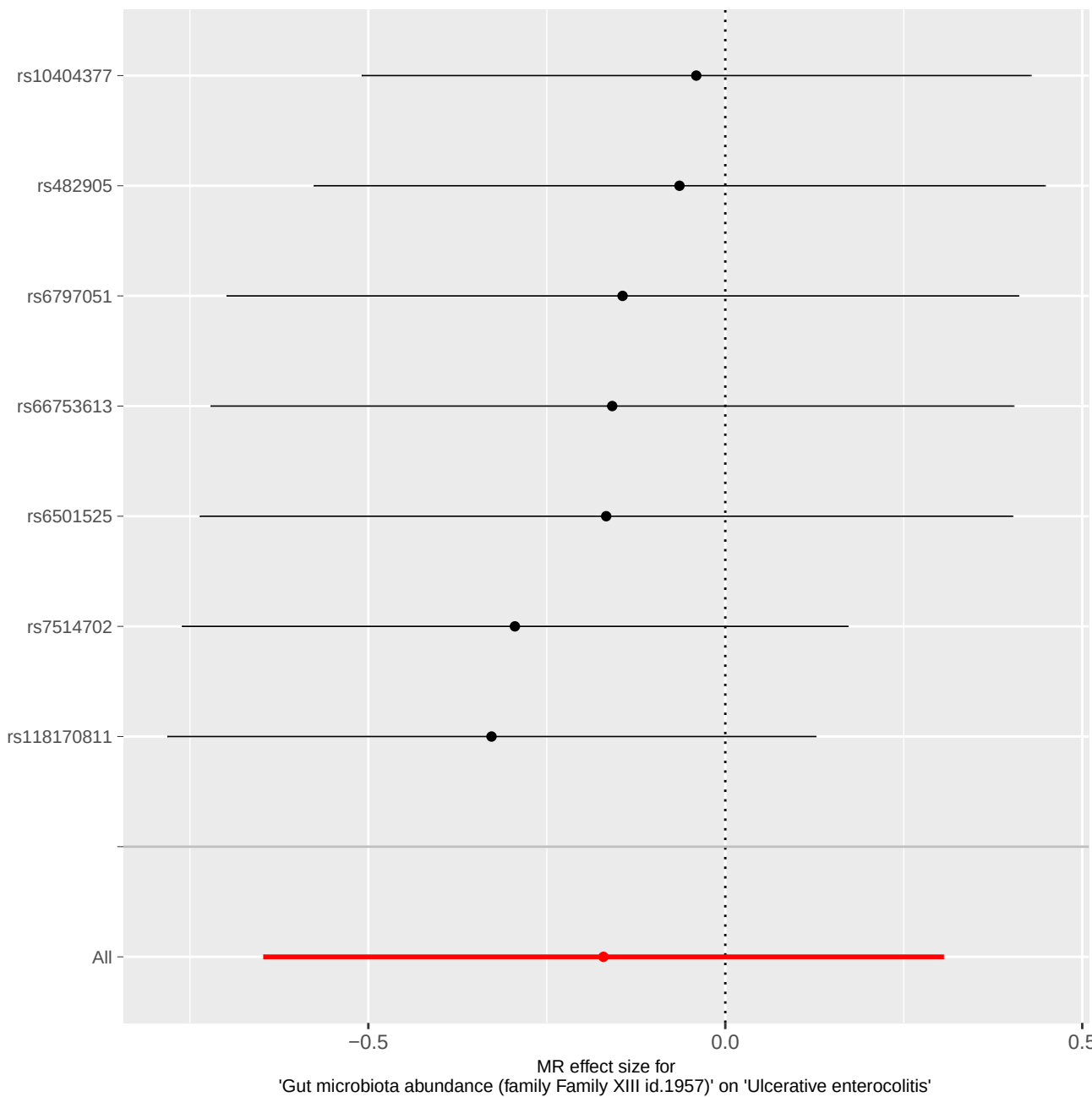


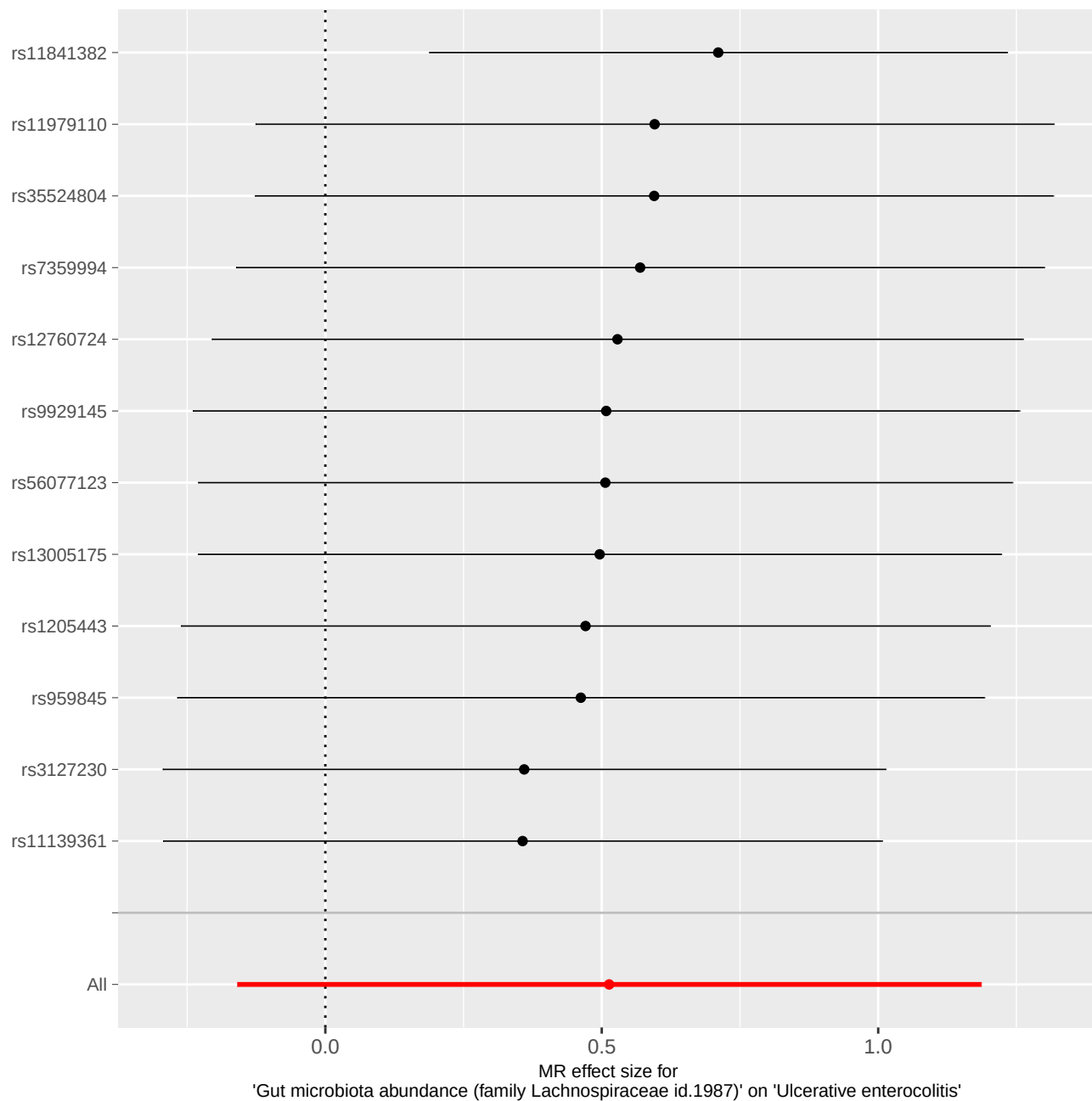


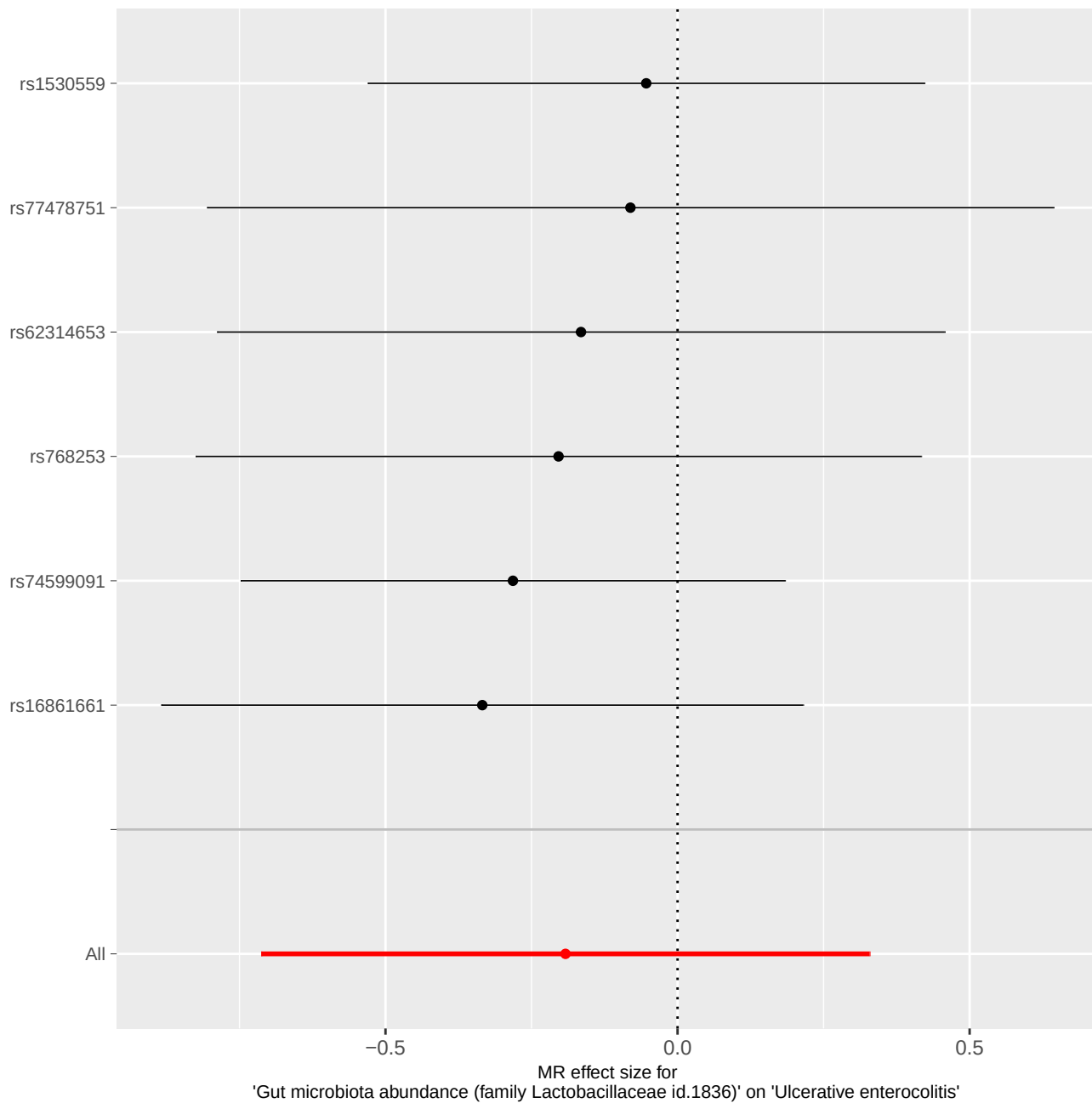
MR effect size for
'Gut microbiota abundance (family Erysipelotrichaceae id.2149)' on 'Ulcerative enterocolitis'

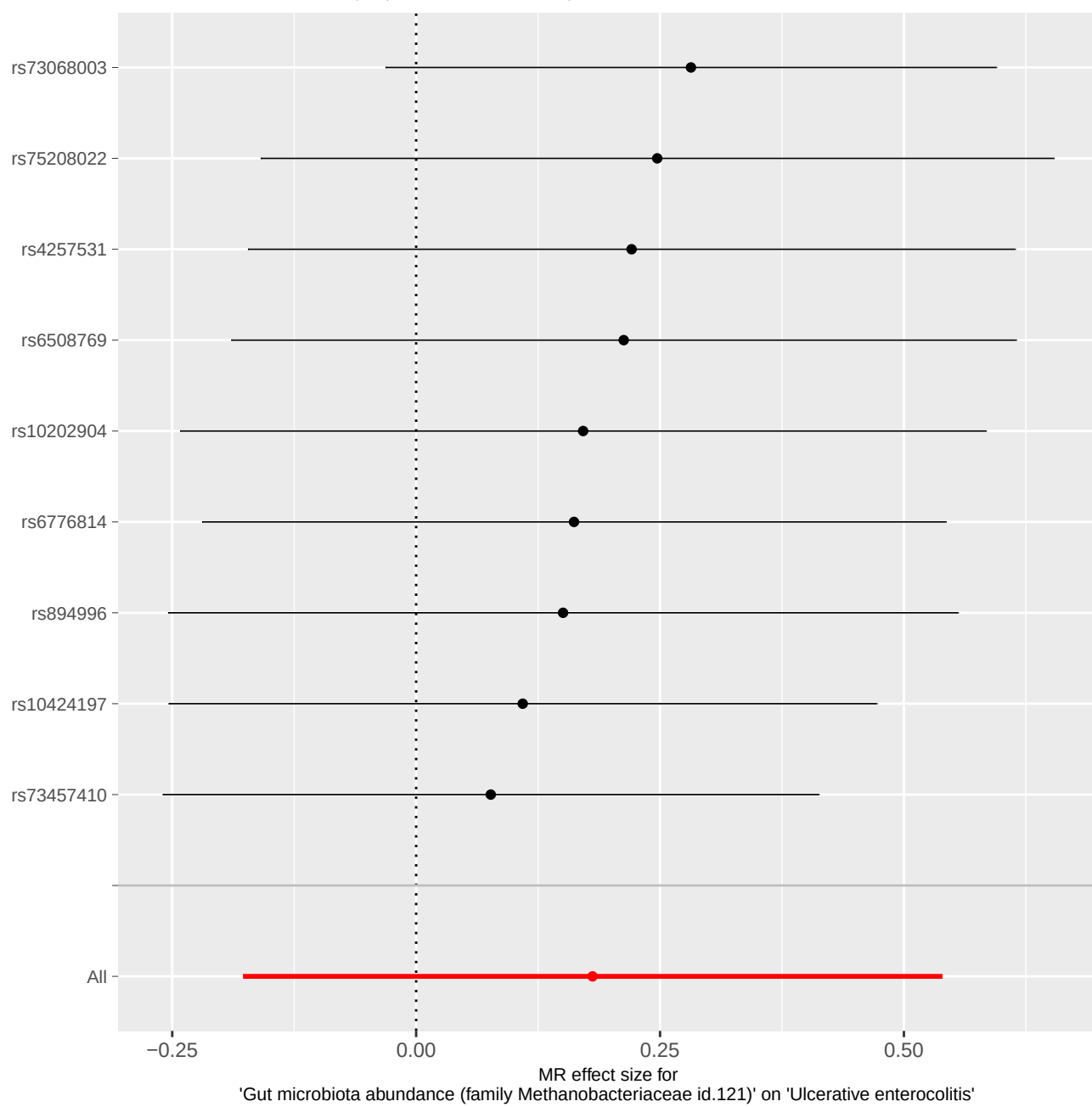
Batch 915 : Gut microbiota abundance (family Family XI id.1936) on Ulcerative enterocolitis

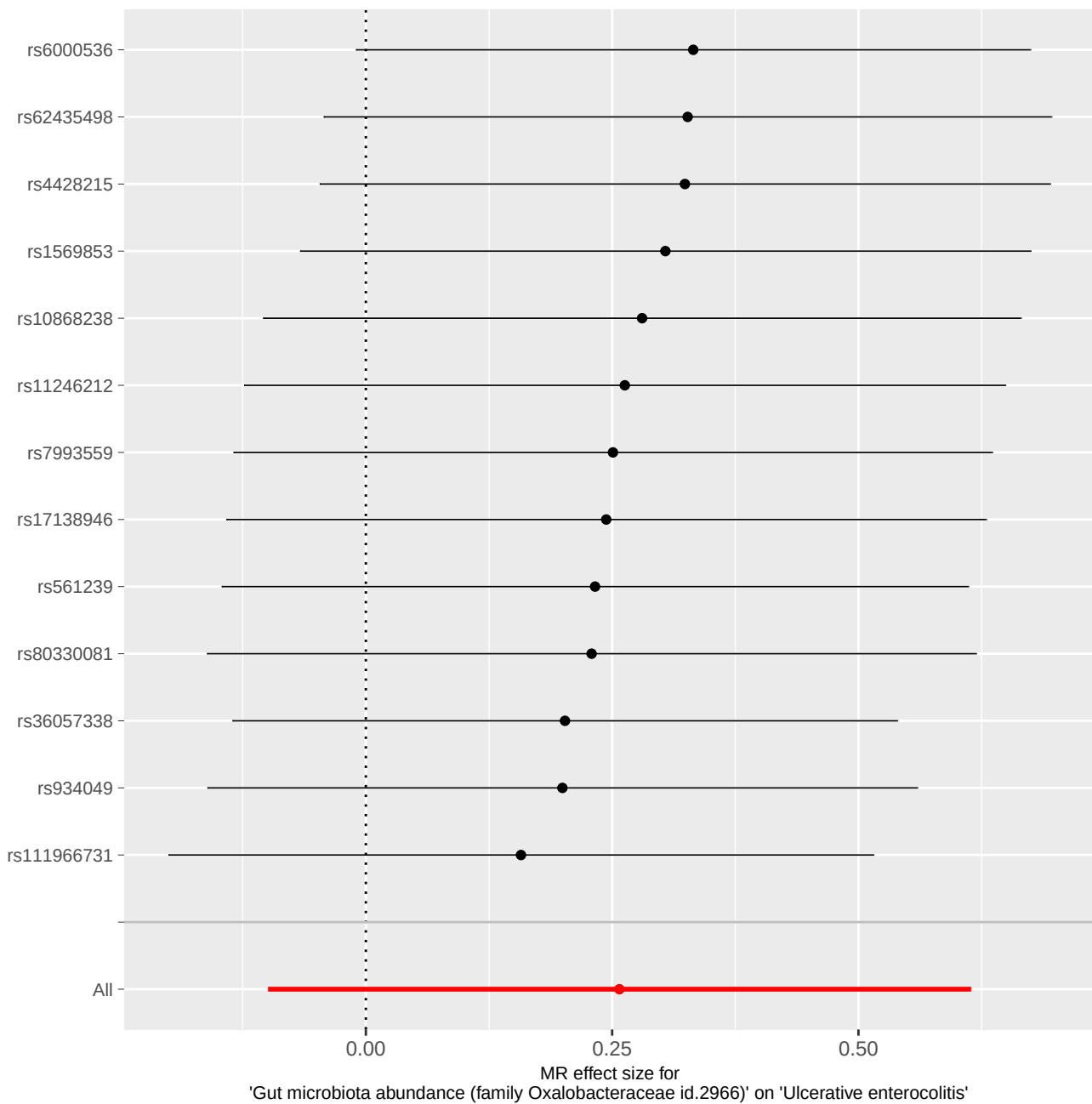


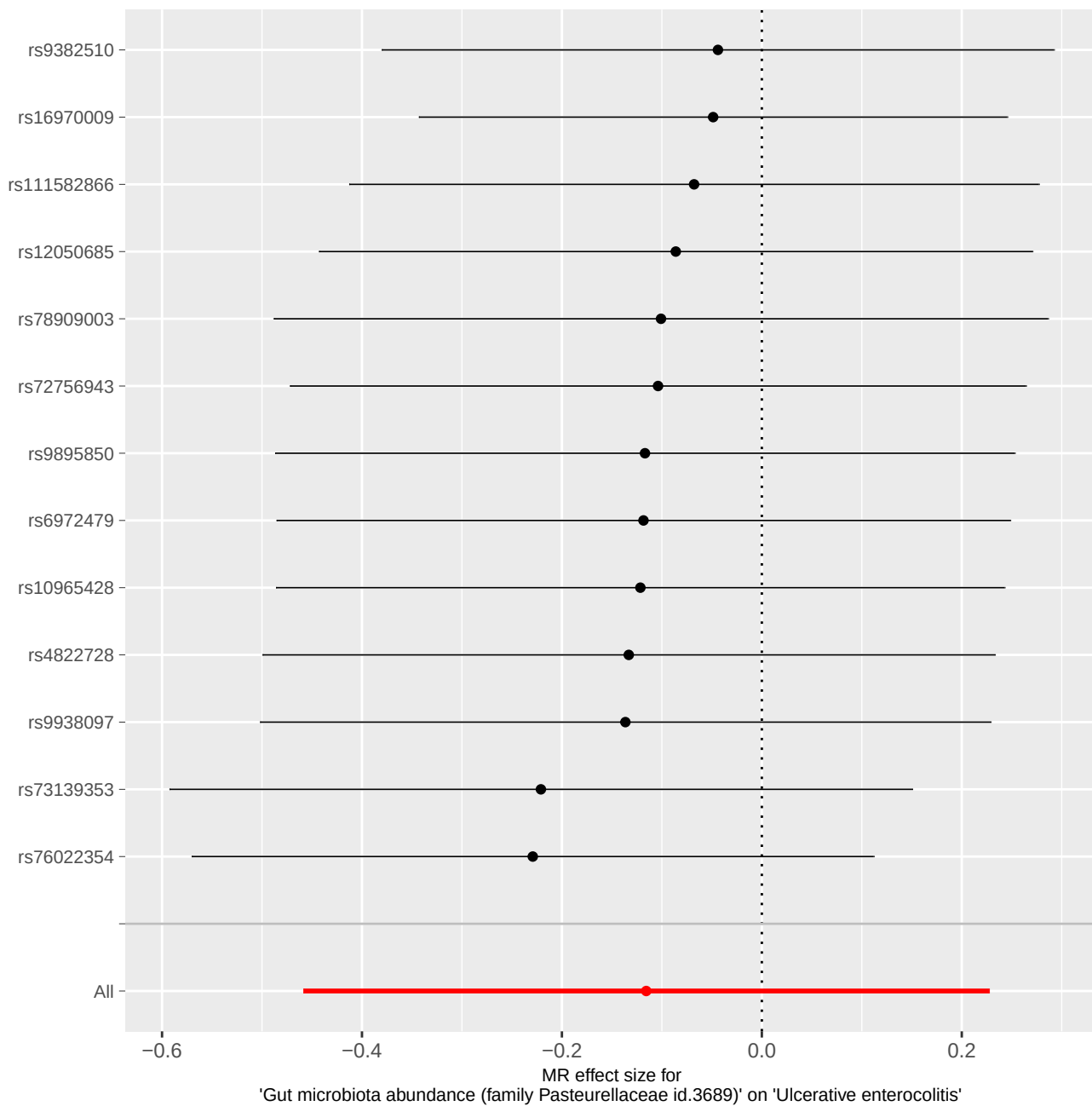


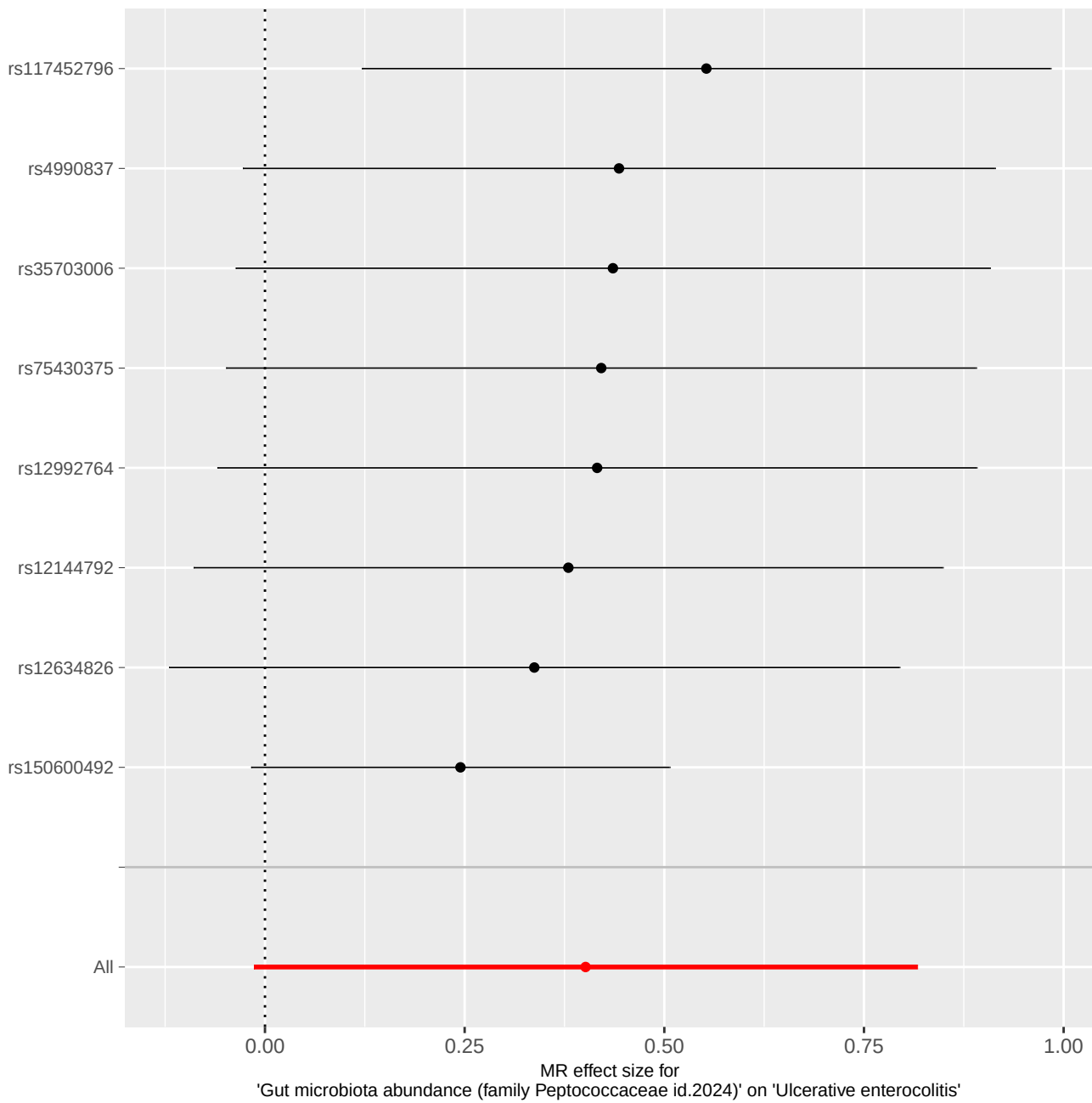


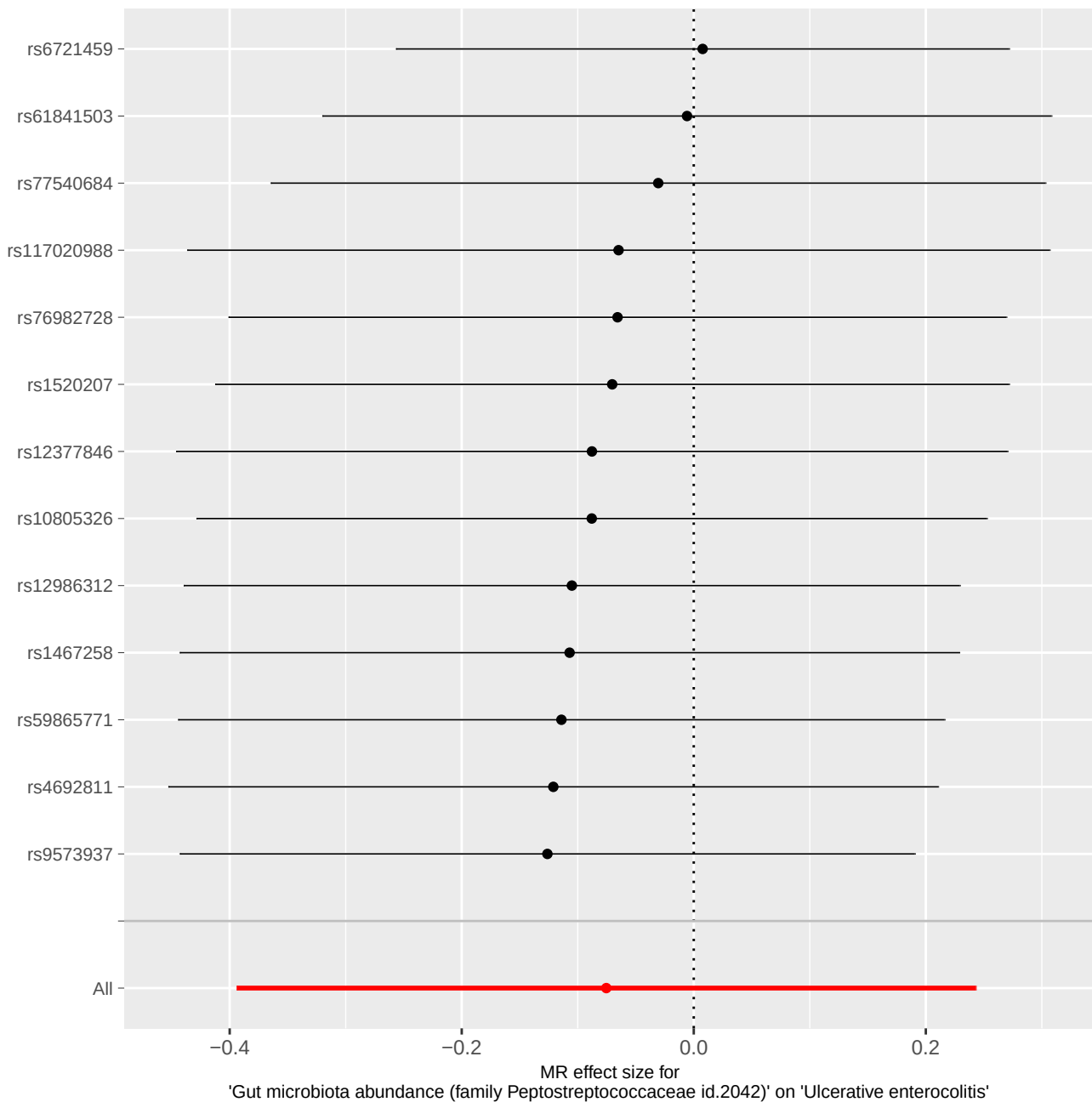


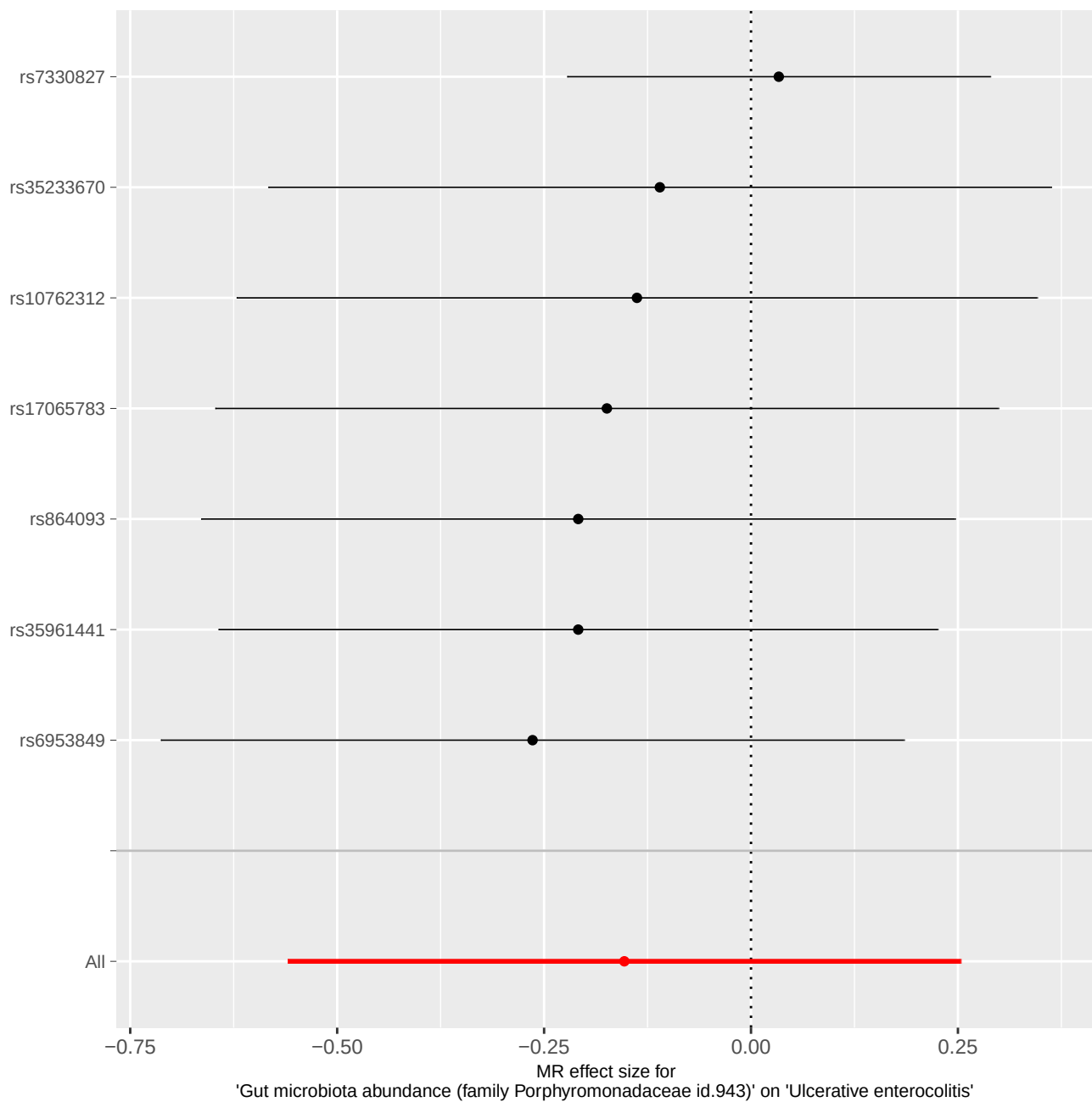


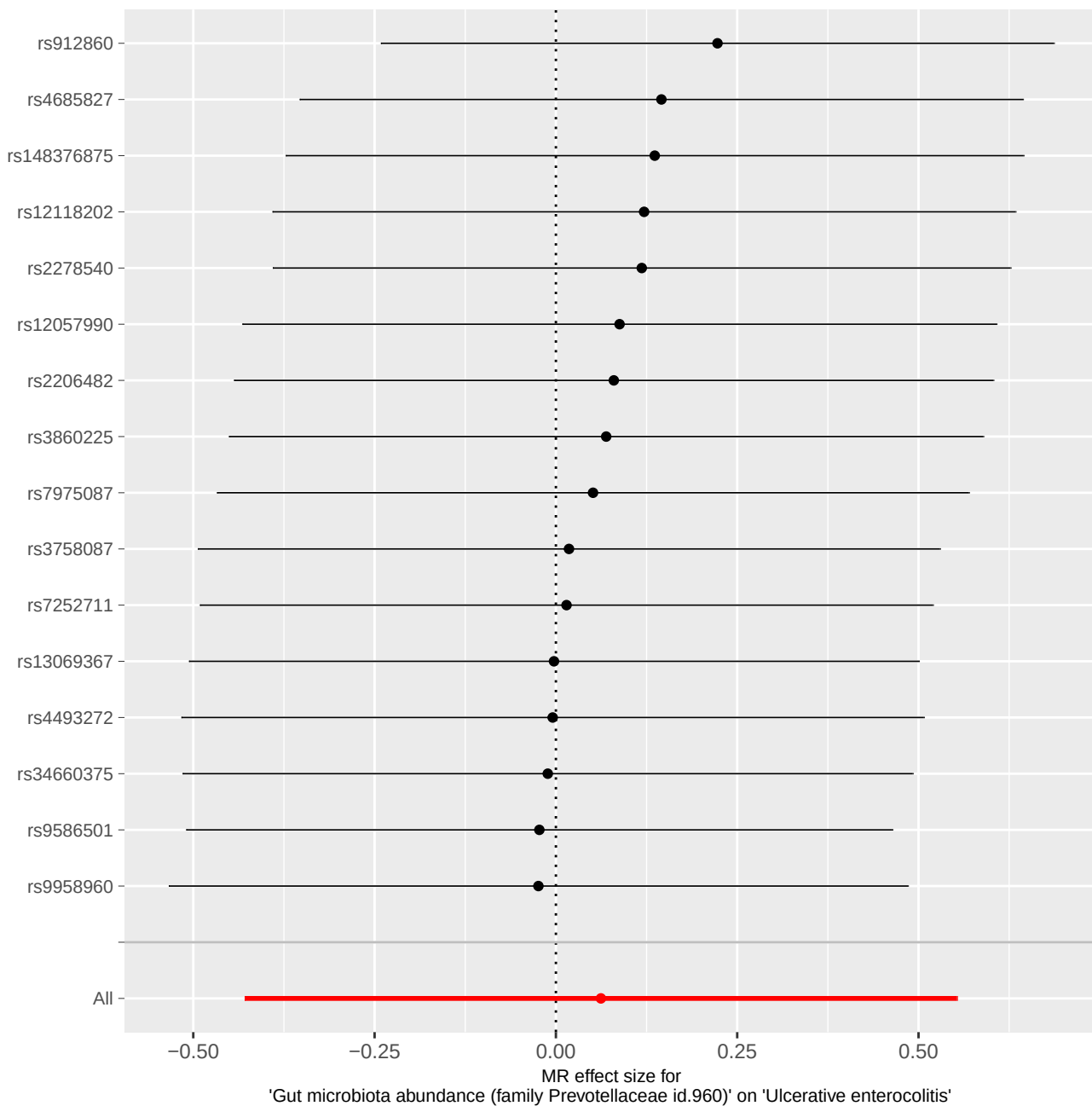


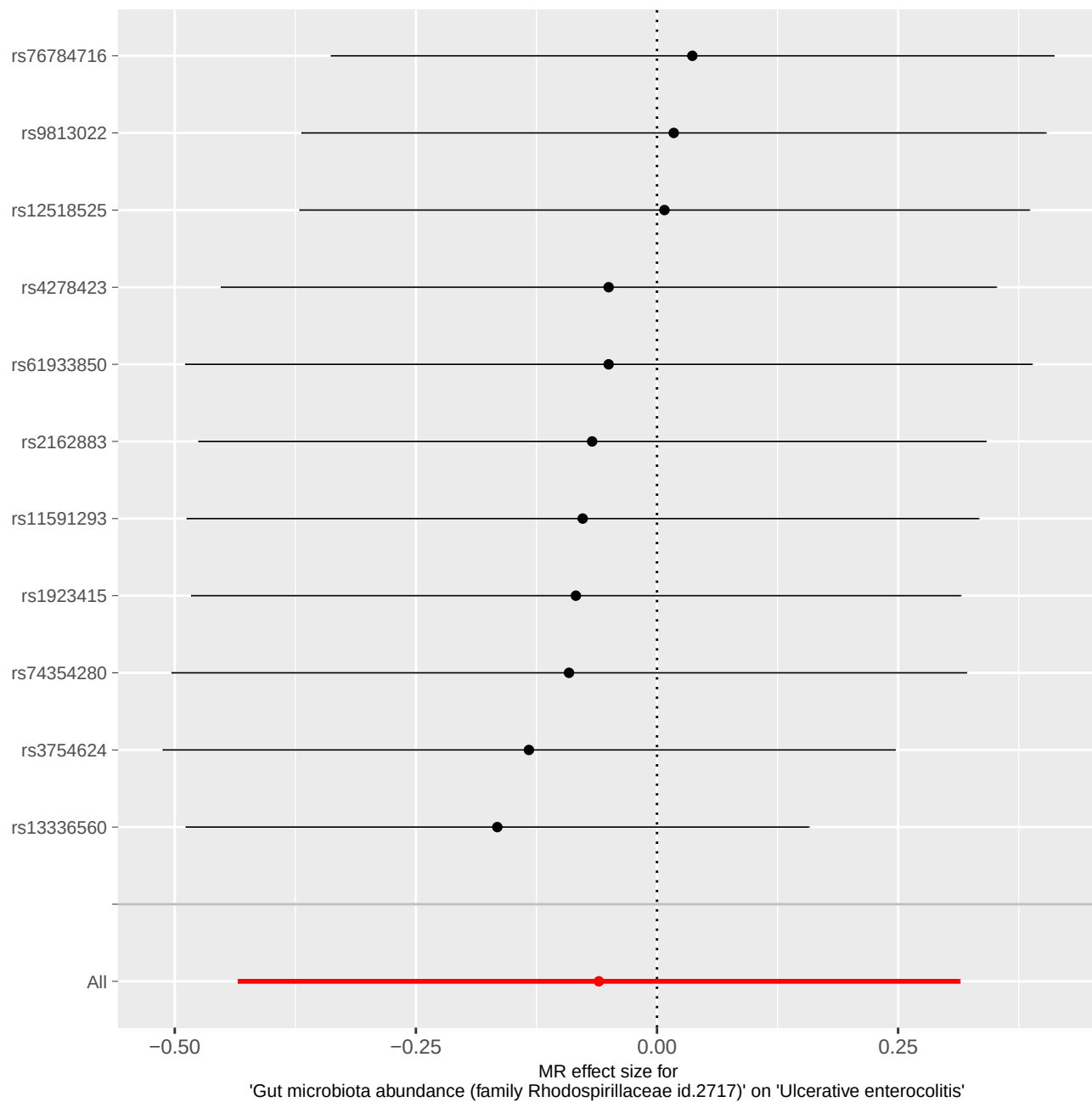


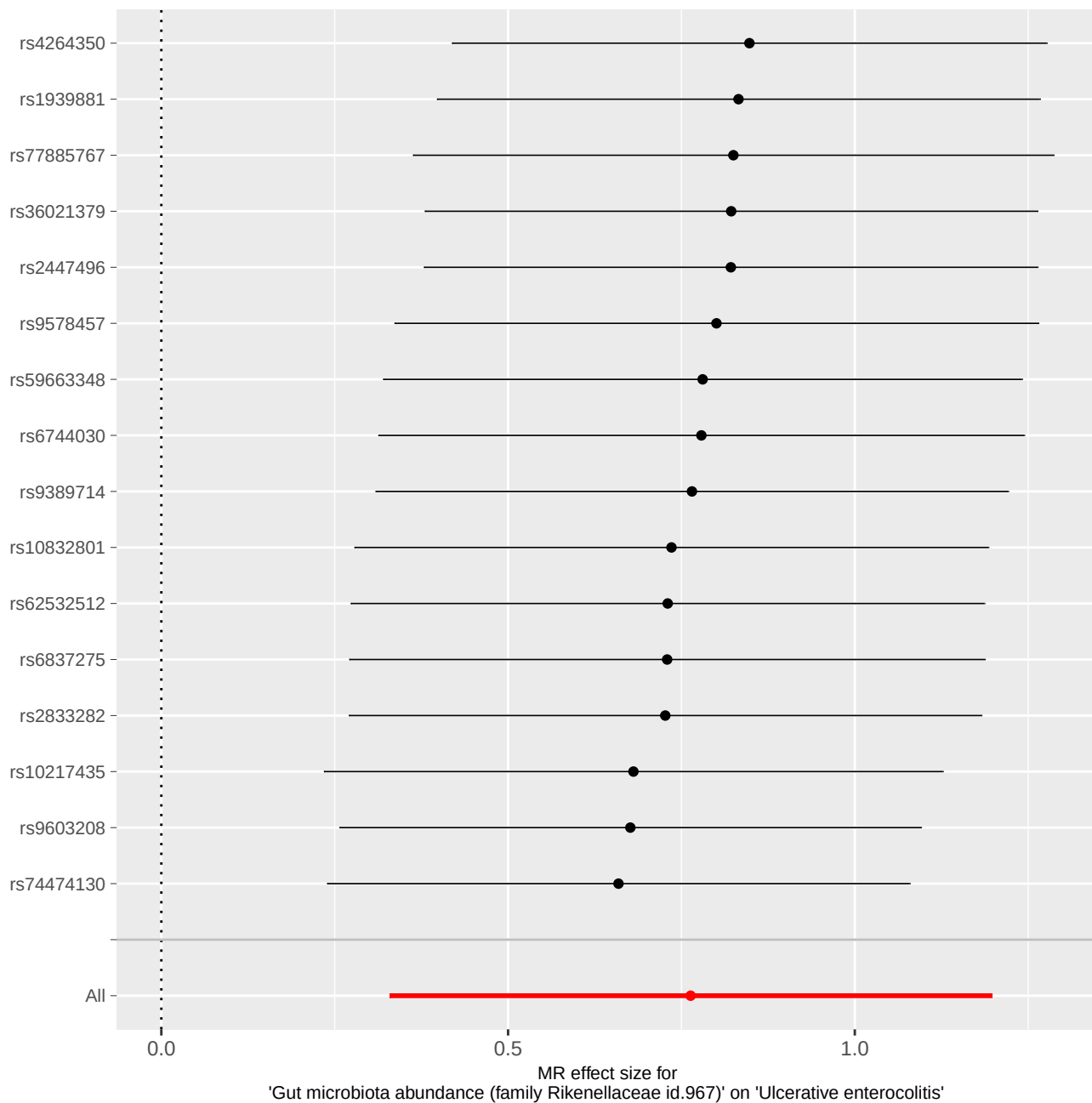


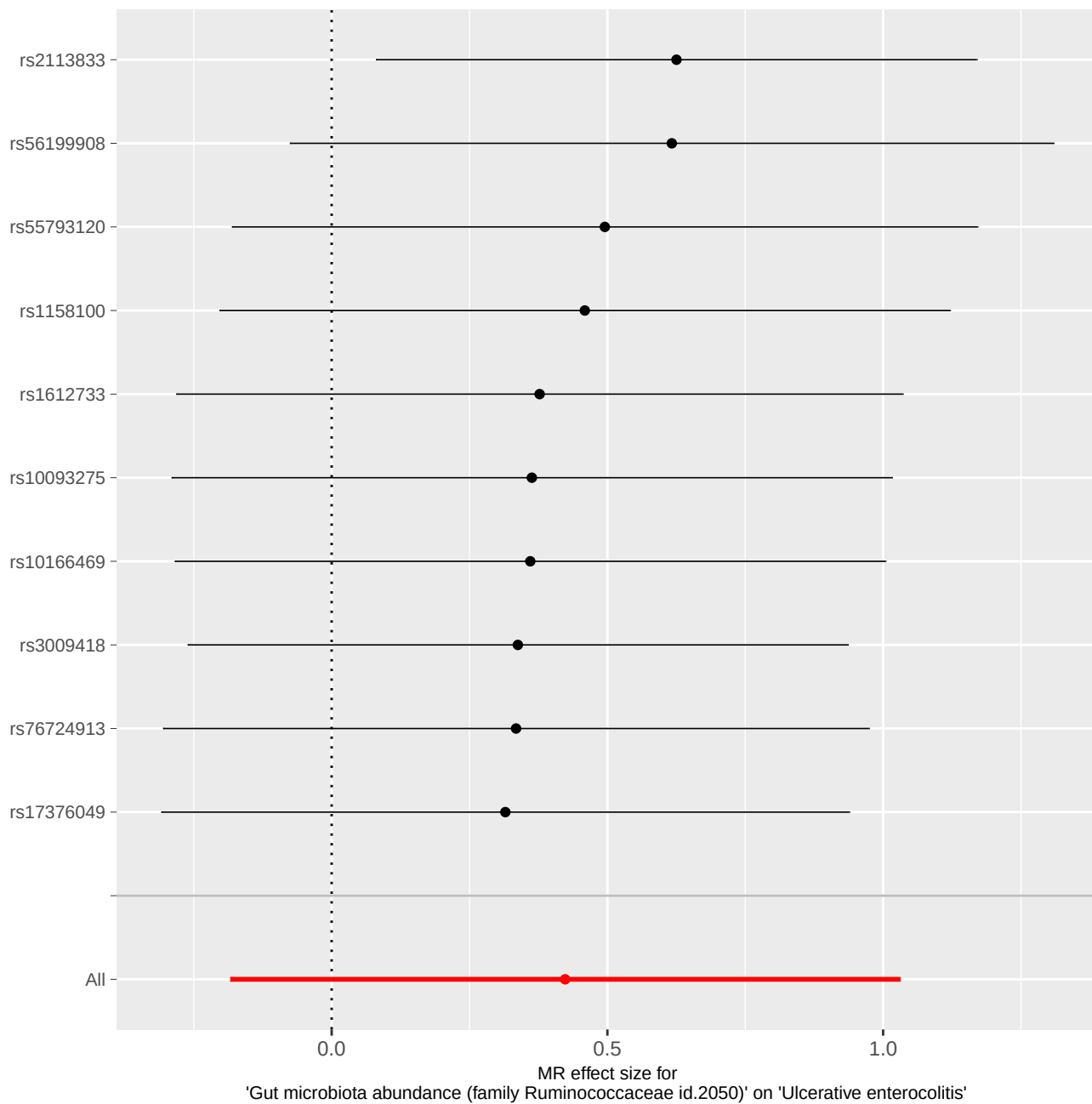


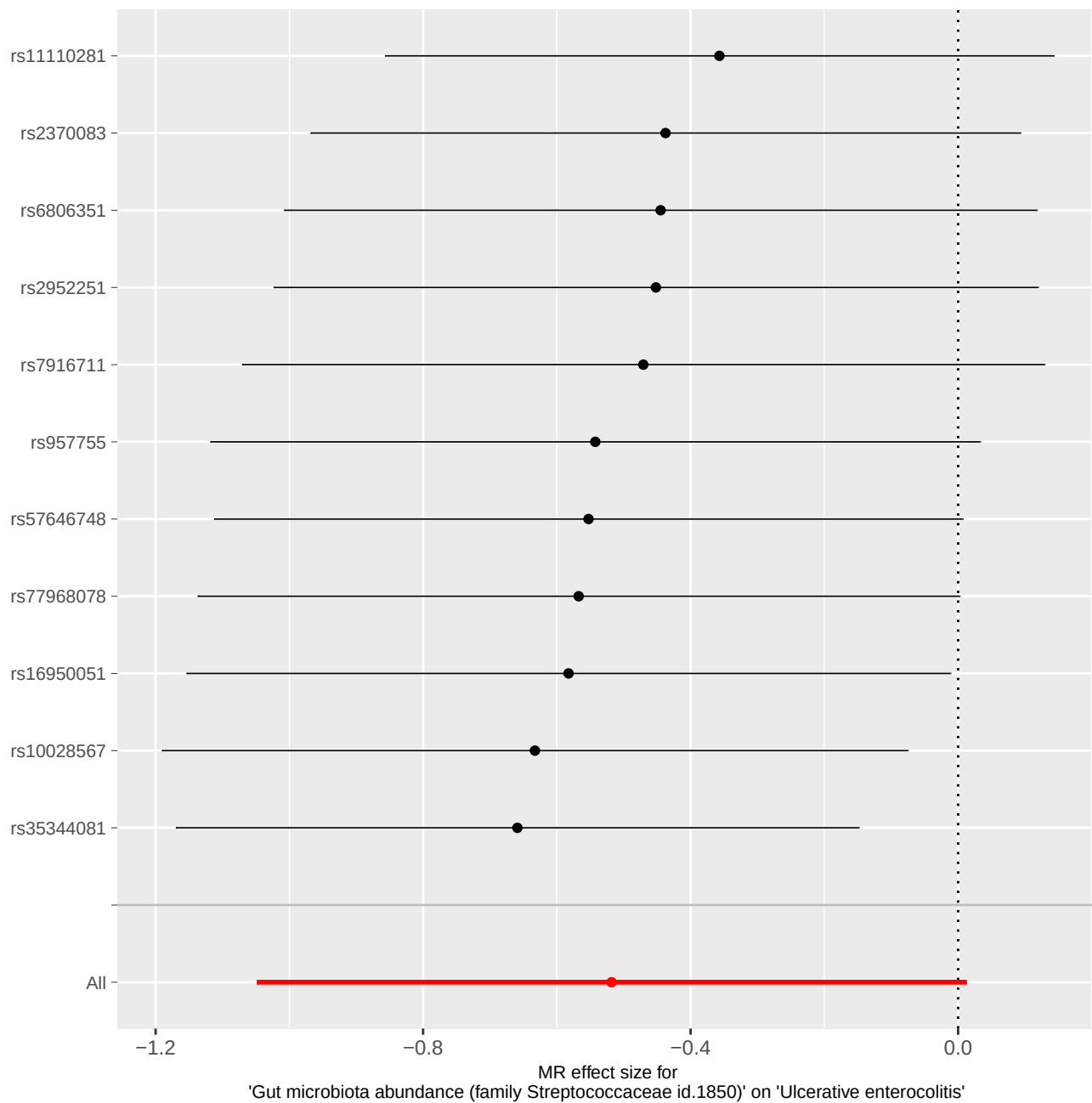


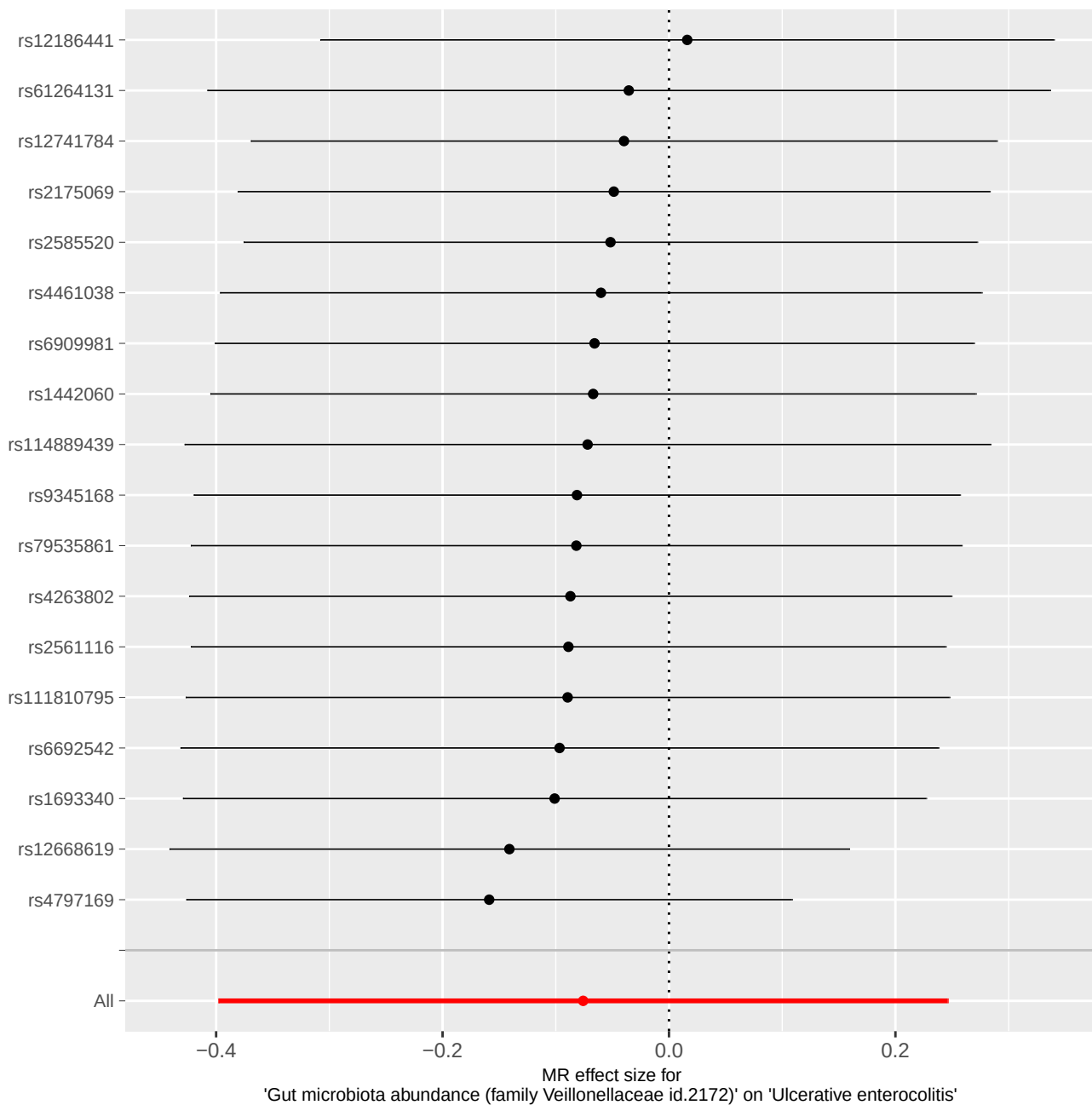


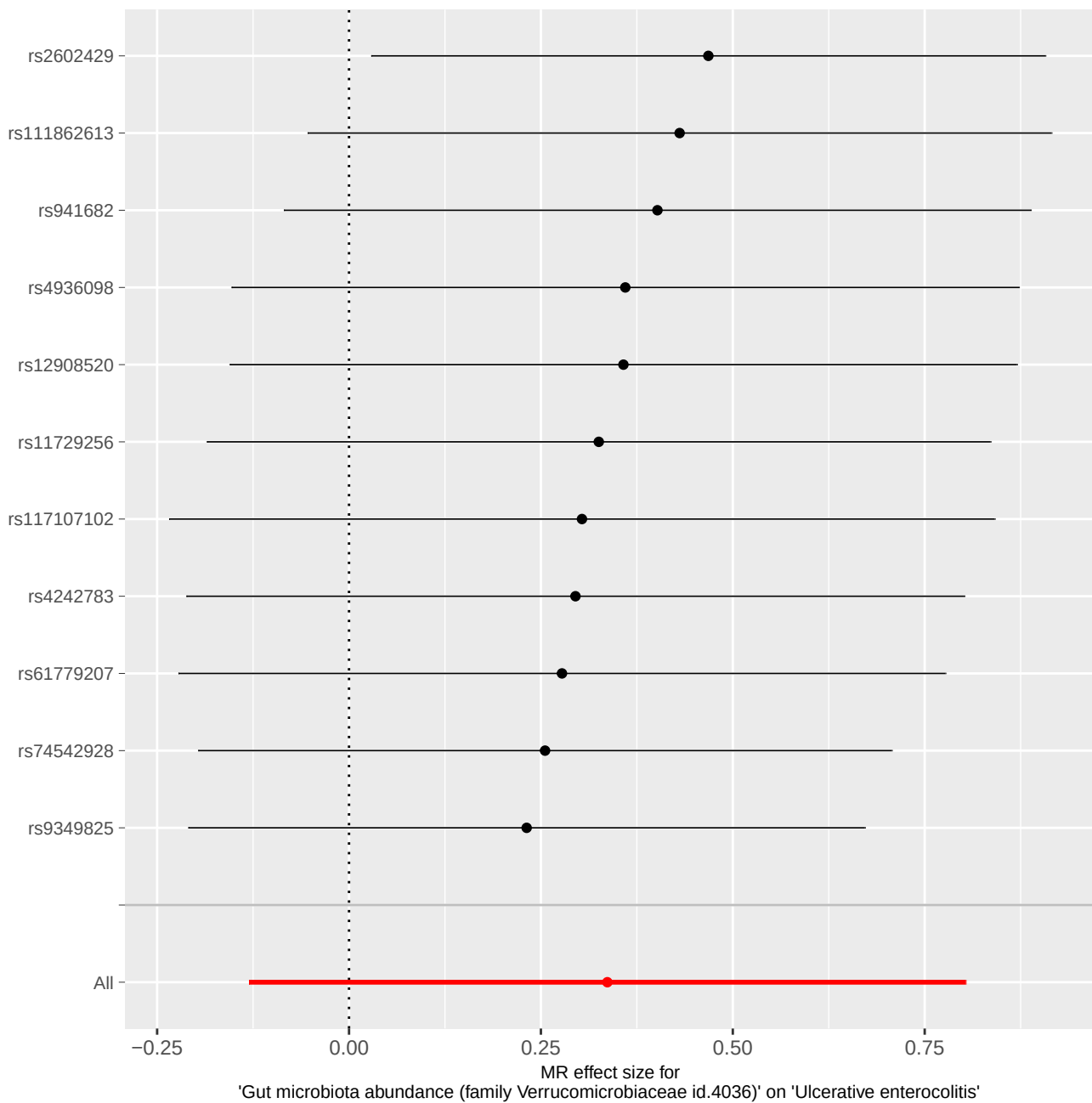


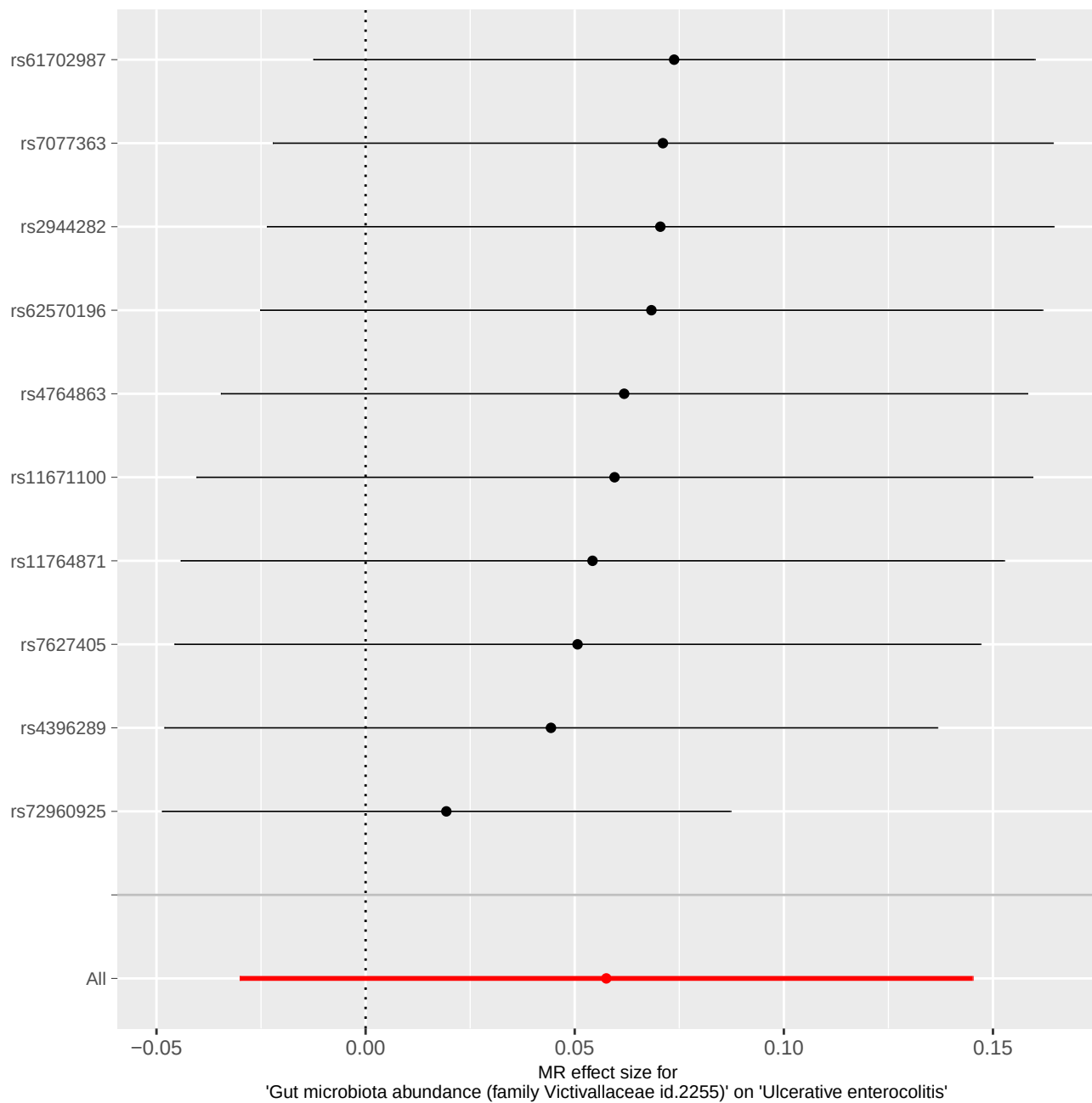




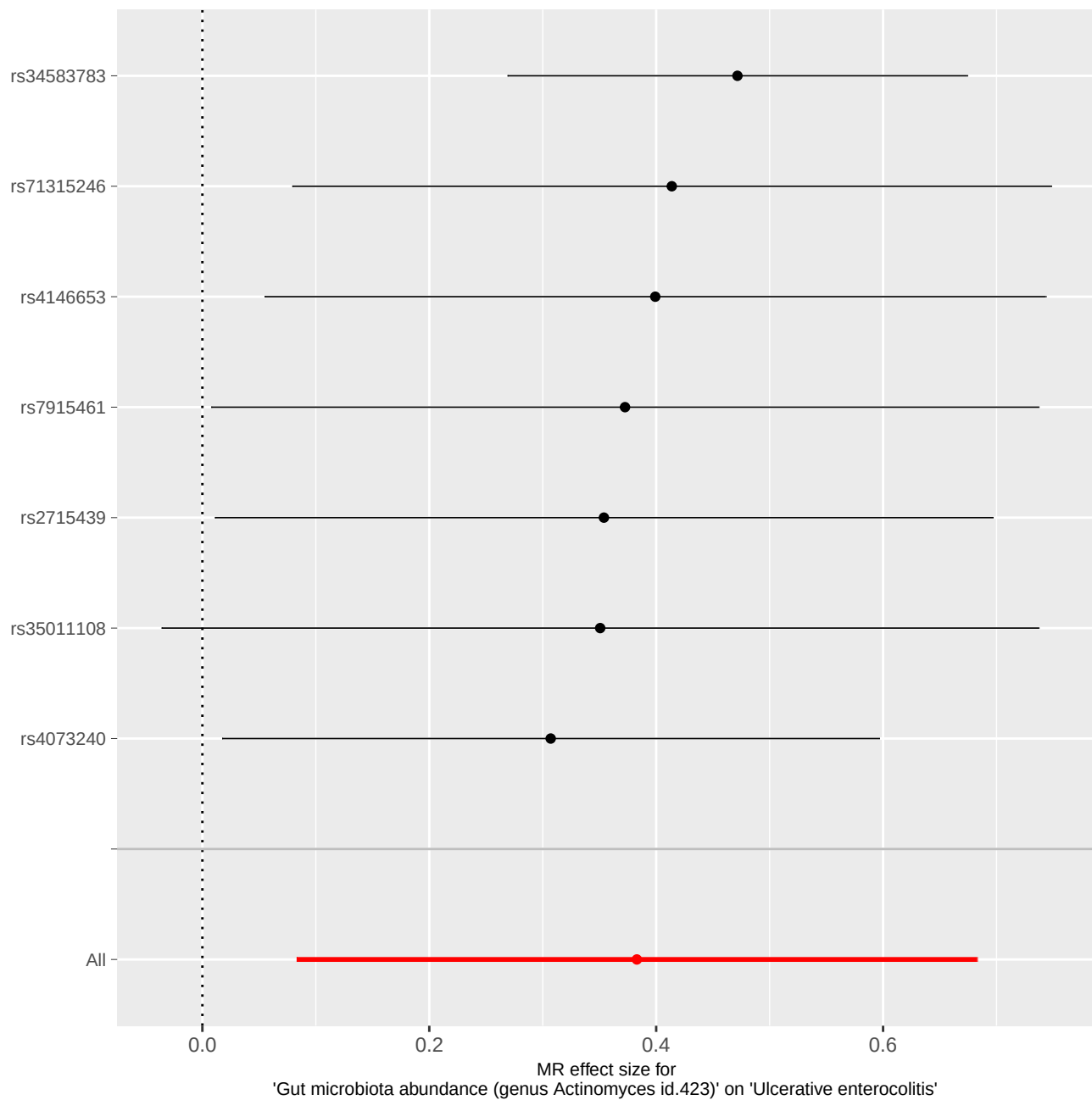


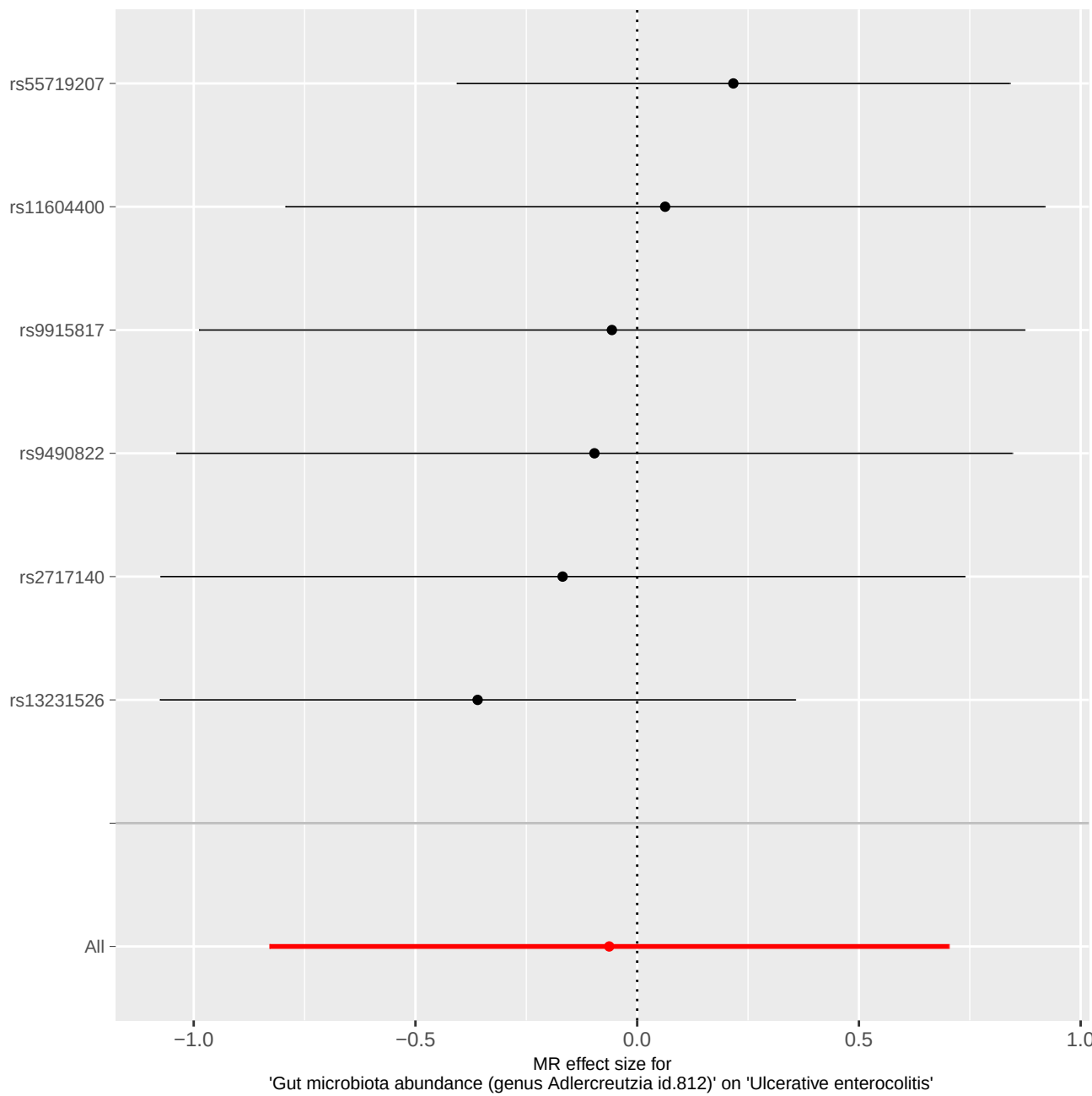


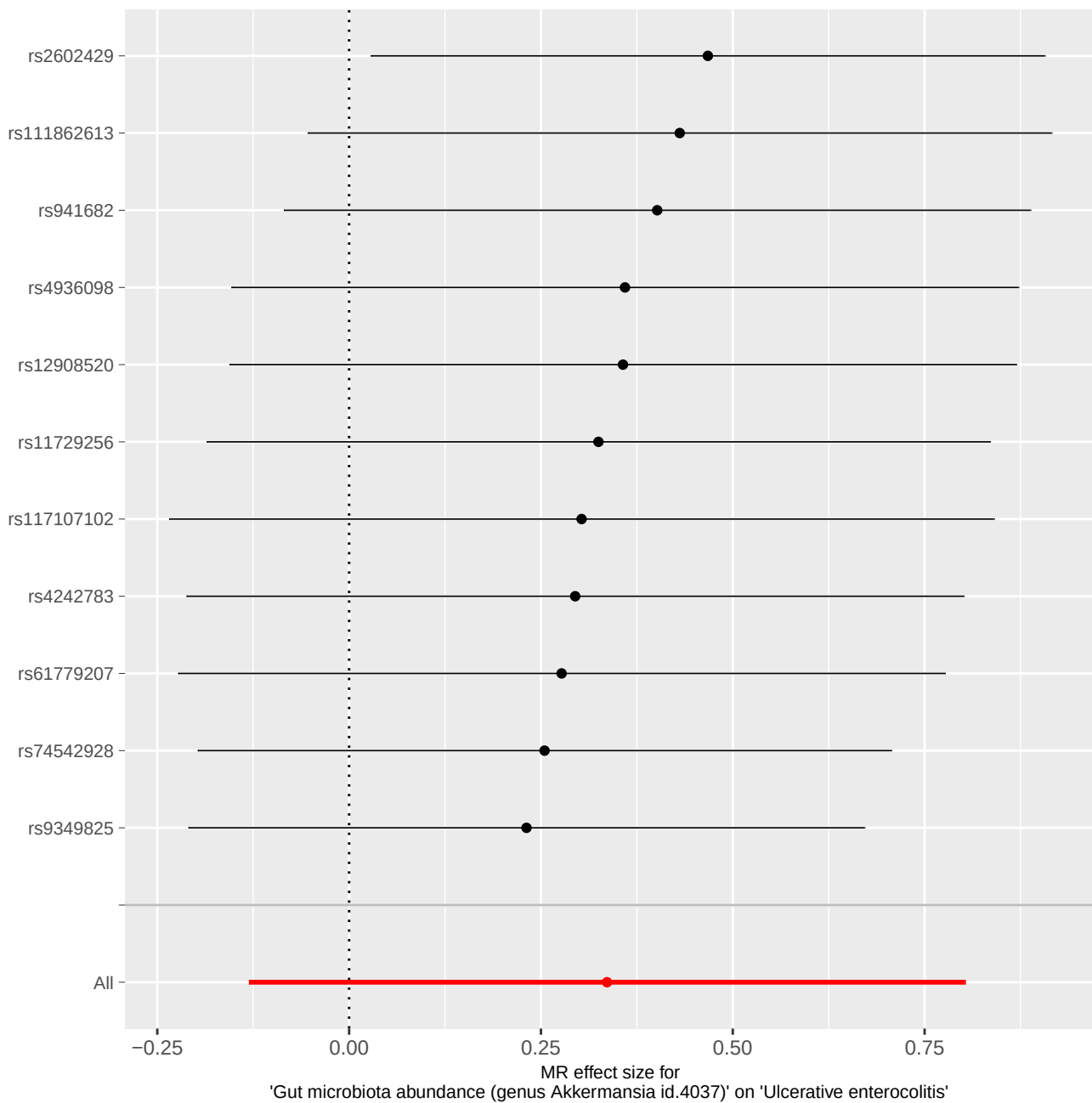




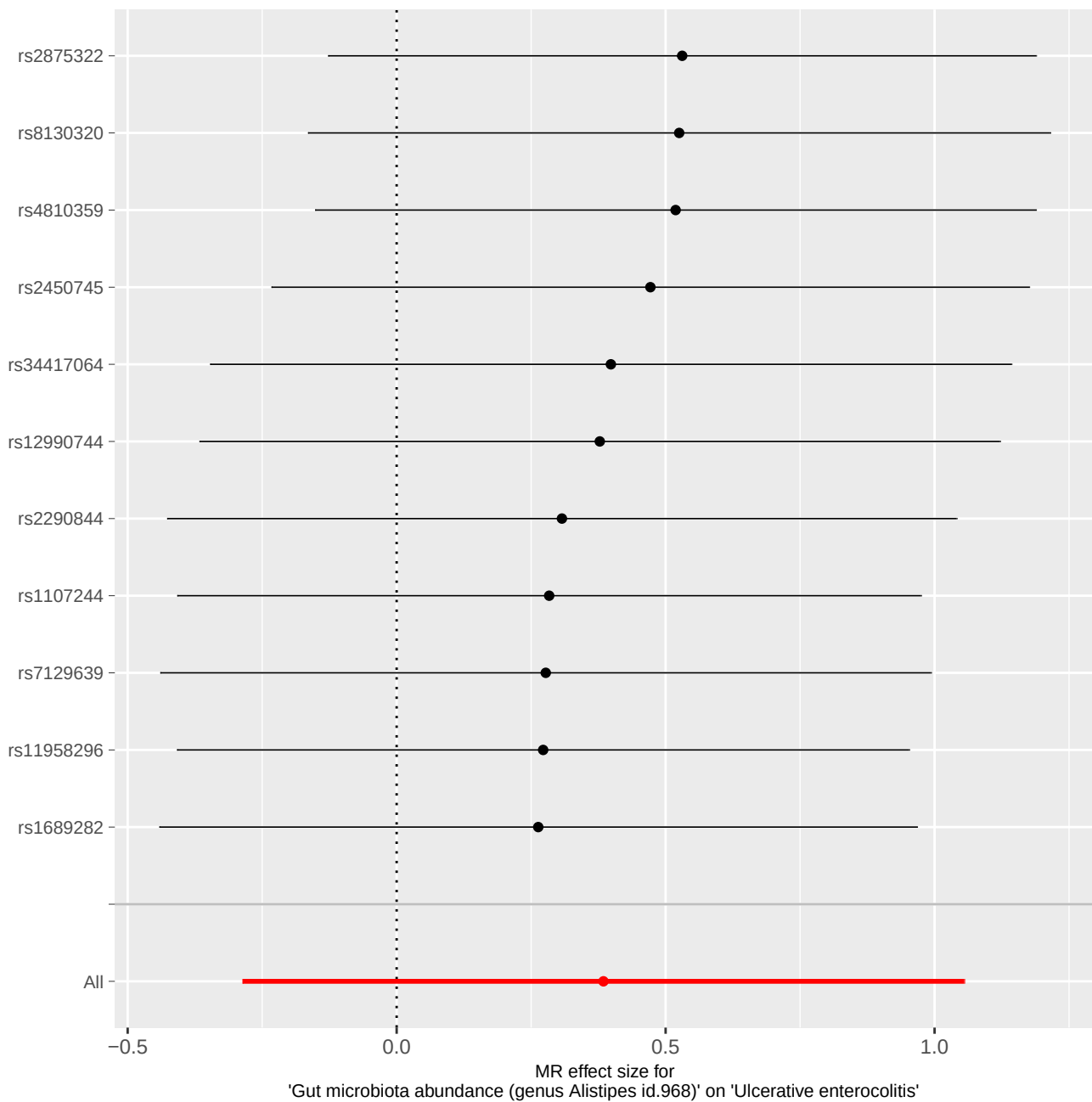
Batch 933 : Gut microbiota abundance (genus Actinomyces id.423) on Ulcerative enterocolitis

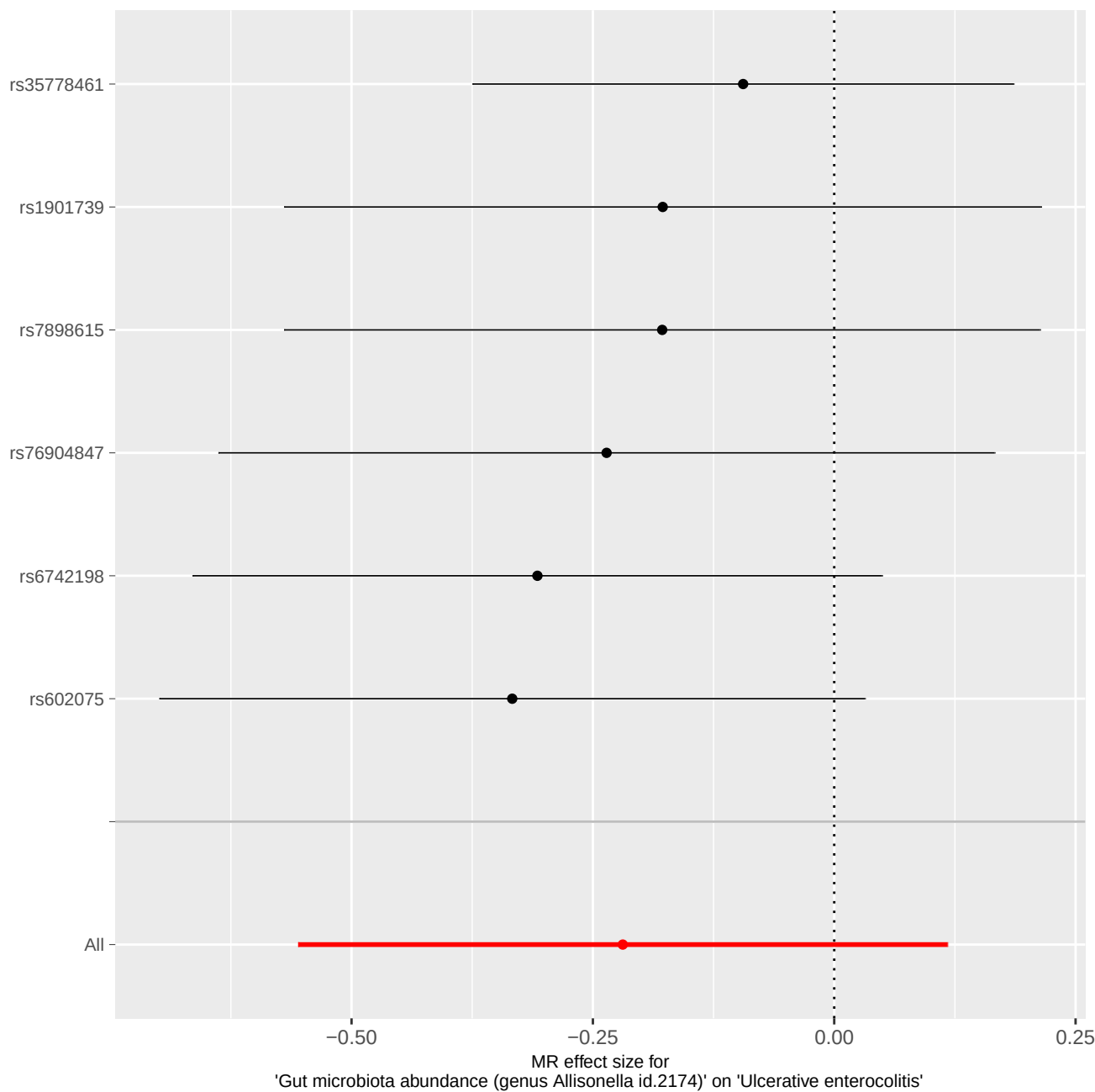


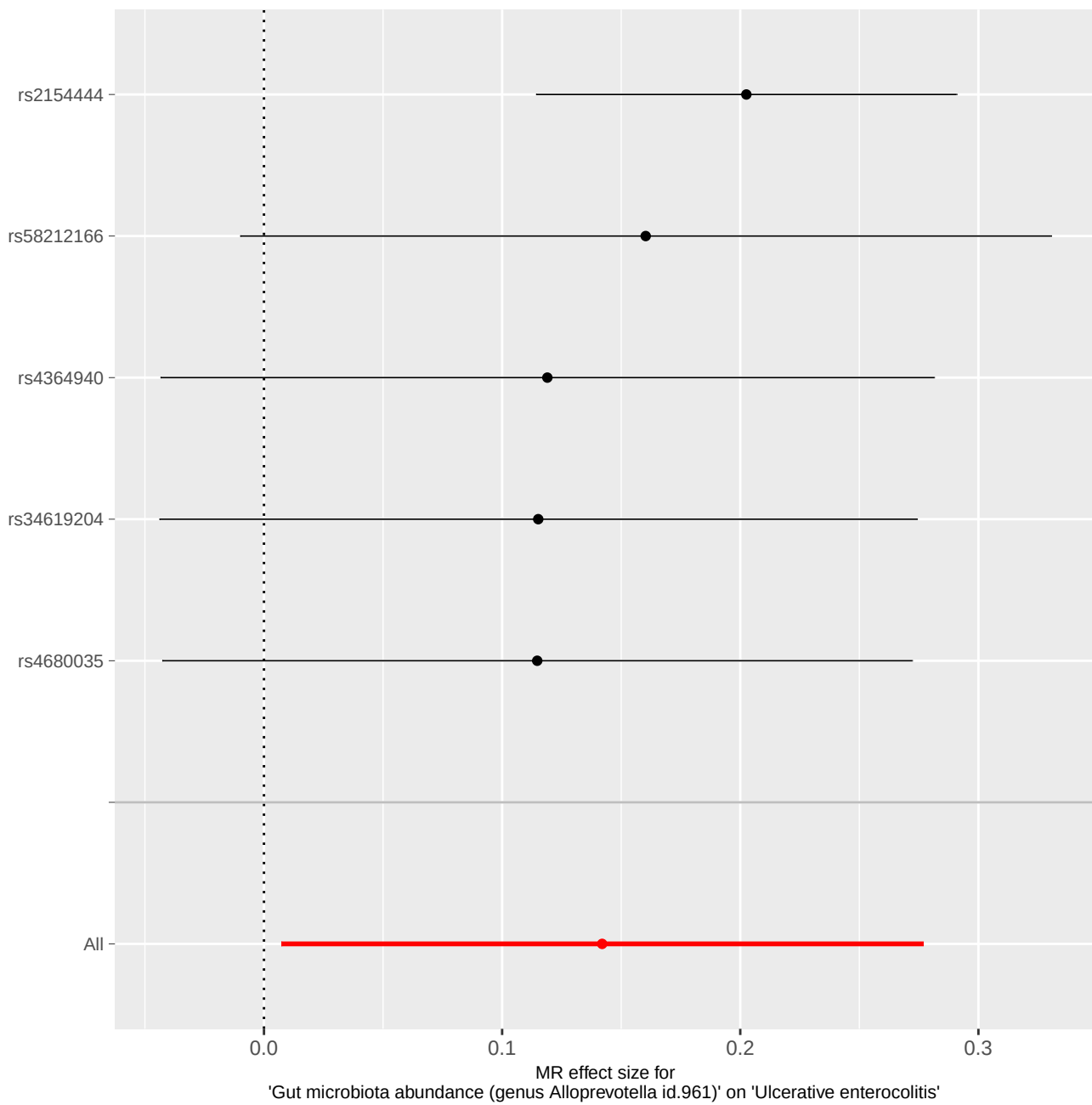




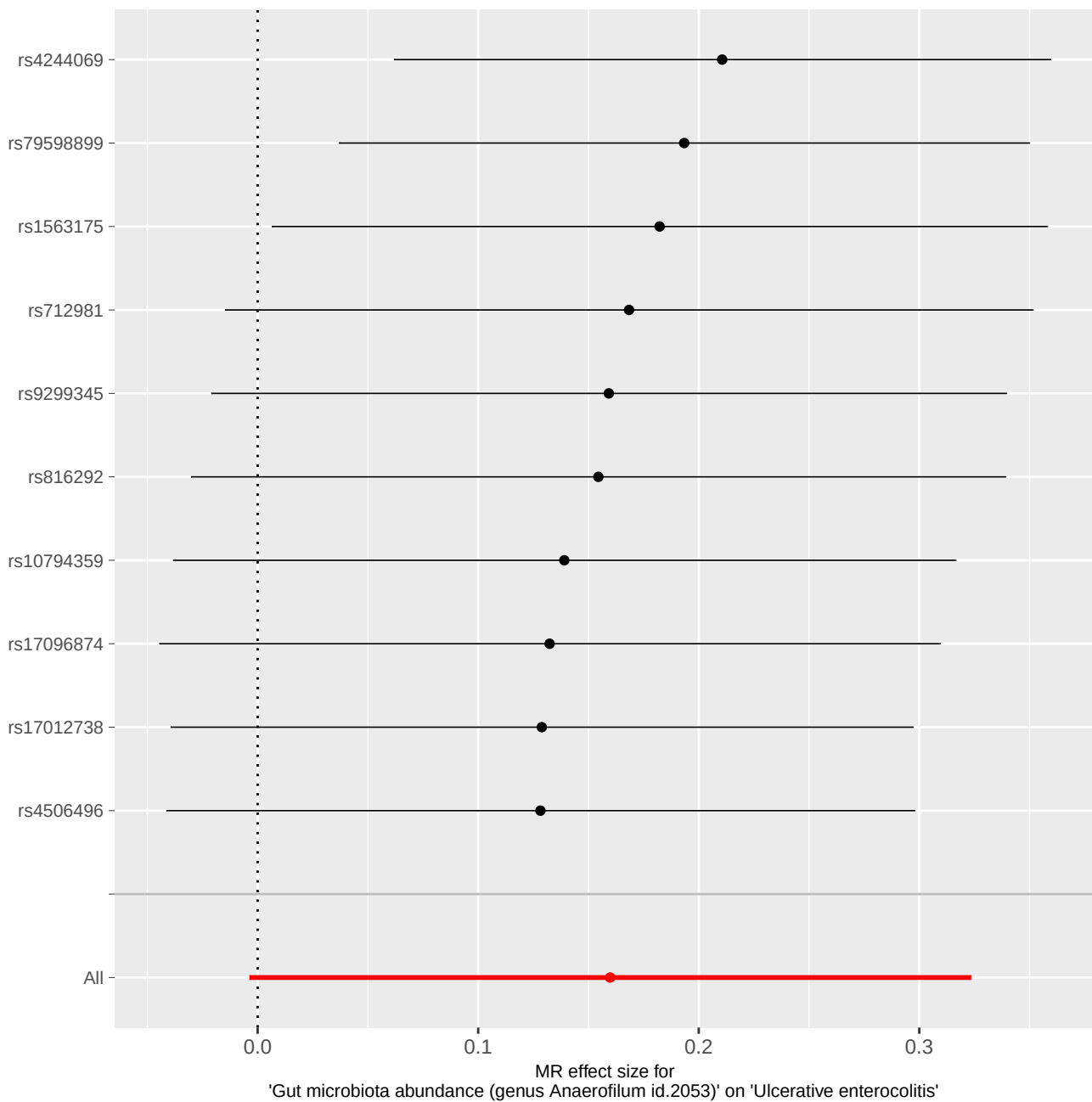
Batch 936 : Gut microbiota abundance (genus Alistipes id.968) on Ulcerative enterocolitis

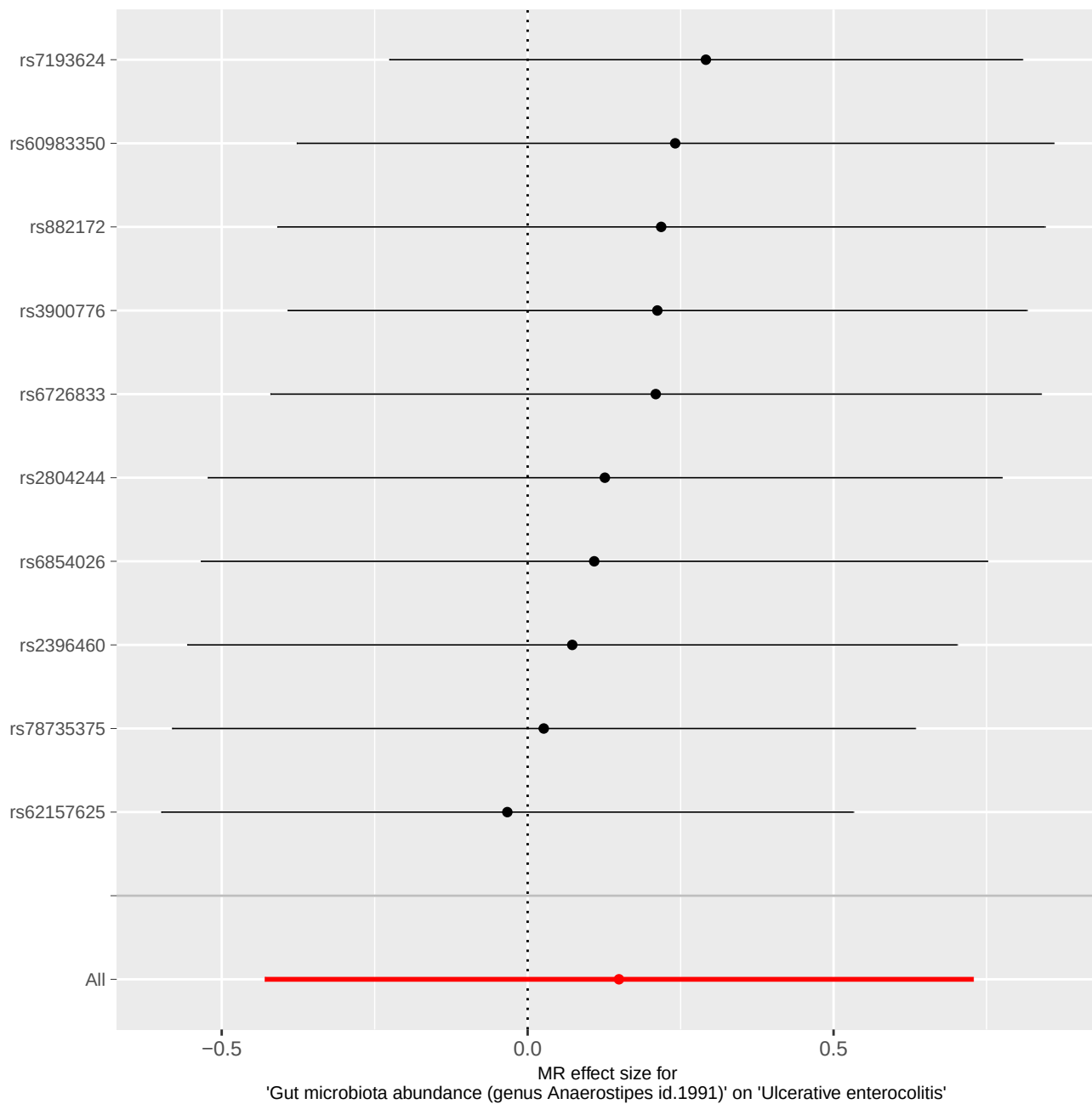


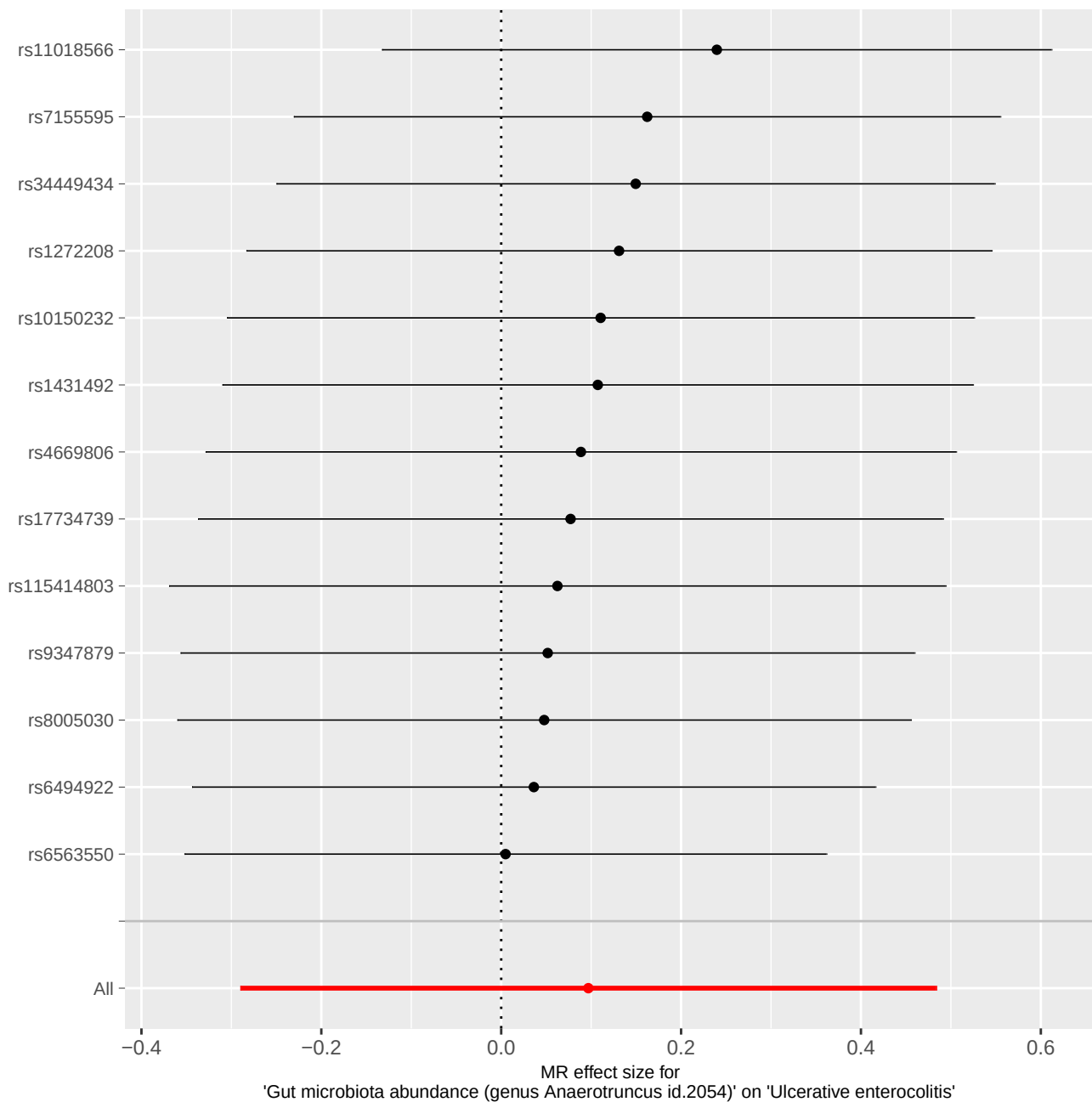


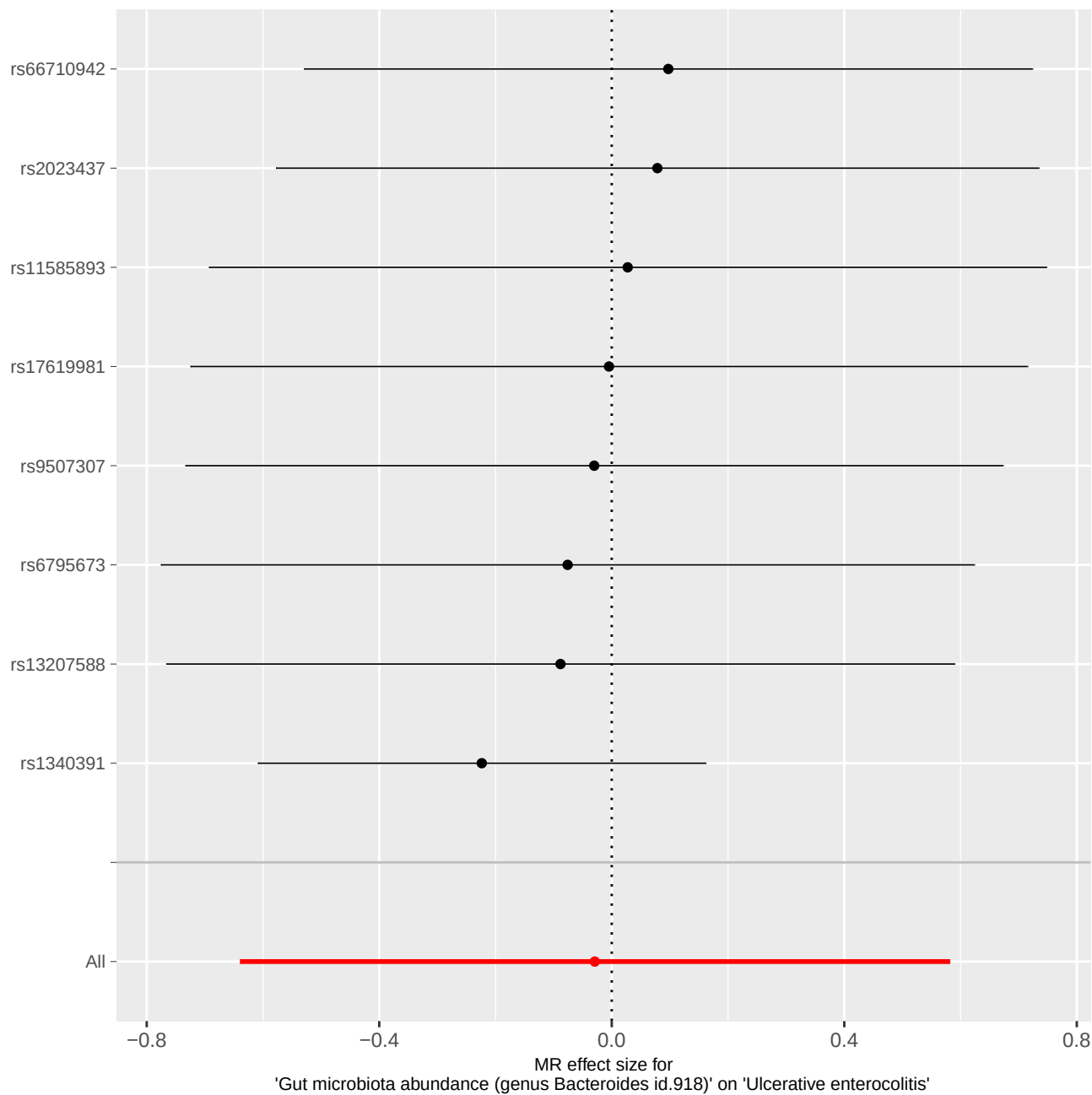


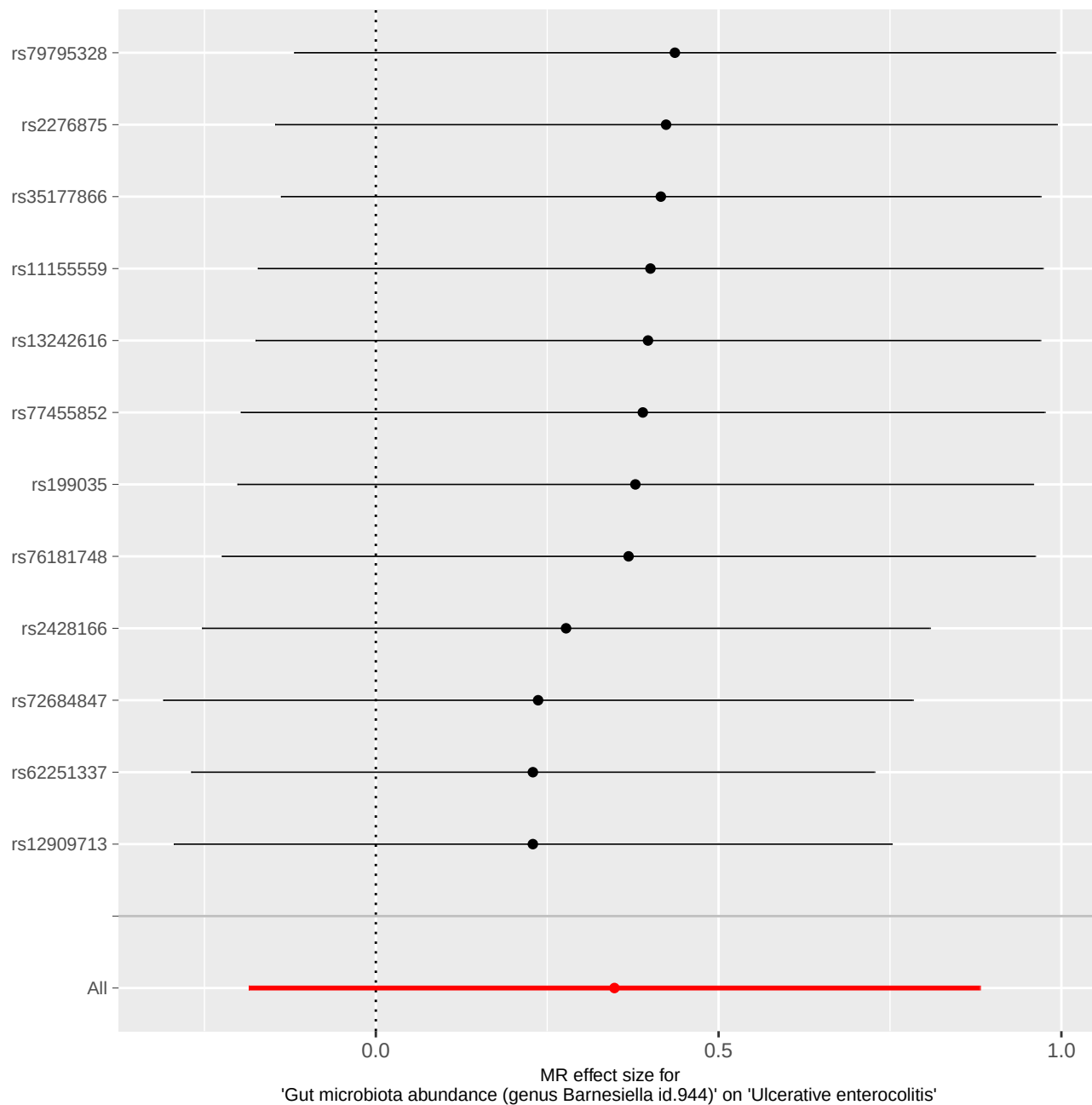
Batch 939 : Gut microbiota abundance (genus Anaerofilum id.2053) on Ulcerative enterocolitis

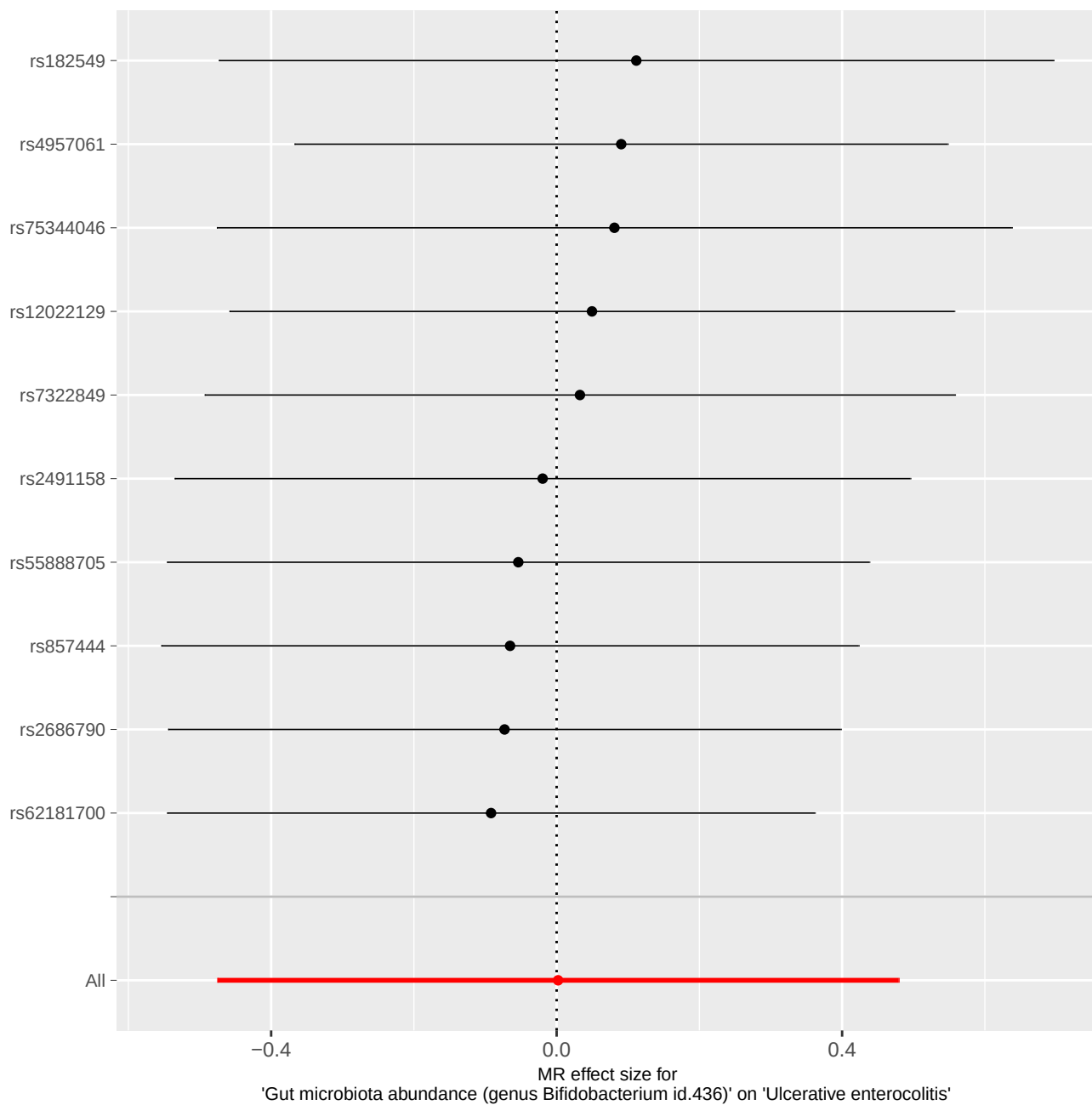


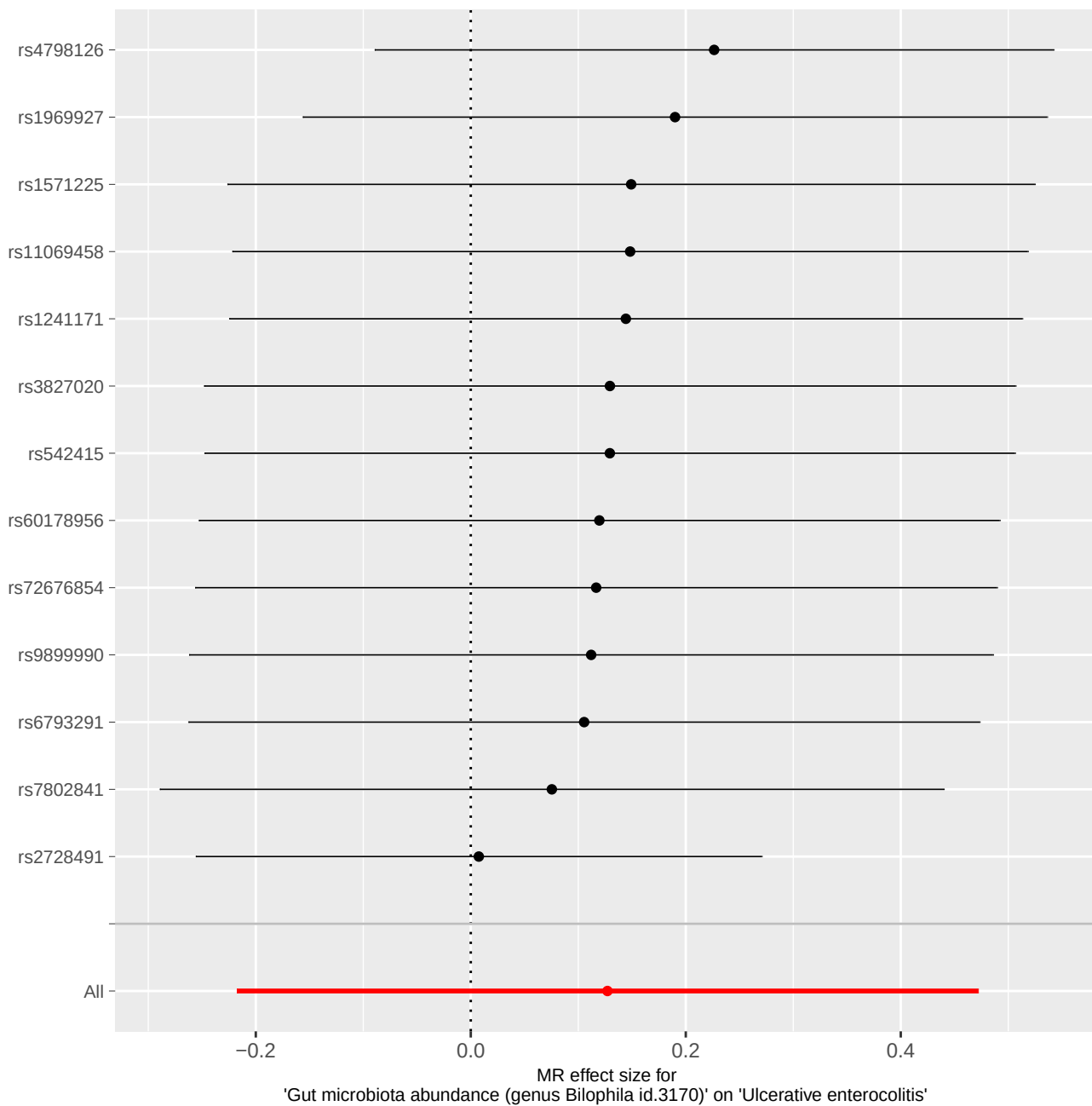


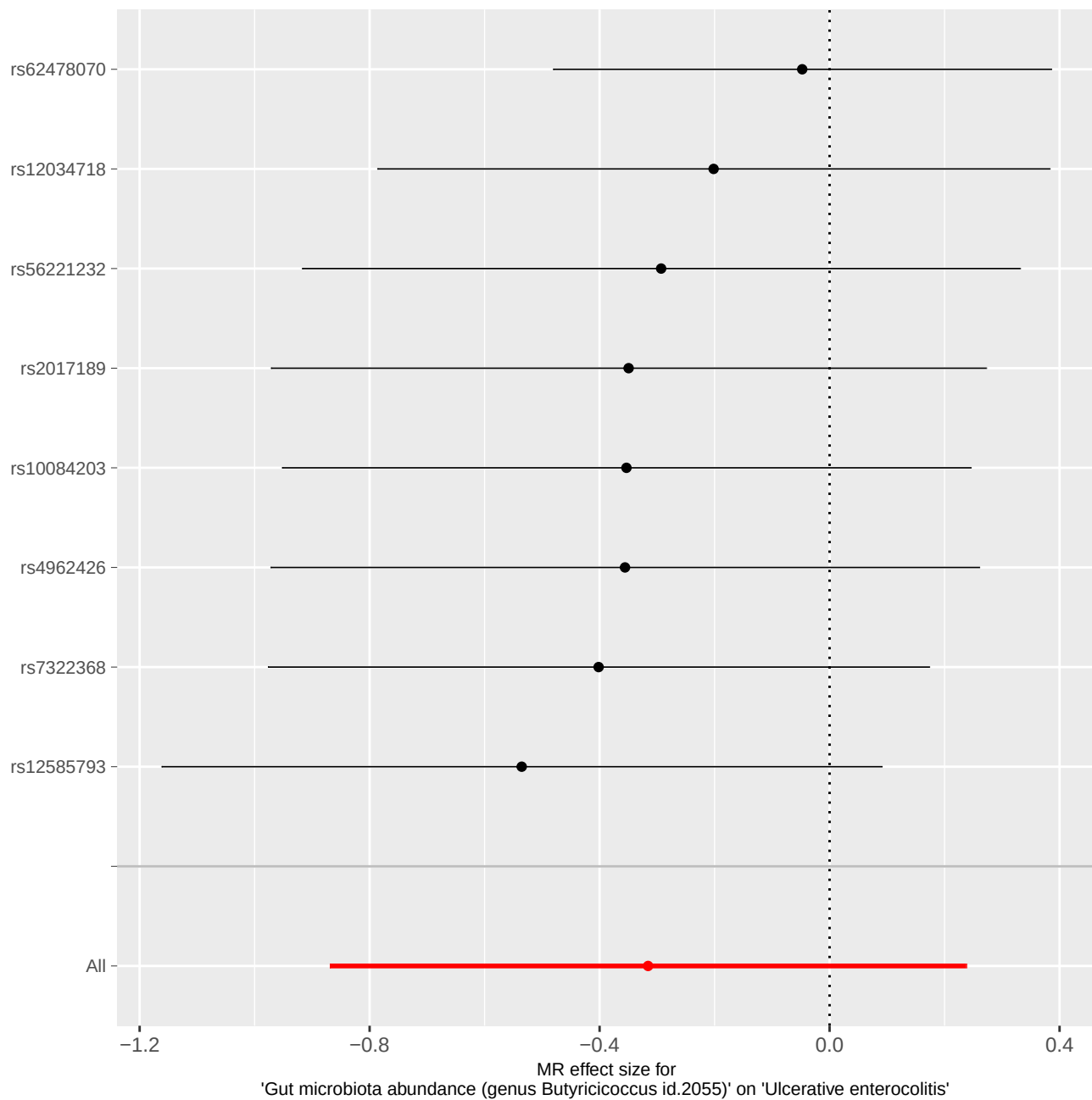


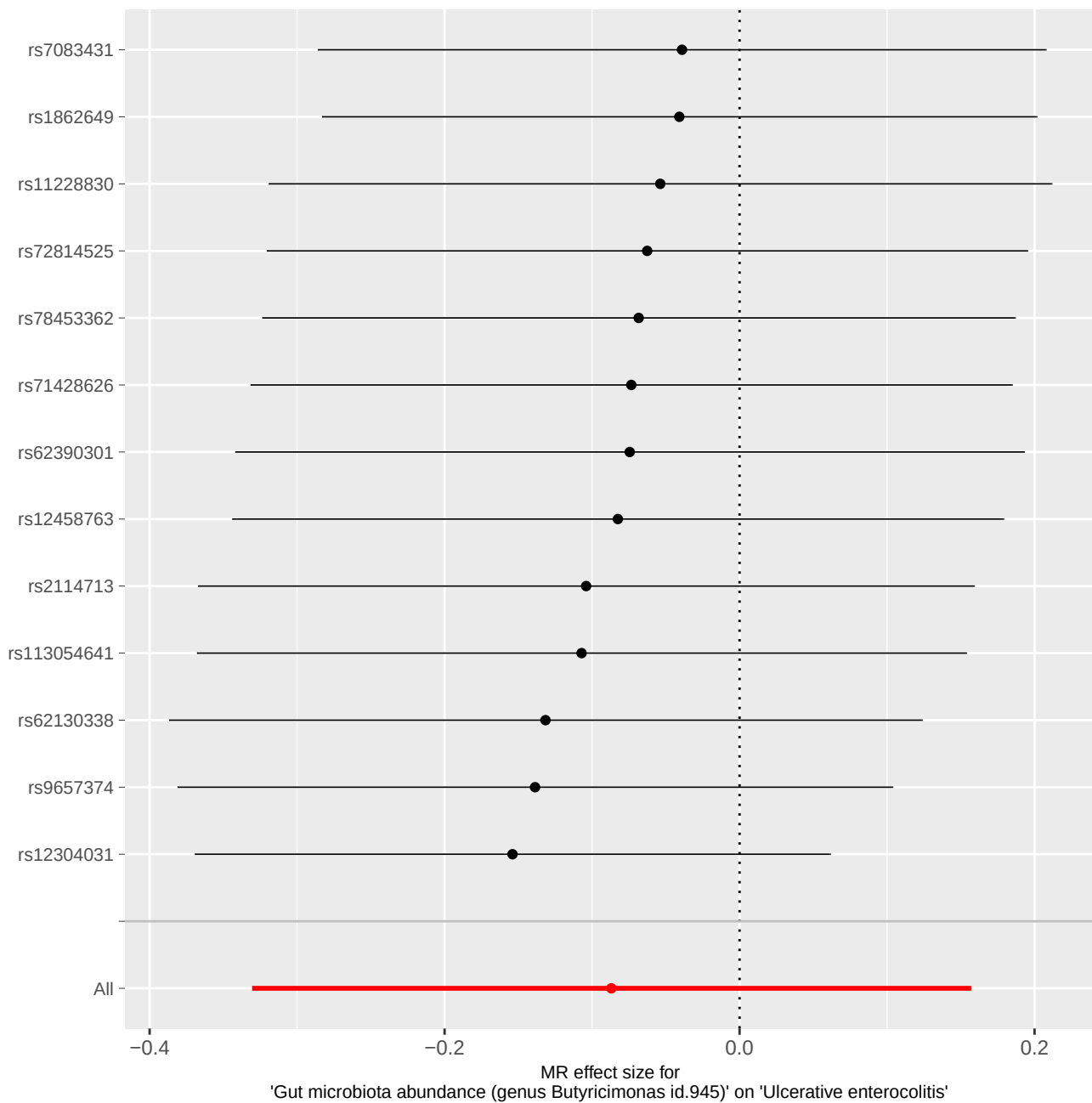


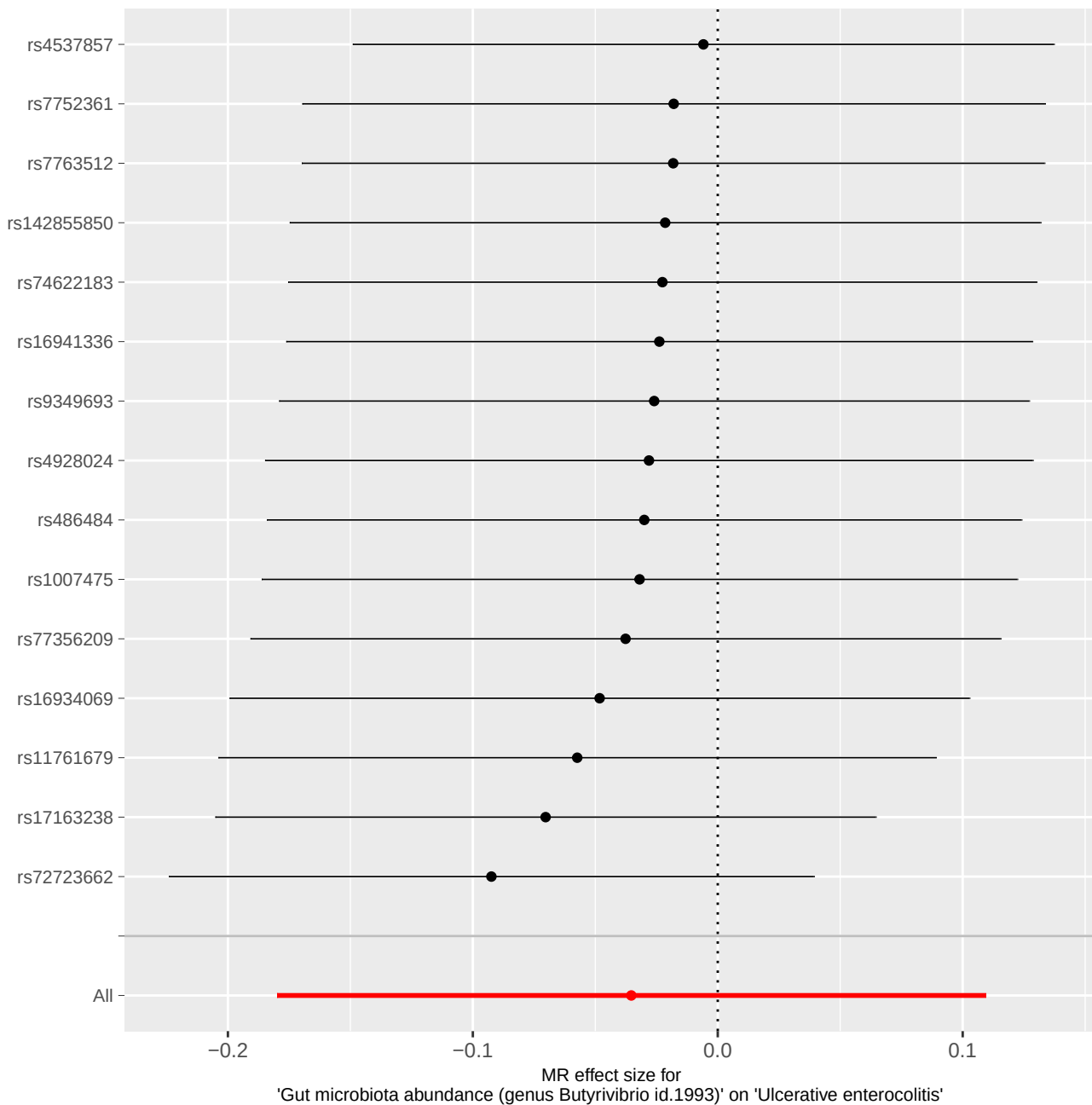


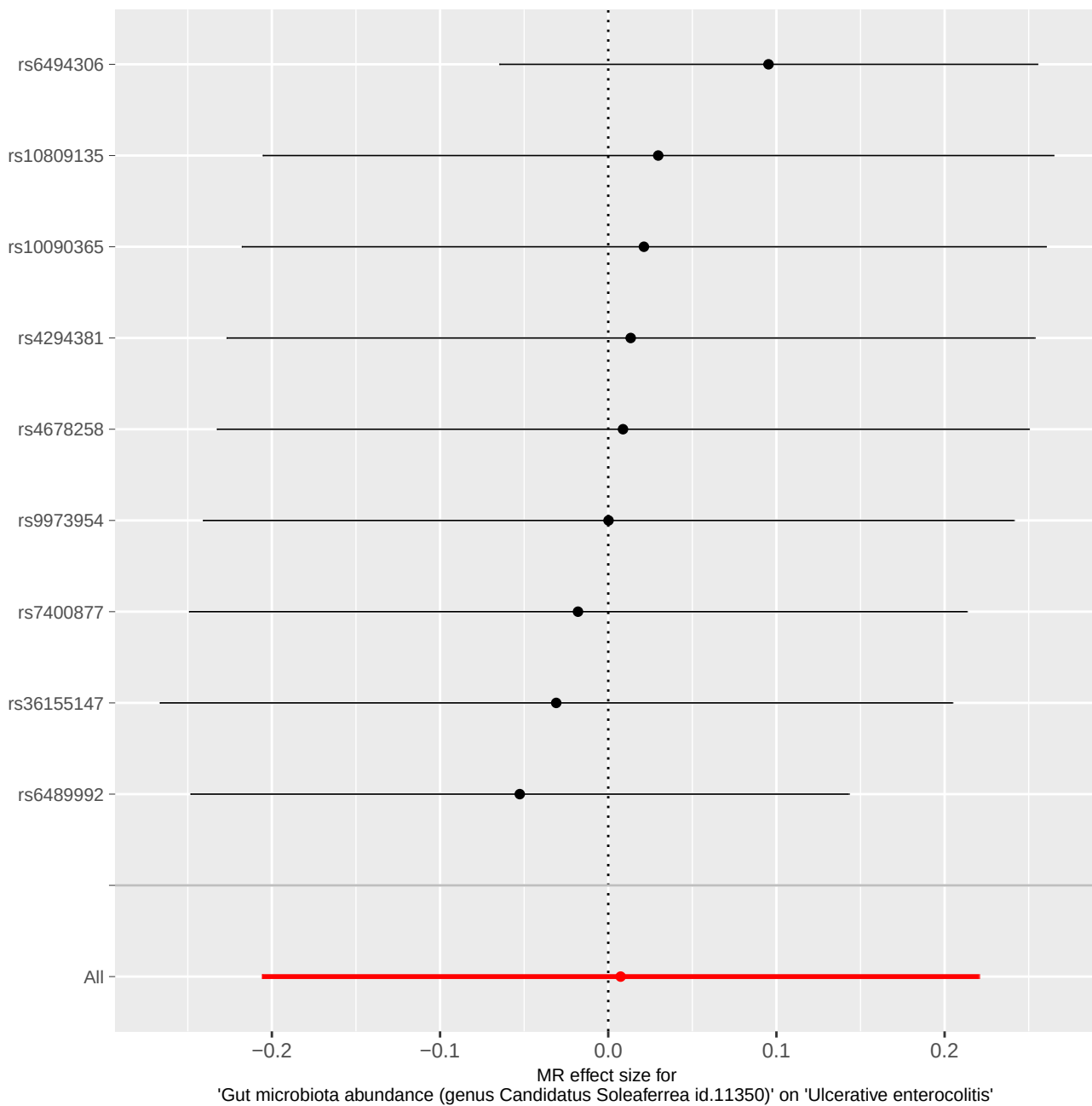


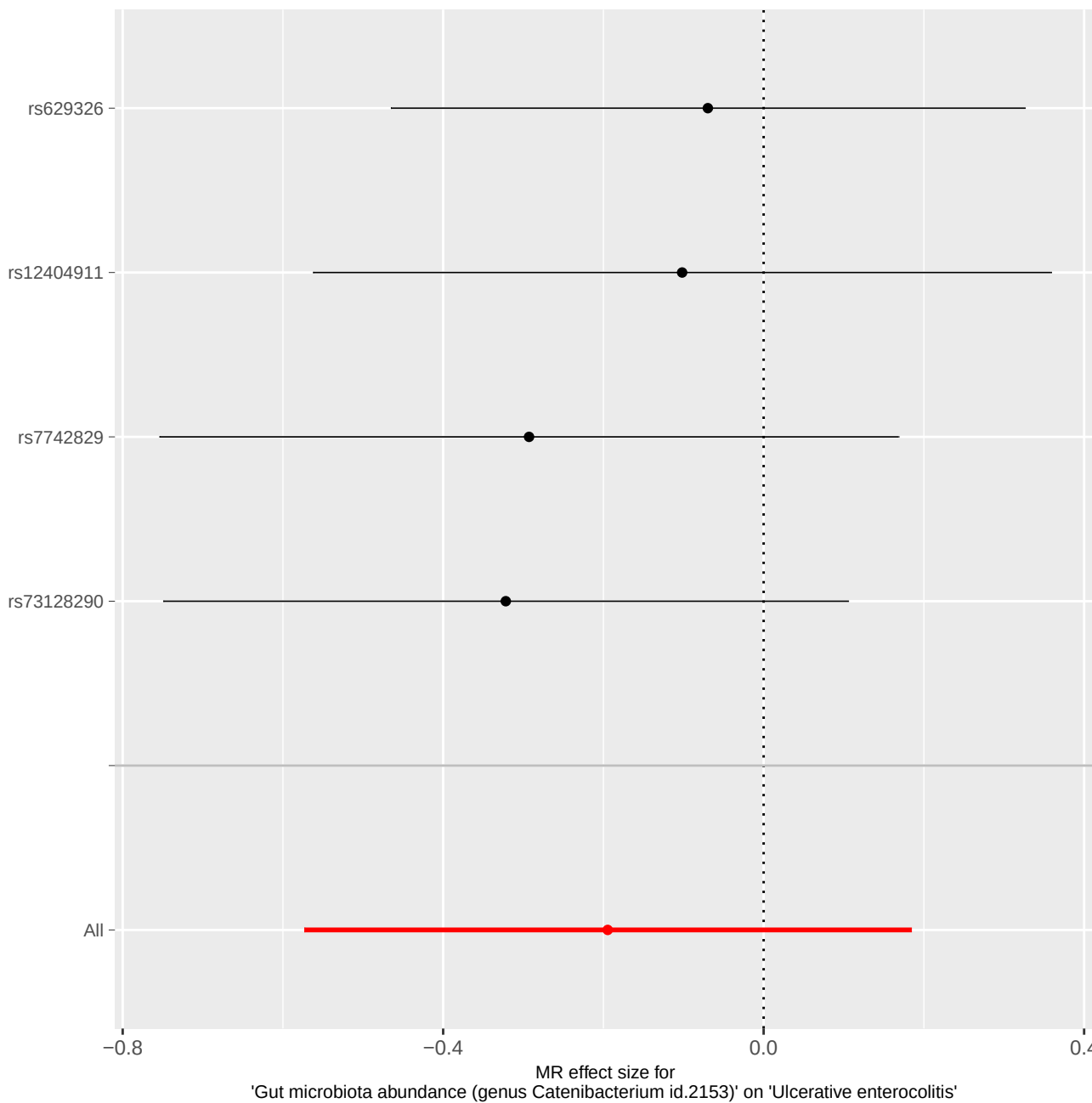


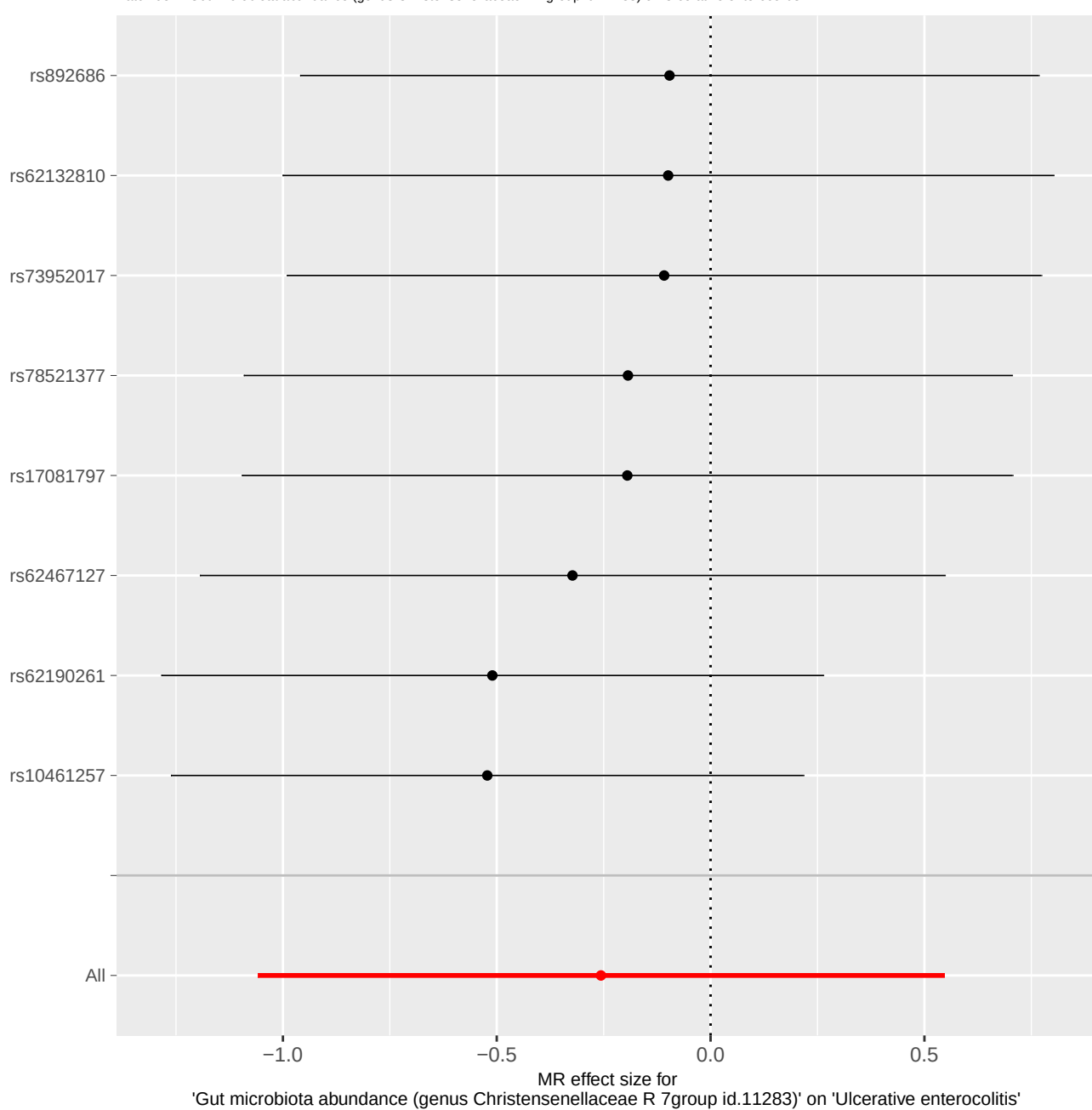


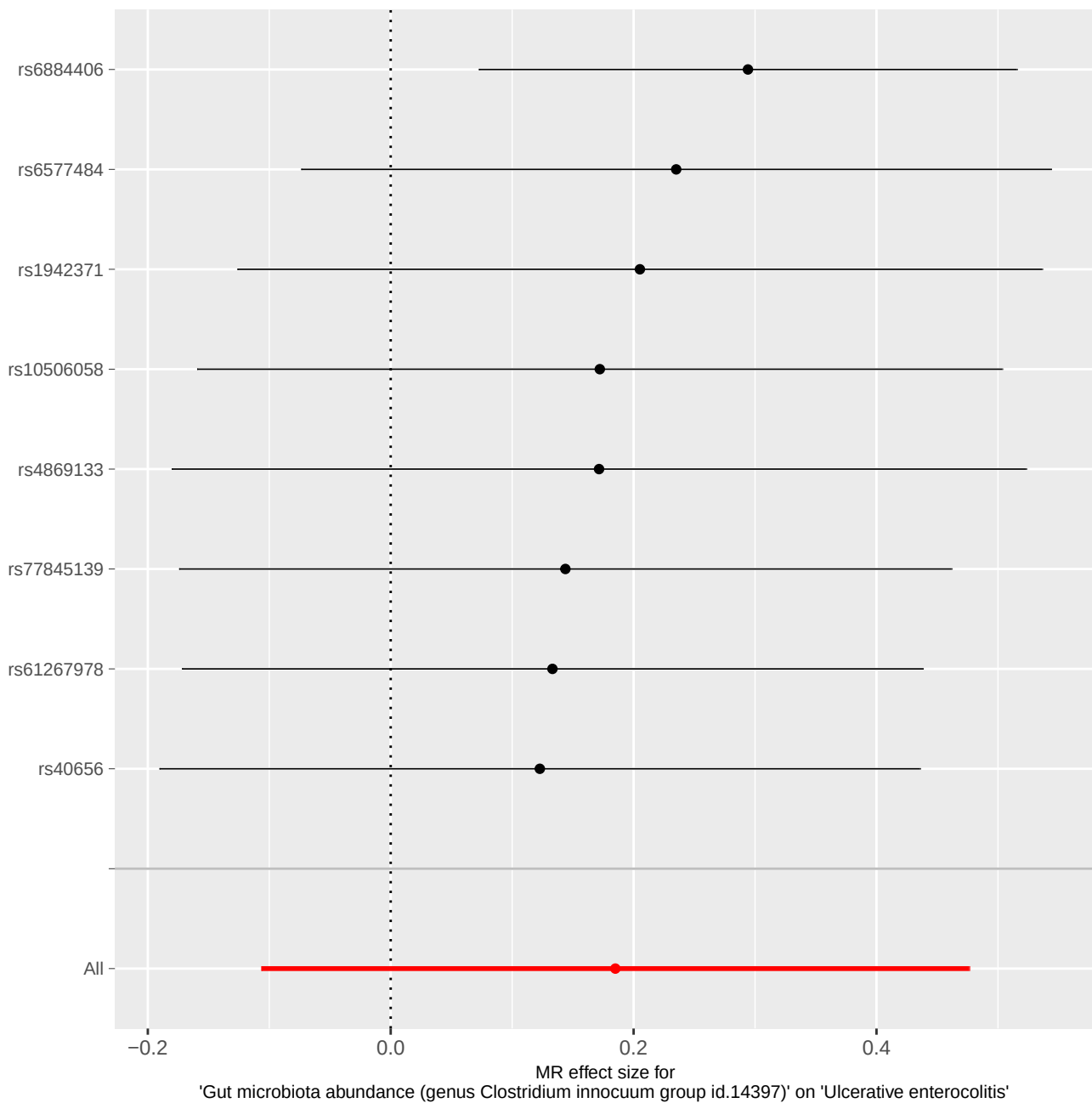


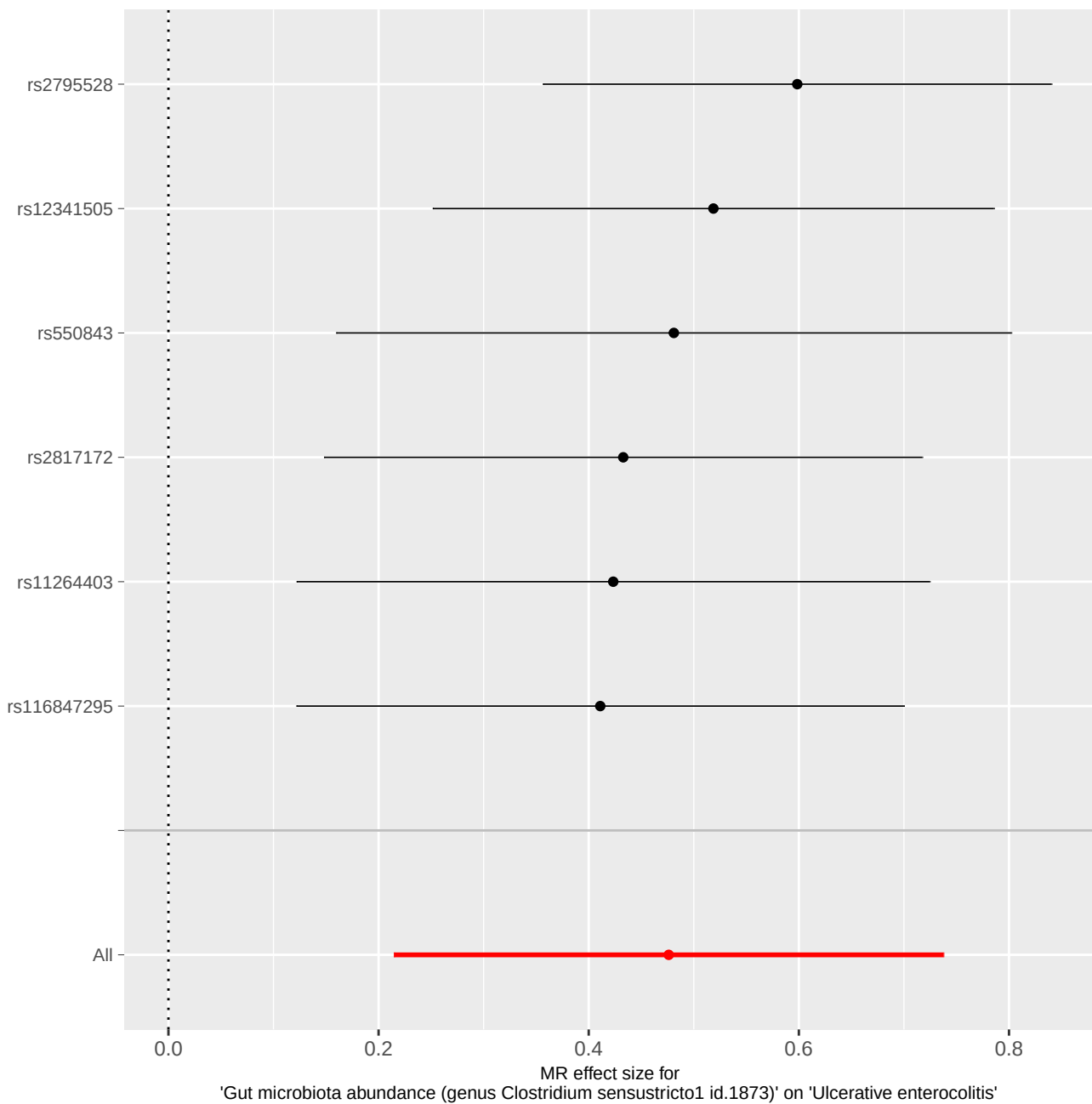


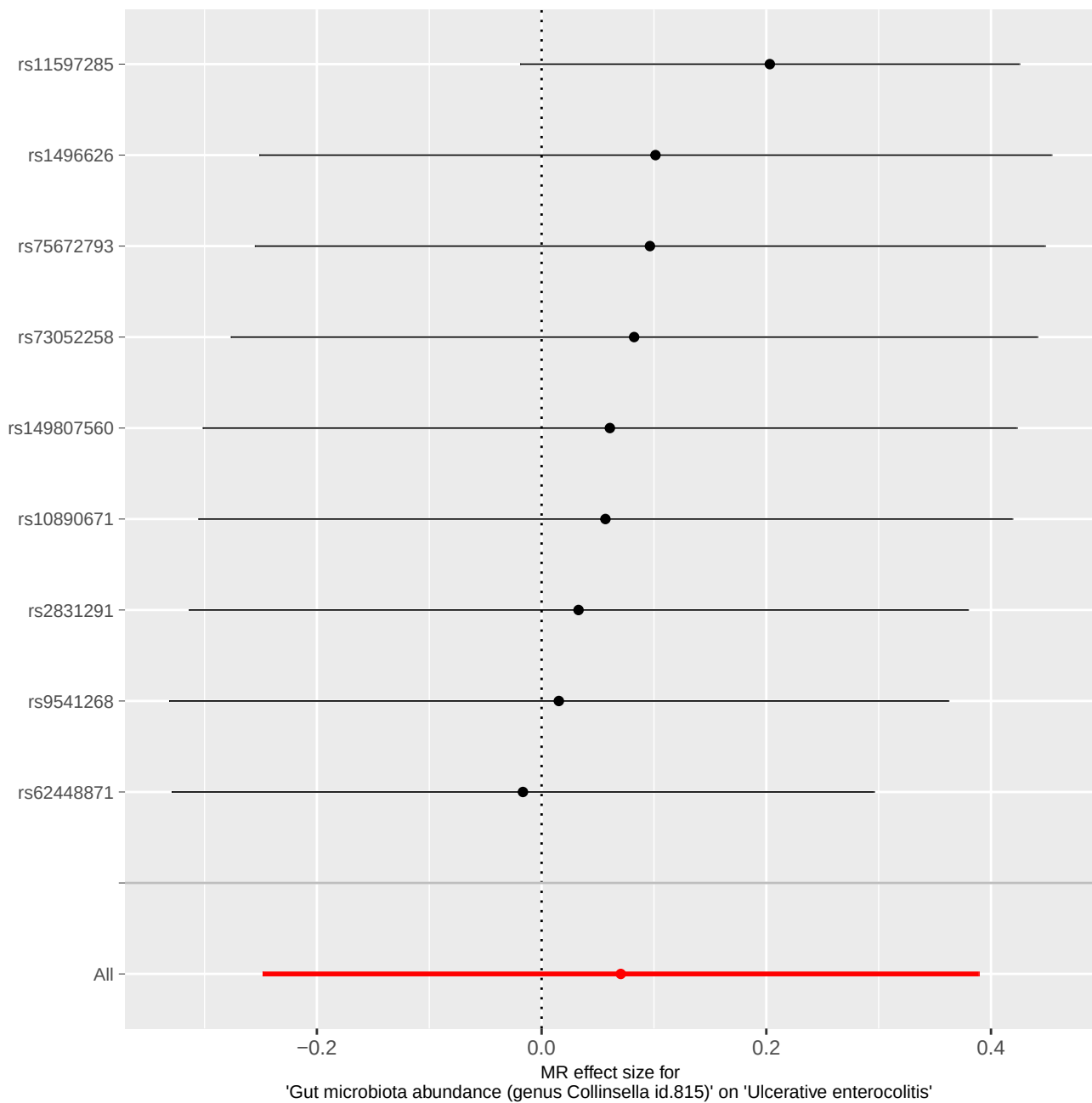


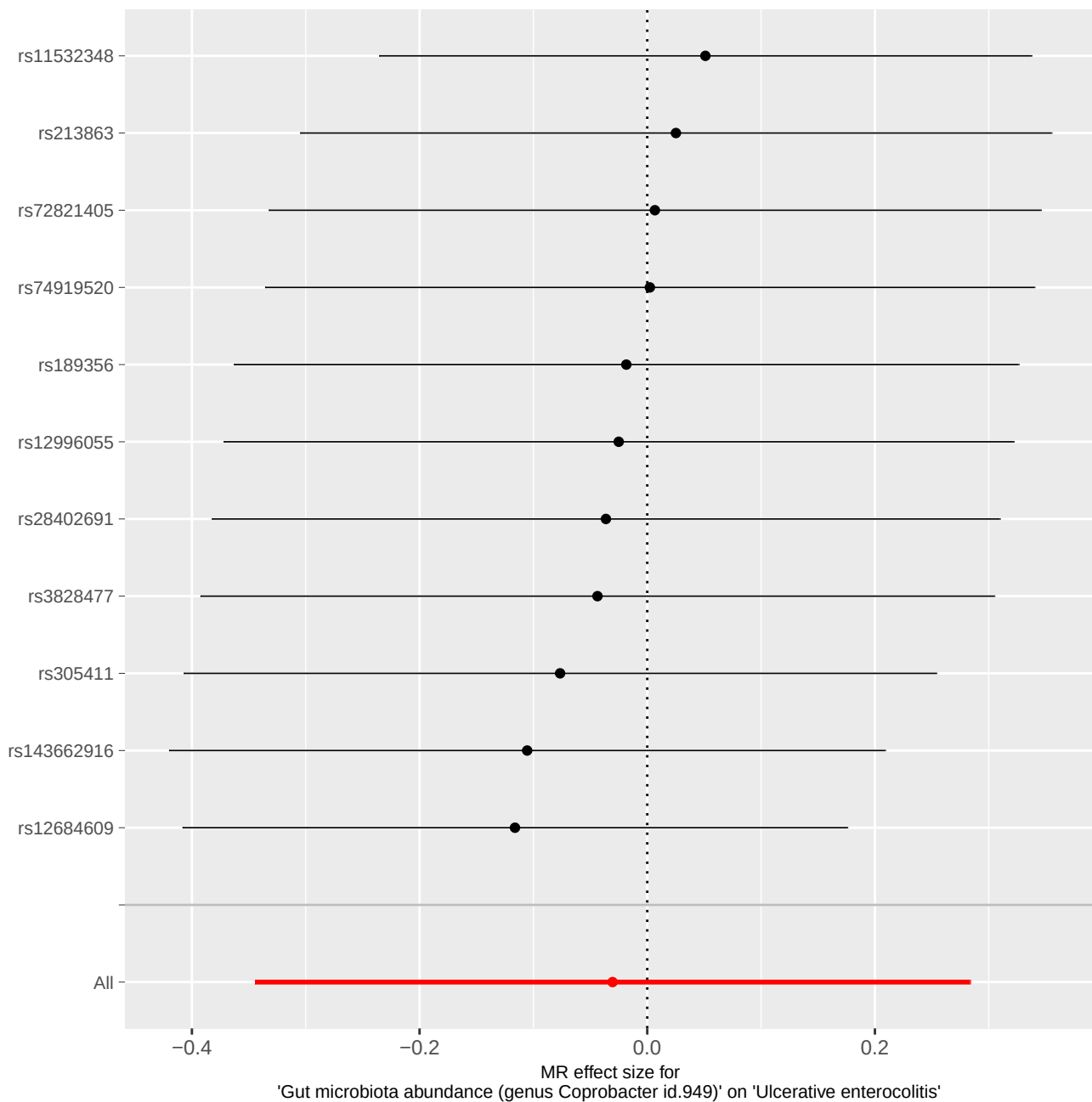


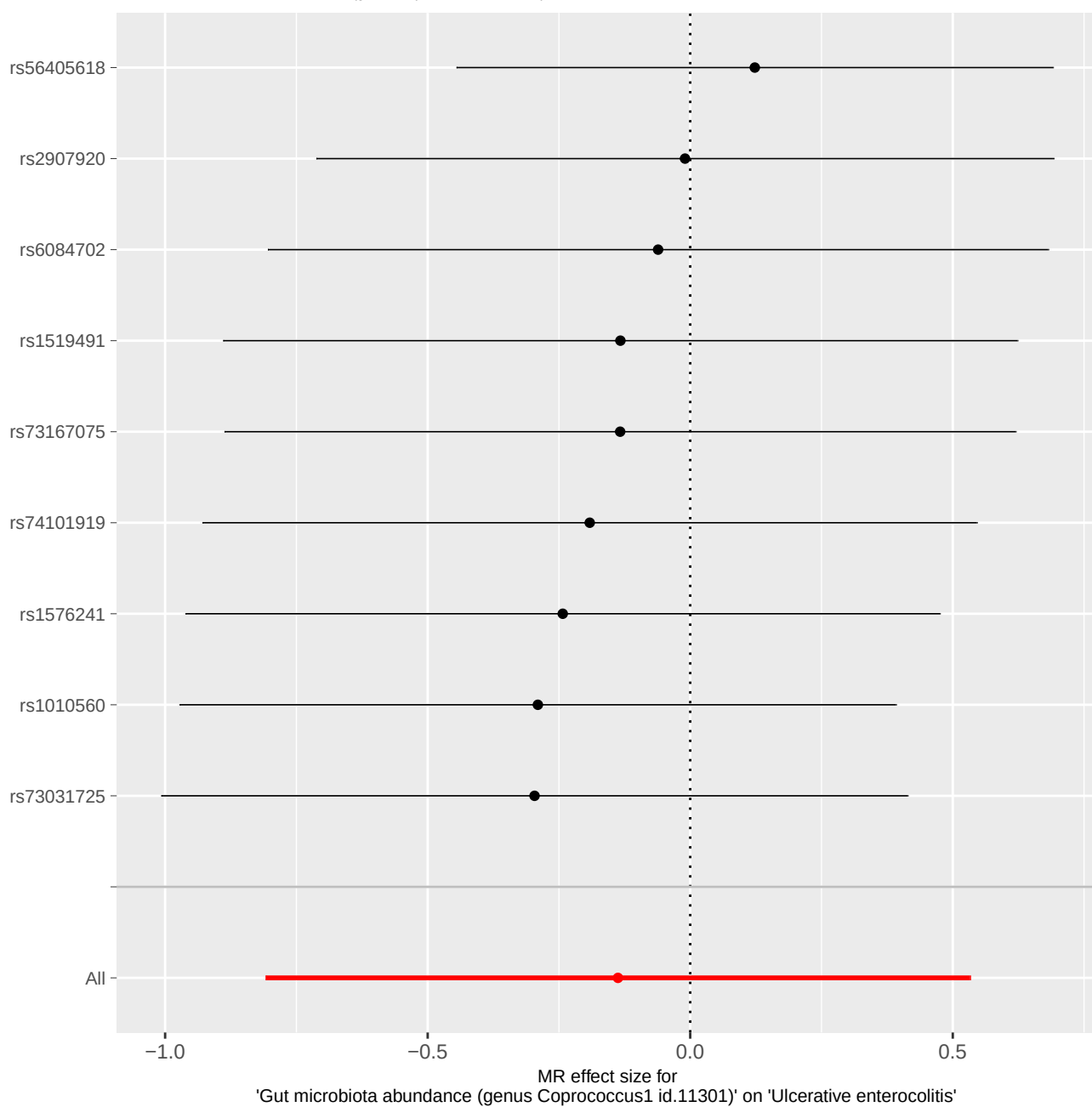


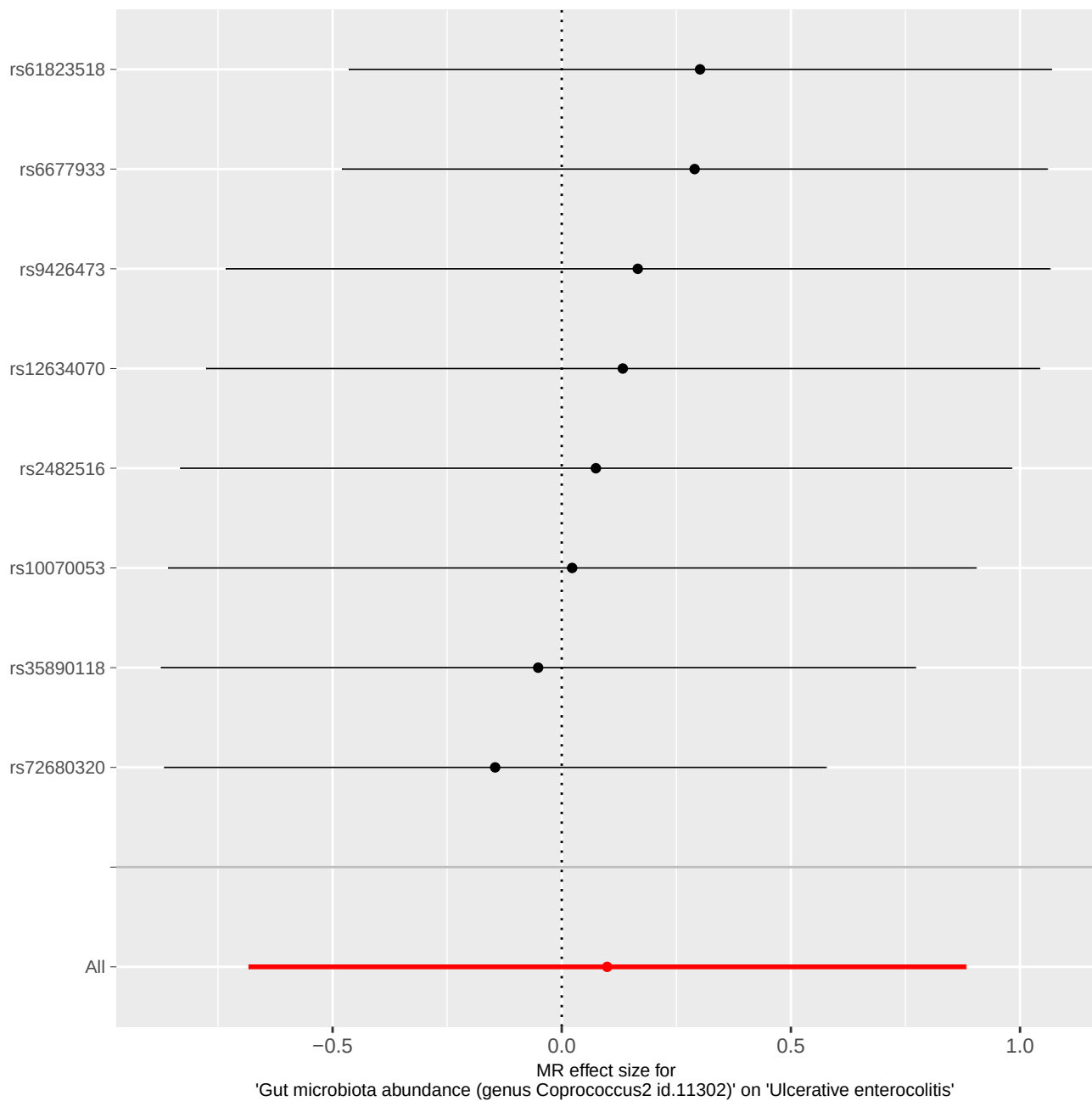


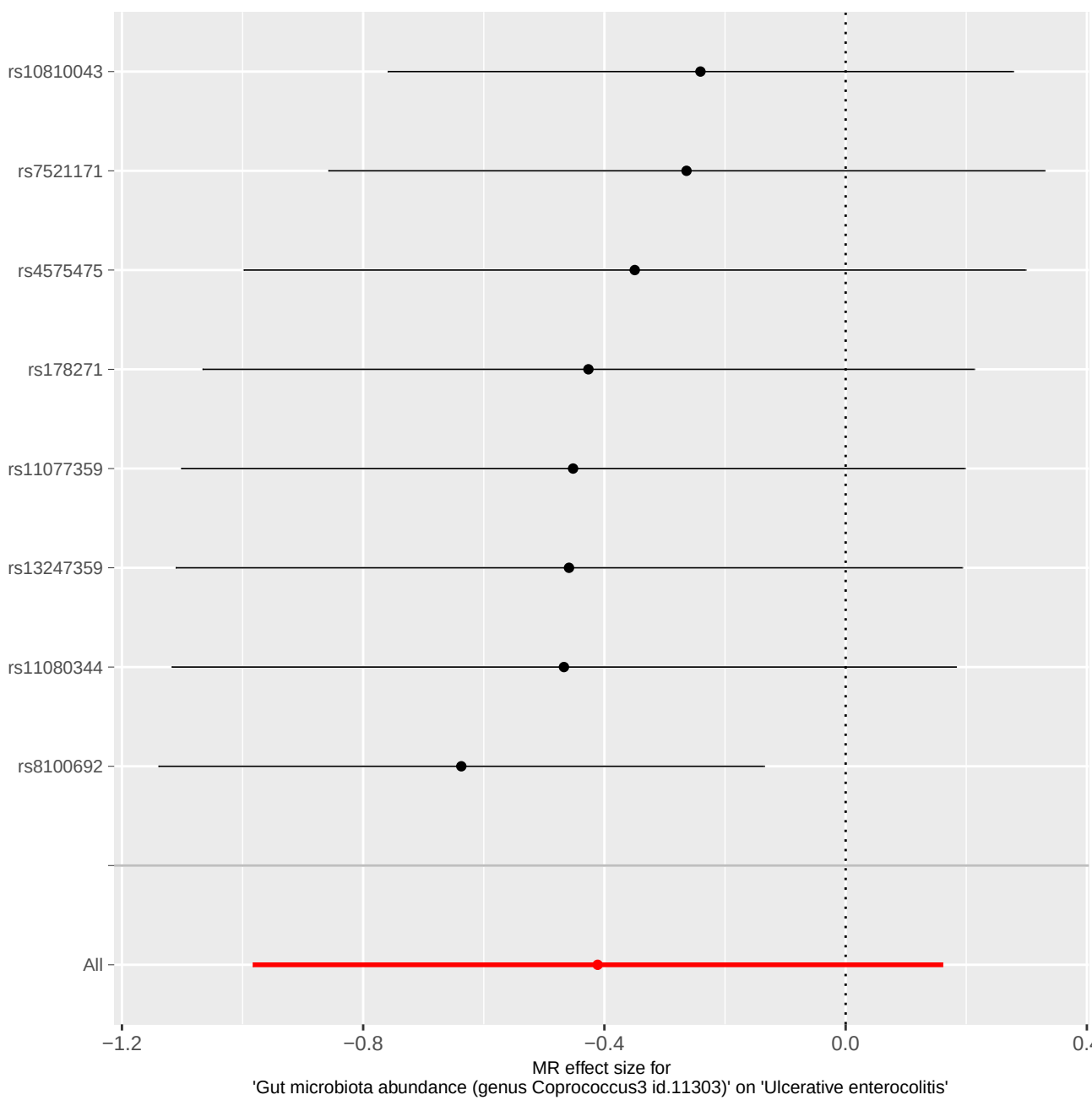


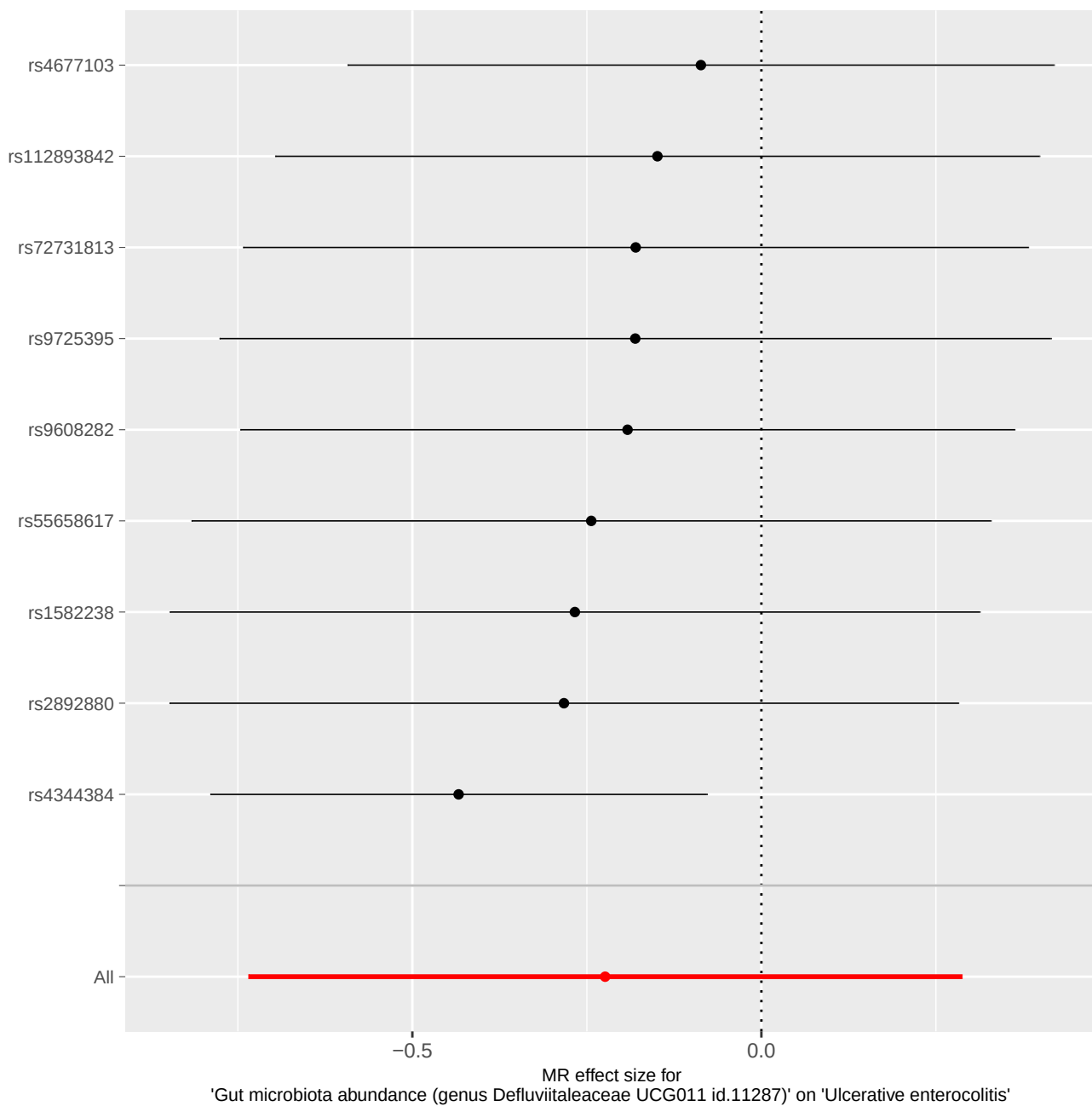


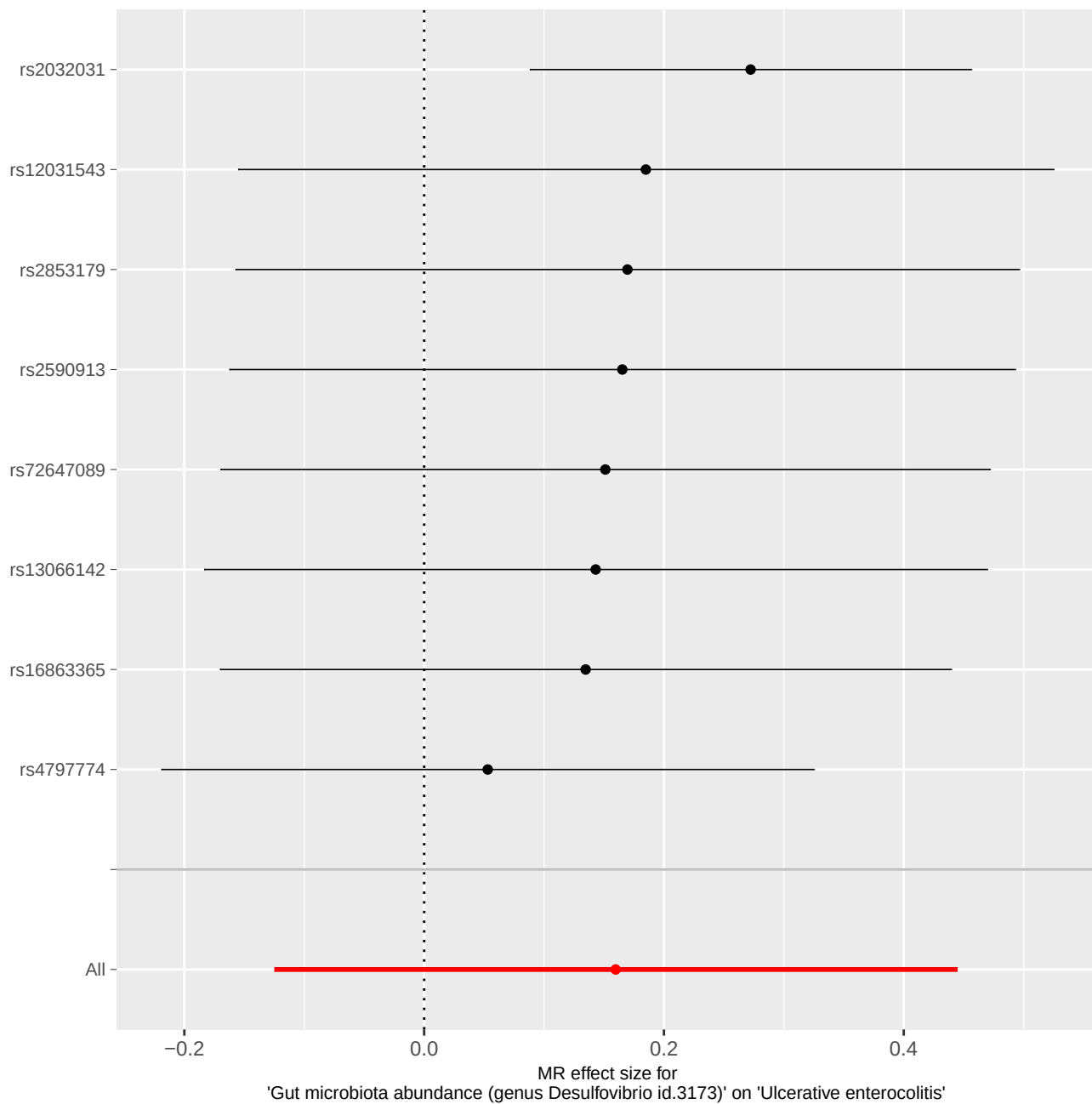




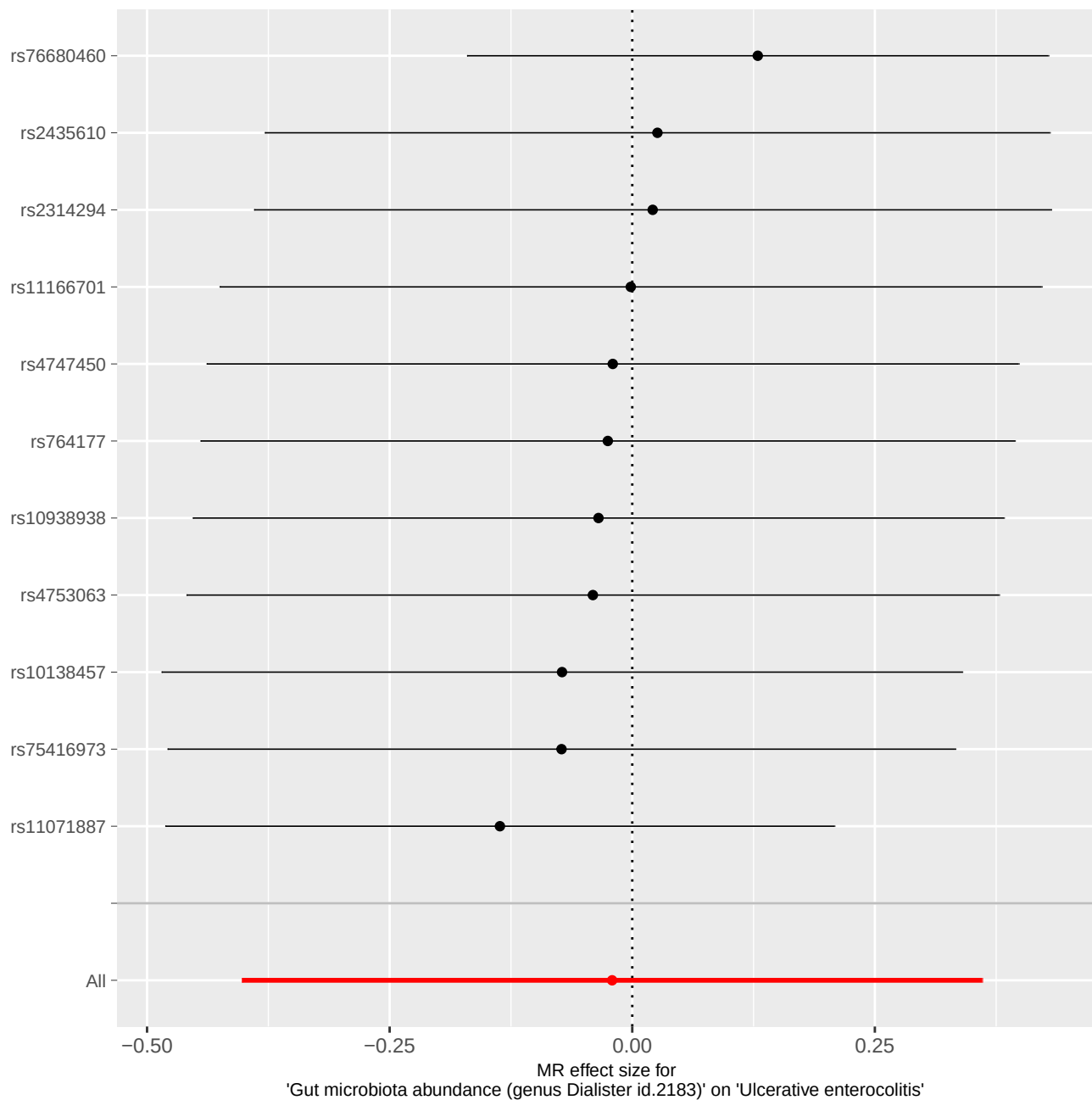


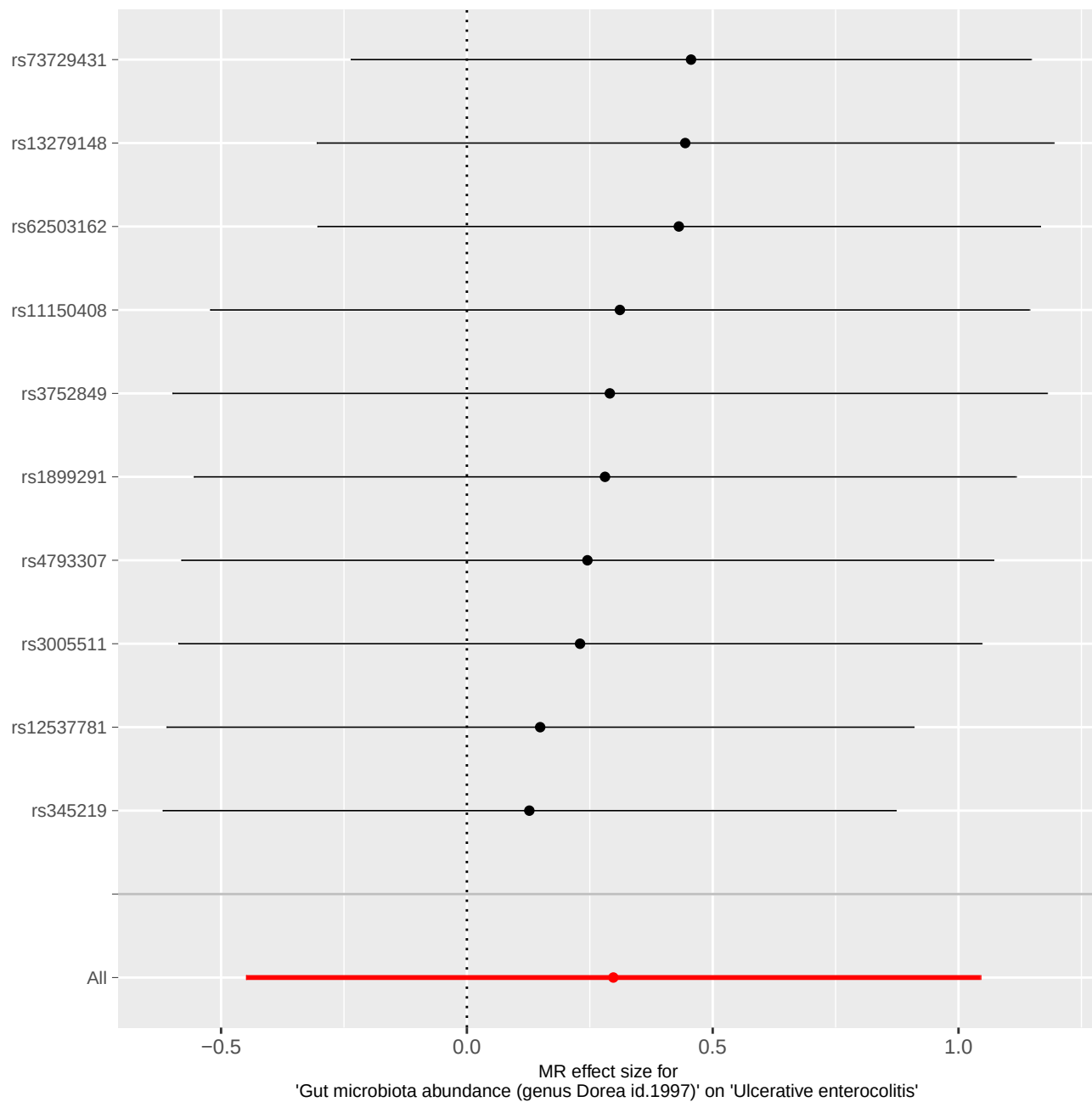


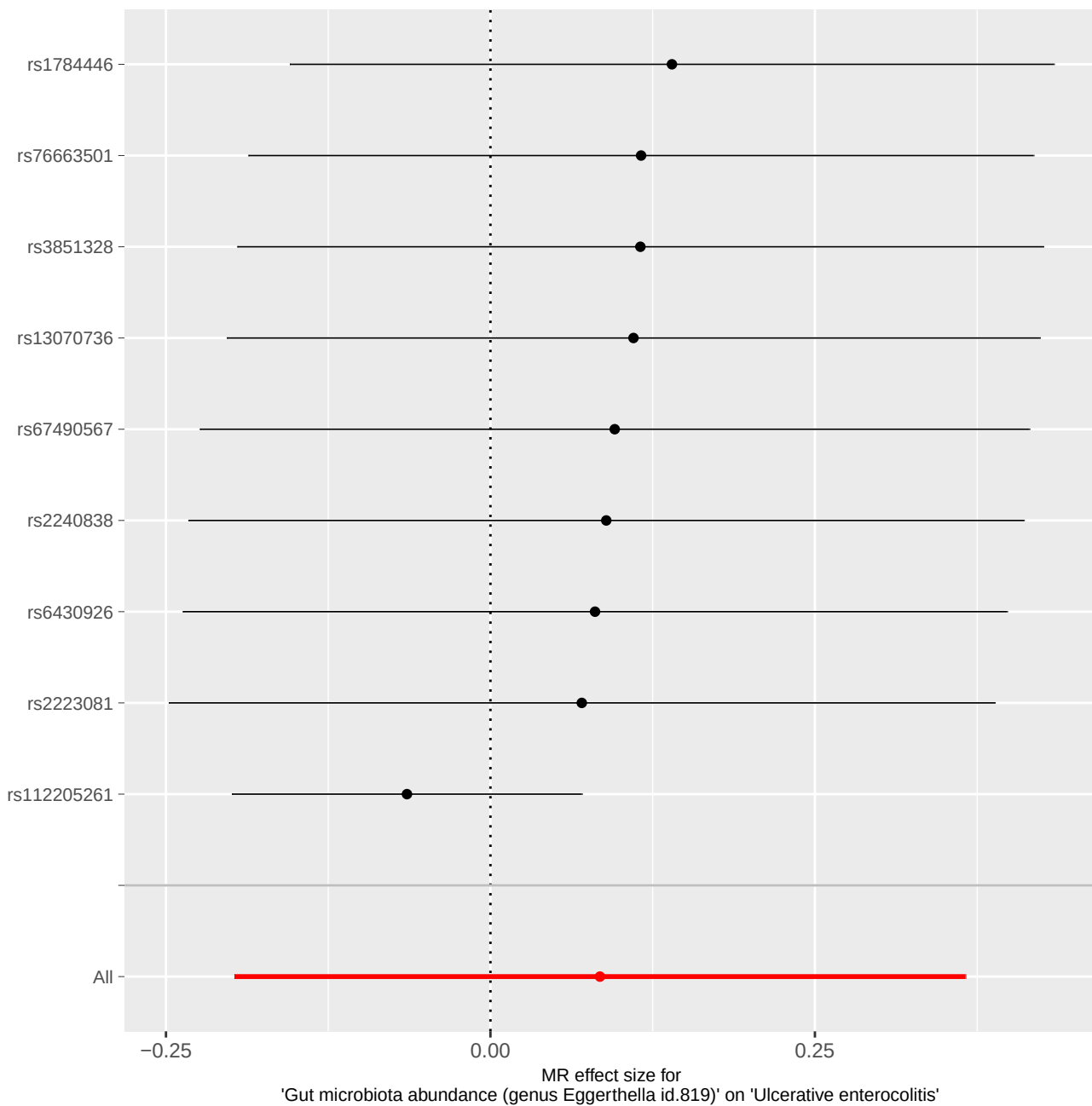


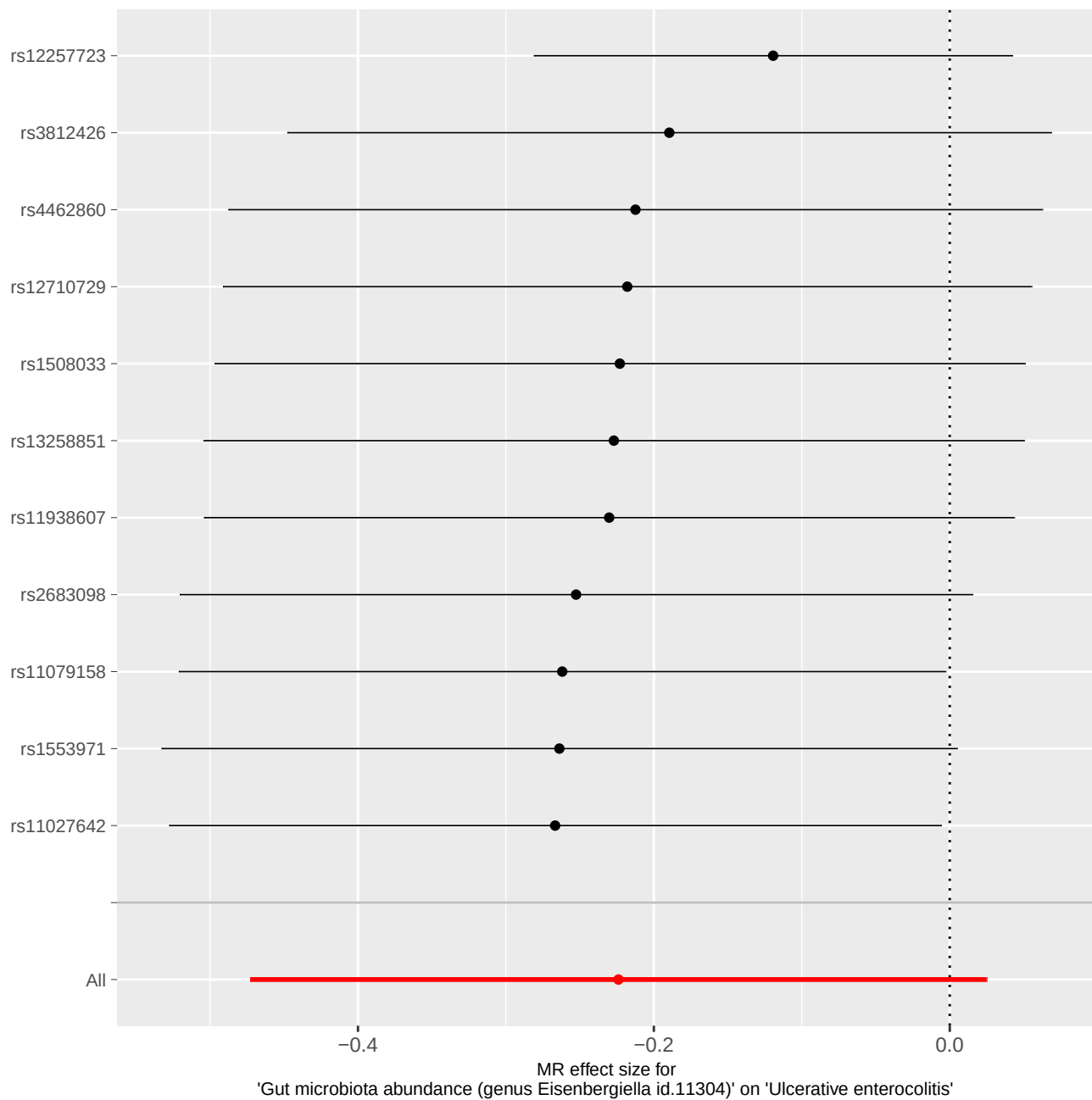


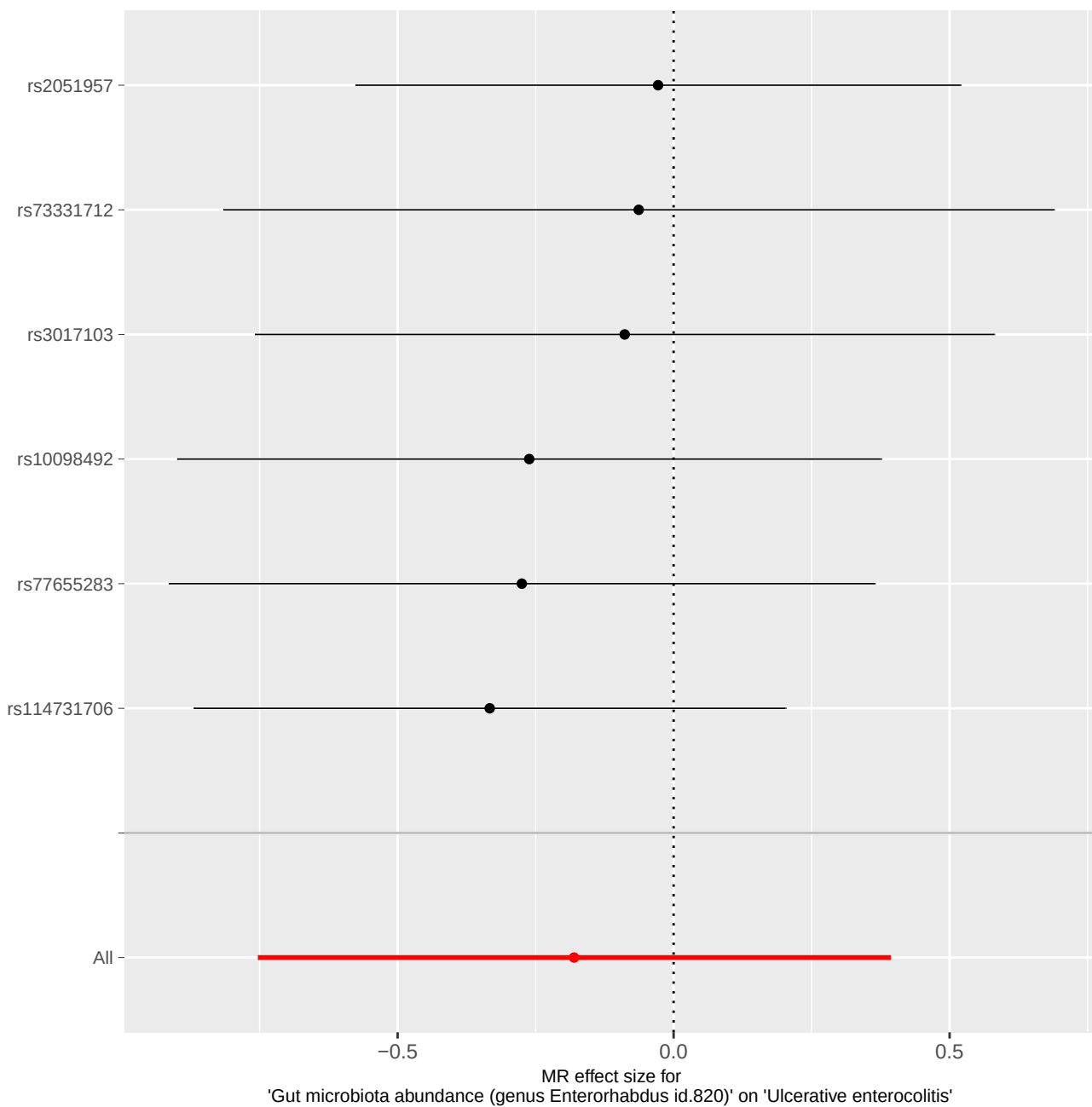
Batch 962 : Gut microbiota abundance (genus Dialister id.2183) on Ulcerative enterocolitis

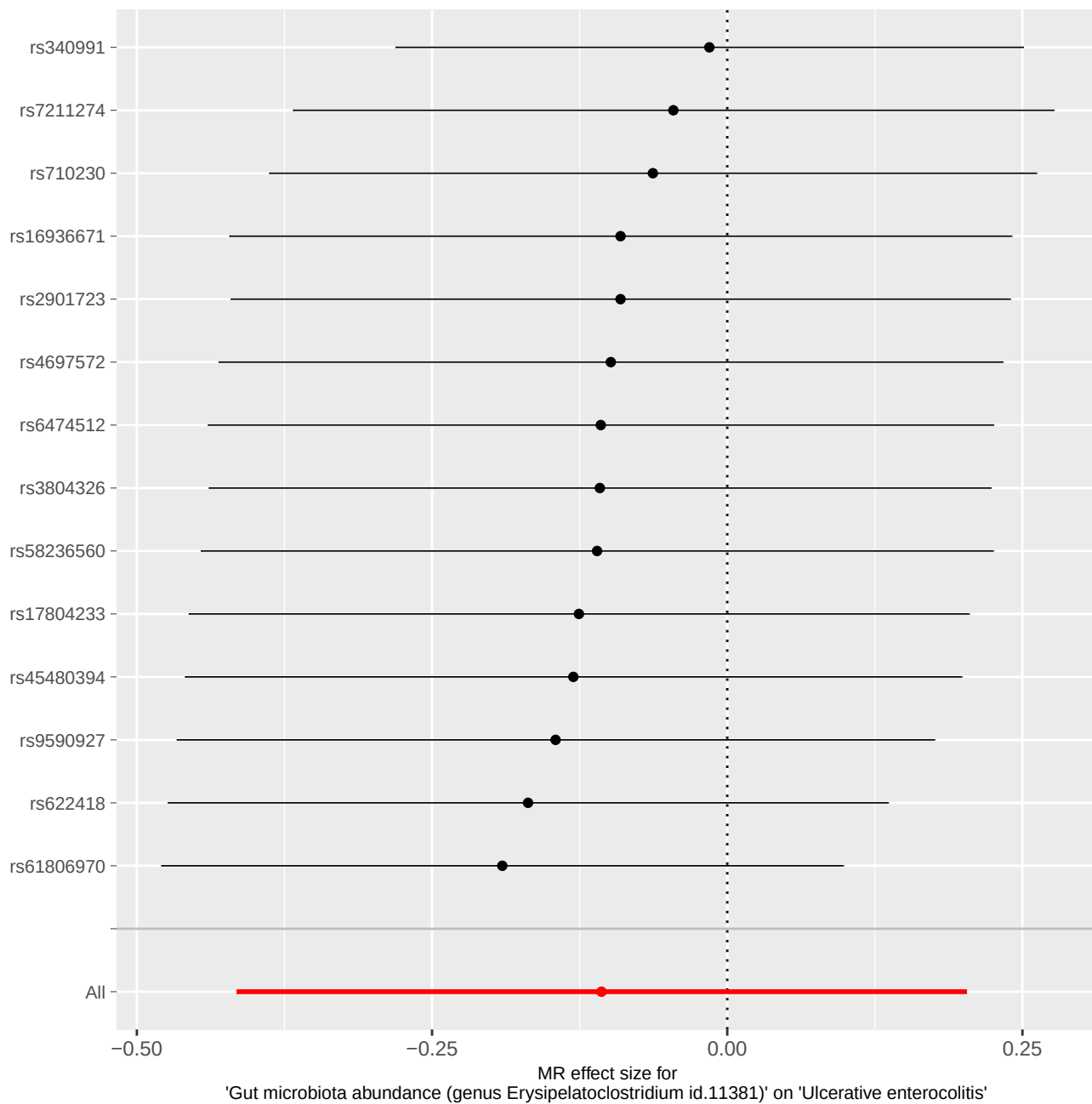


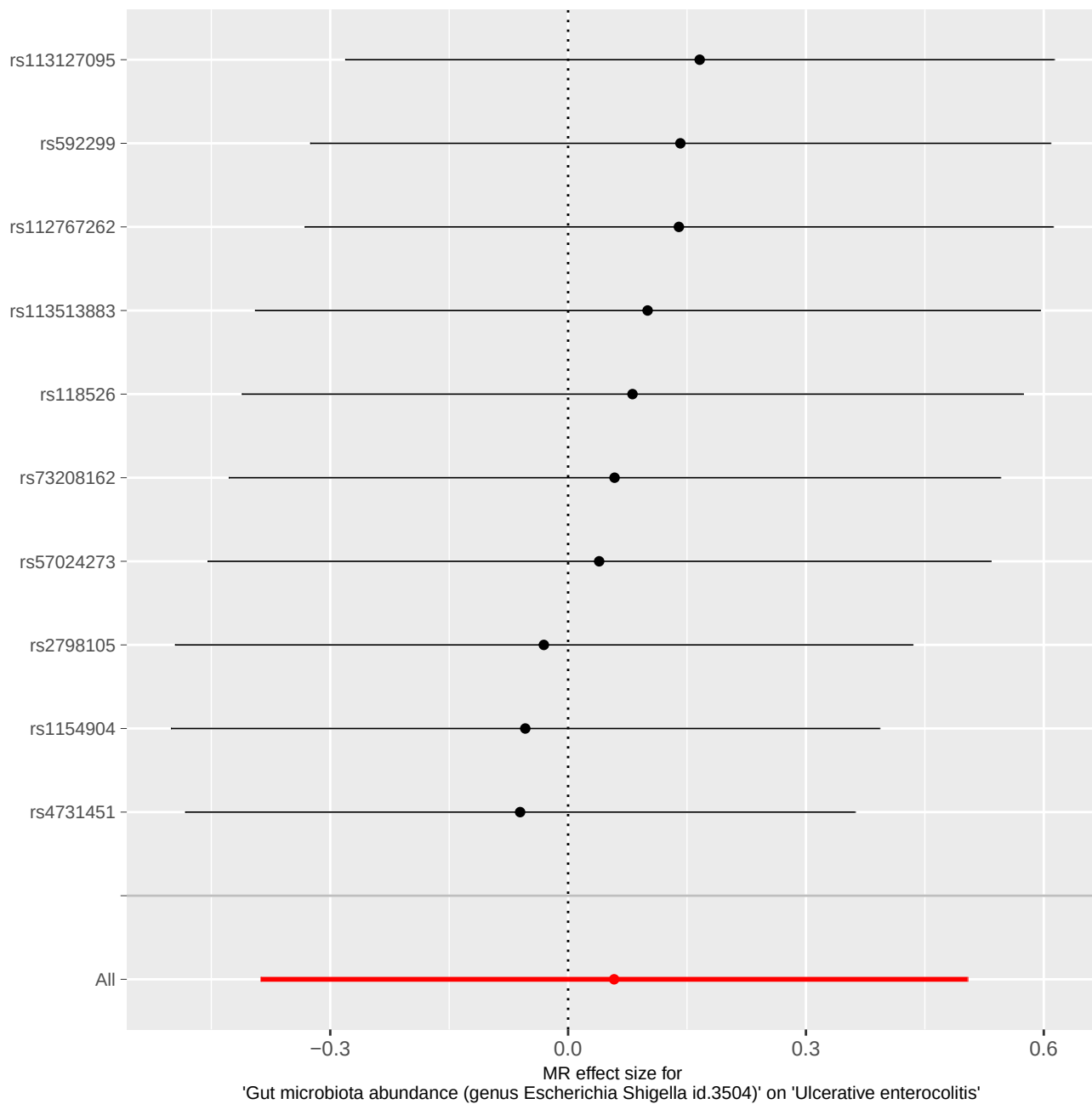


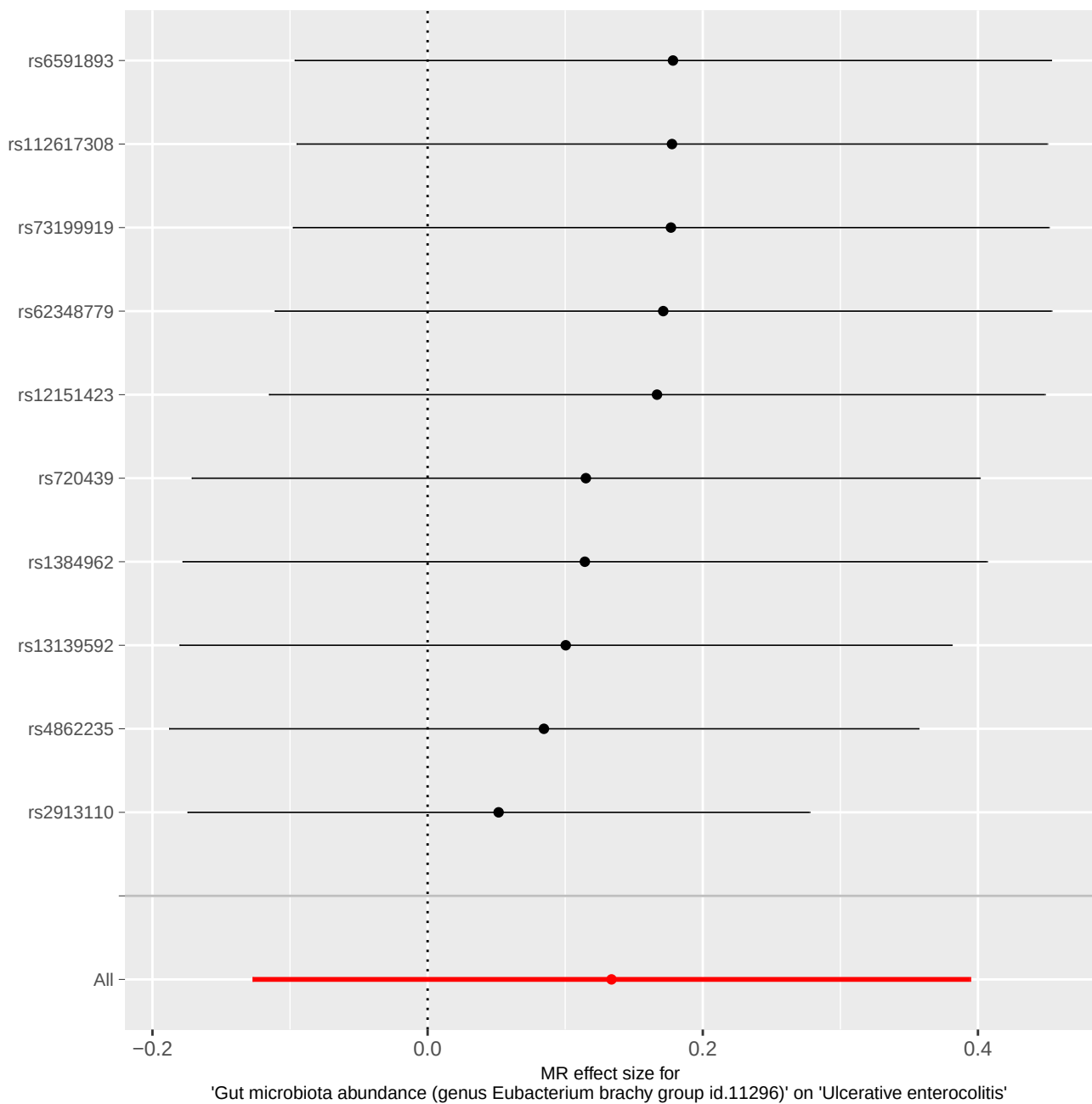


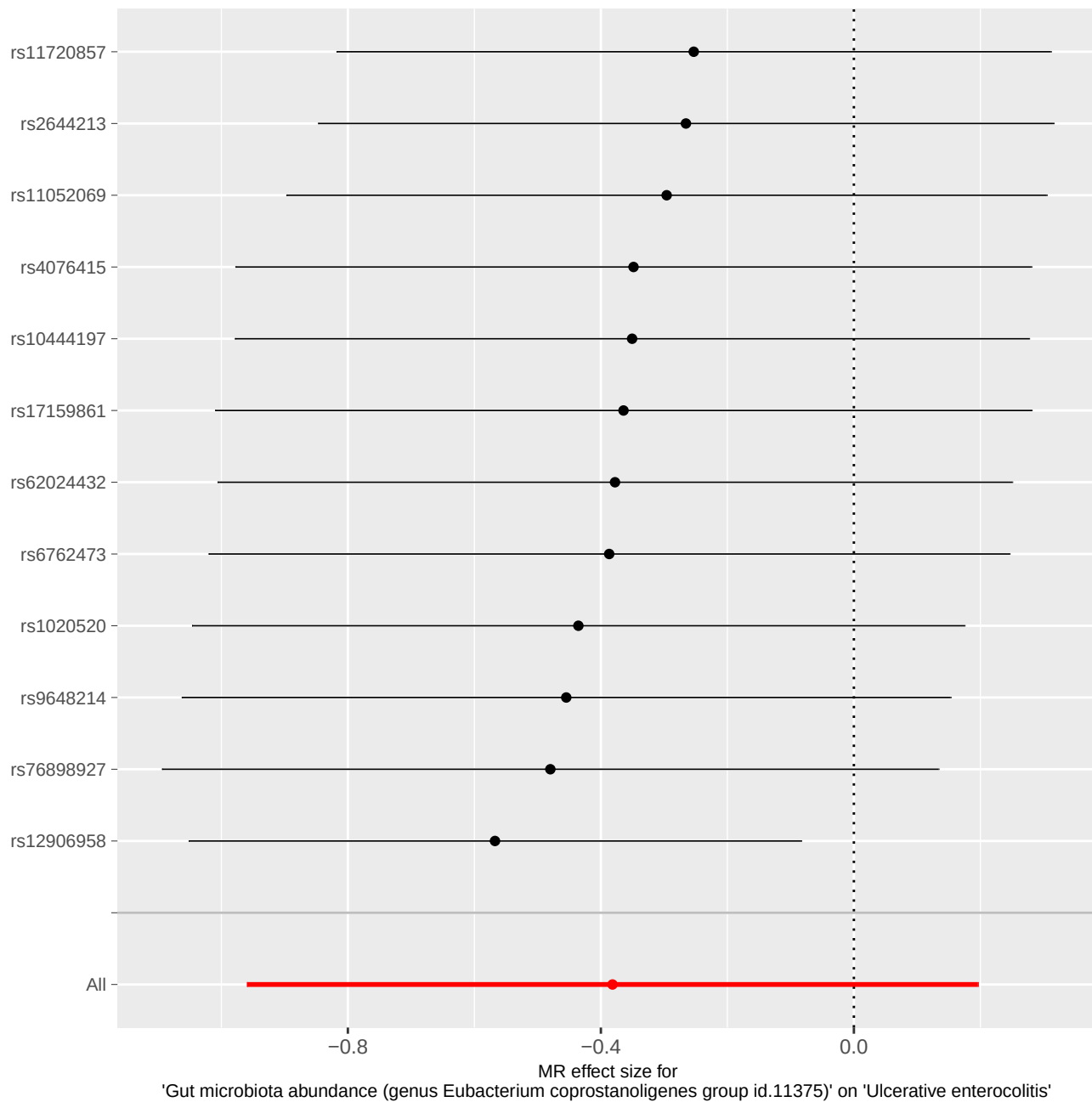


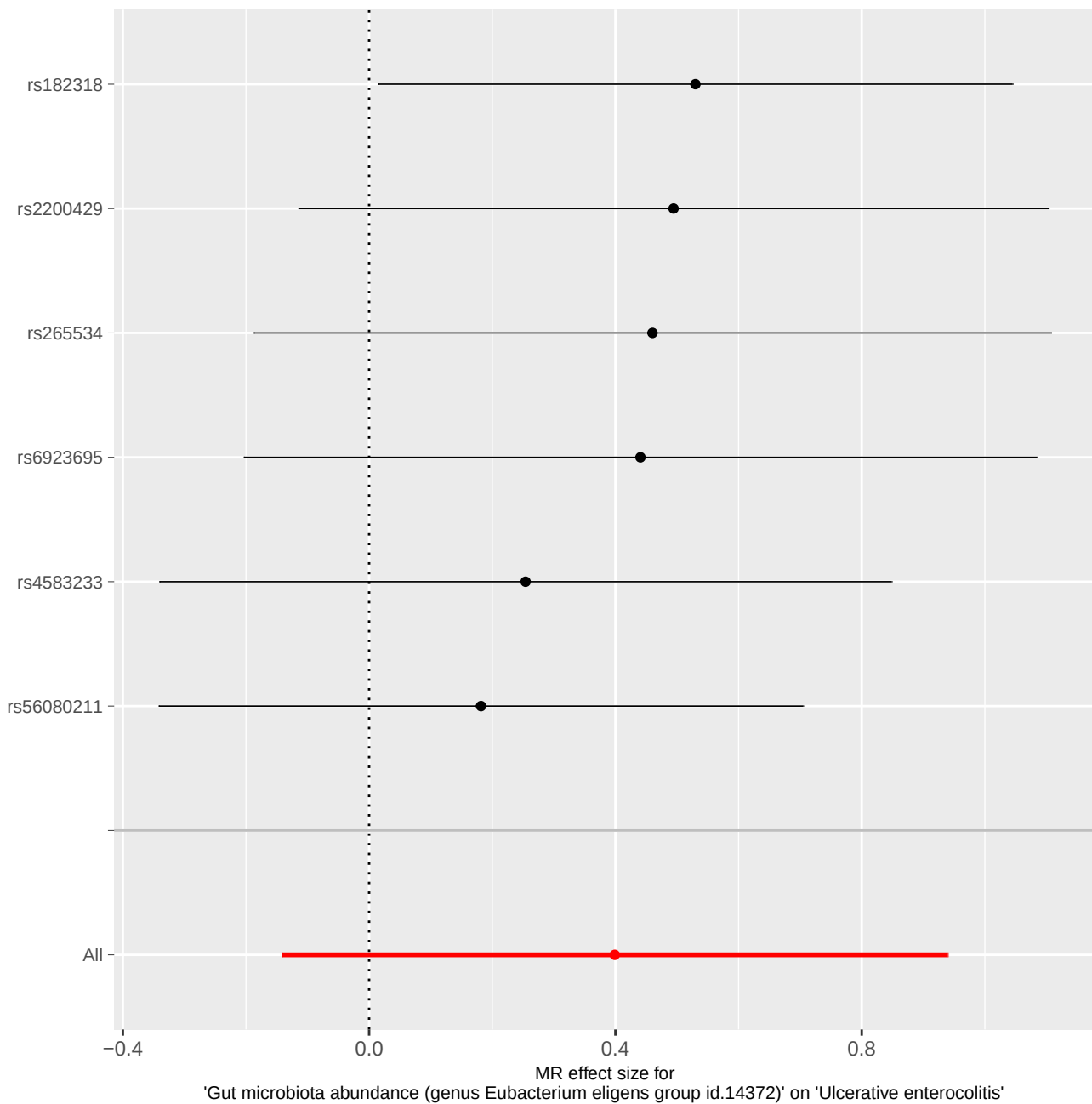


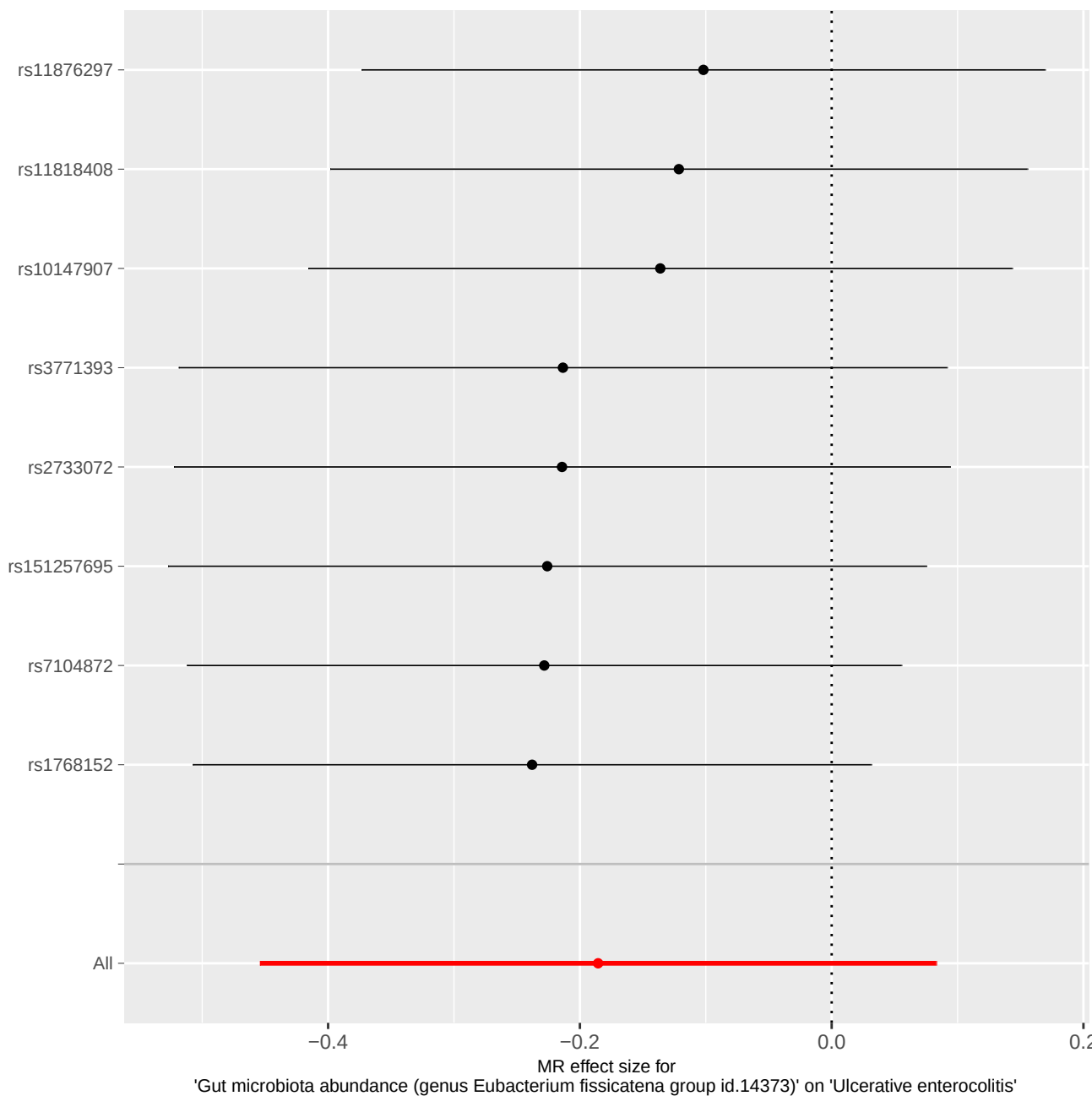


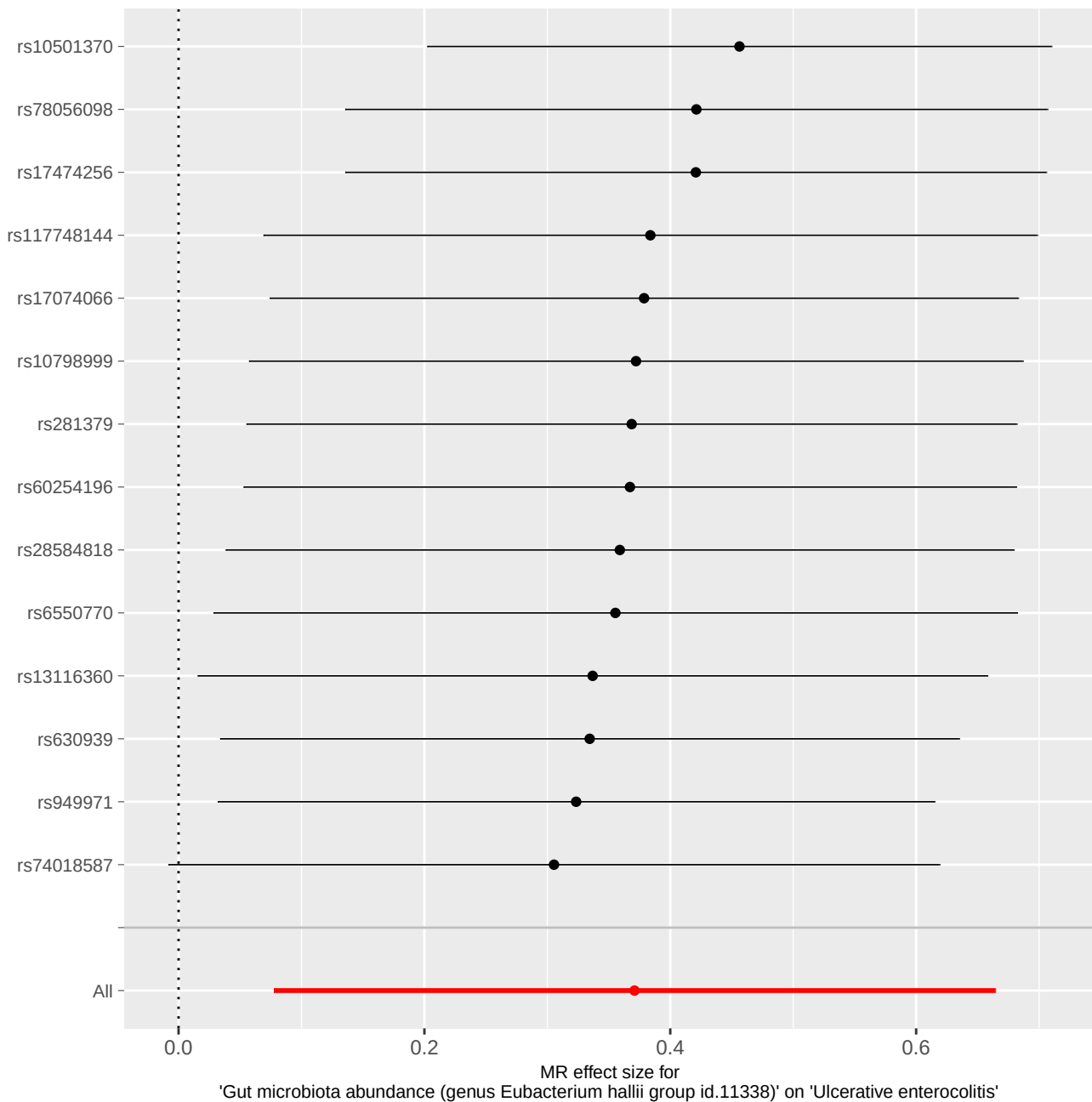


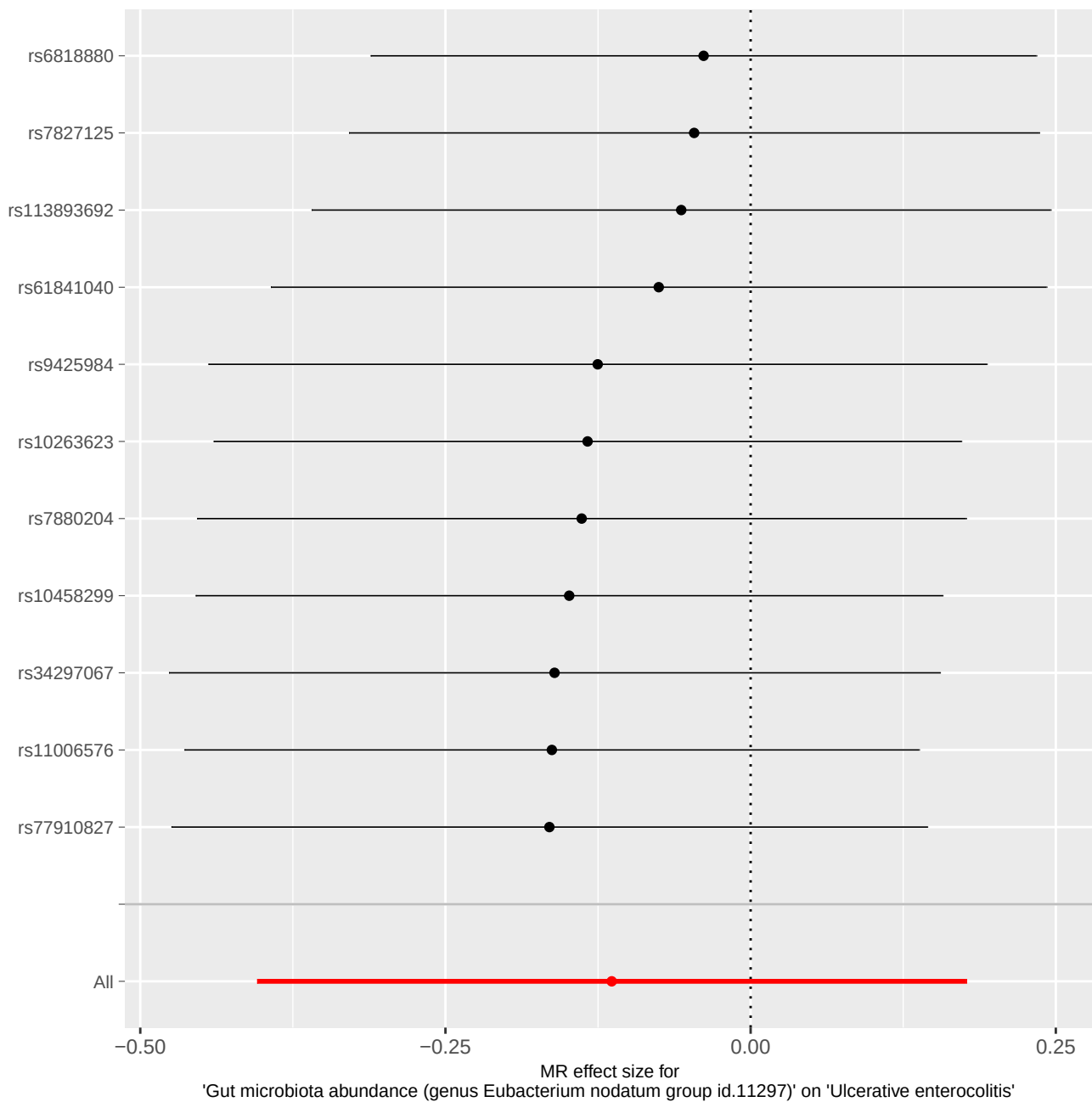


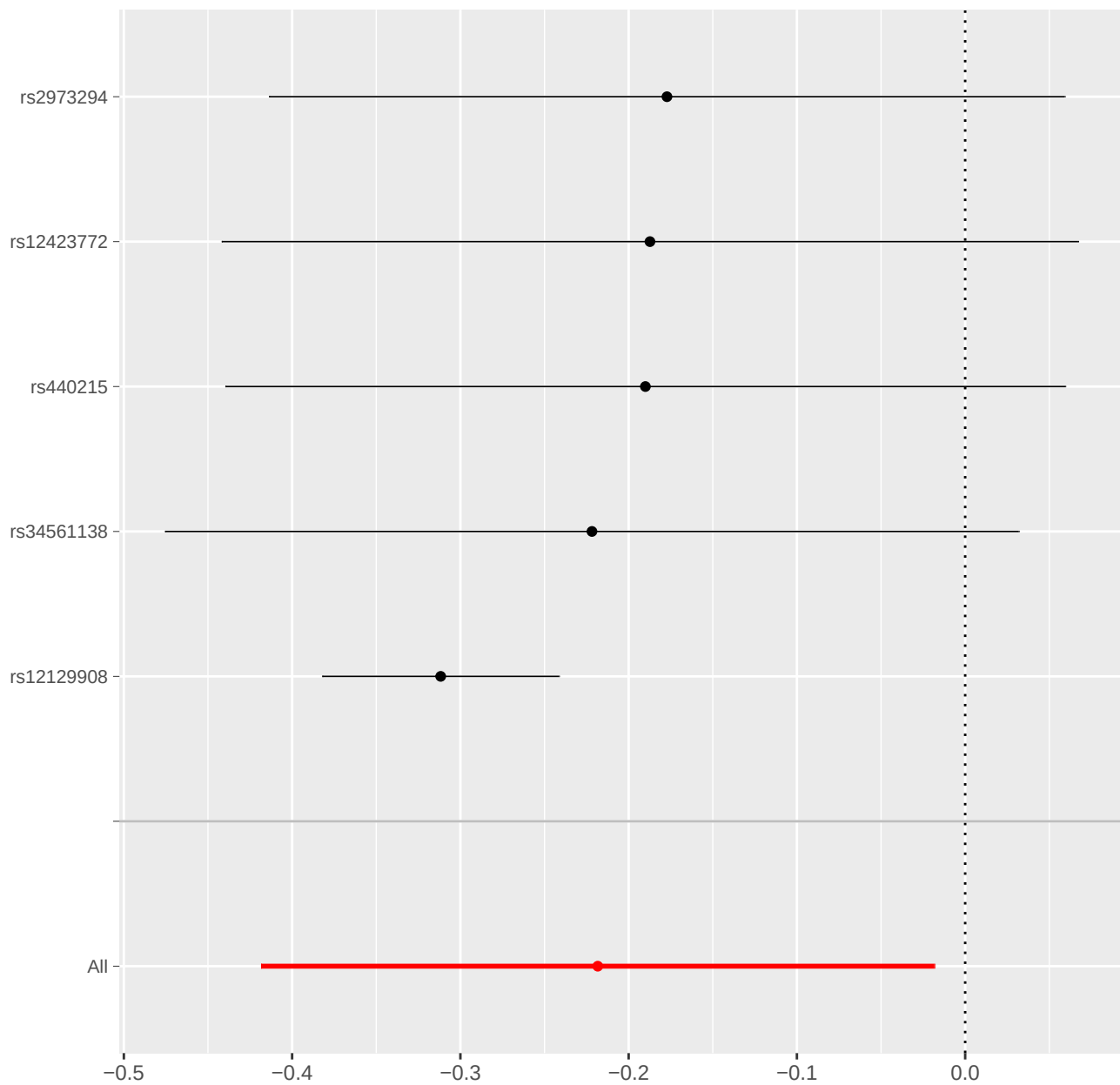




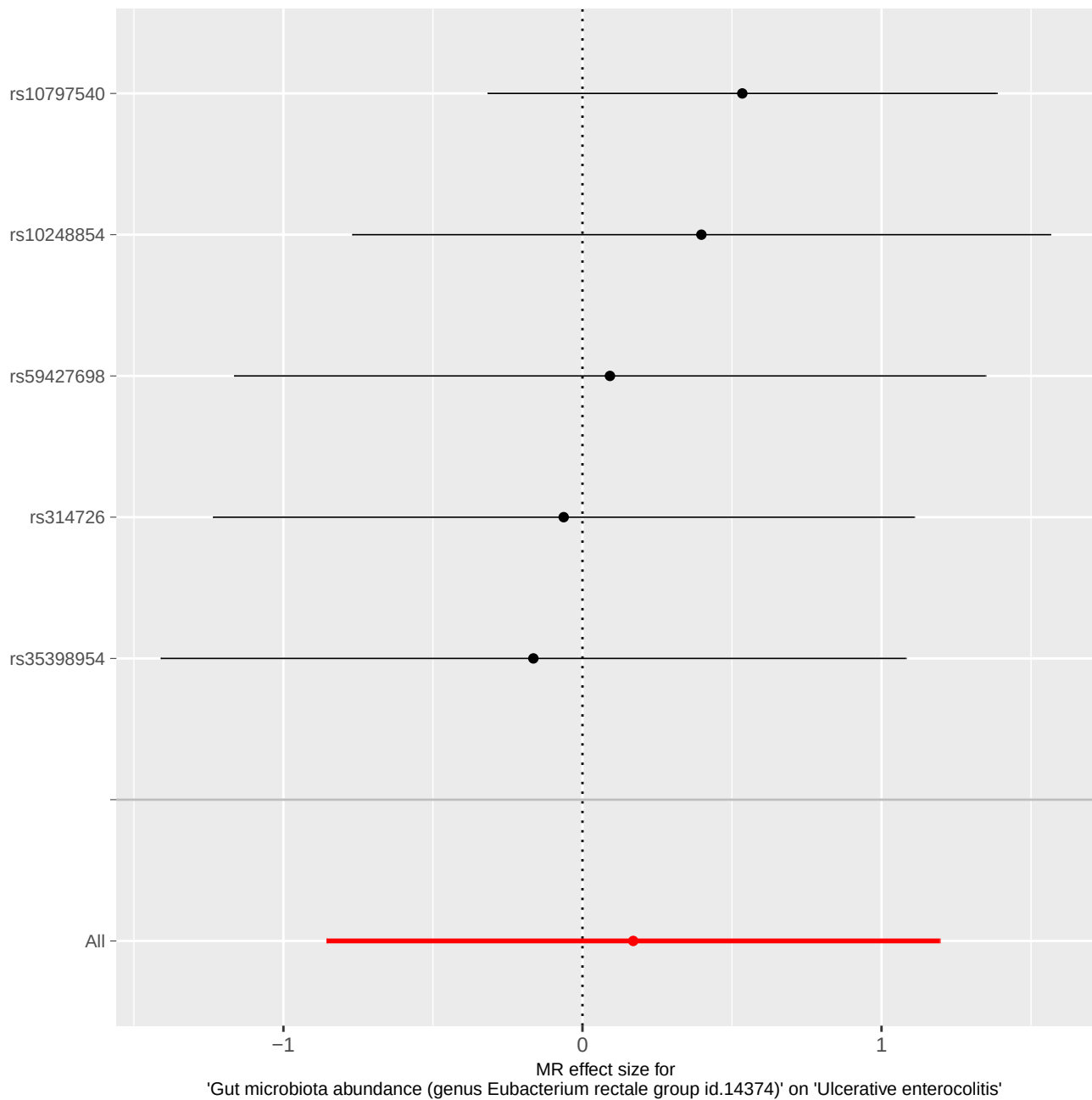


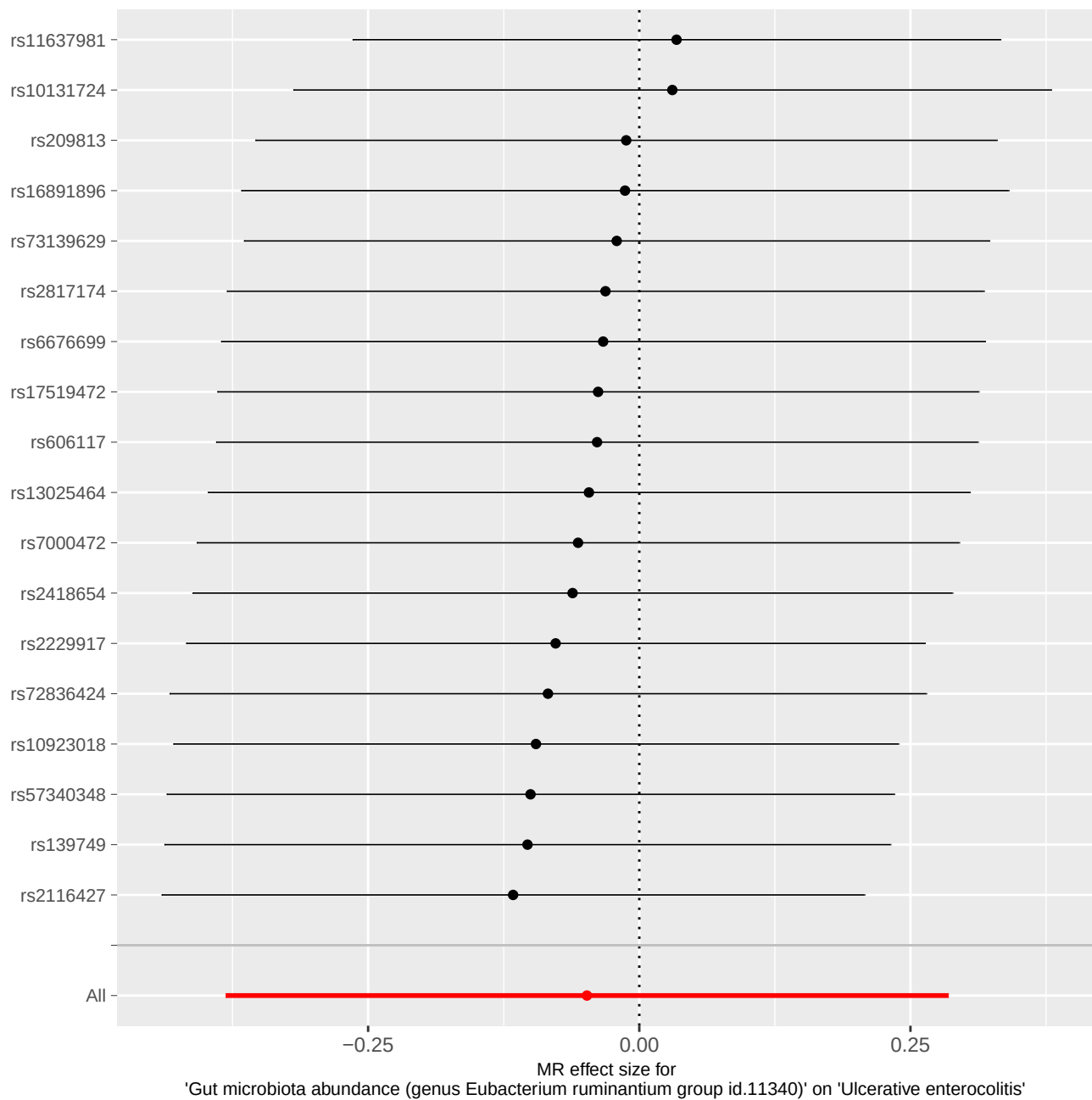


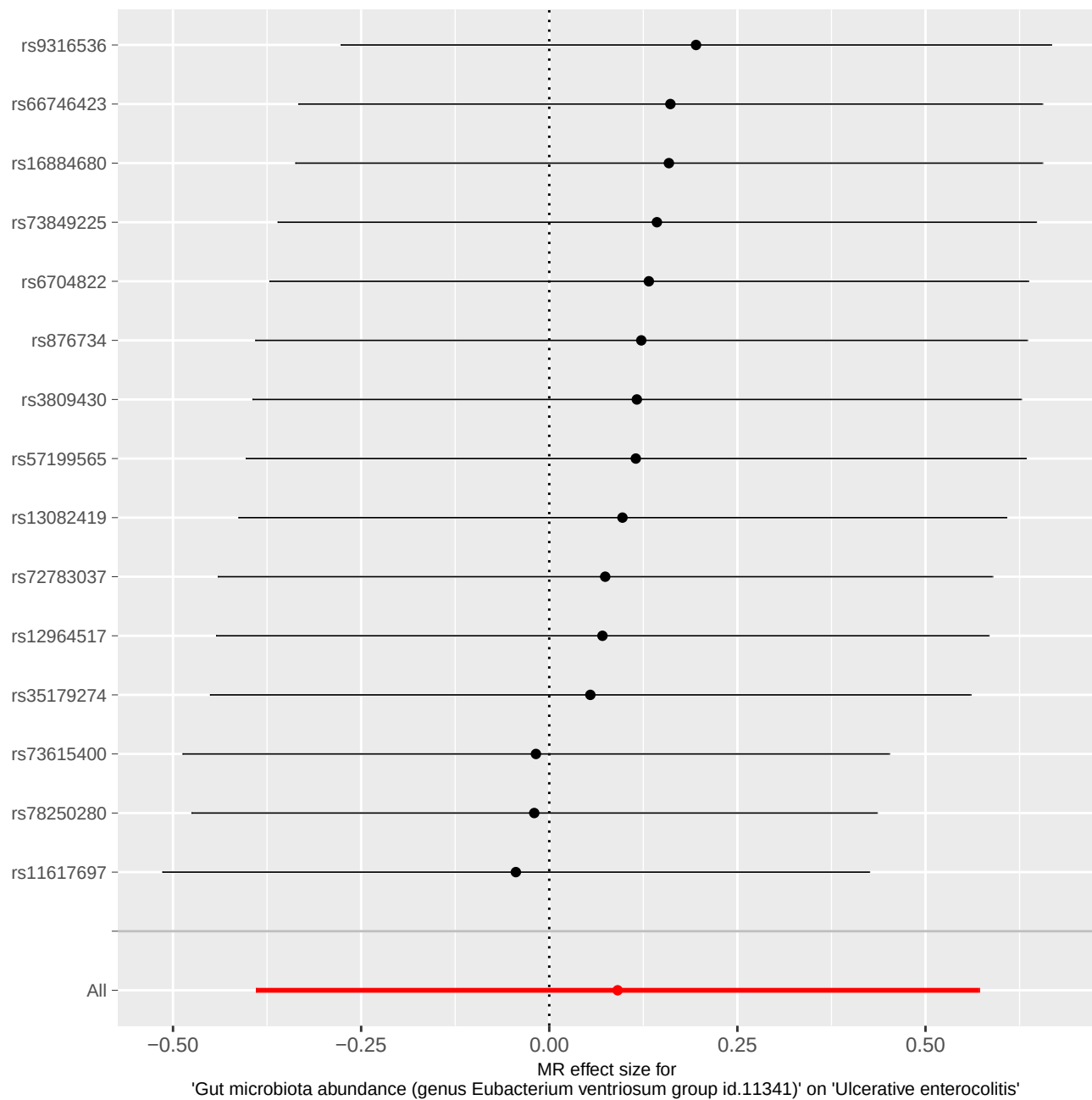


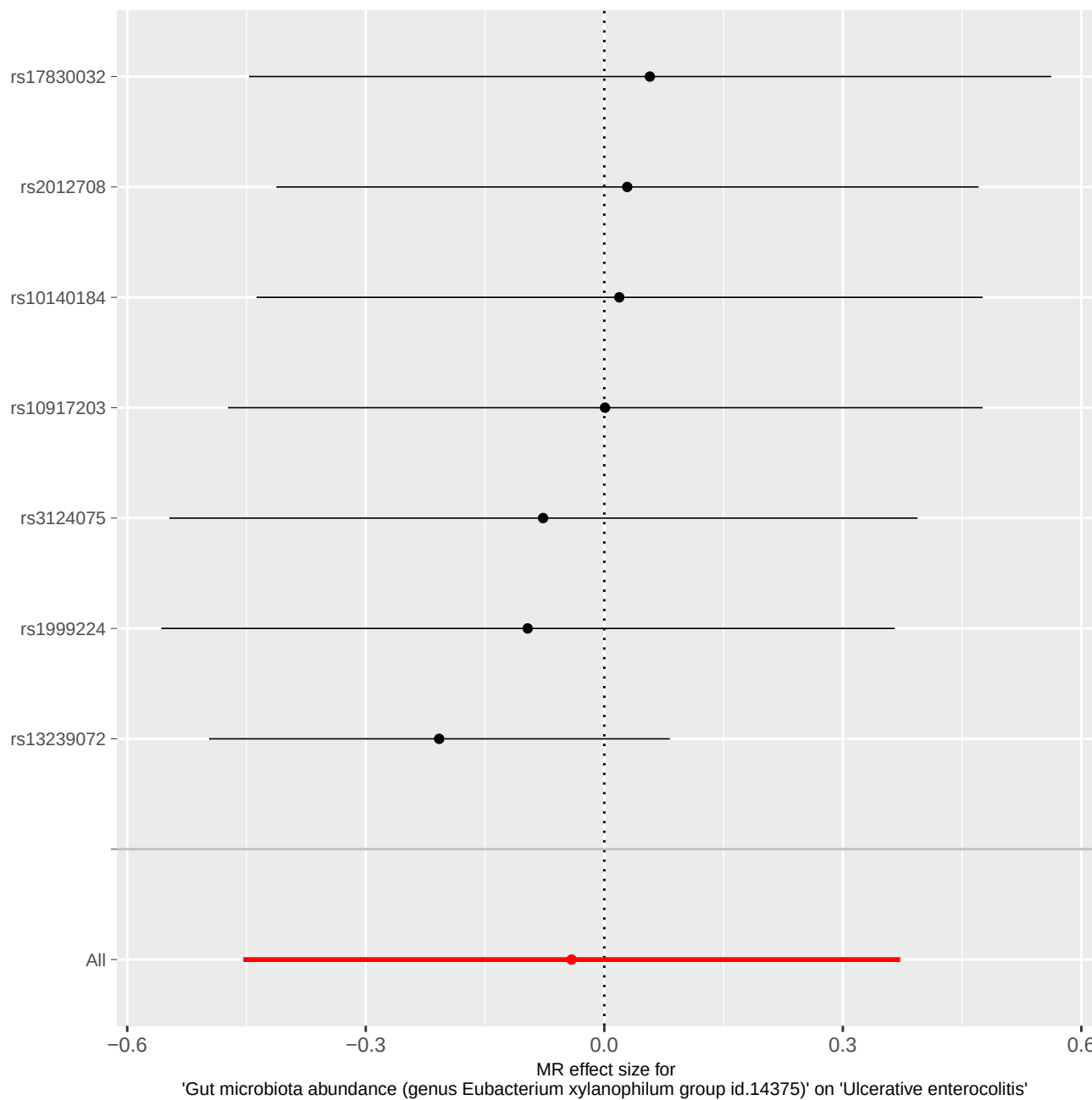


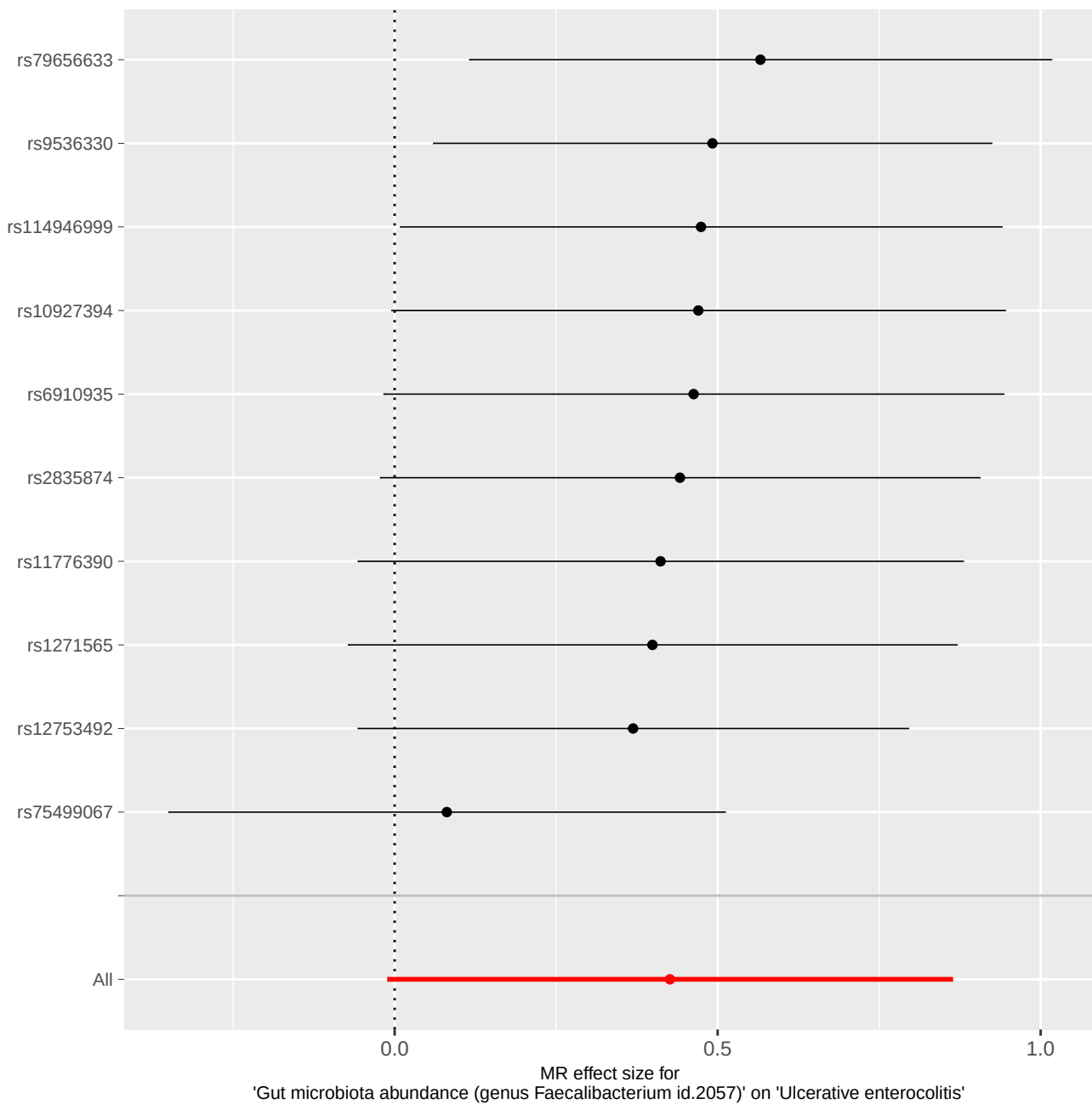
MR effect size for
'Gut microbiota abundance (genus Eubacterium oxidoreducens group id.11339)' on 'Ulcerative enterocolitis'

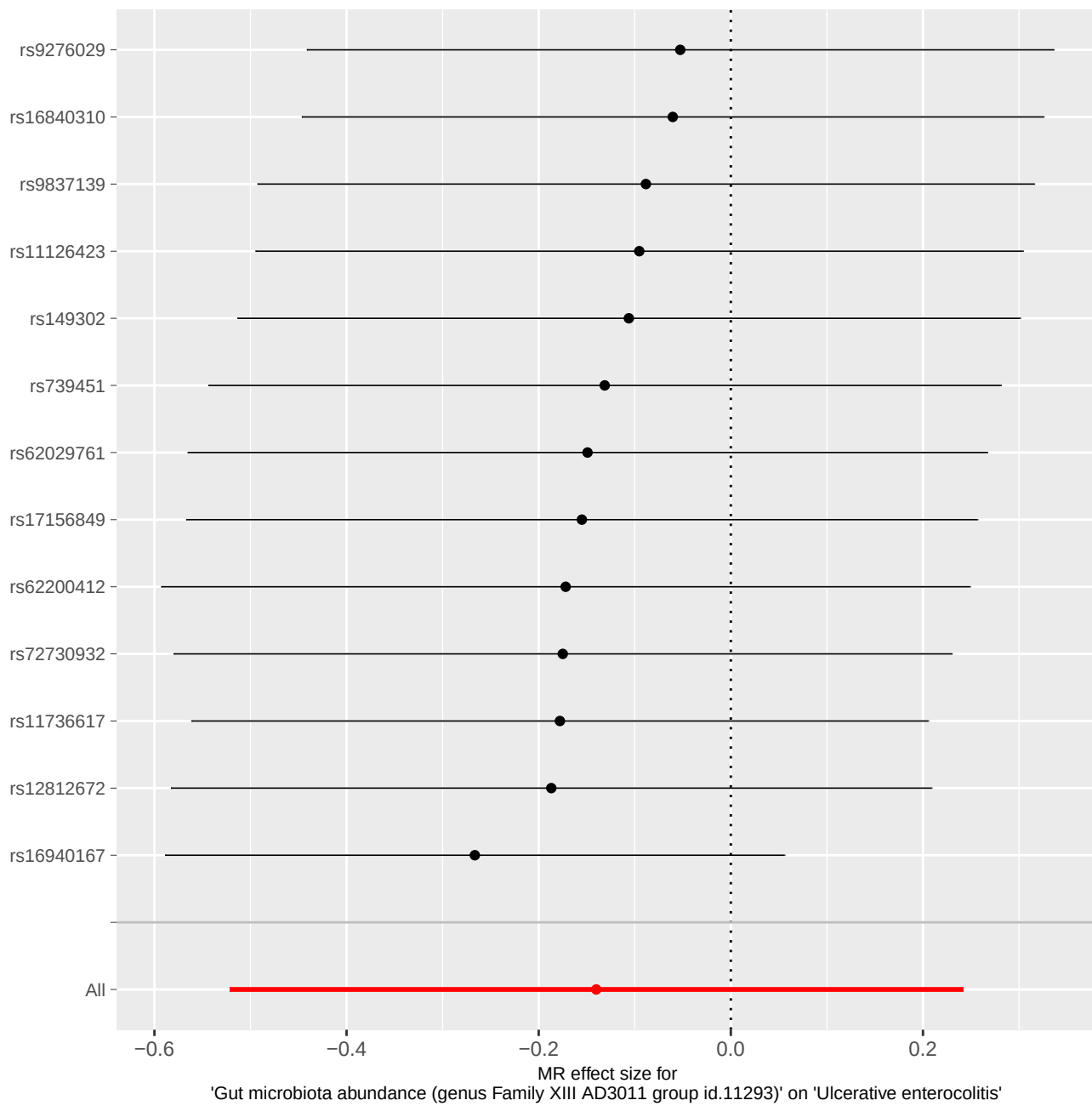


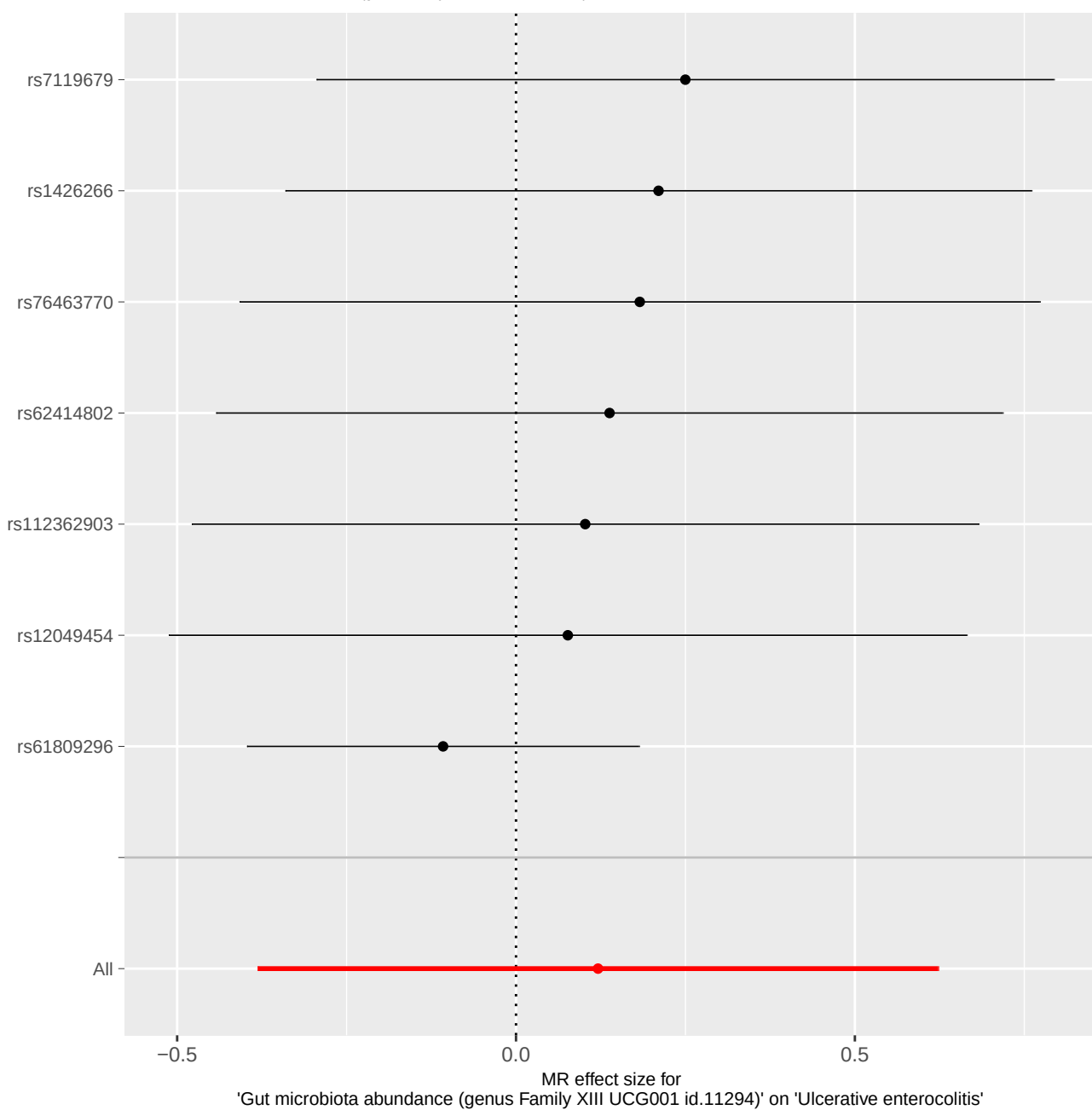


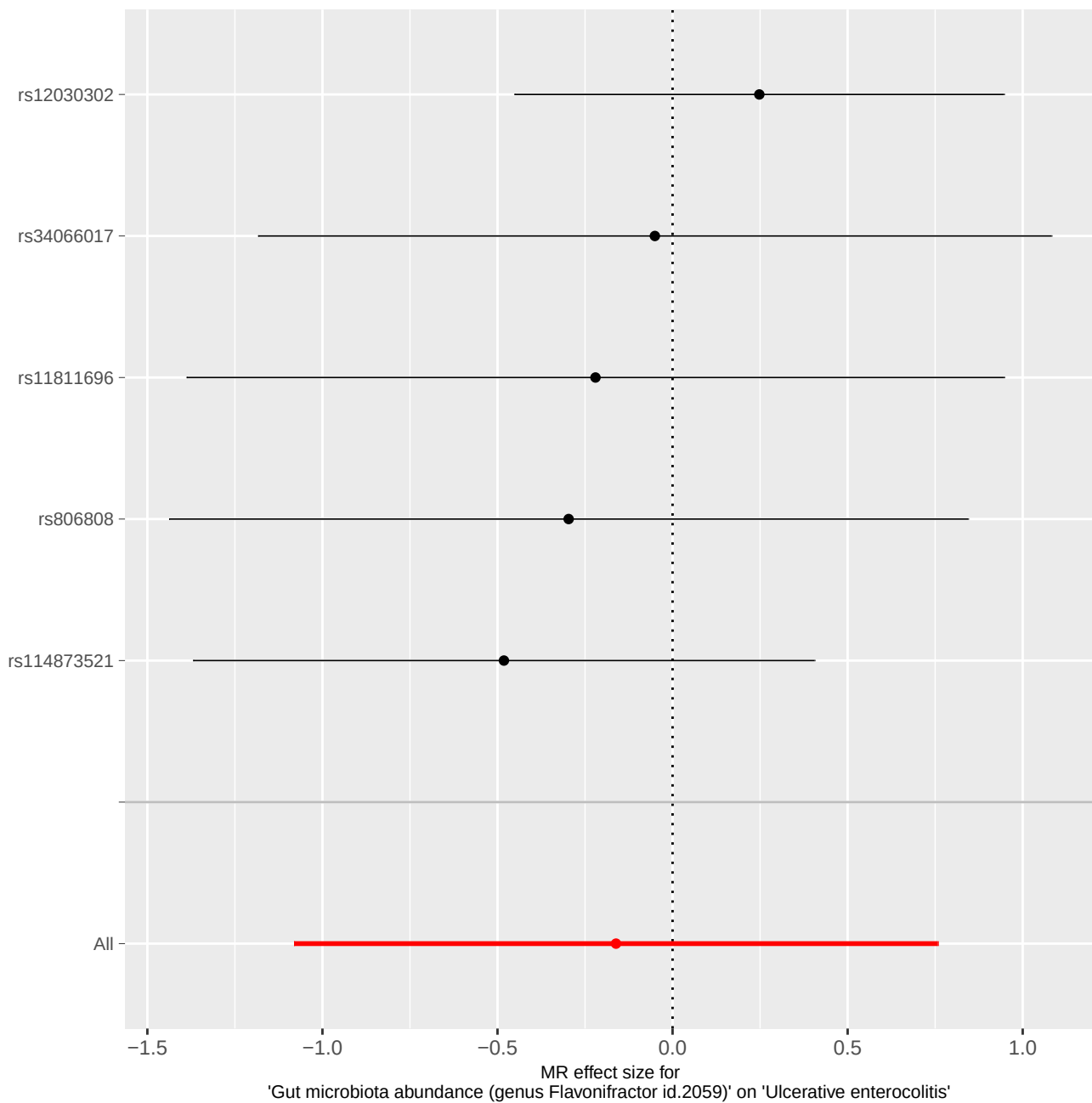


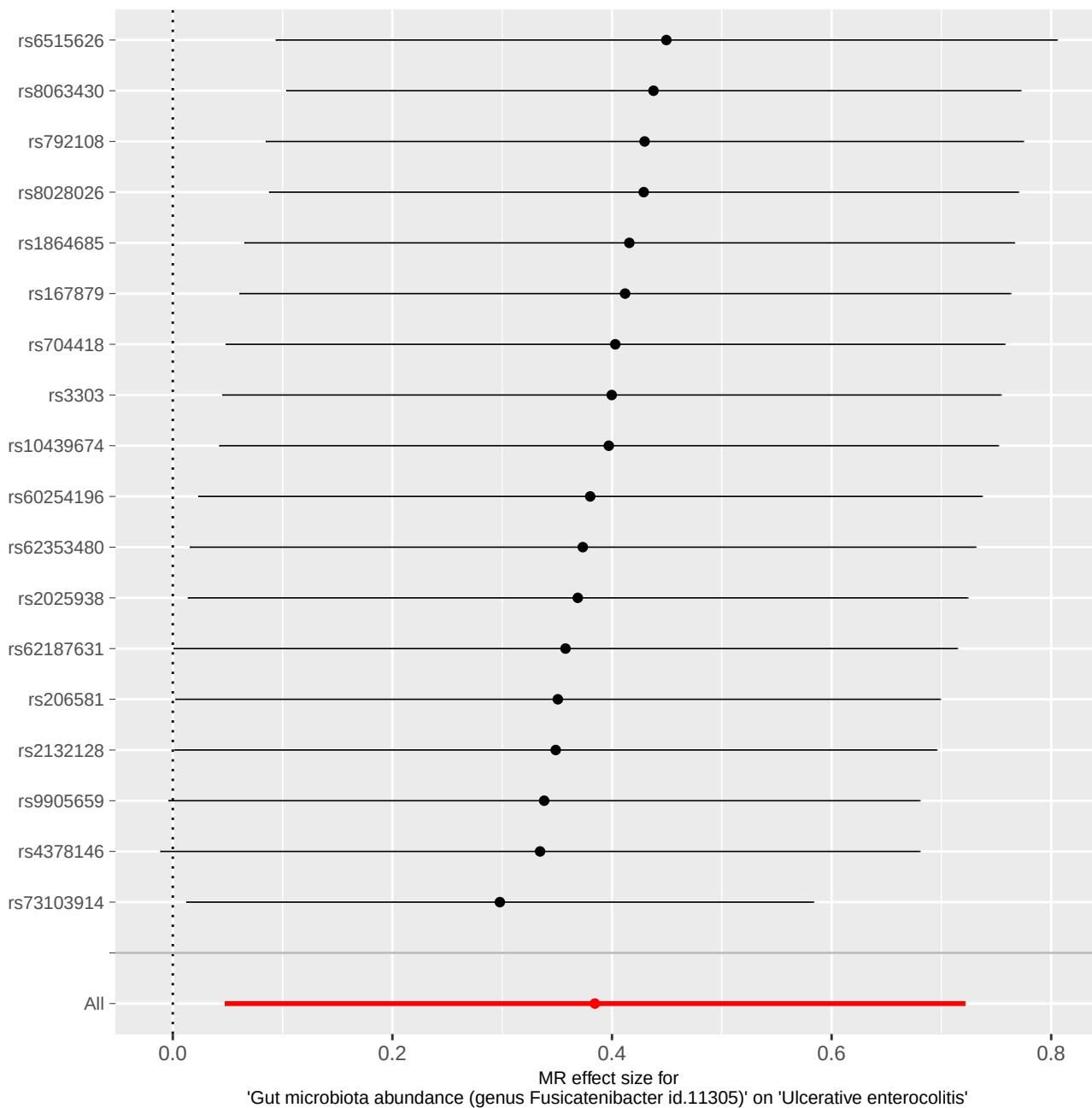


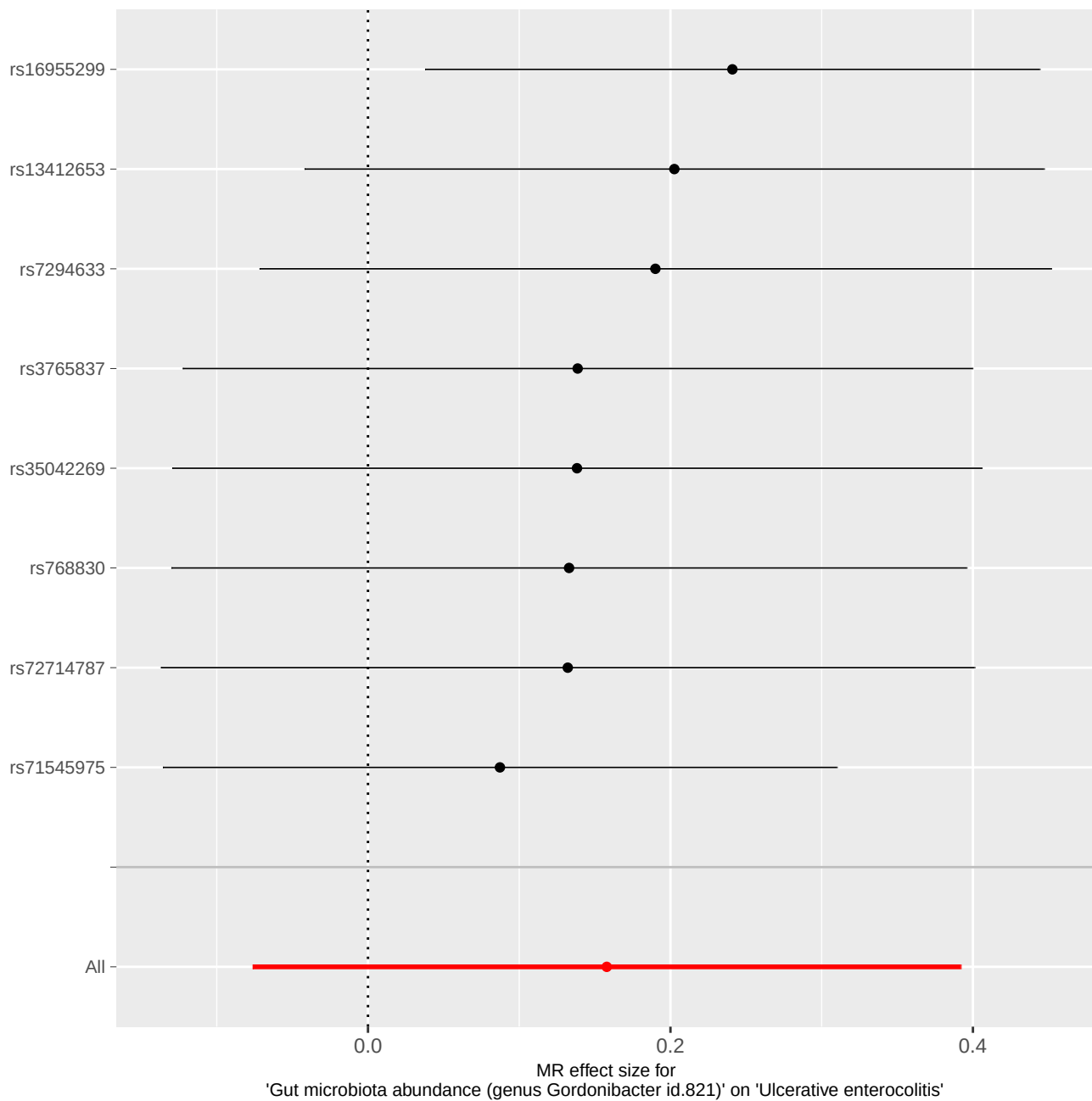


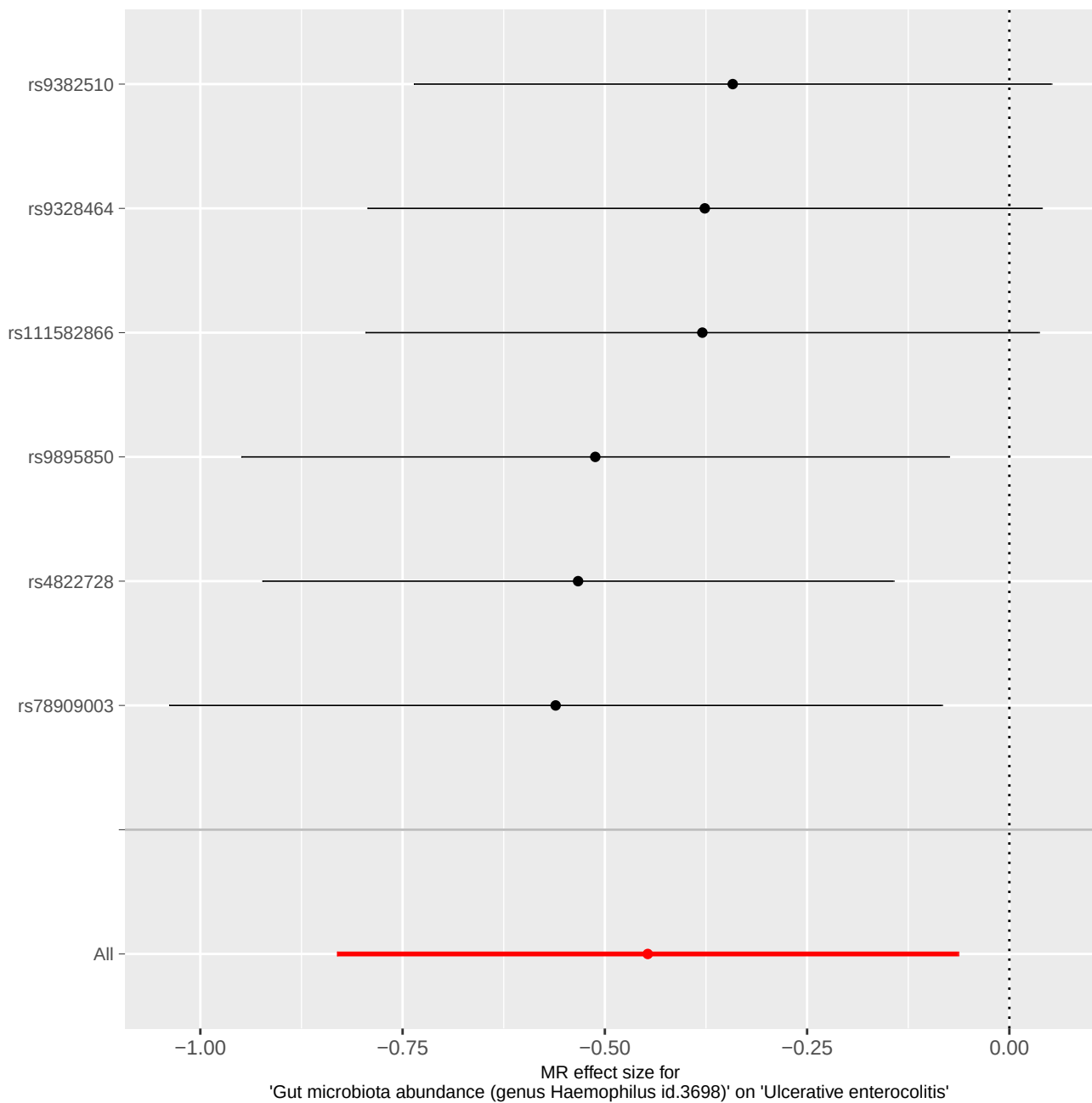


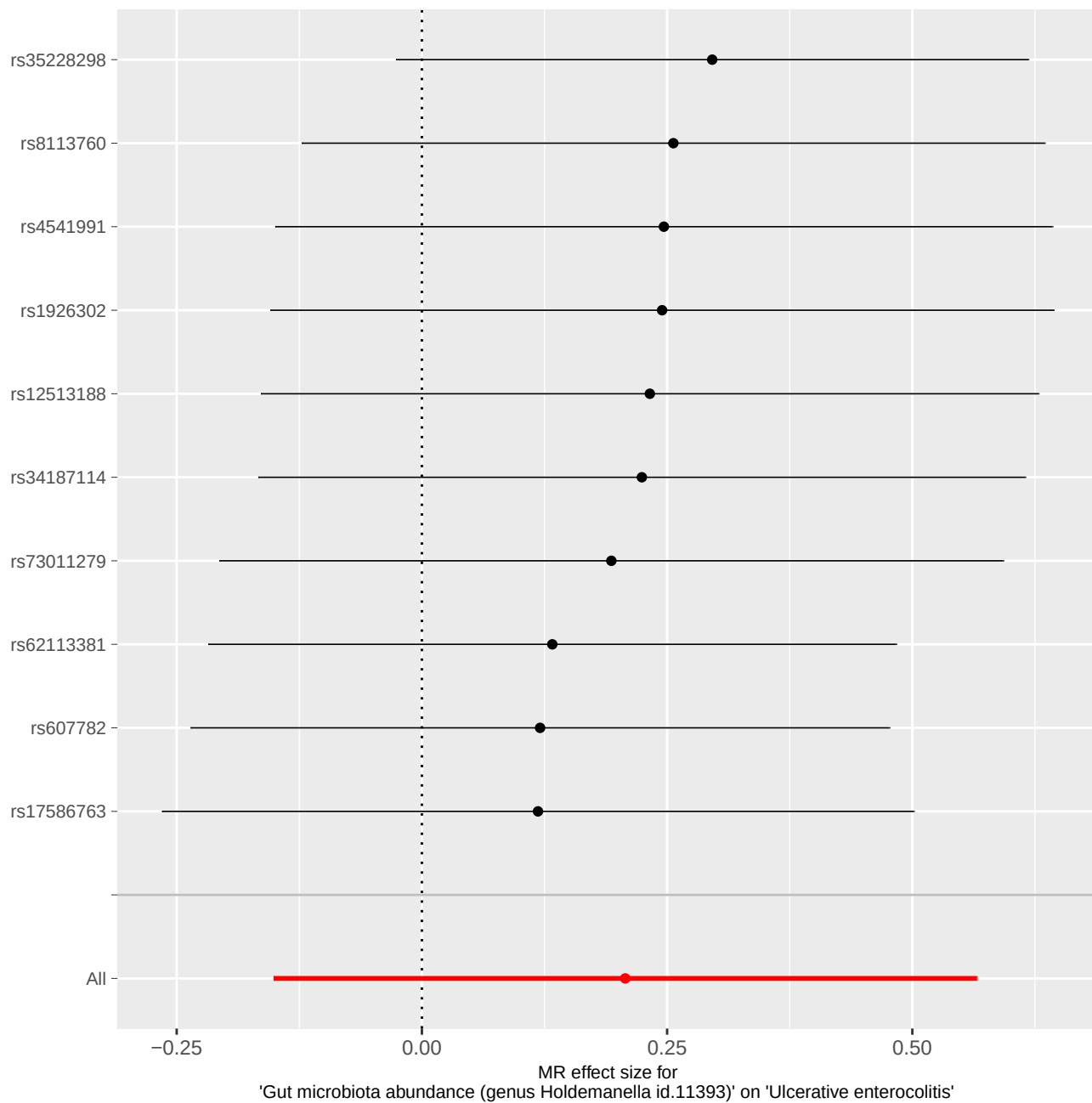


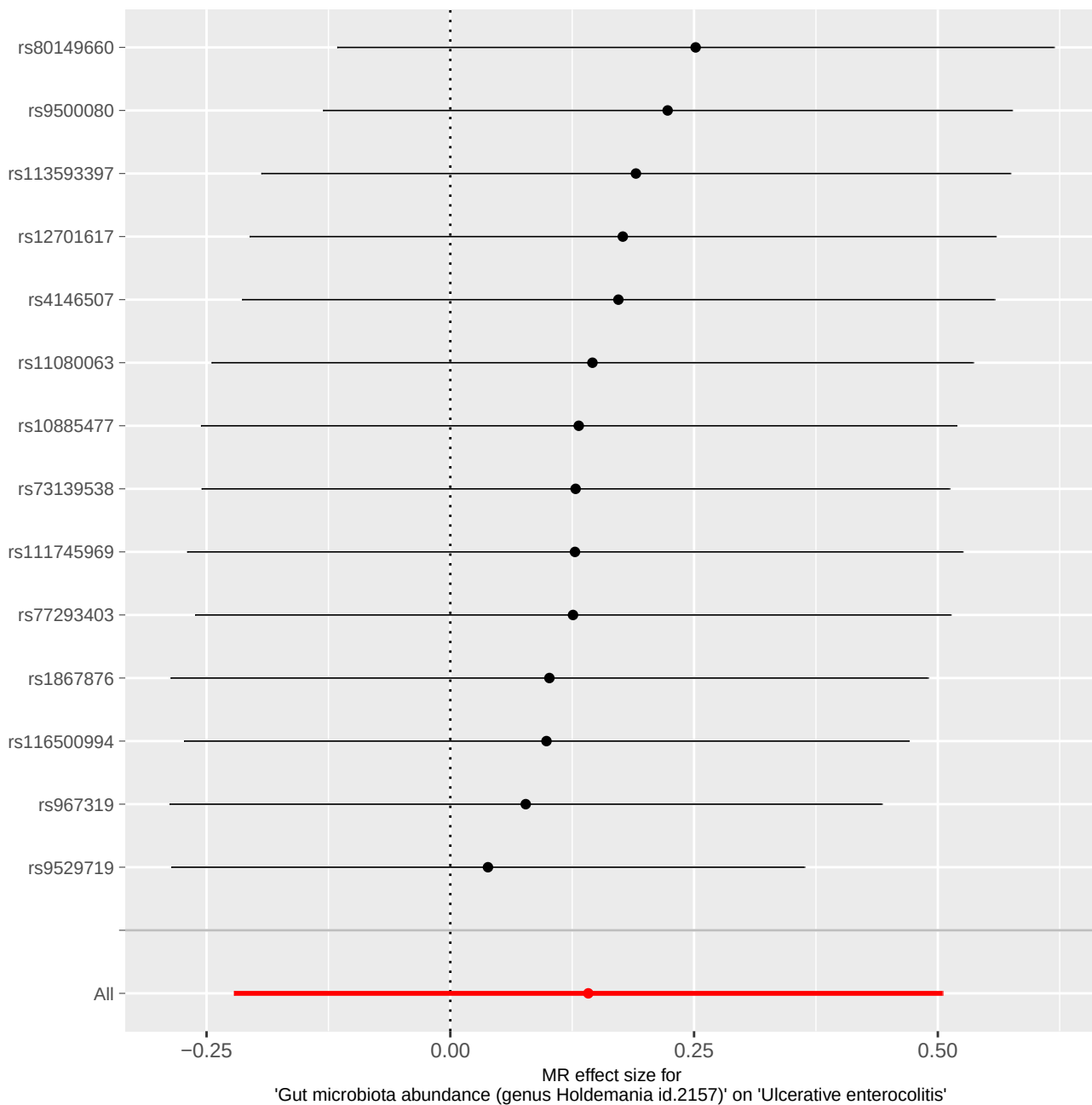


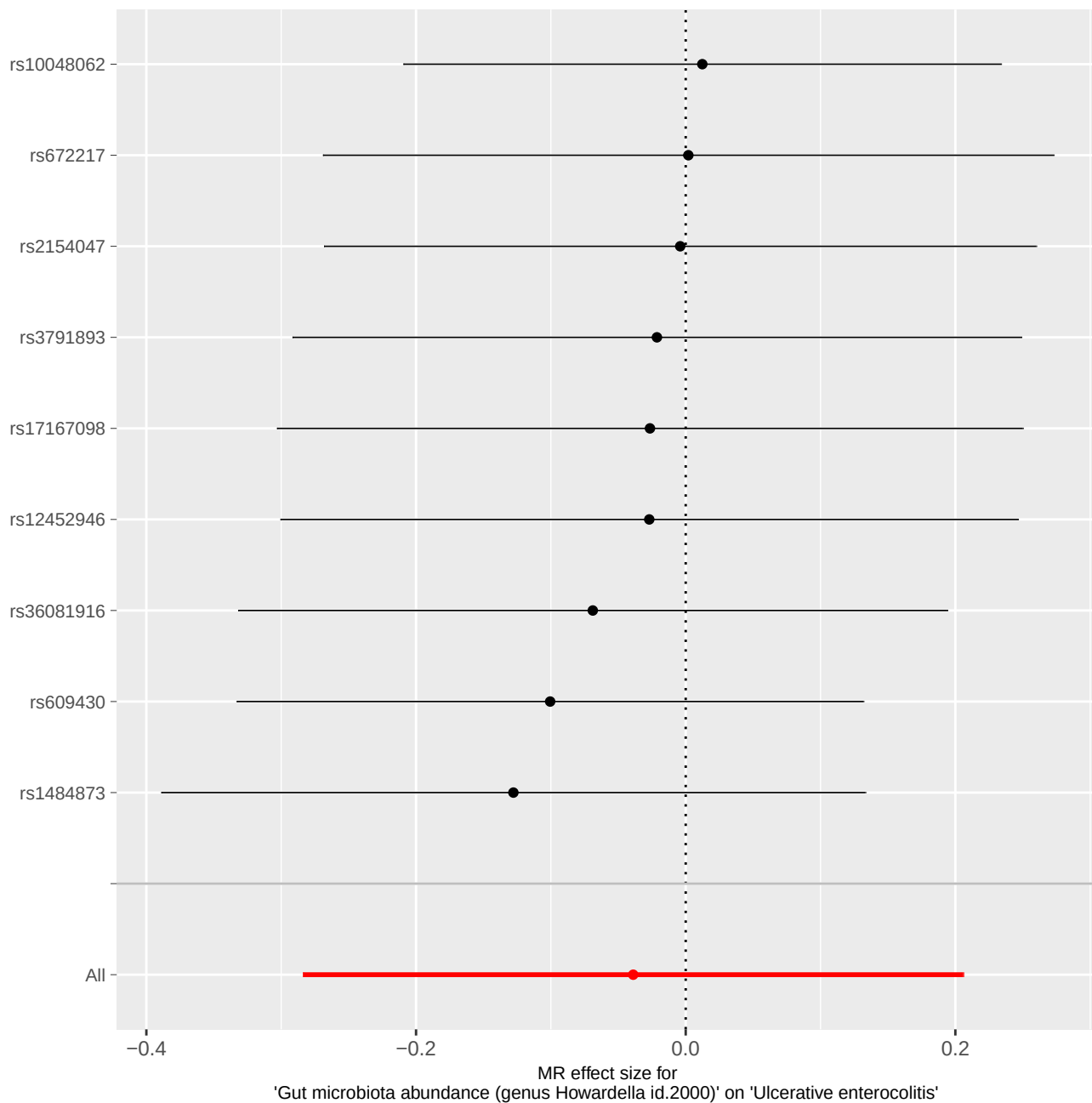


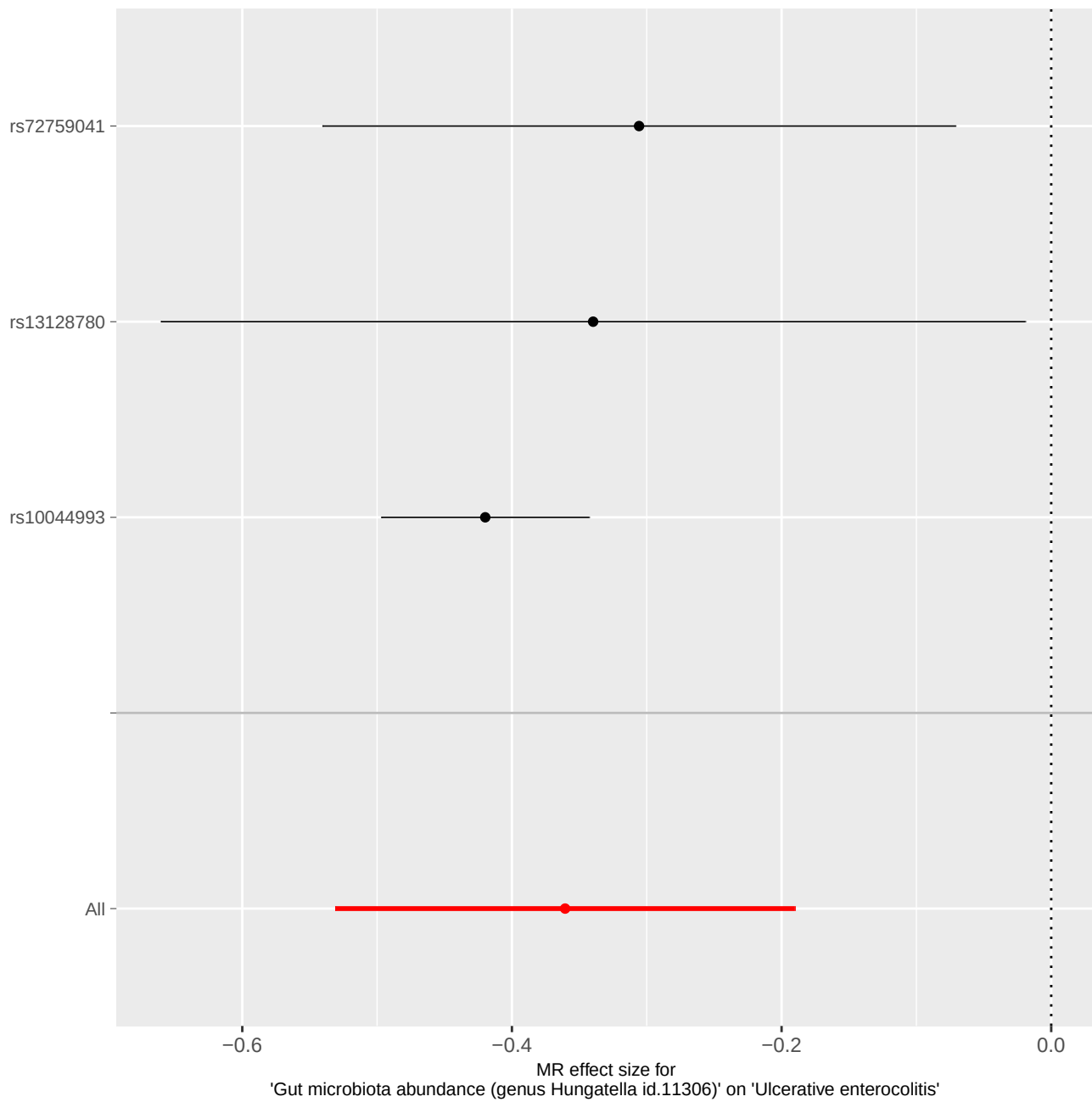


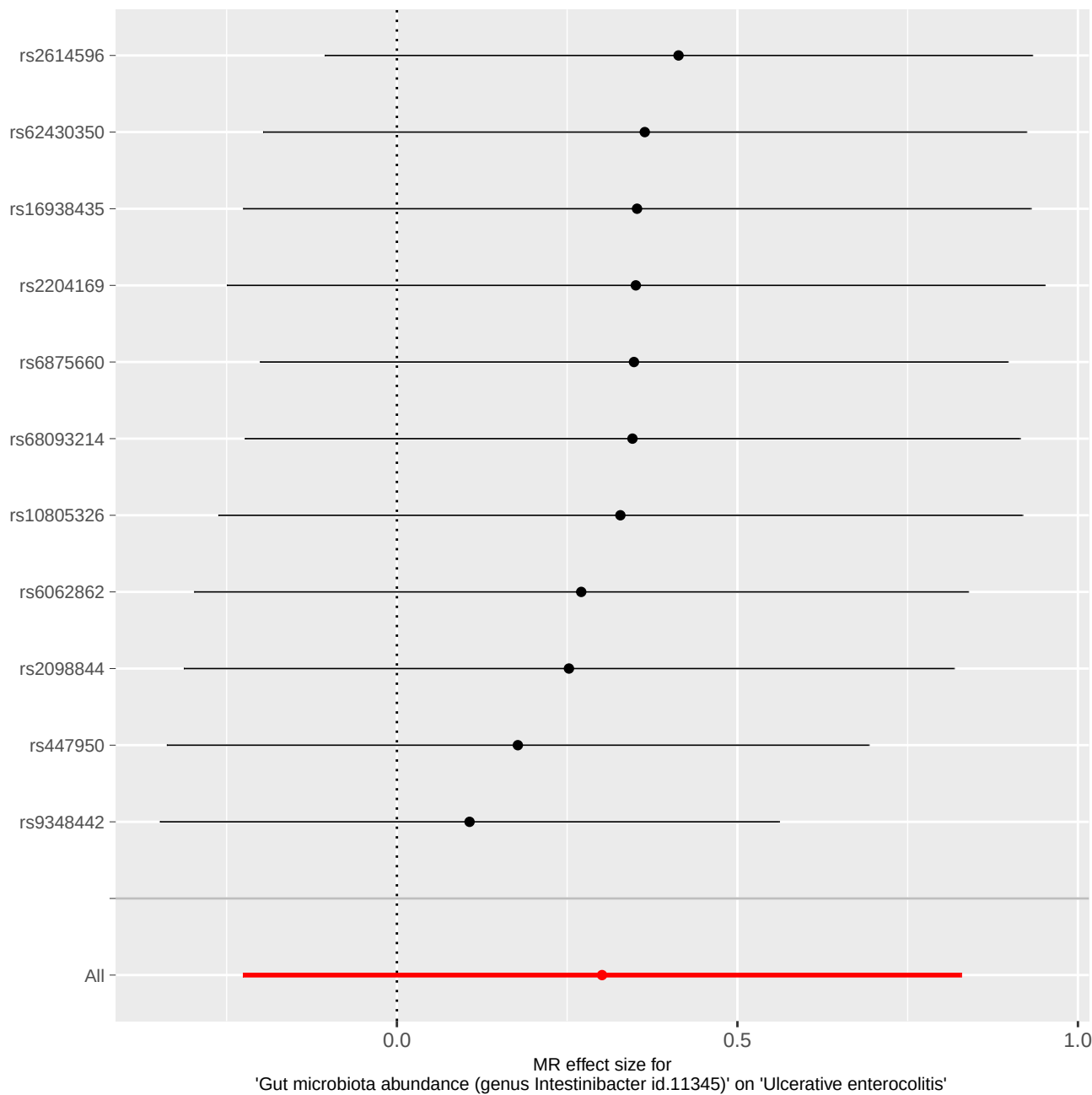


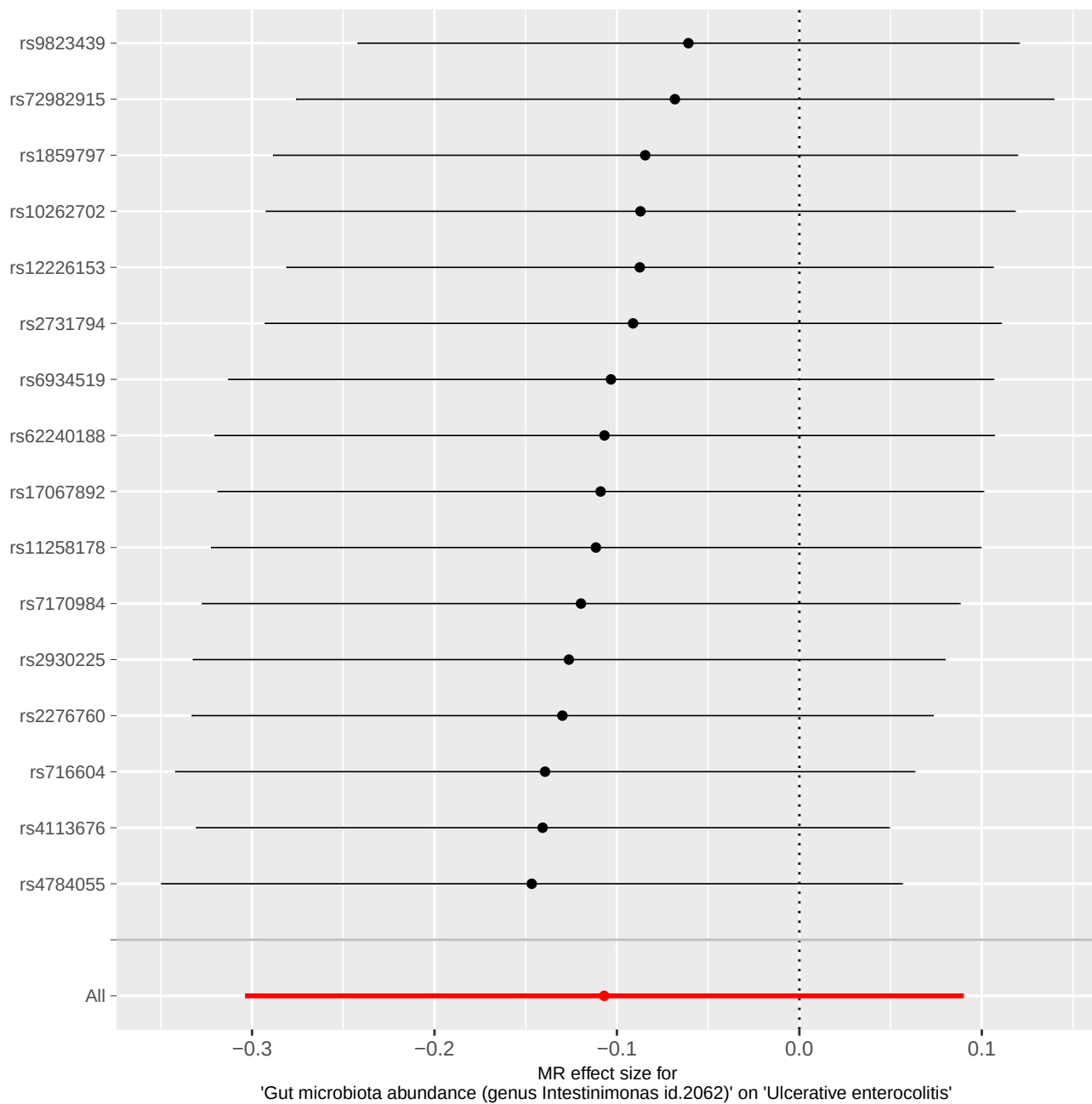


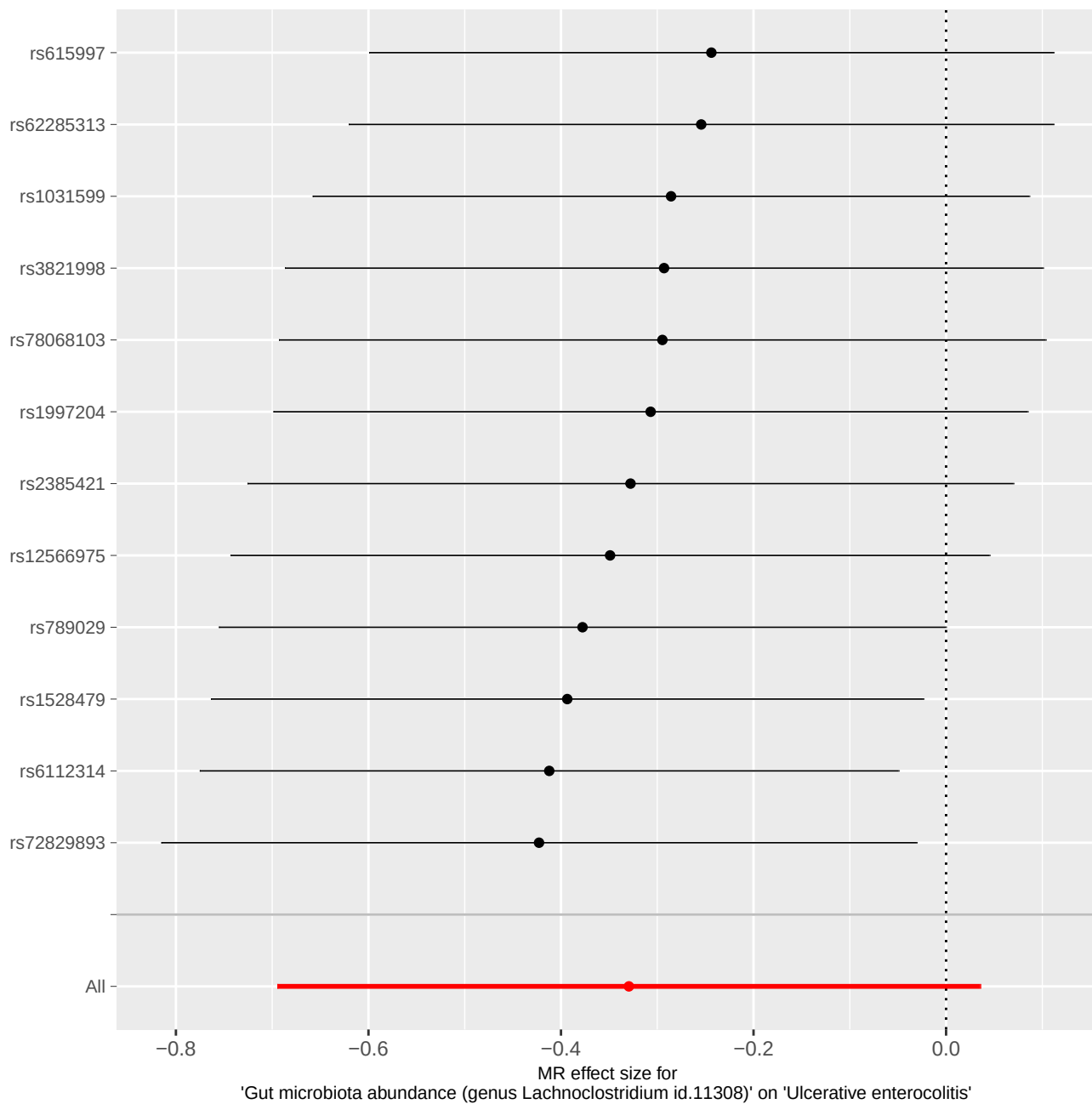


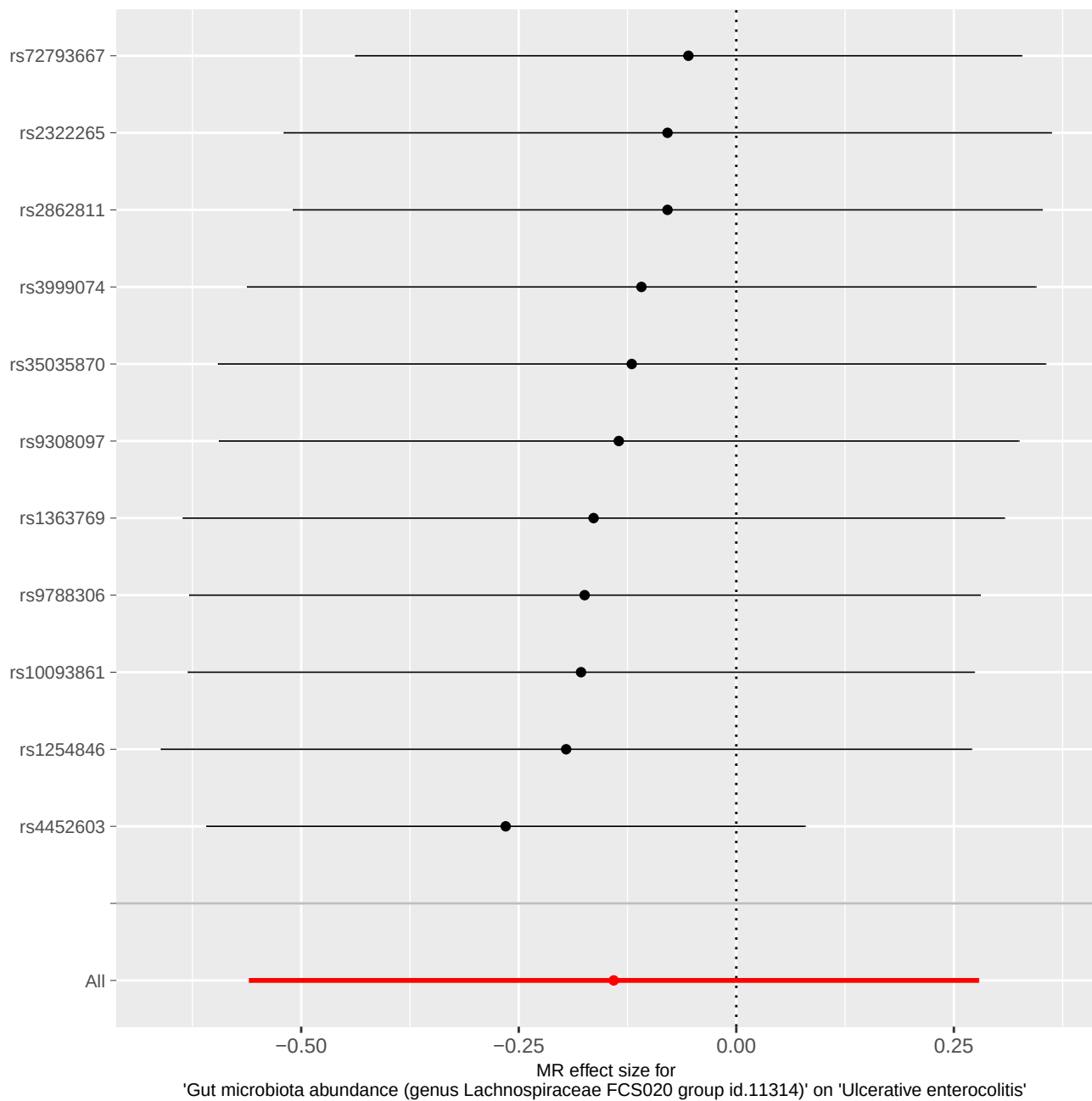


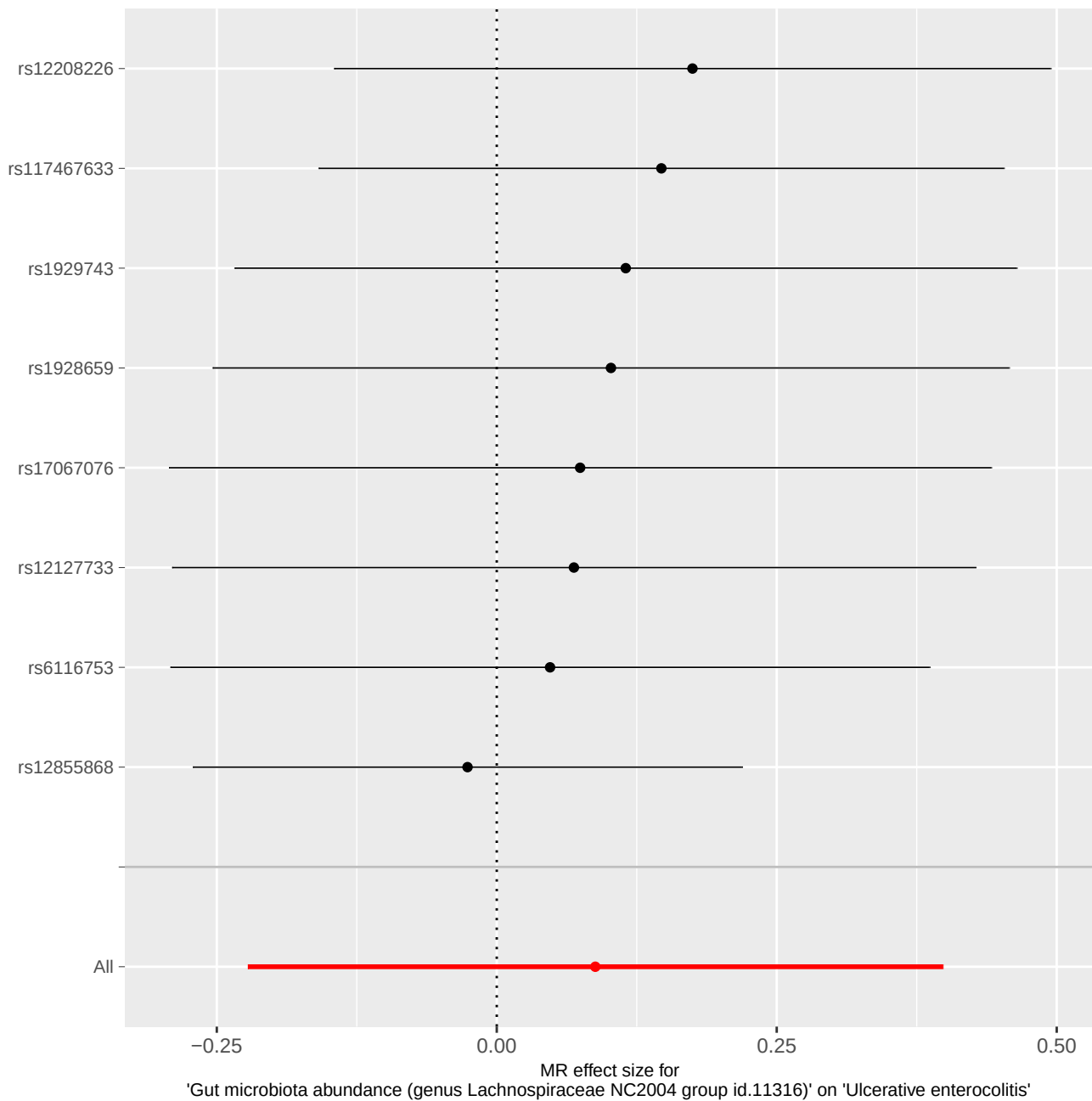


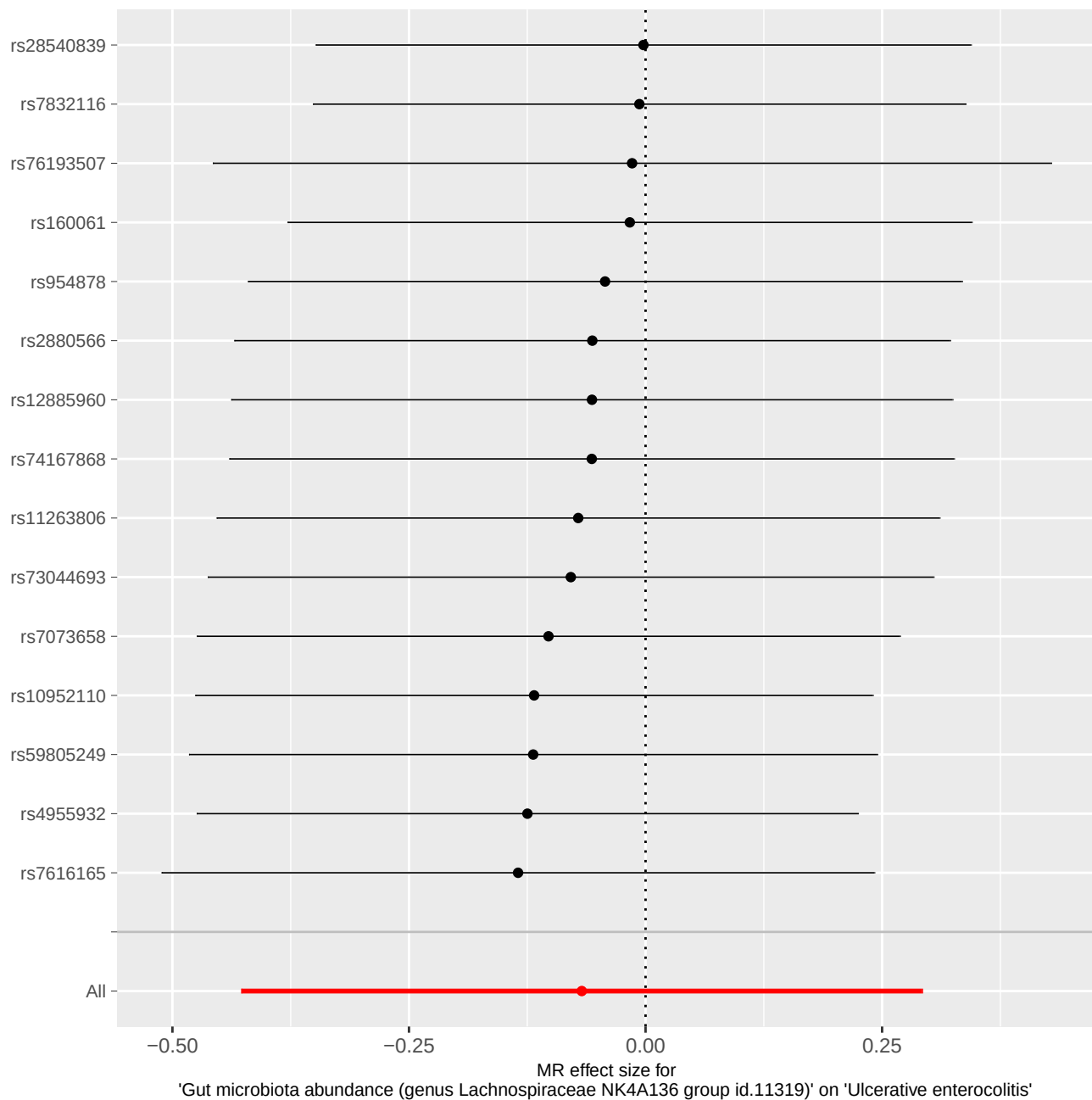




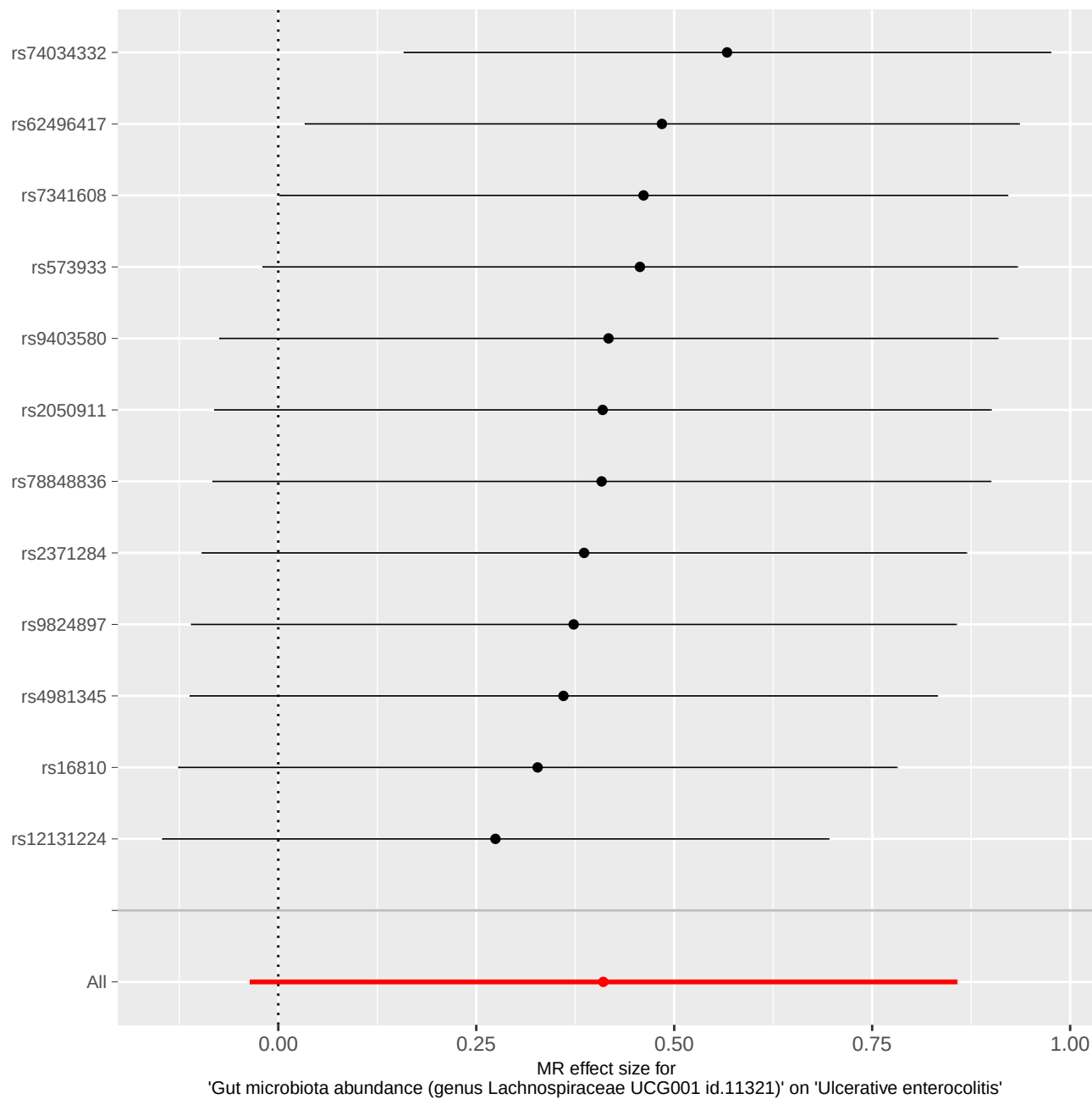


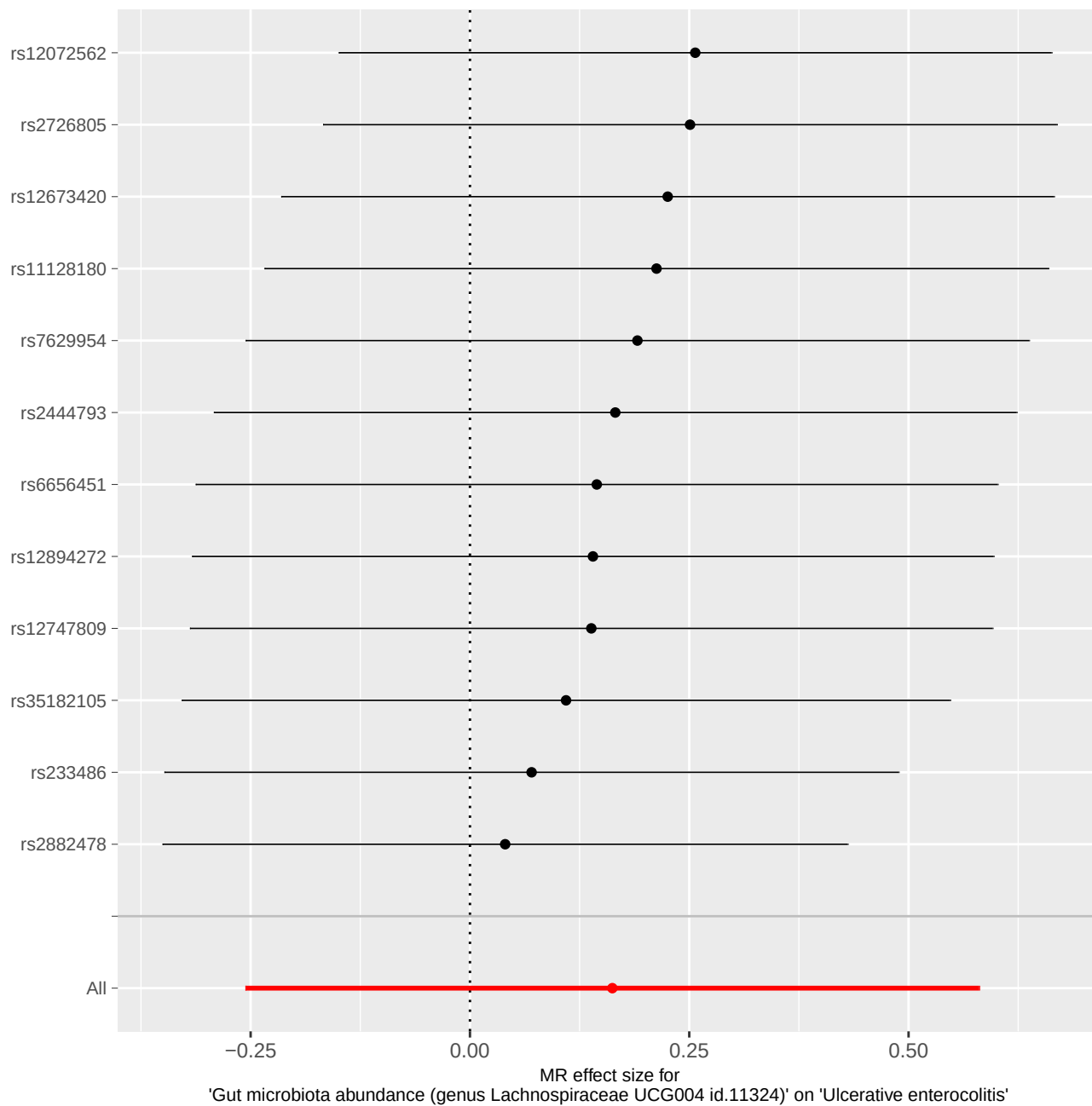


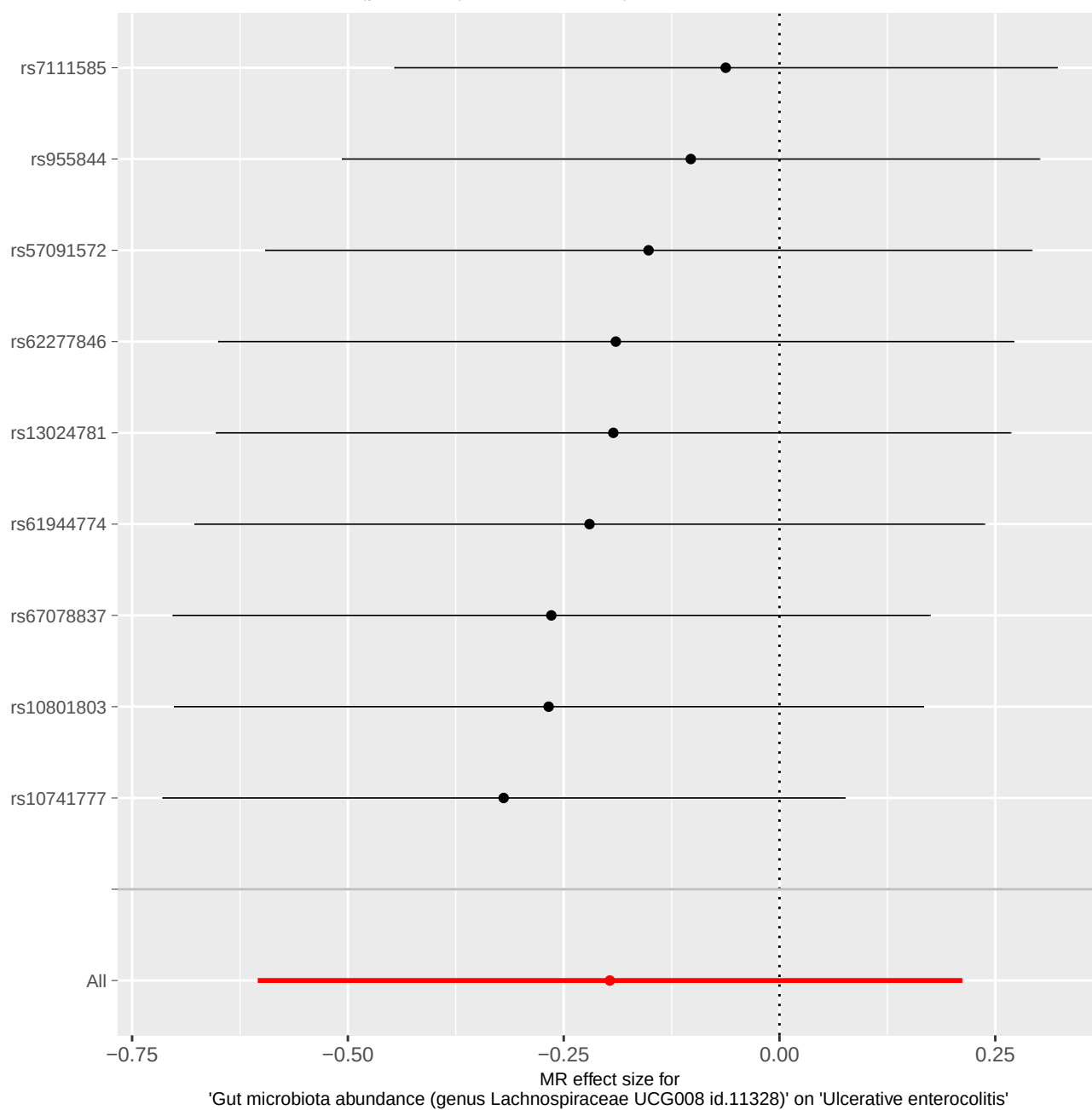


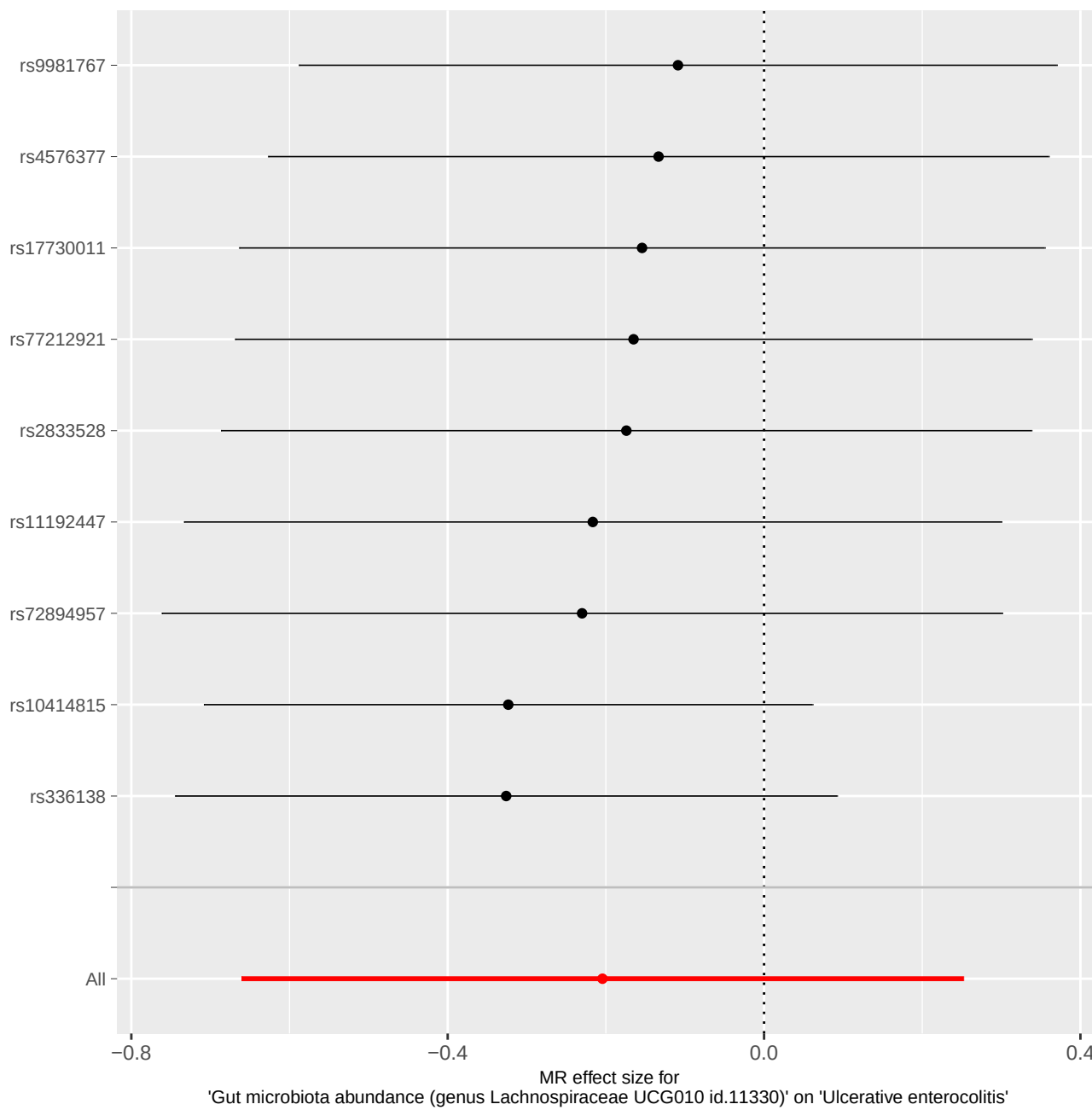


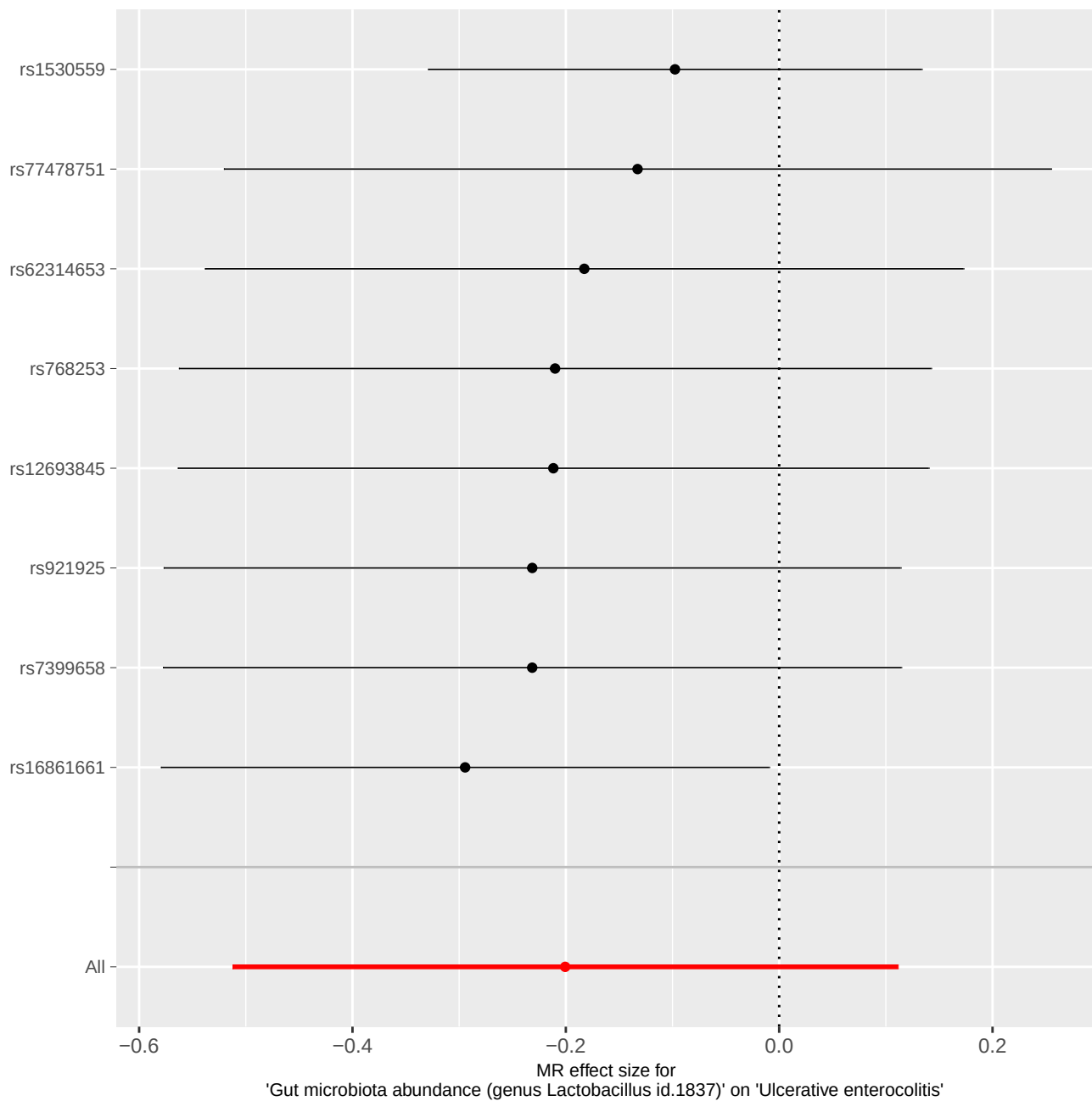
MR effect size for
'Gut microbiota abundance (genus Lachnospiraceae NK4A136 group id.11319)' on 'Ulcerative enterocolitis'

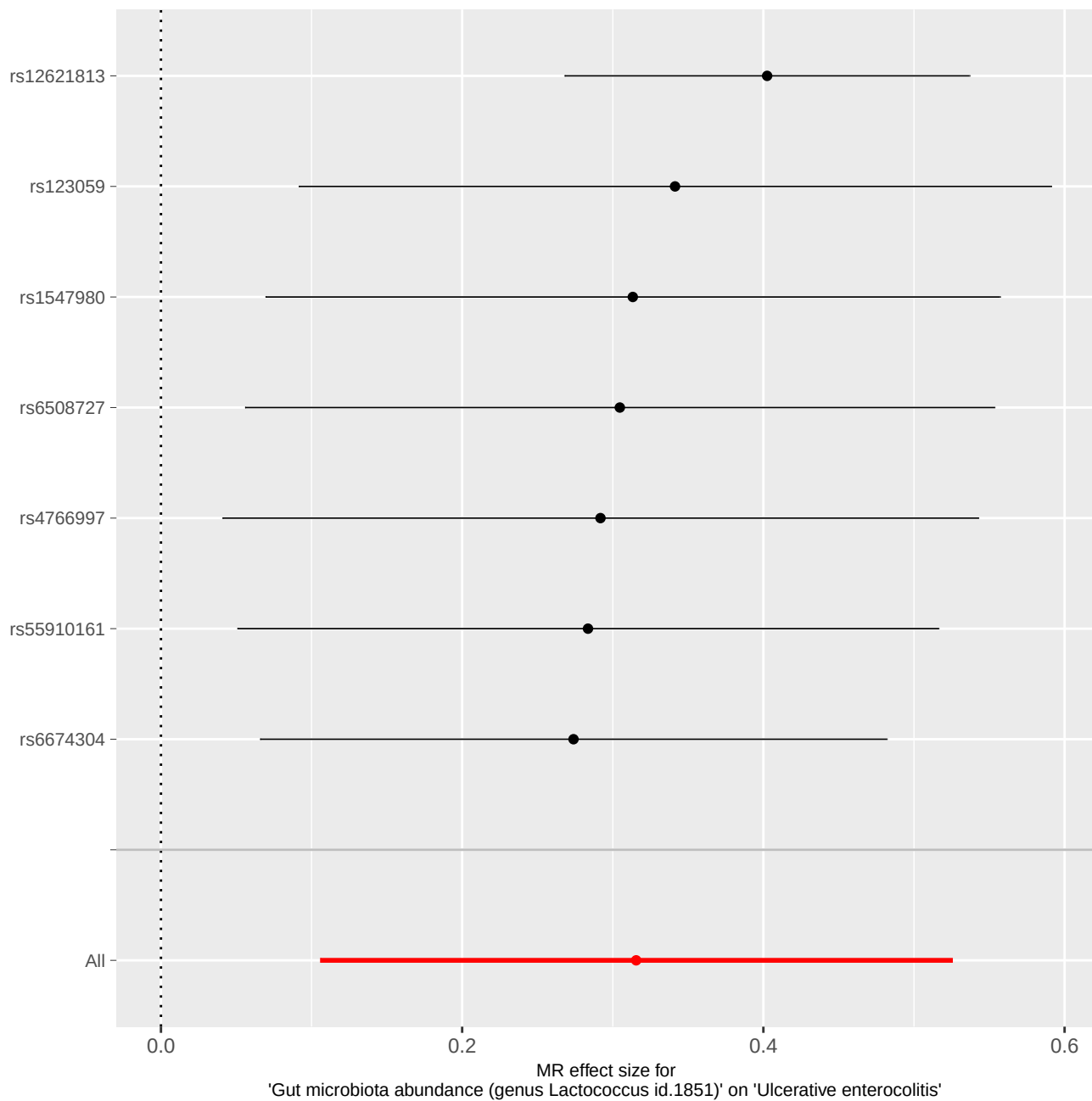


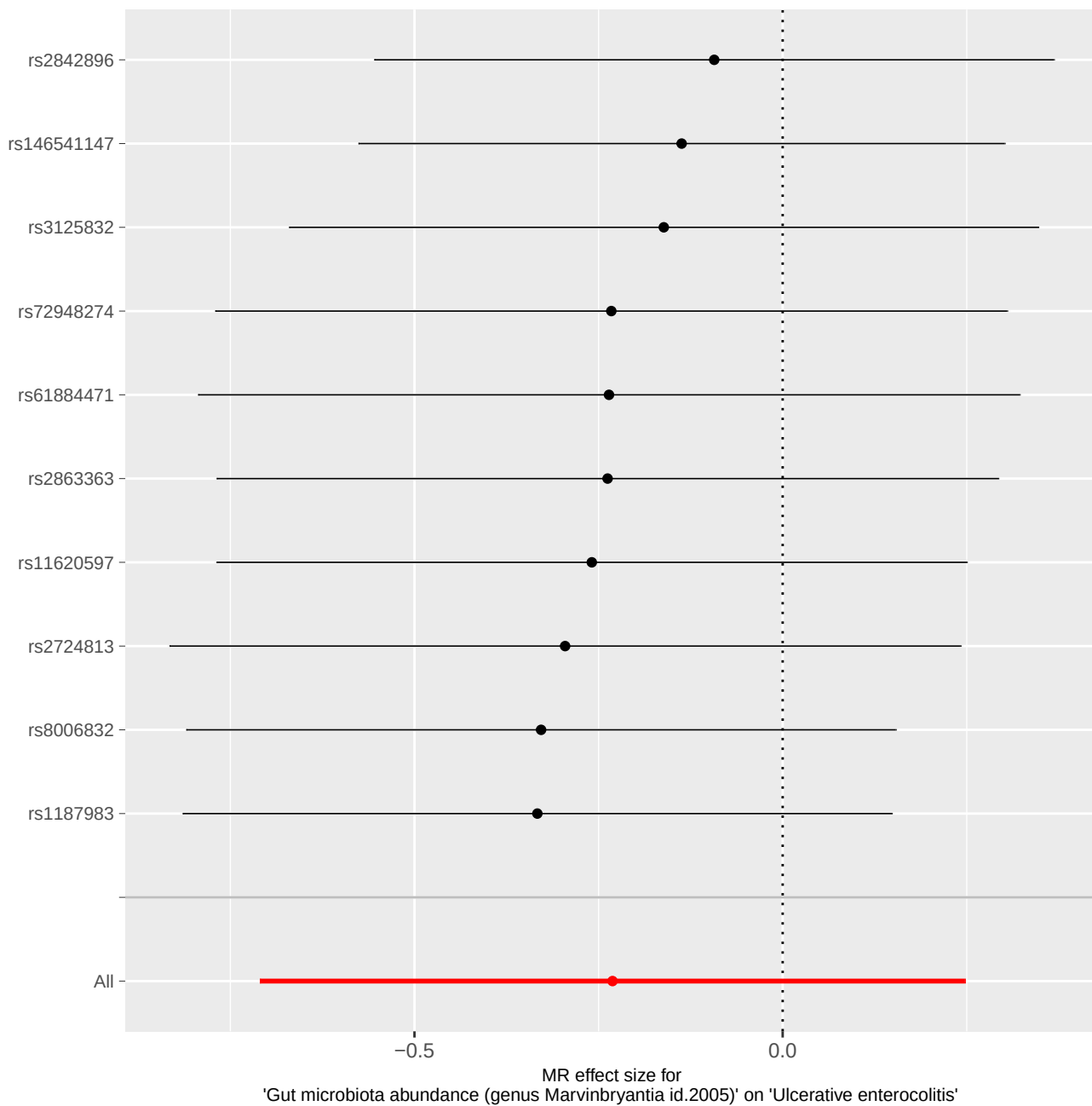


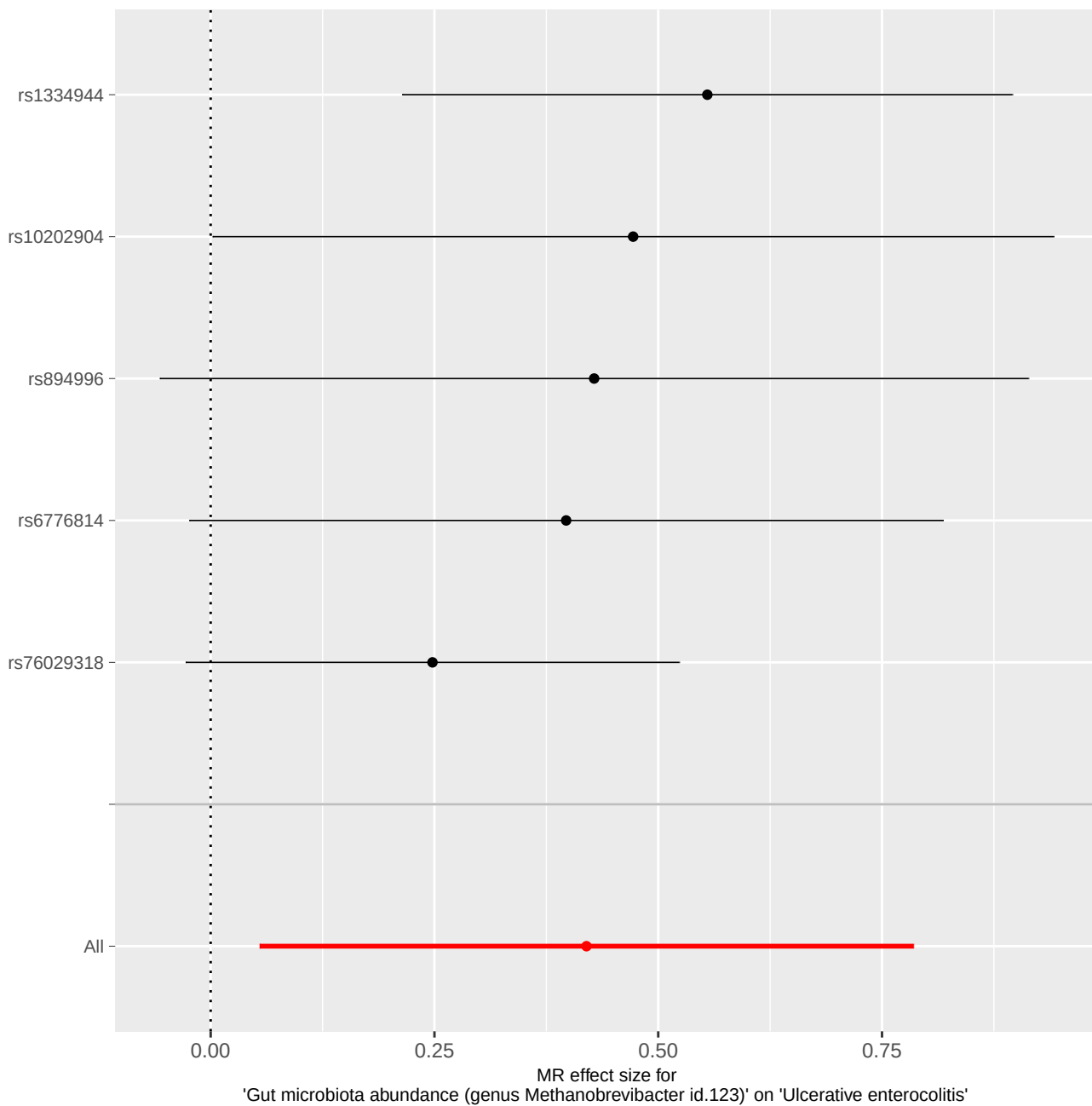


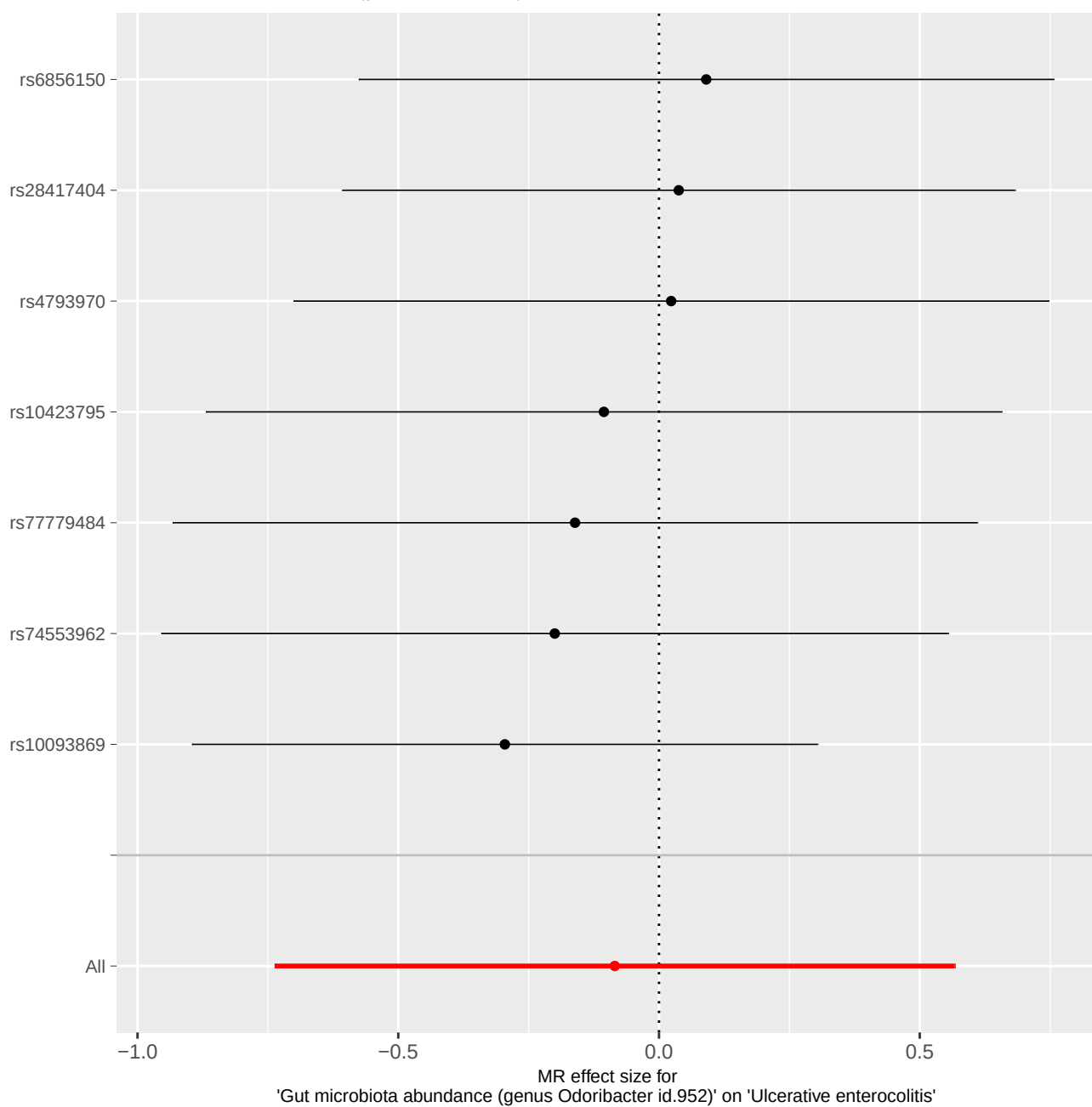


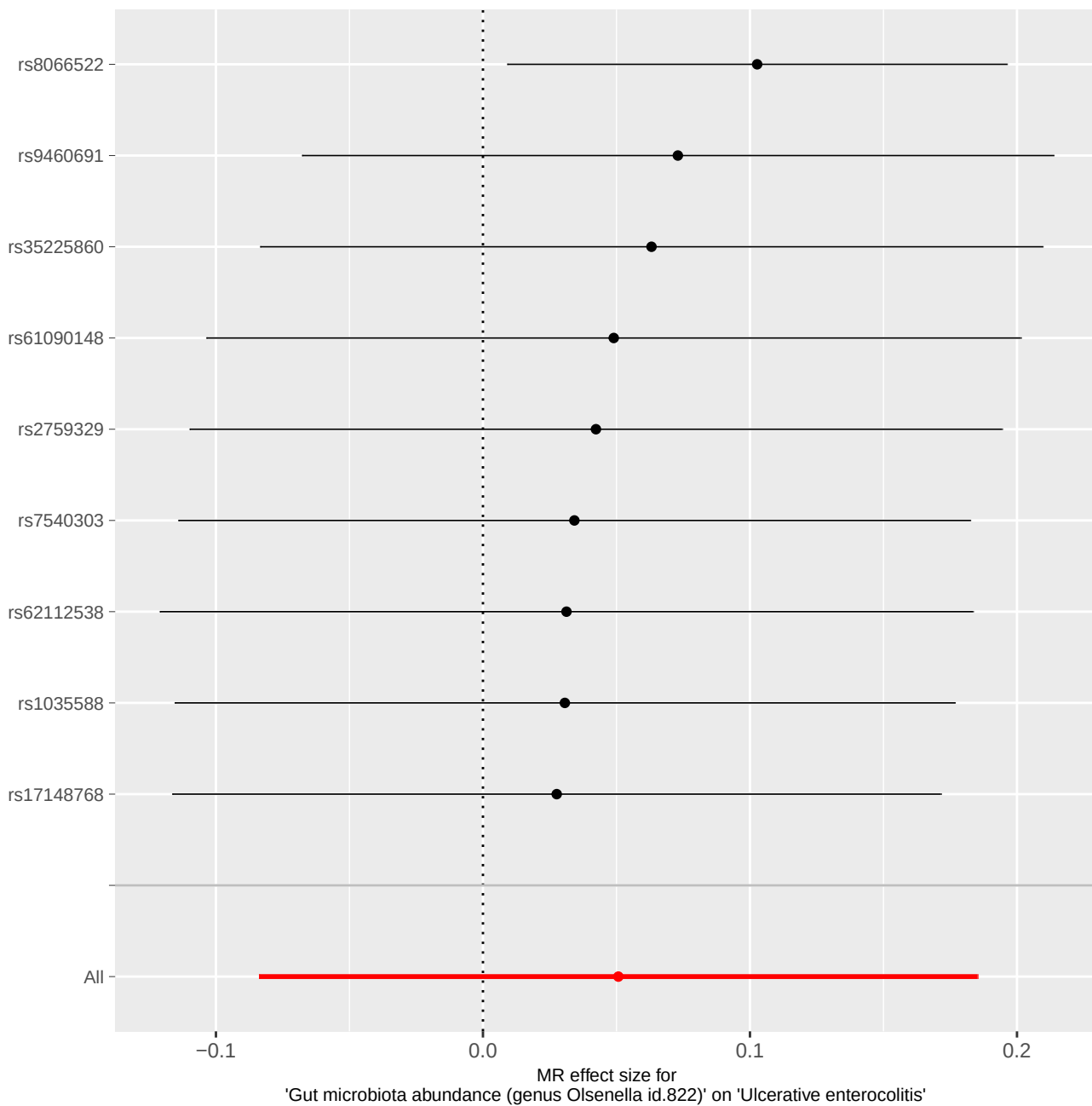


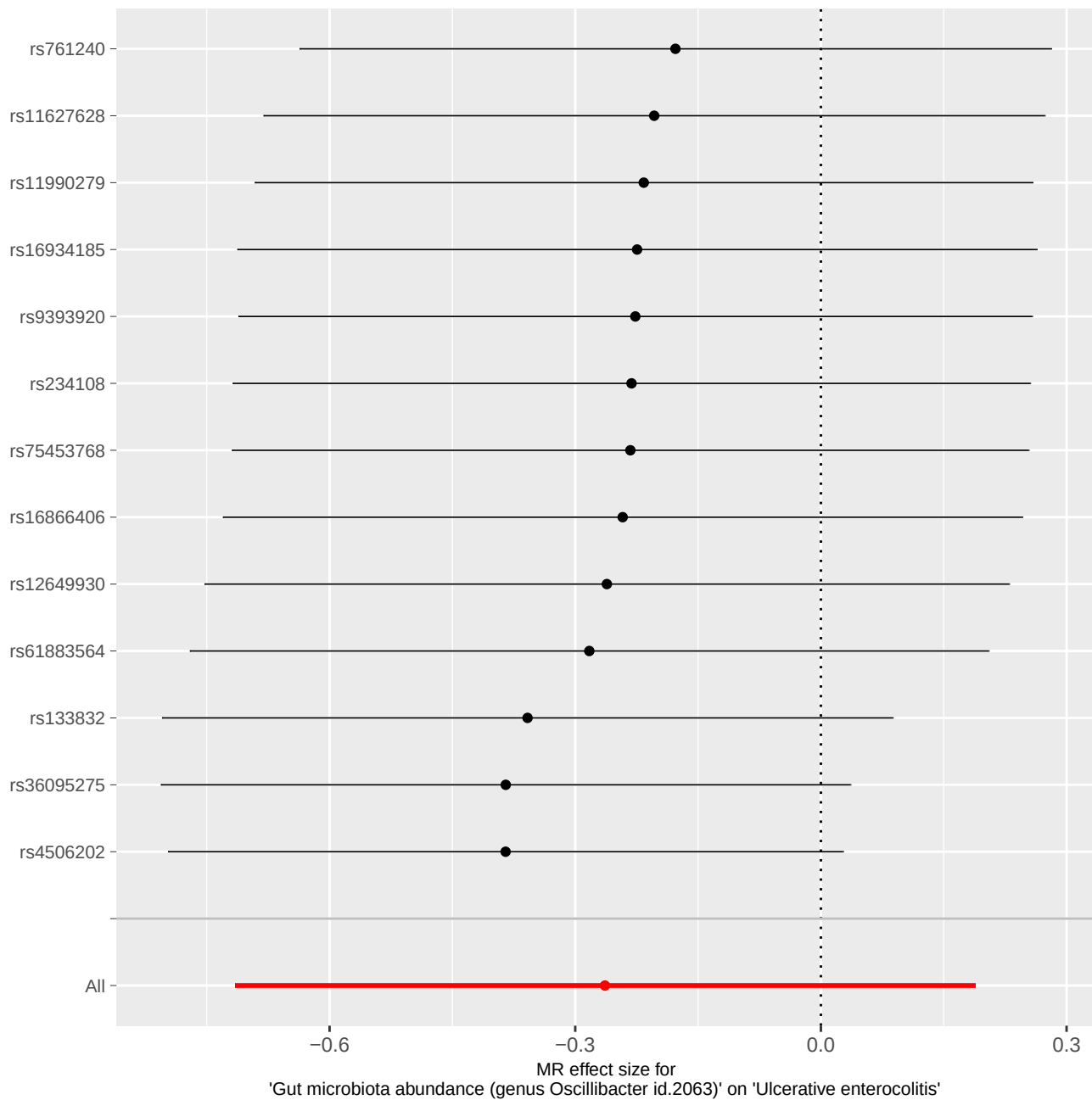


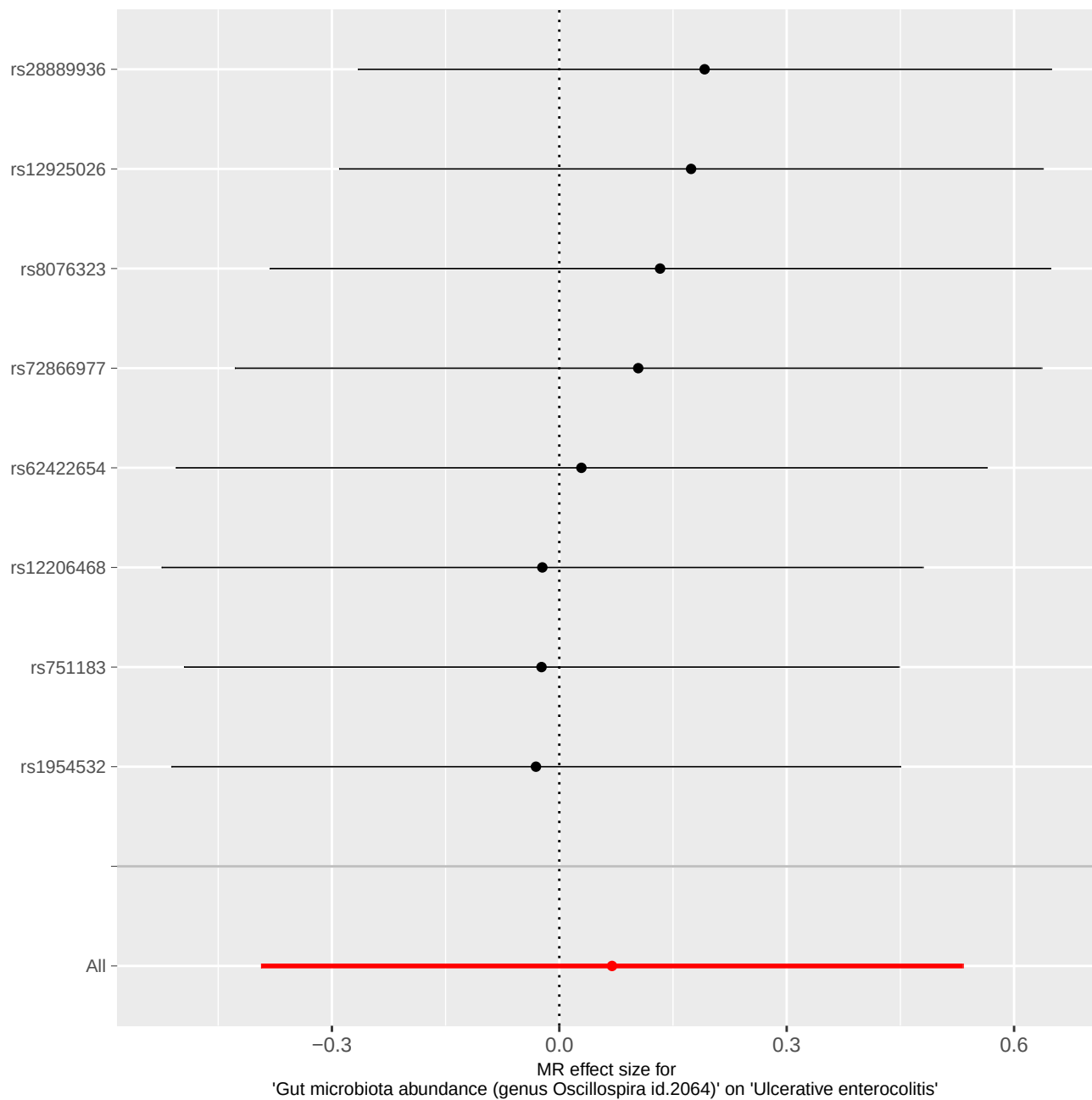


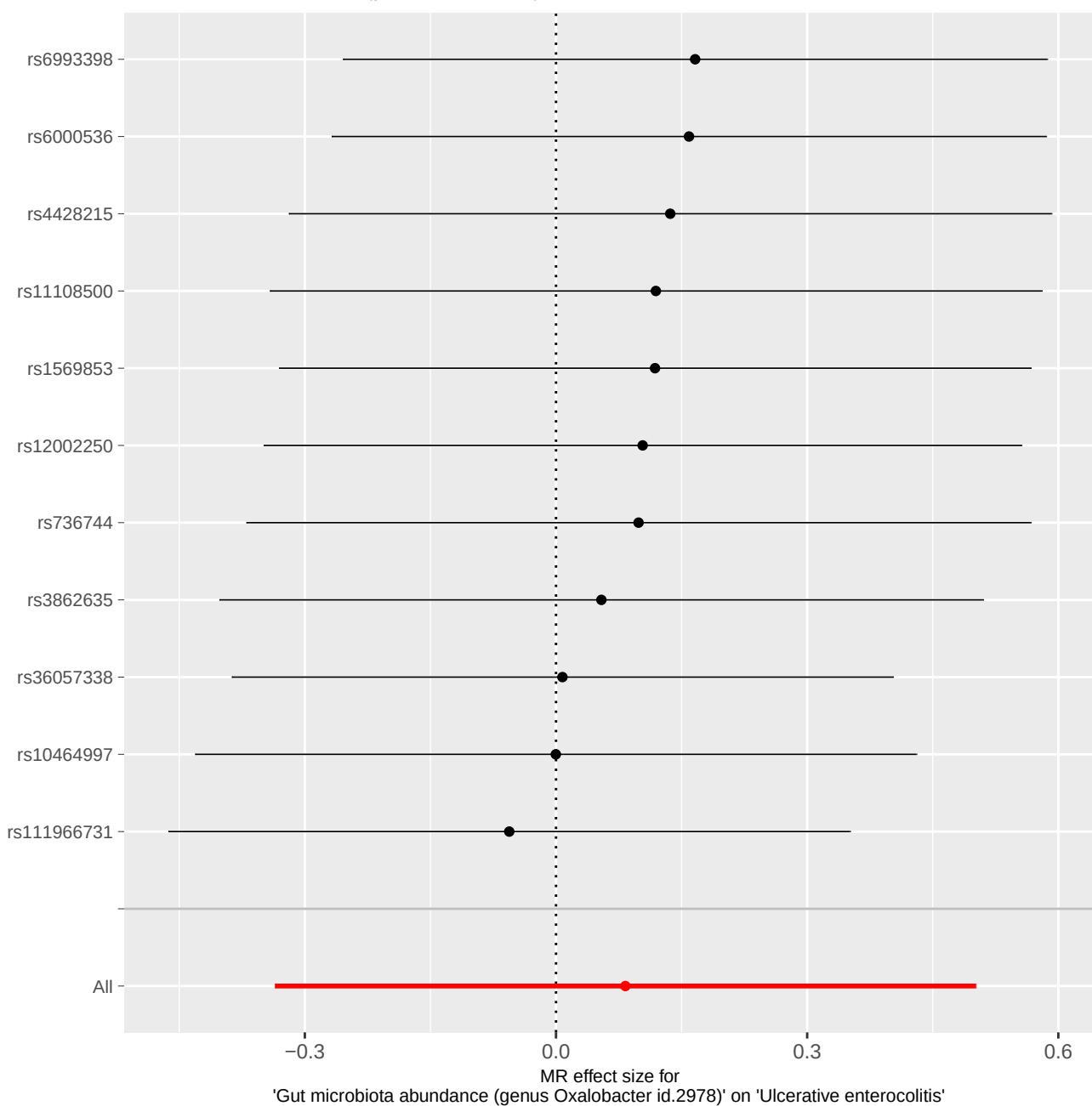


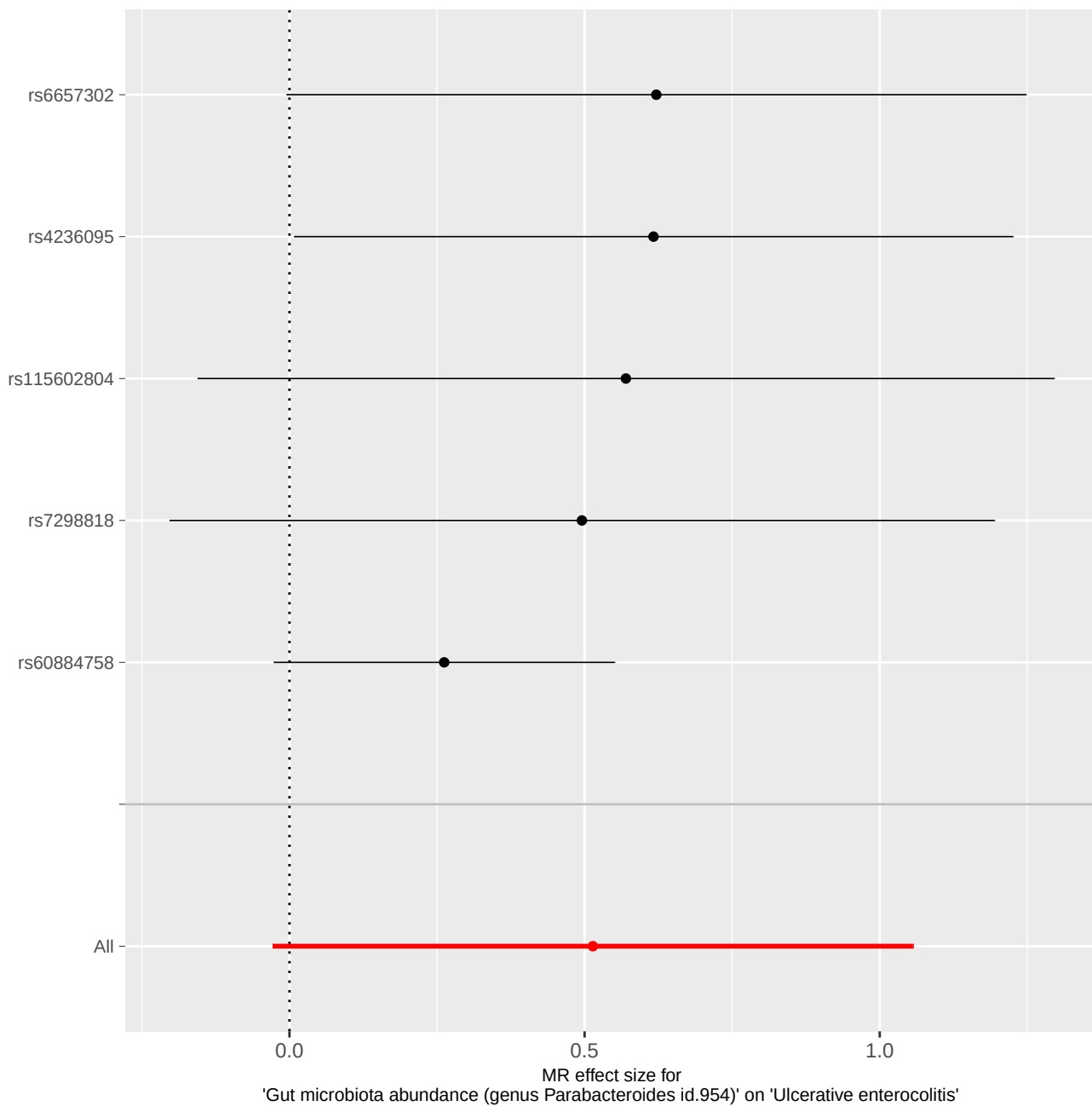


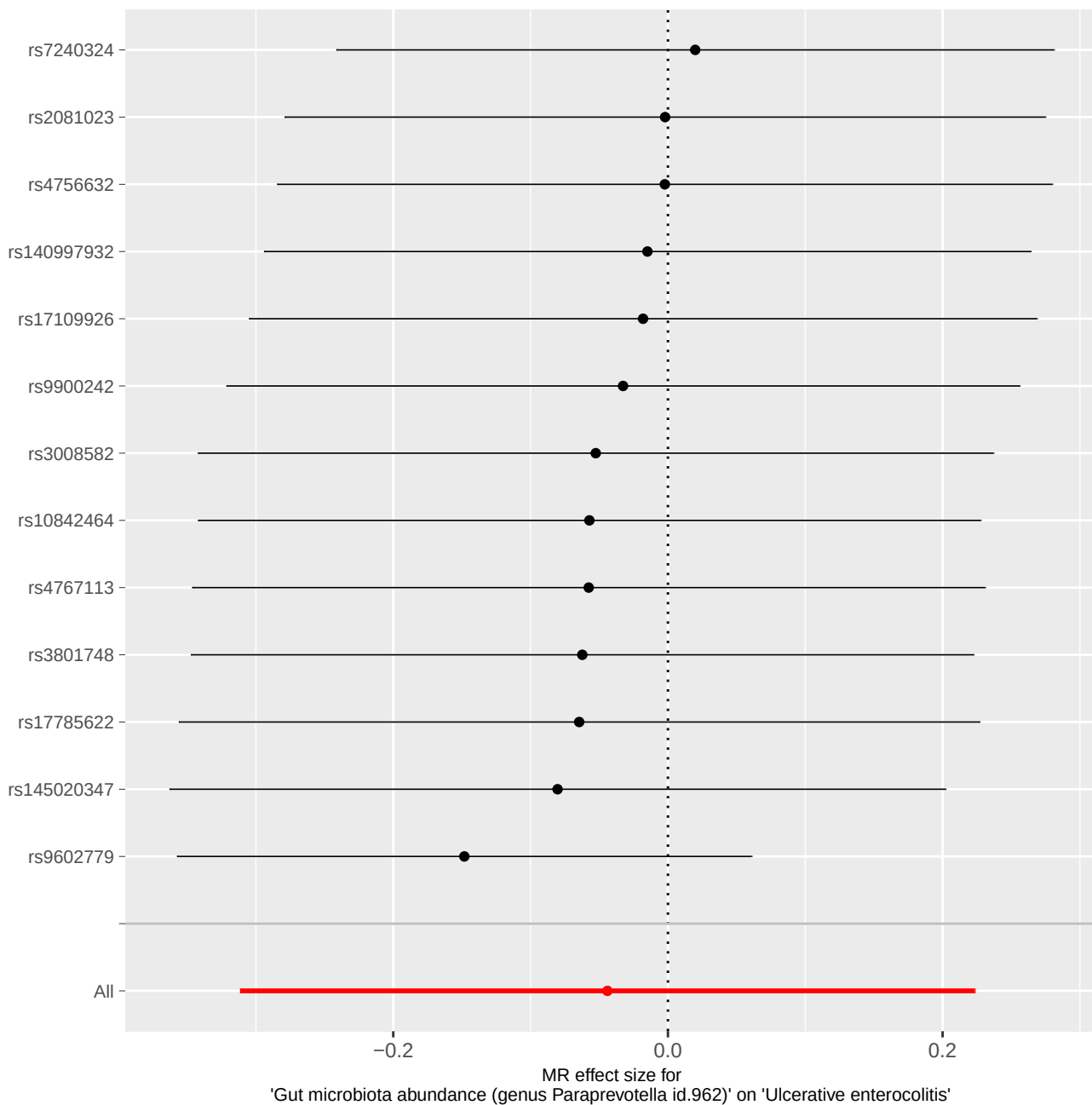


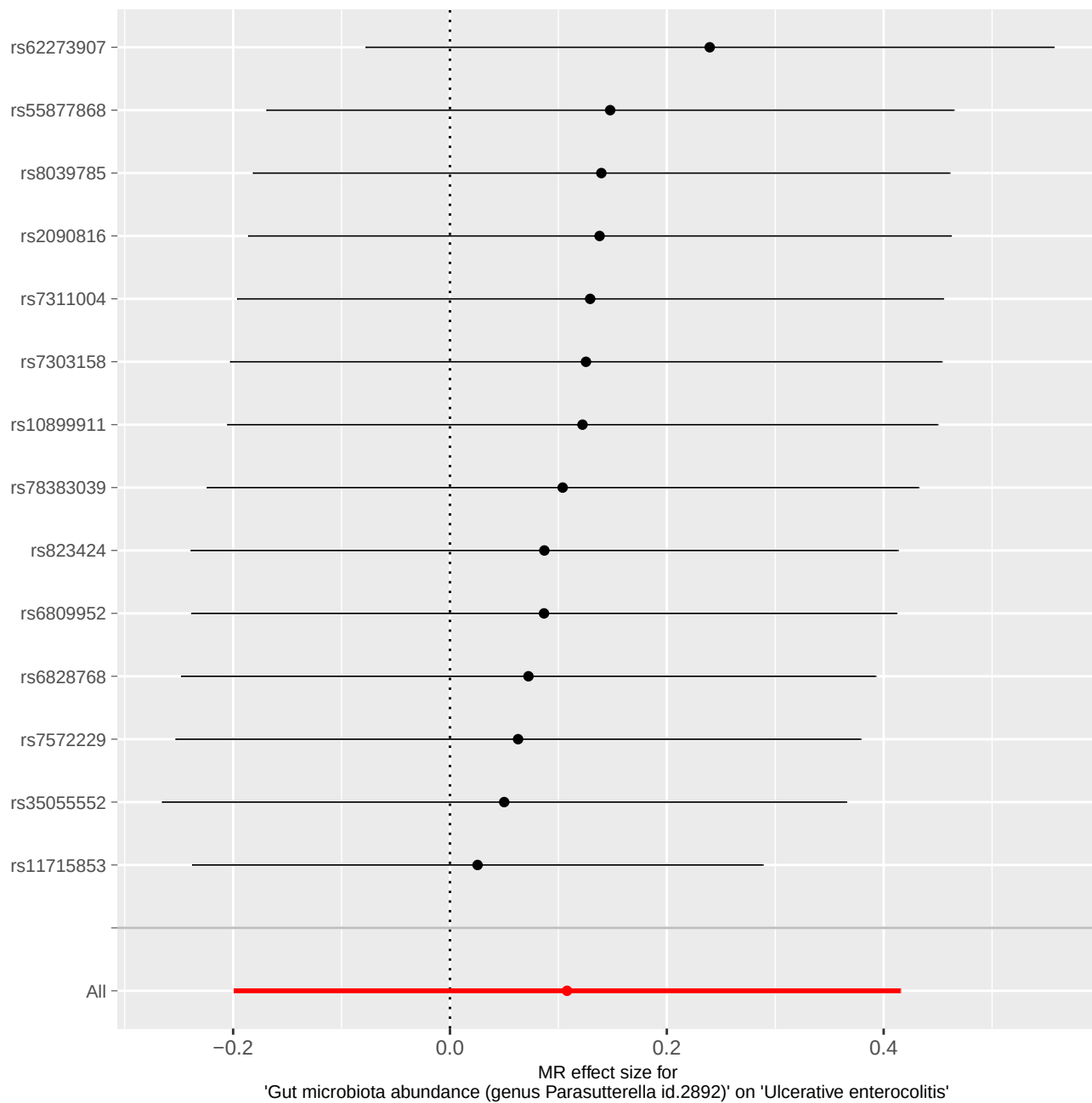


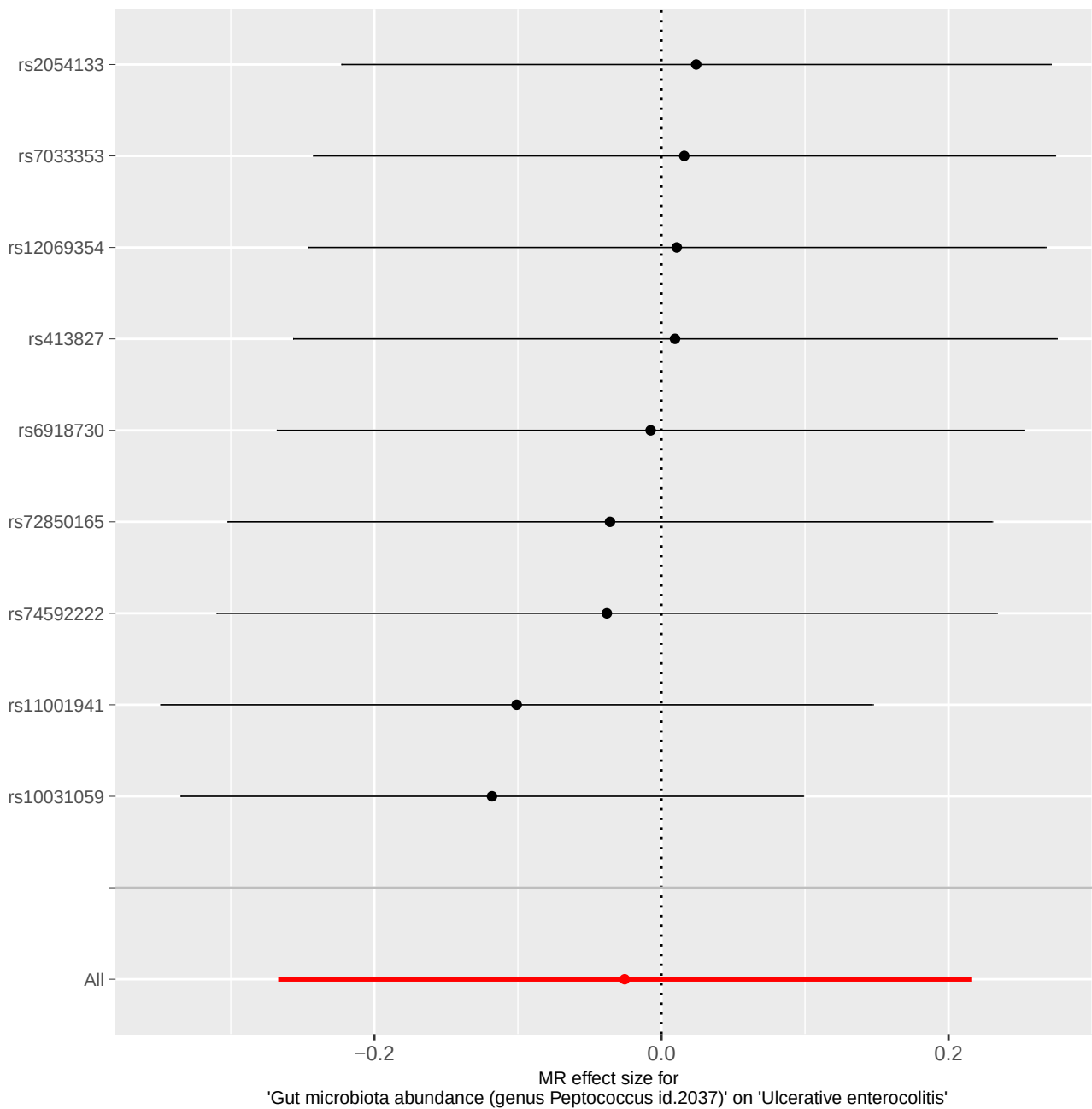


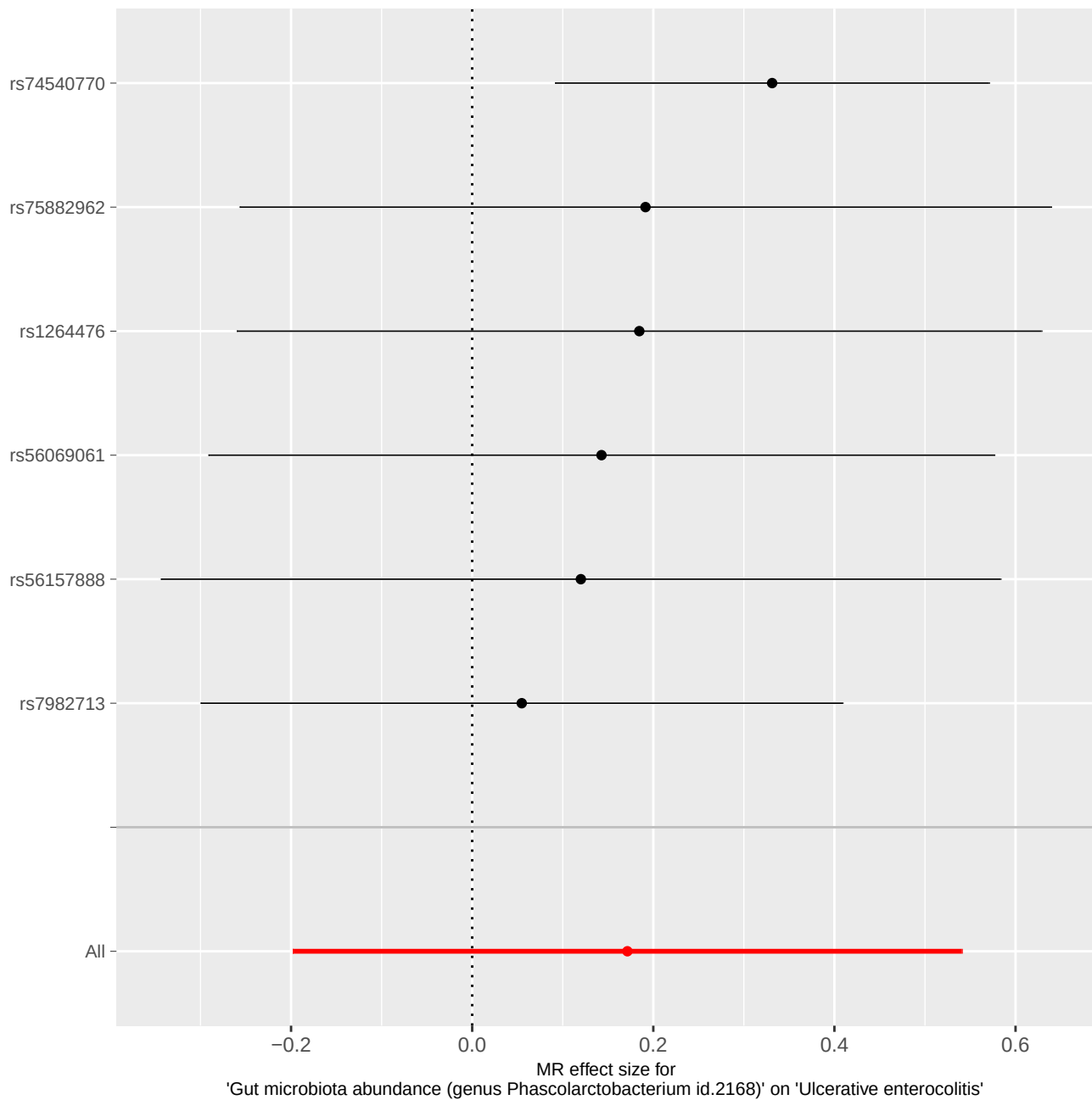


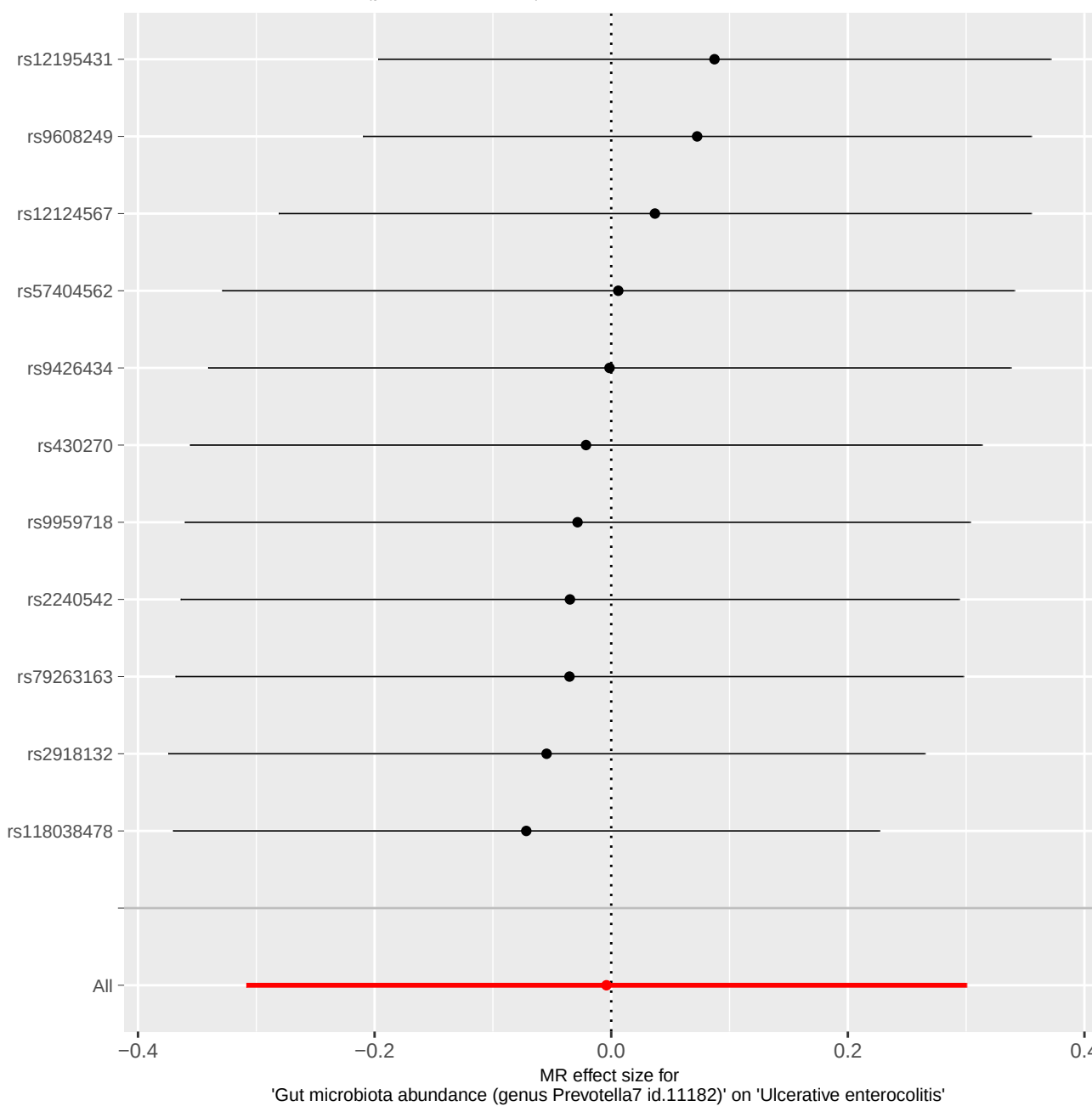


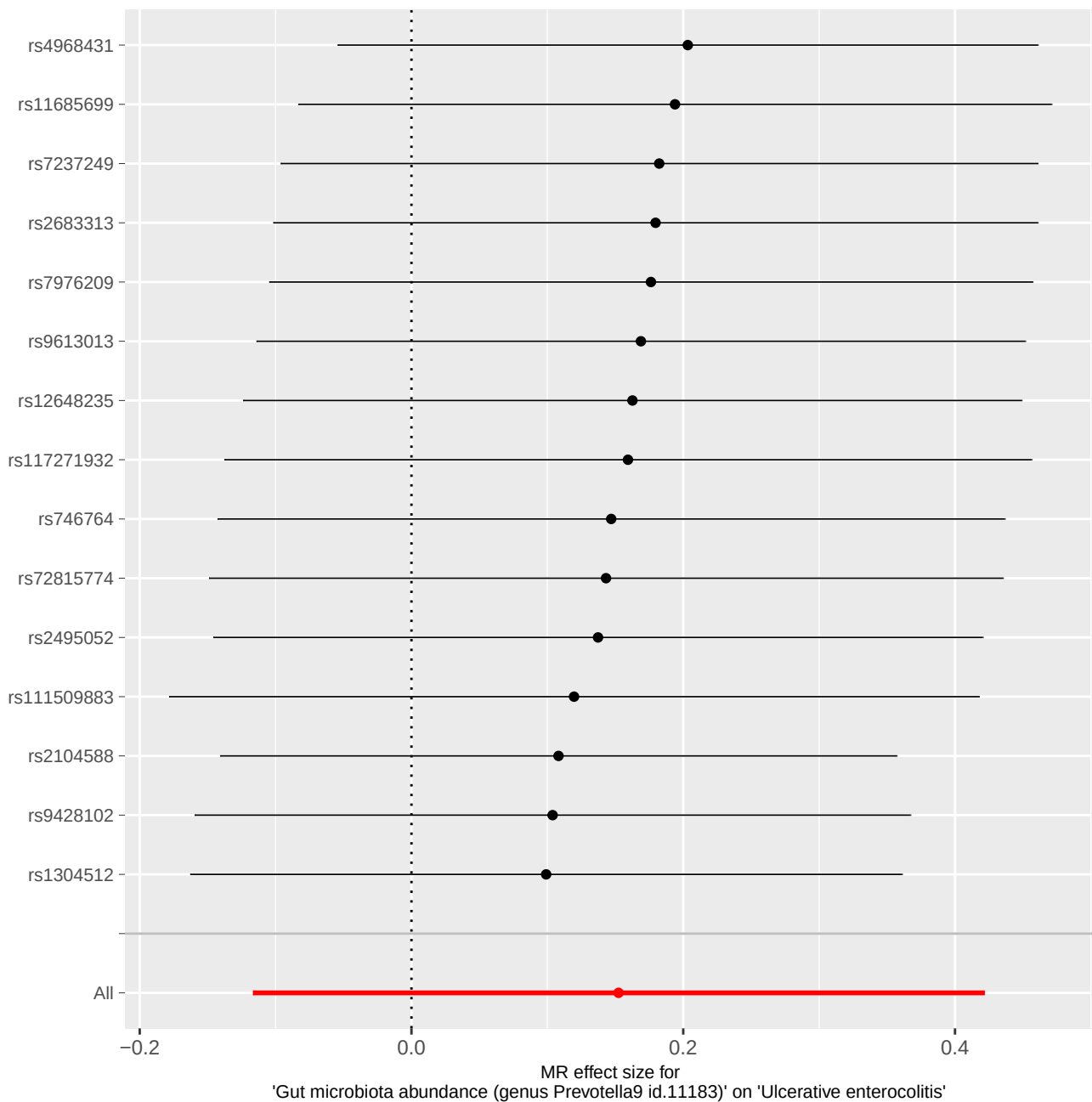


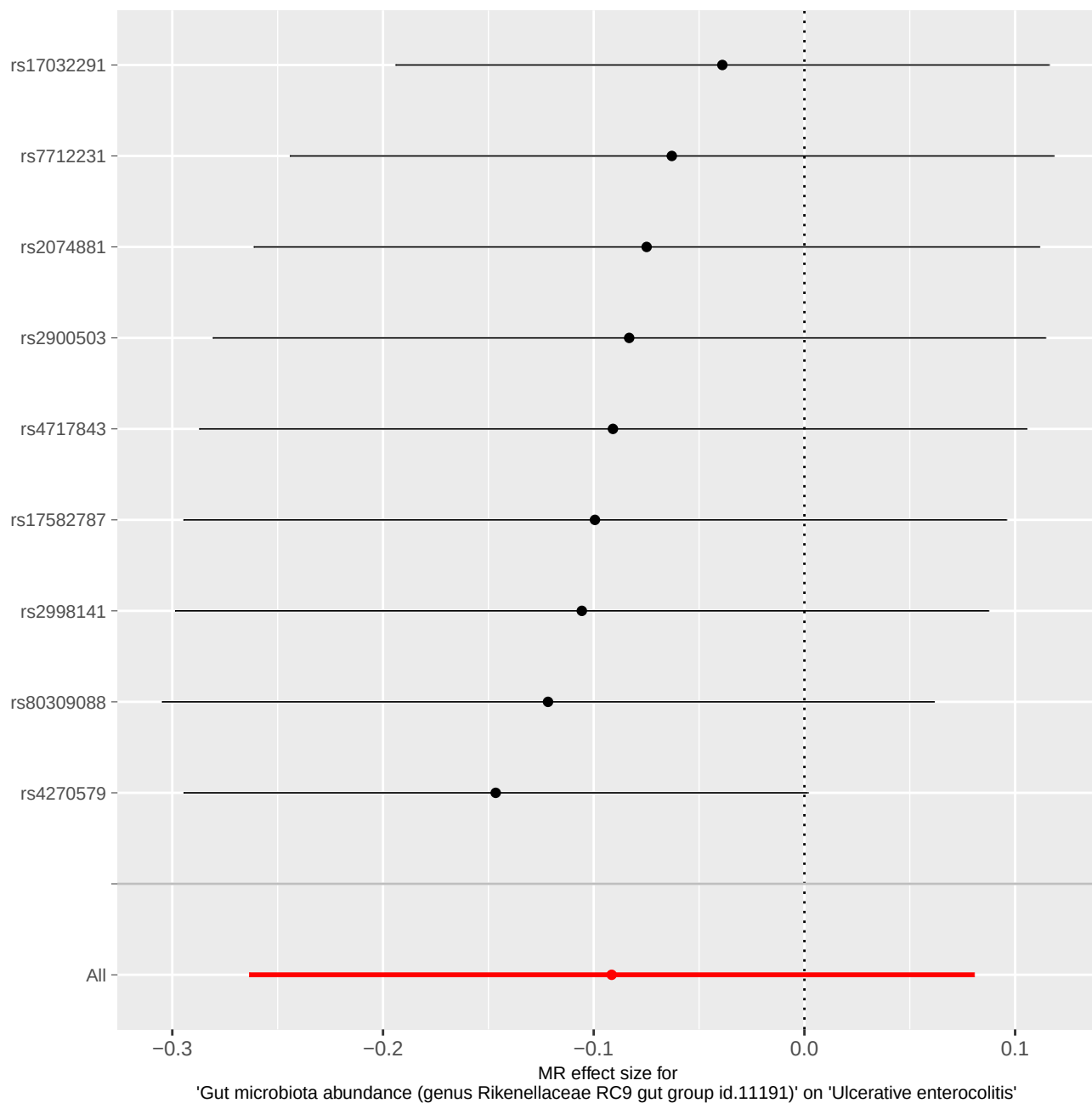


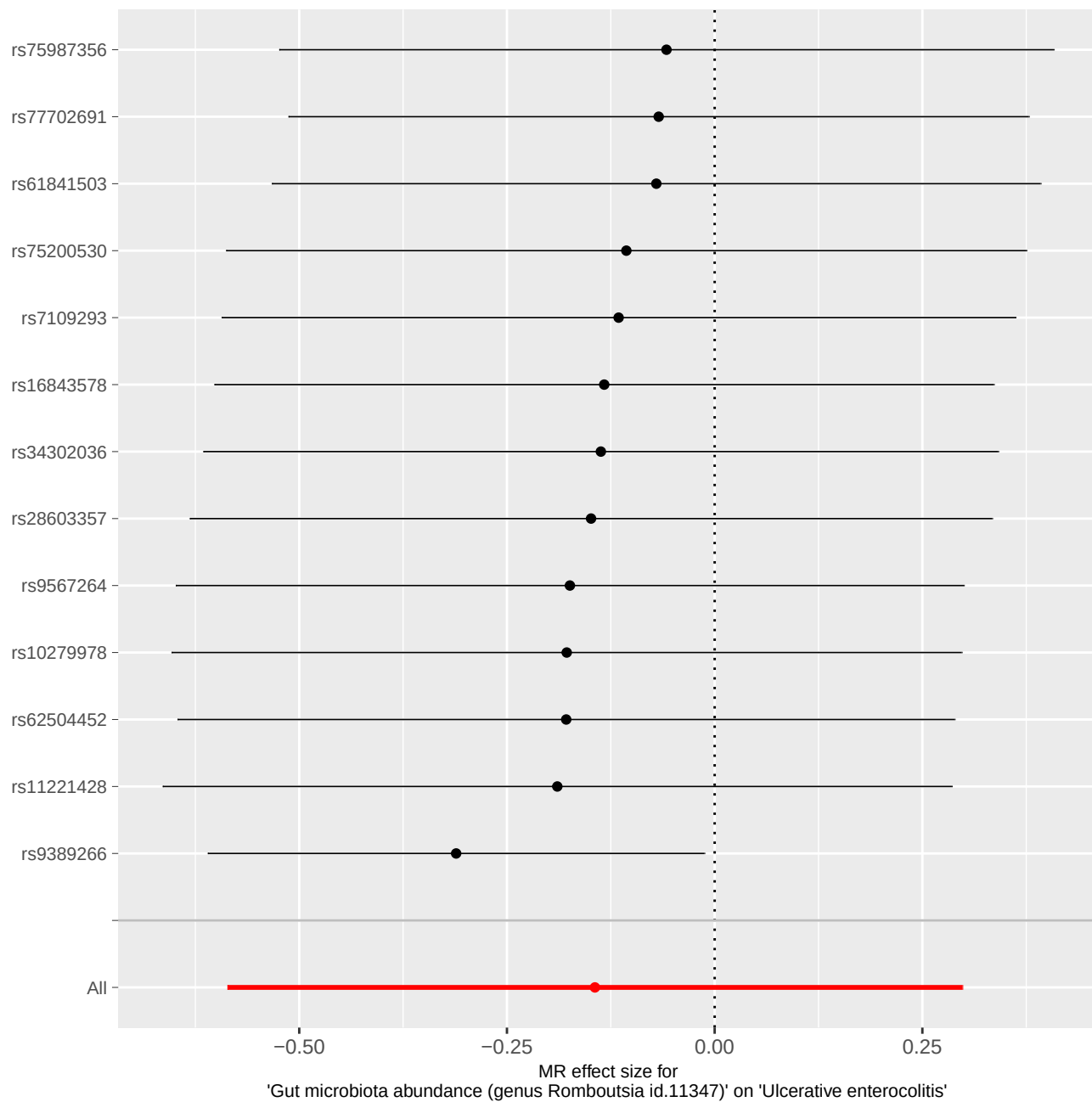




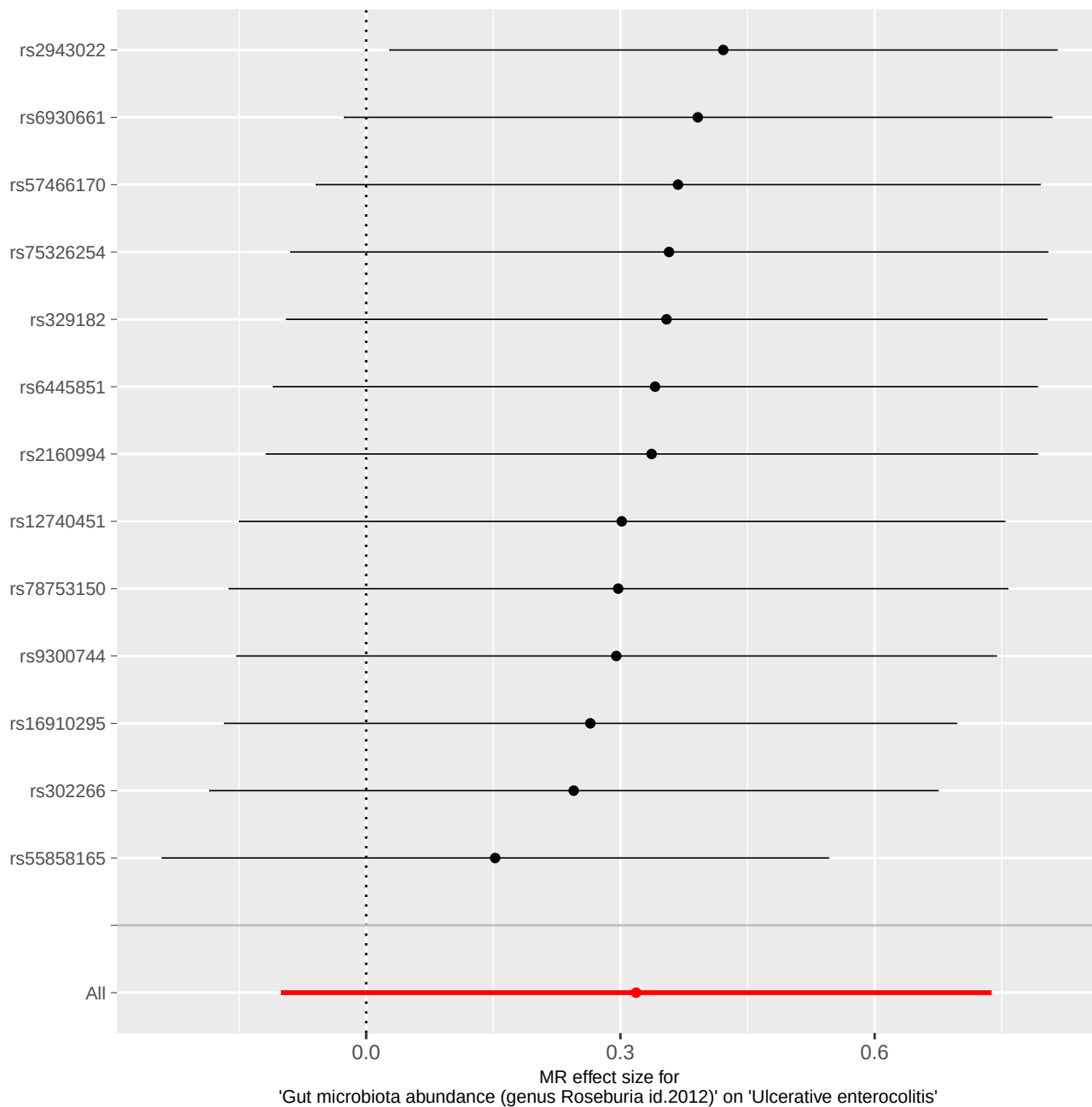




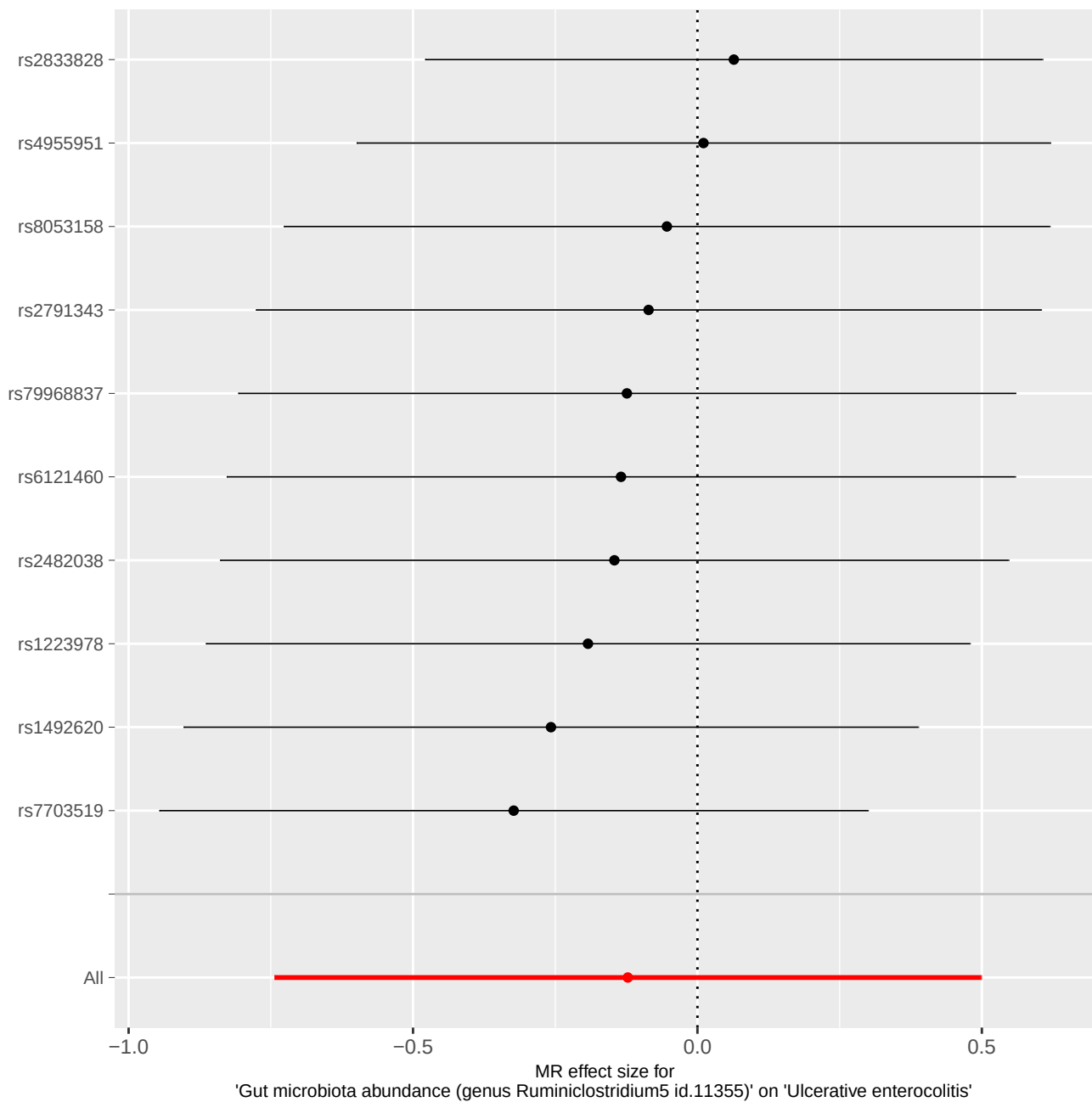


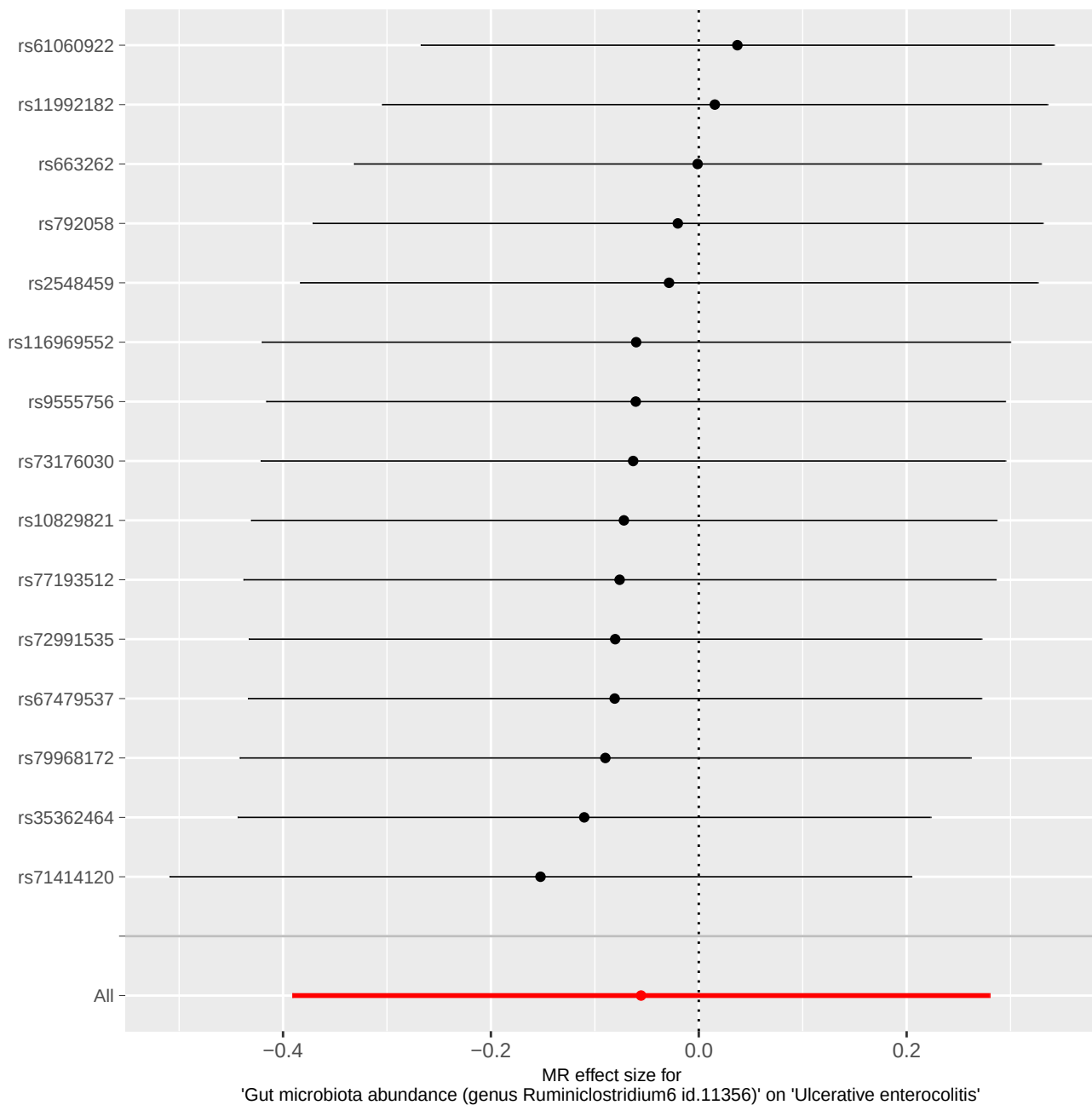


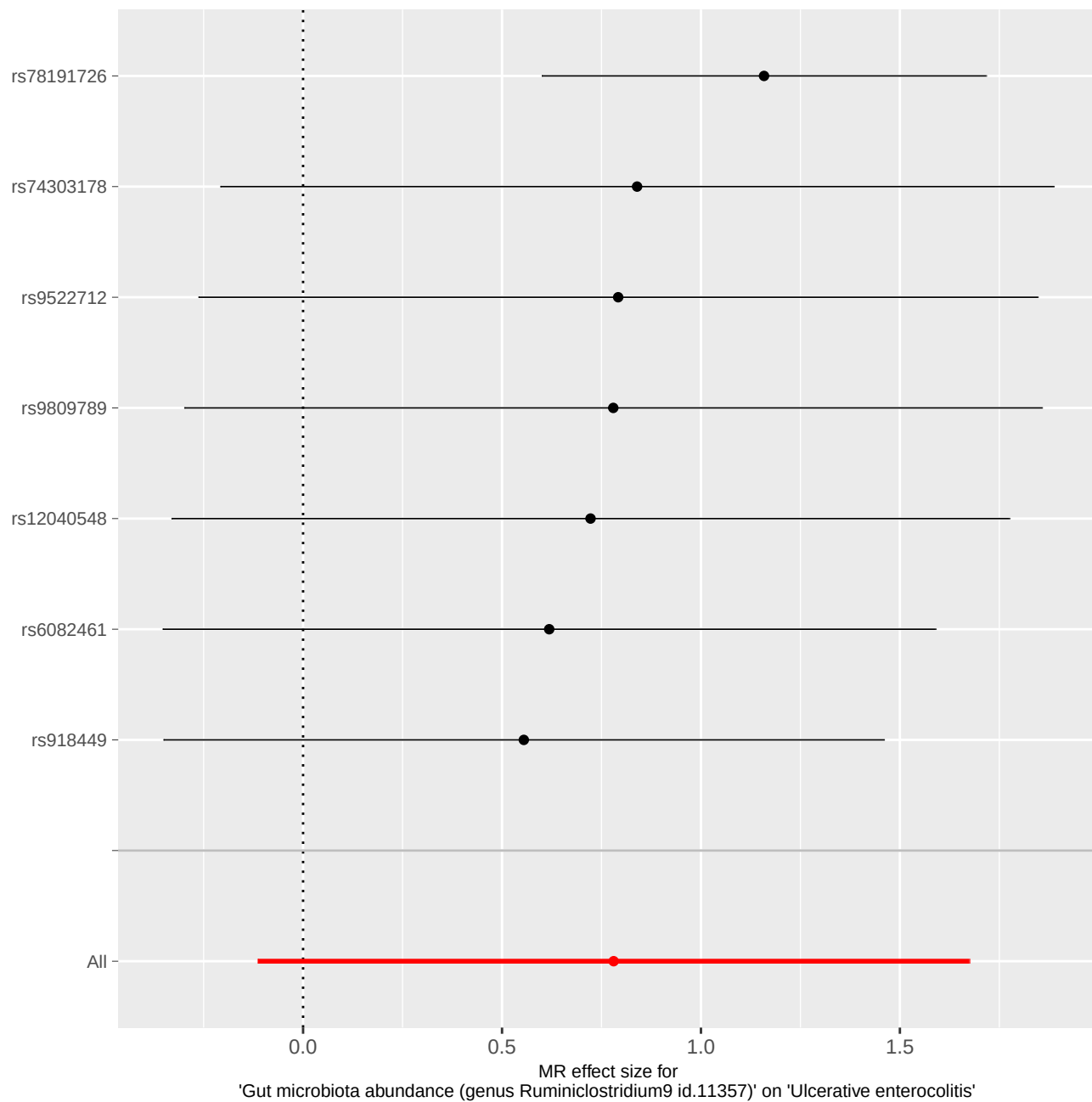
Batch 1022 : Gut microbiota abundance (genus Roseburia id.2012) on Ulcerative enterocolitis

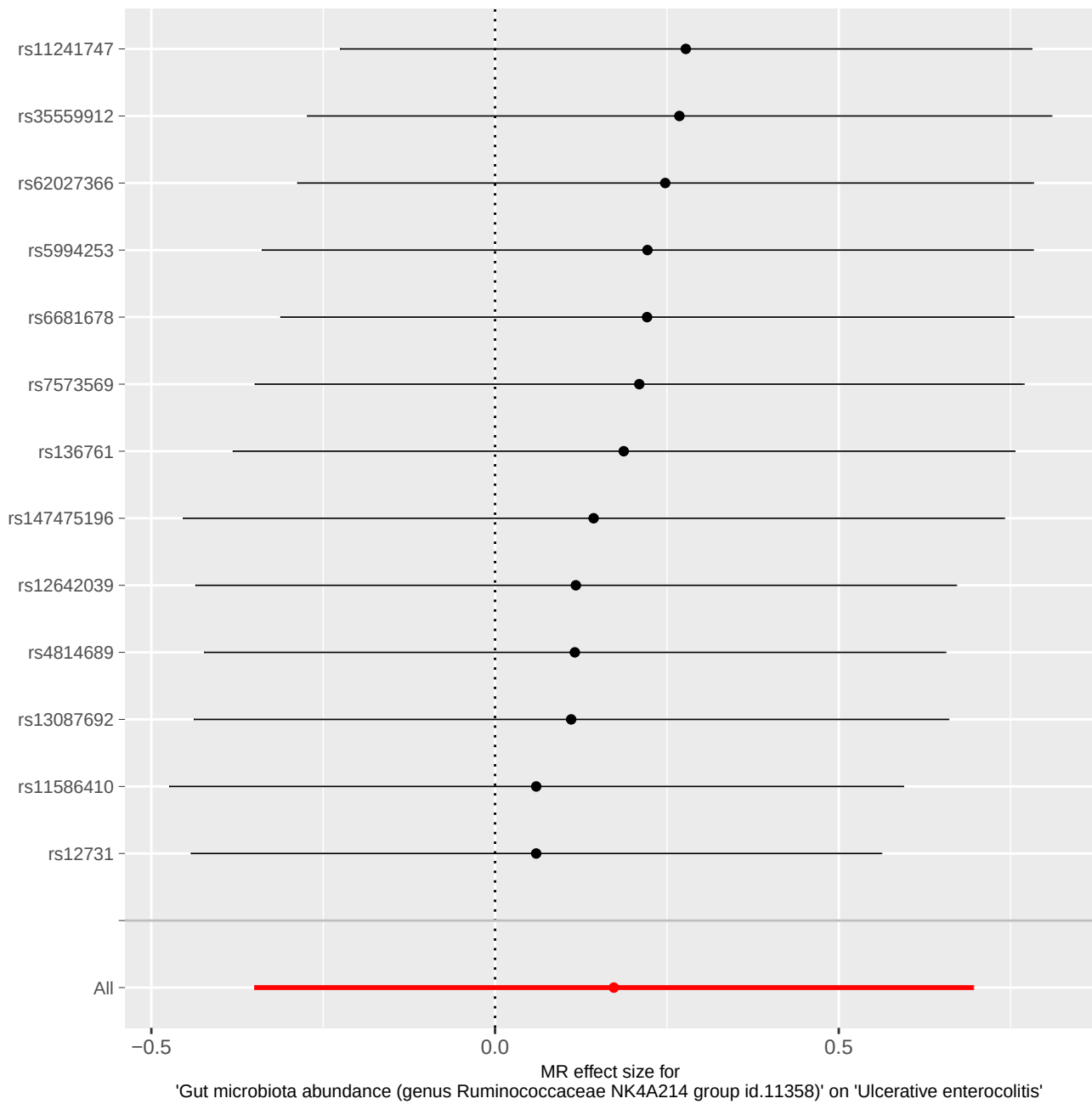


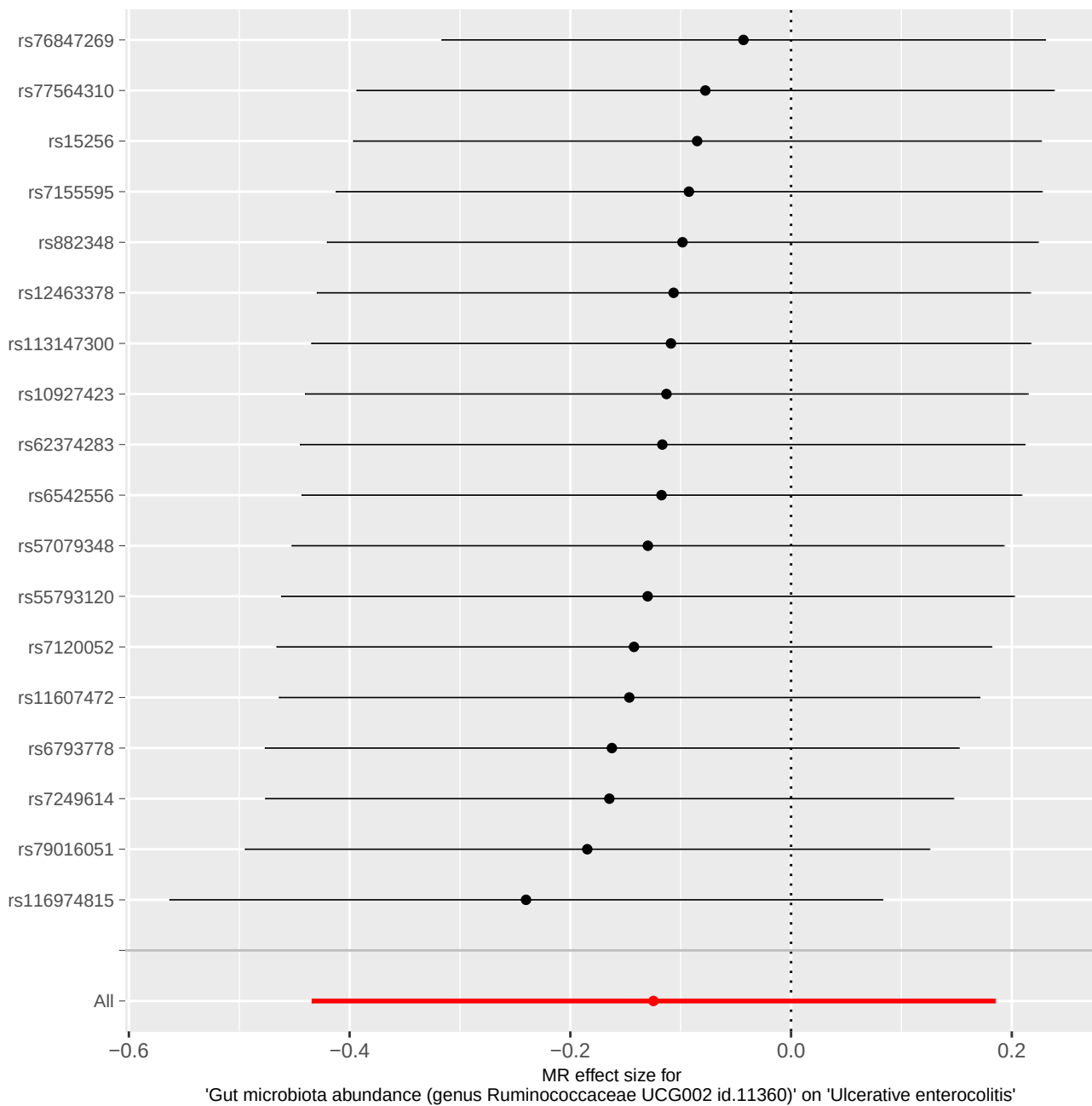
Batch 1023 : Gut microbiota abundance (genus Ruminiclostridium5 id.11355) on Ulcerative enterocolitis

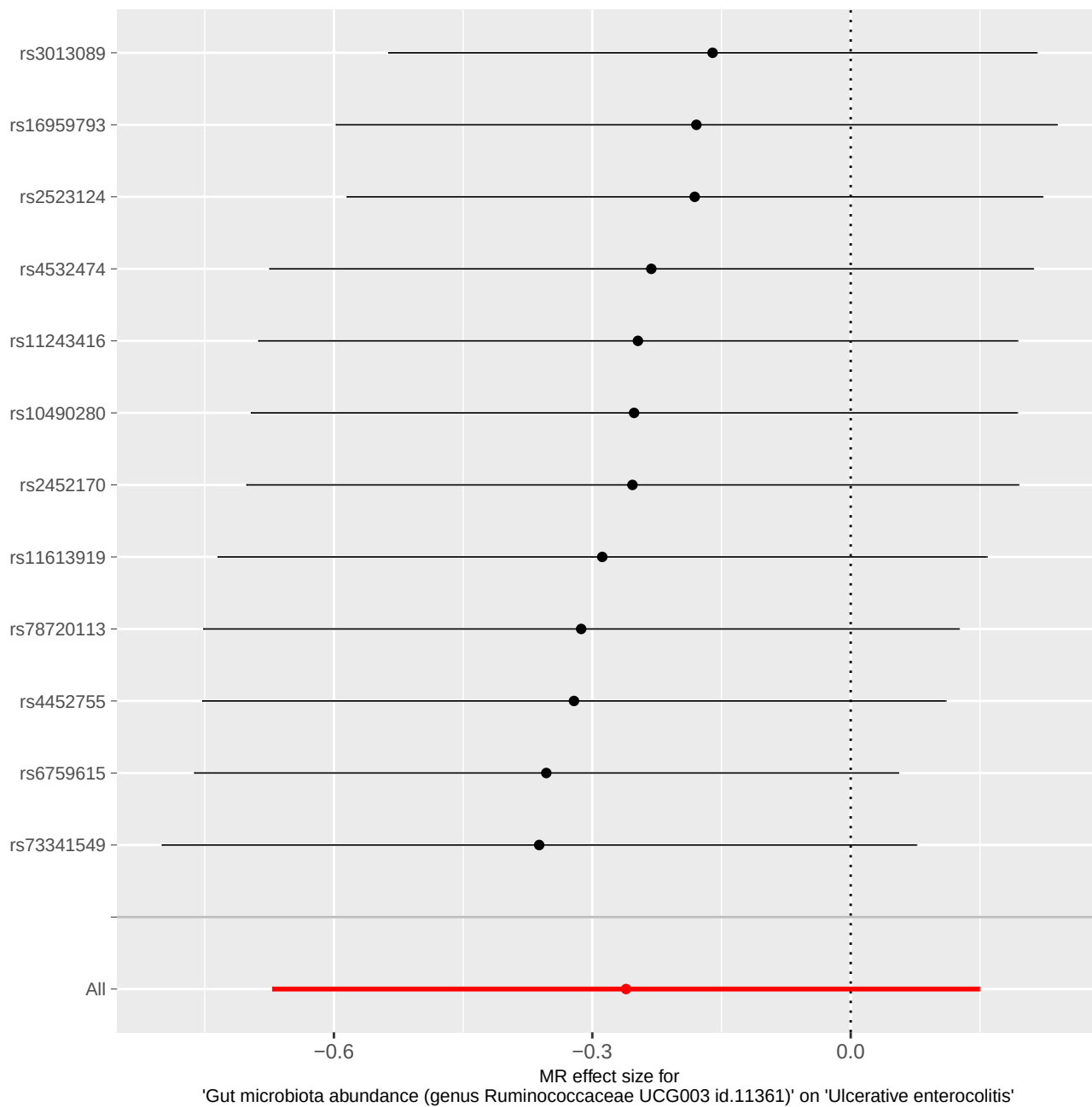


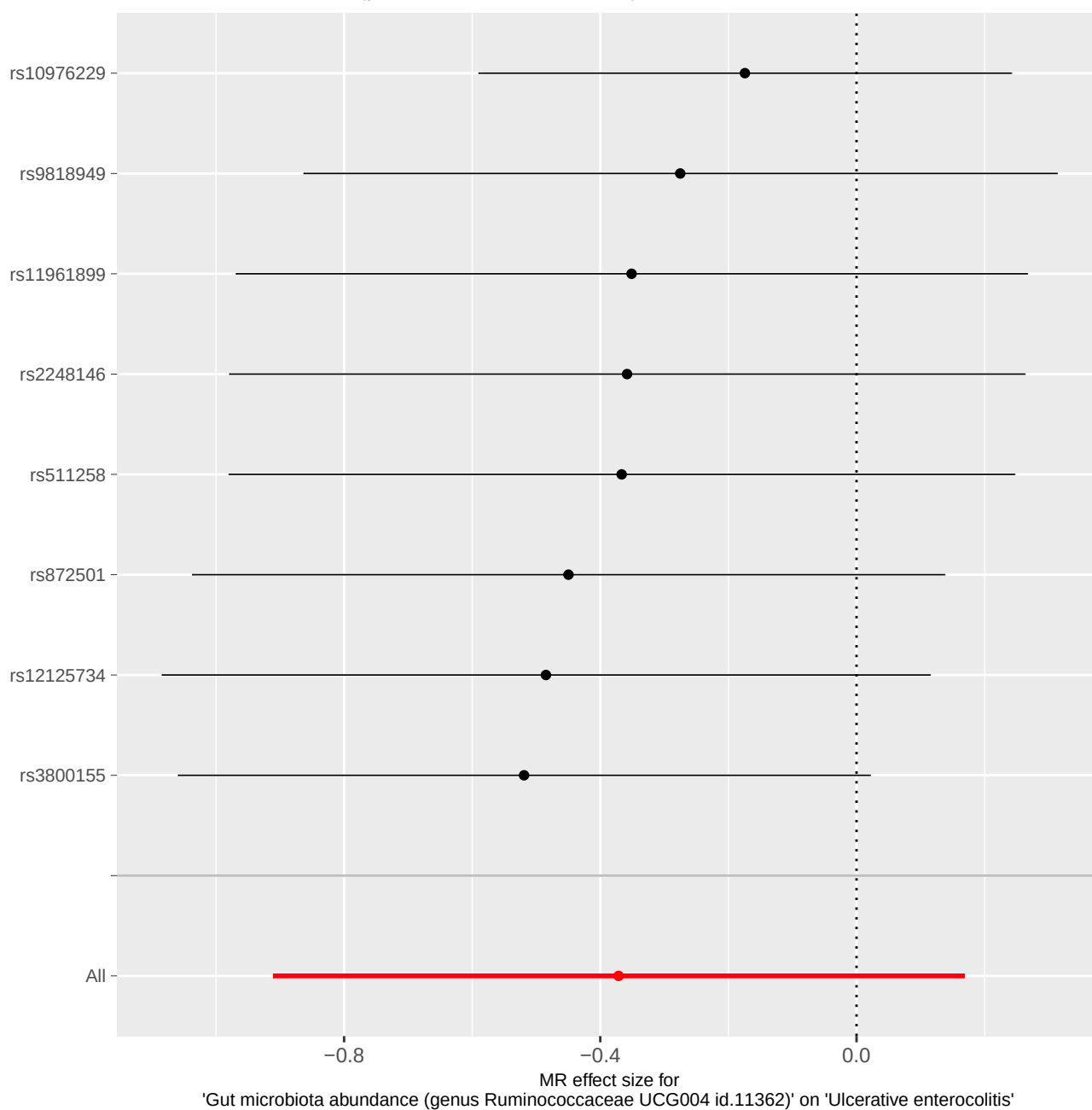


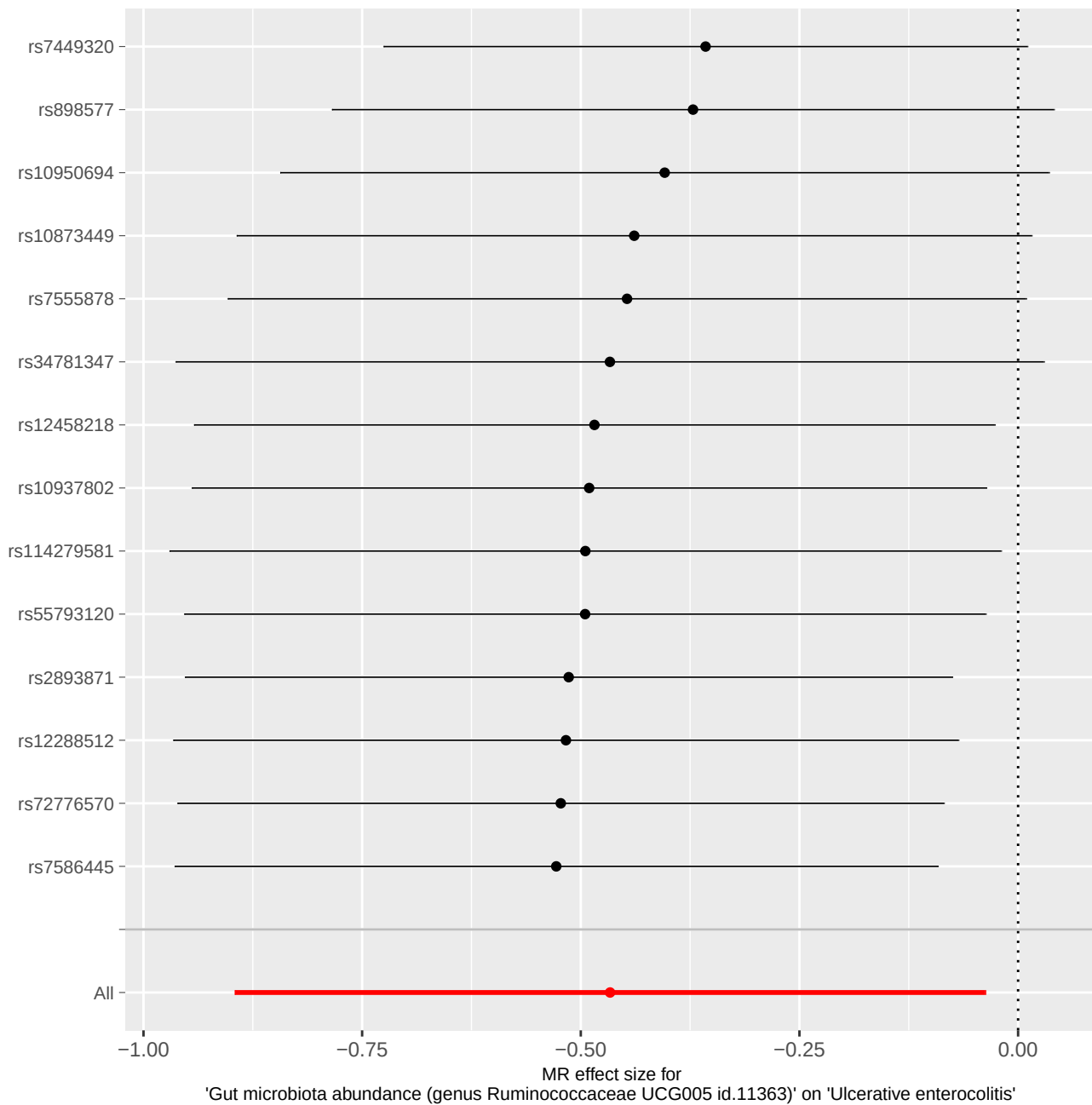


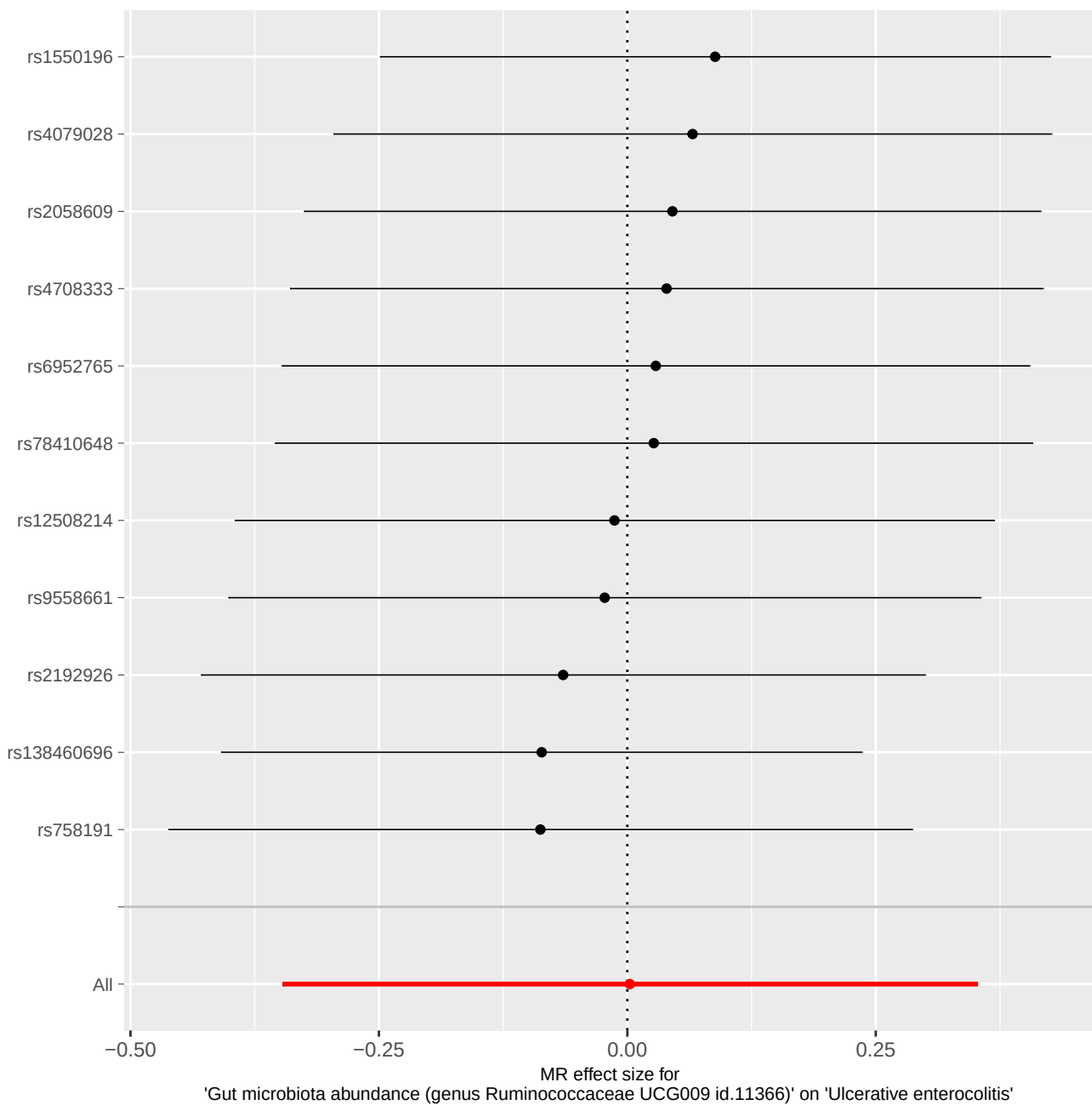


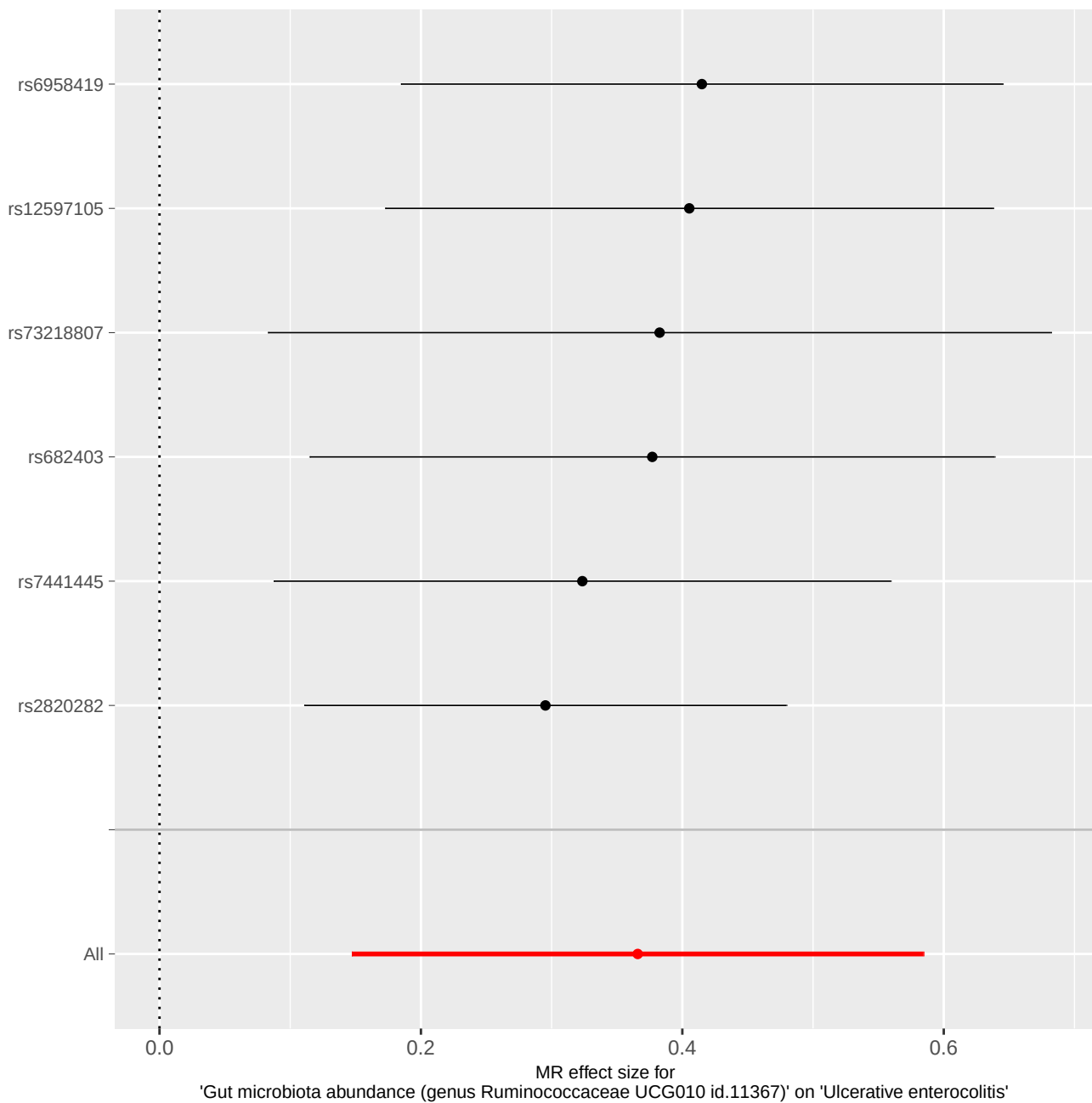


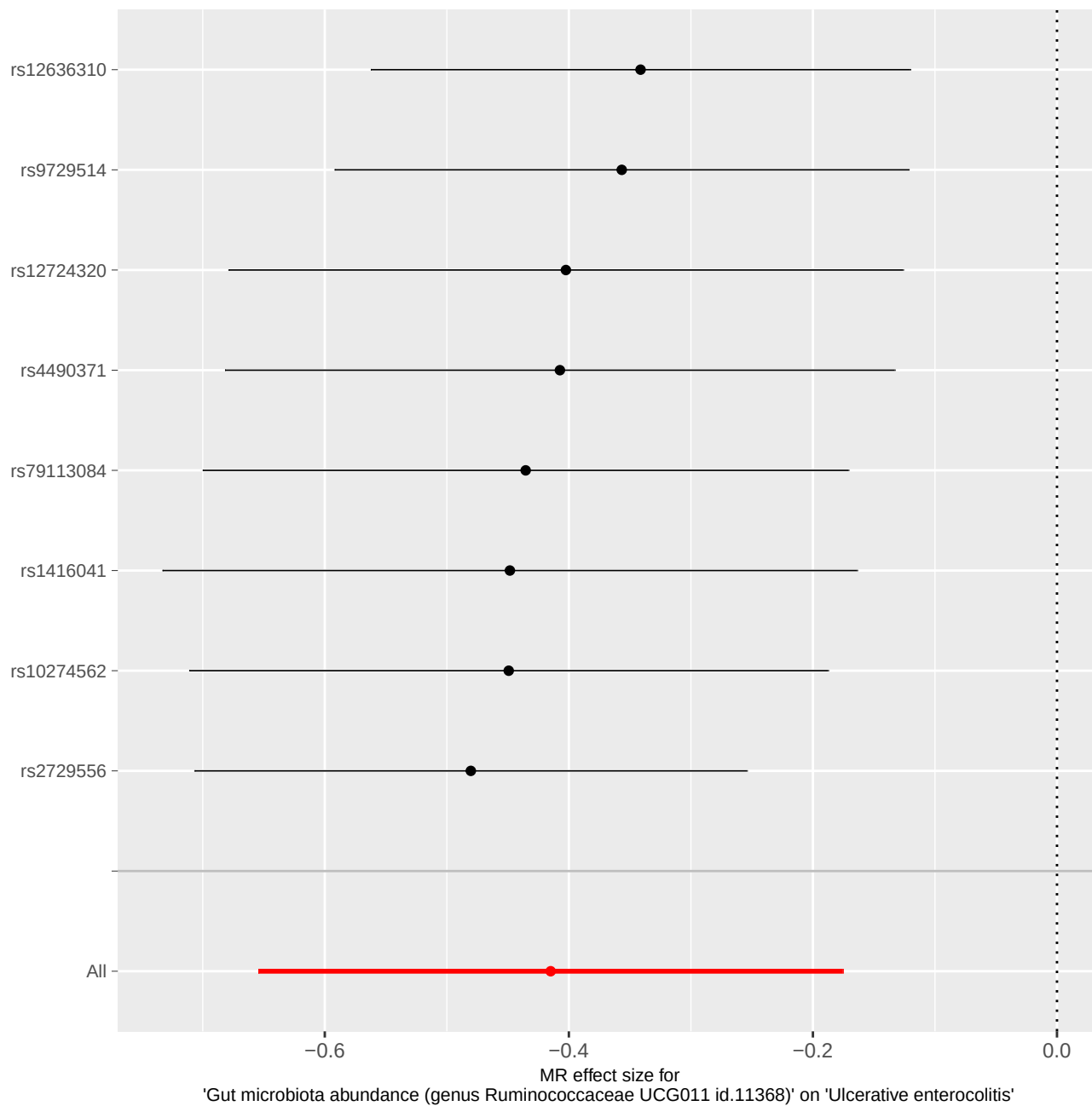


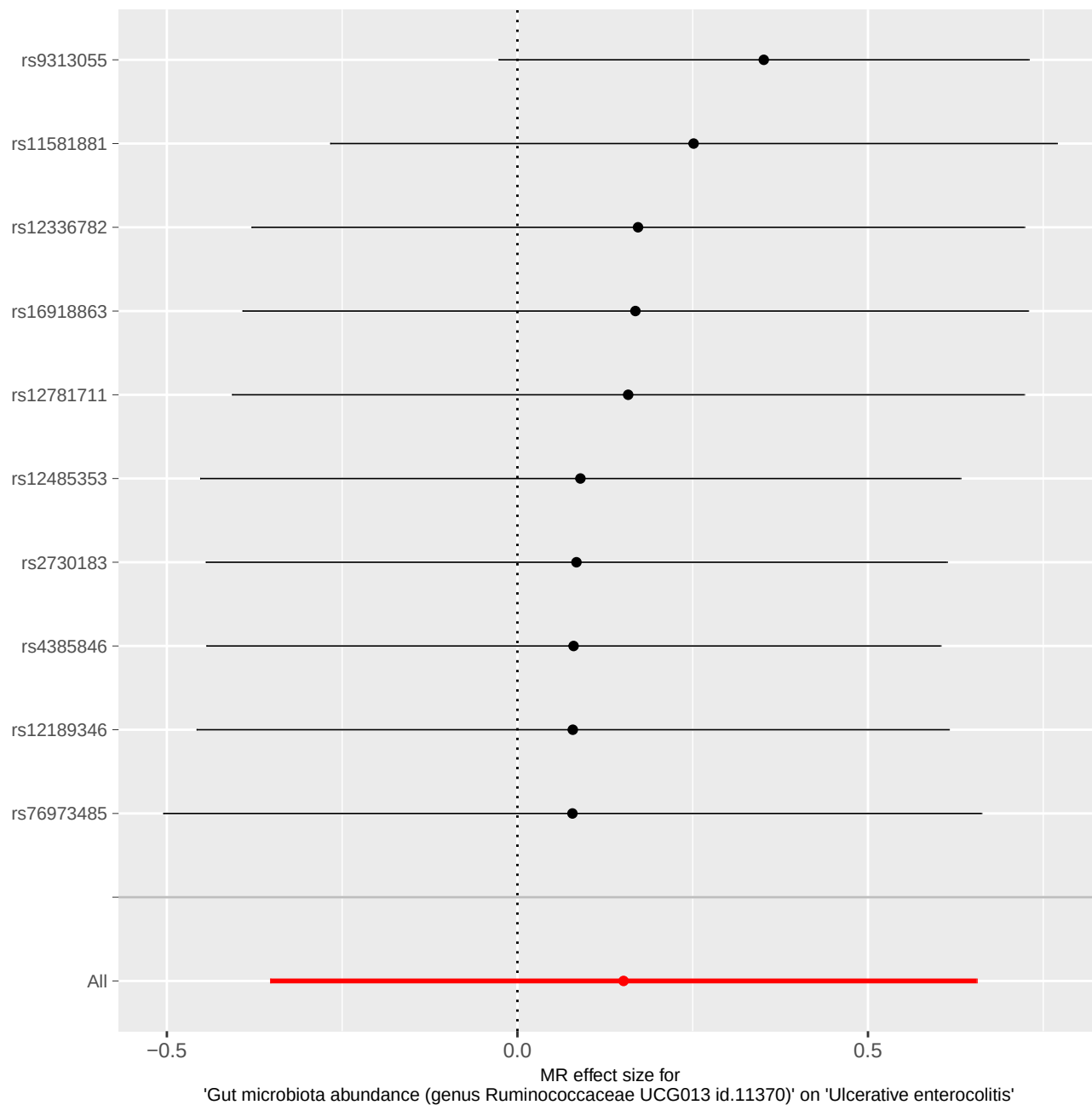


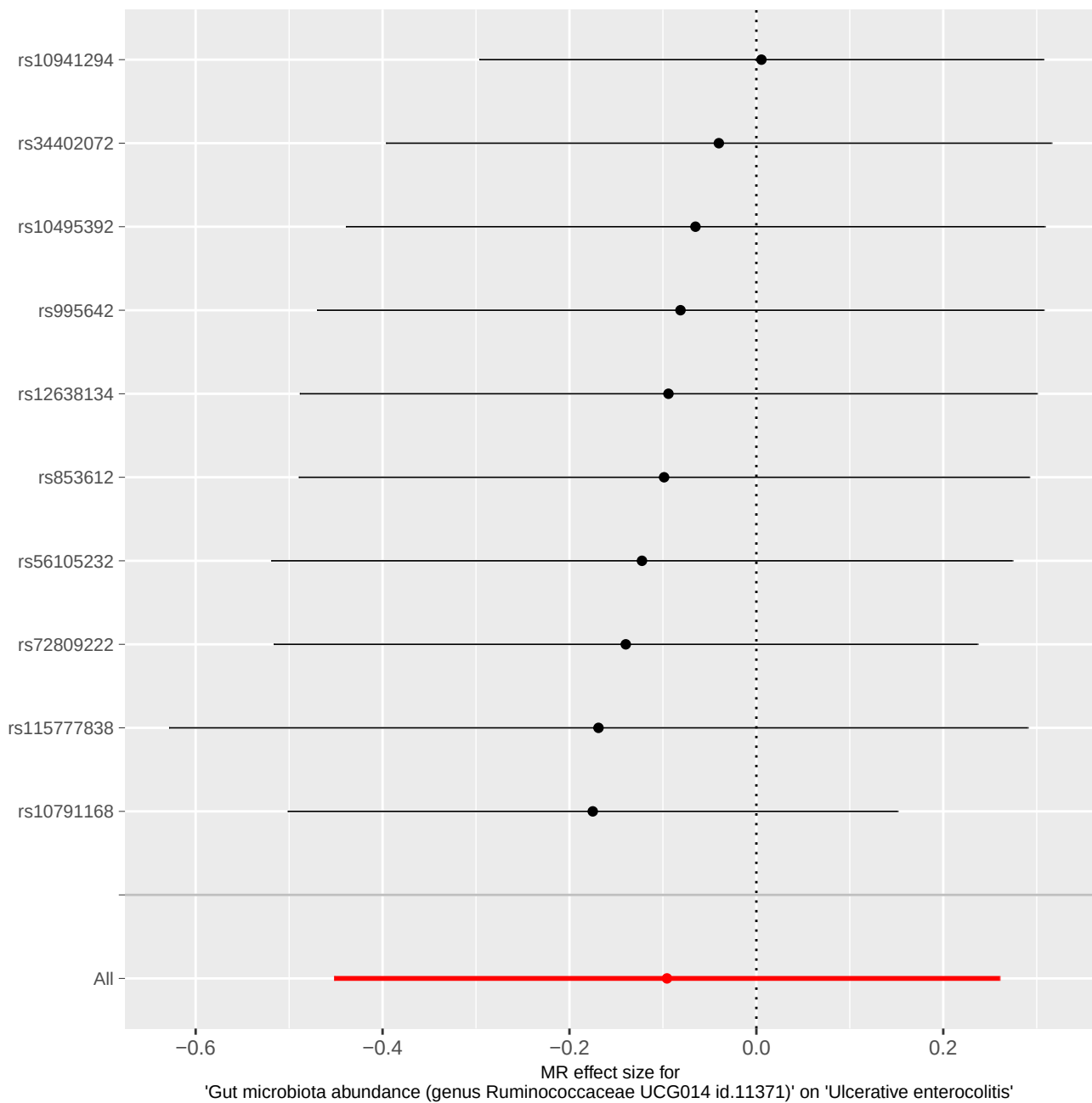


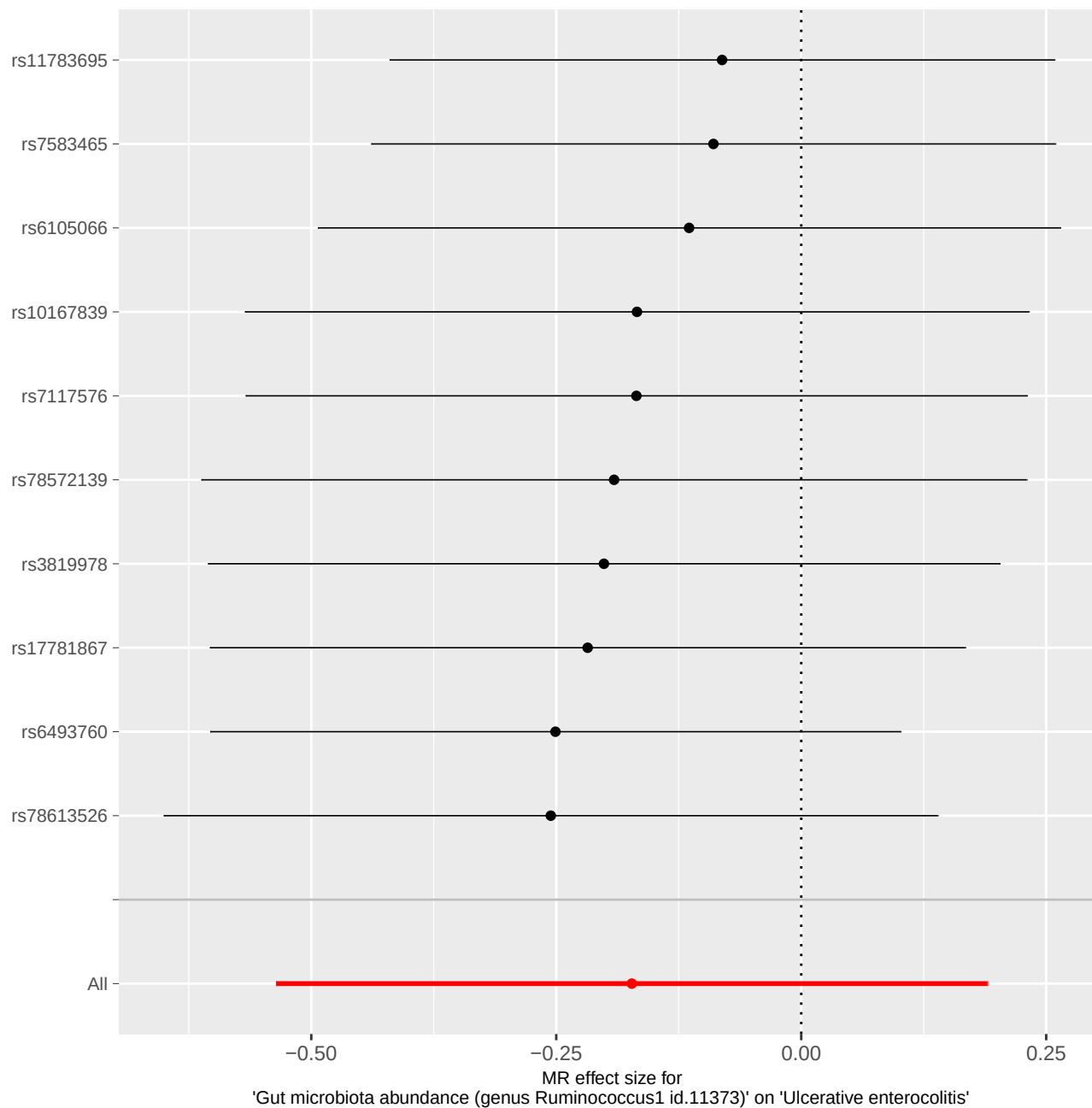


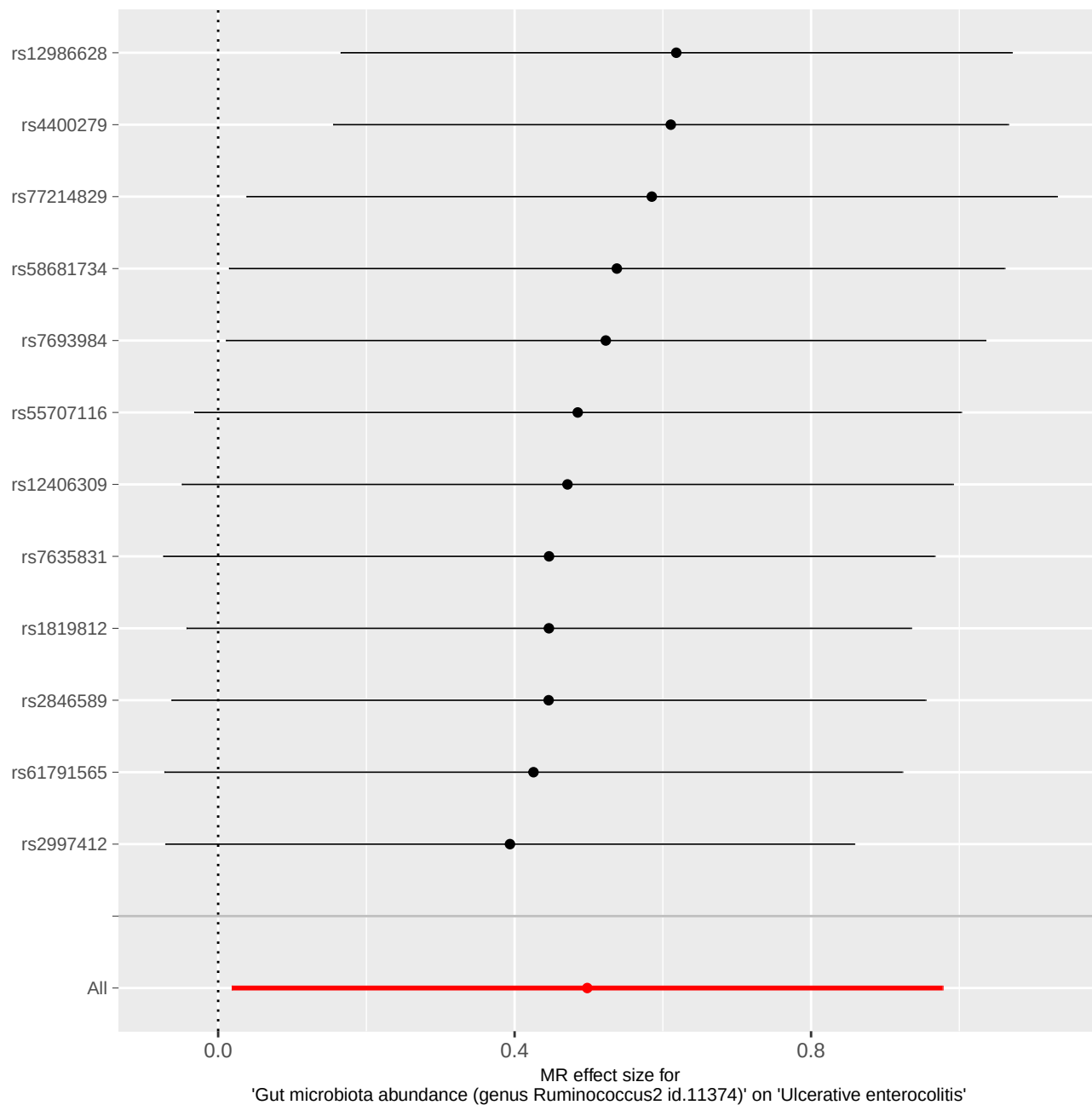


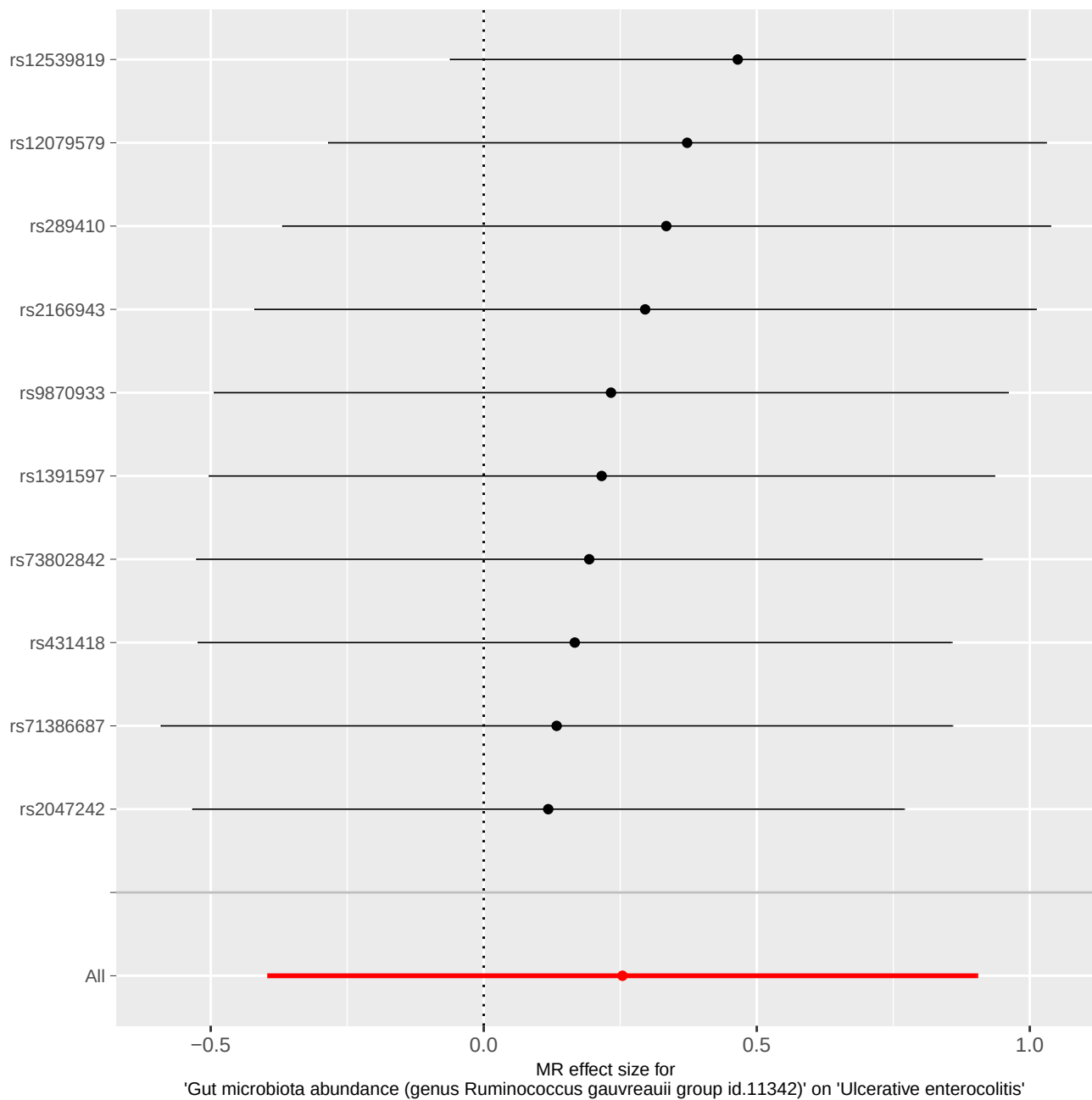


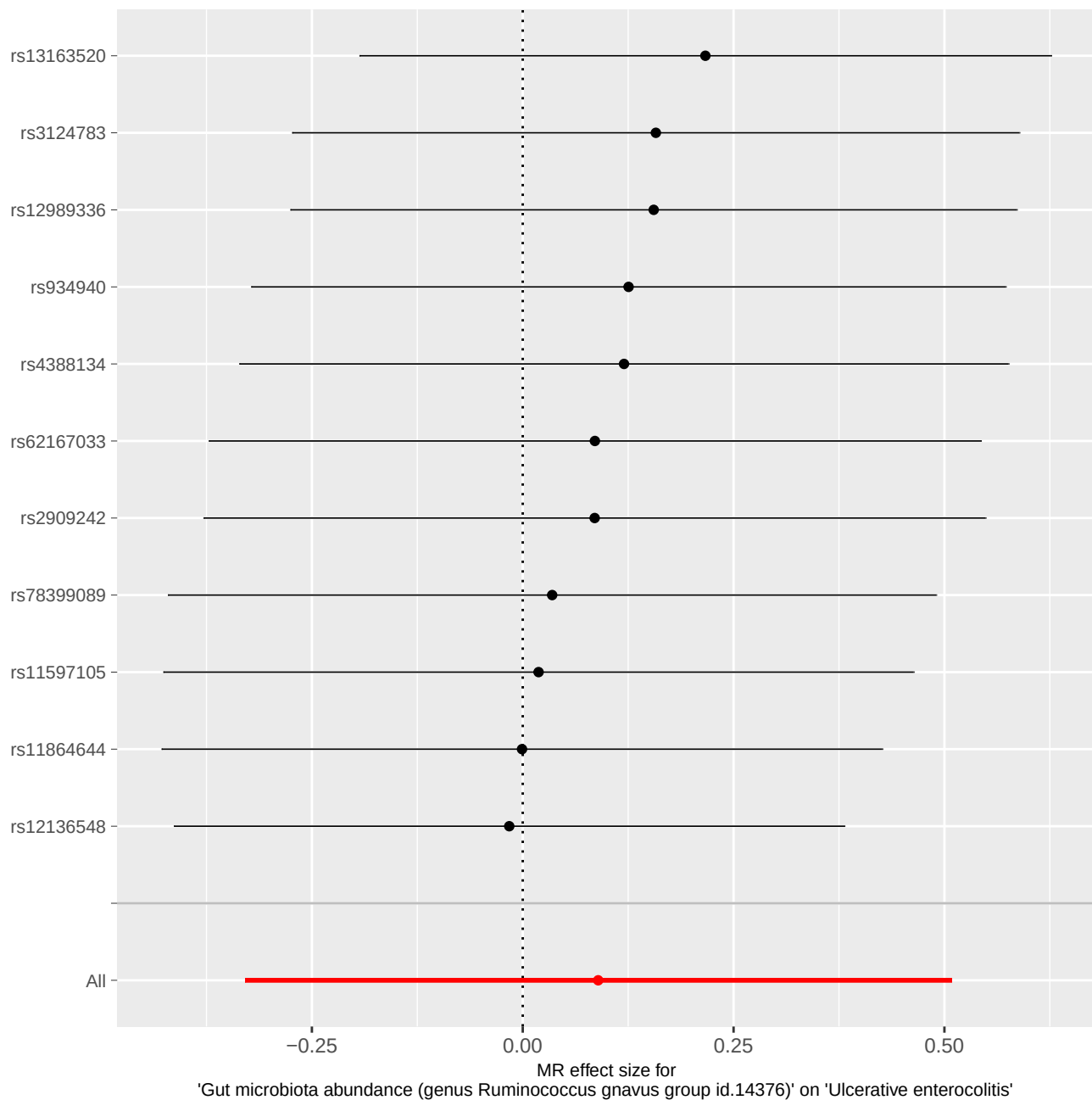


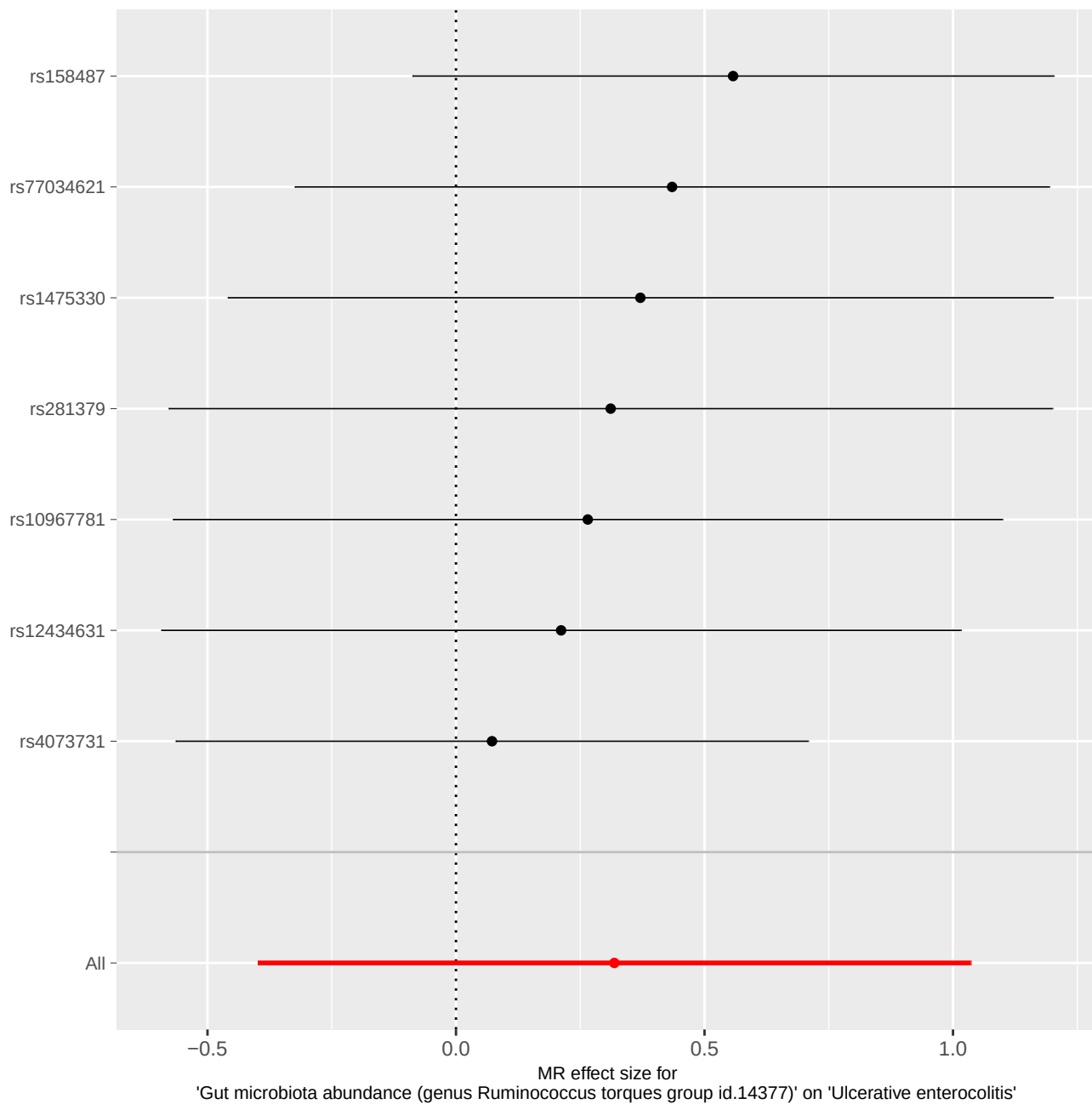




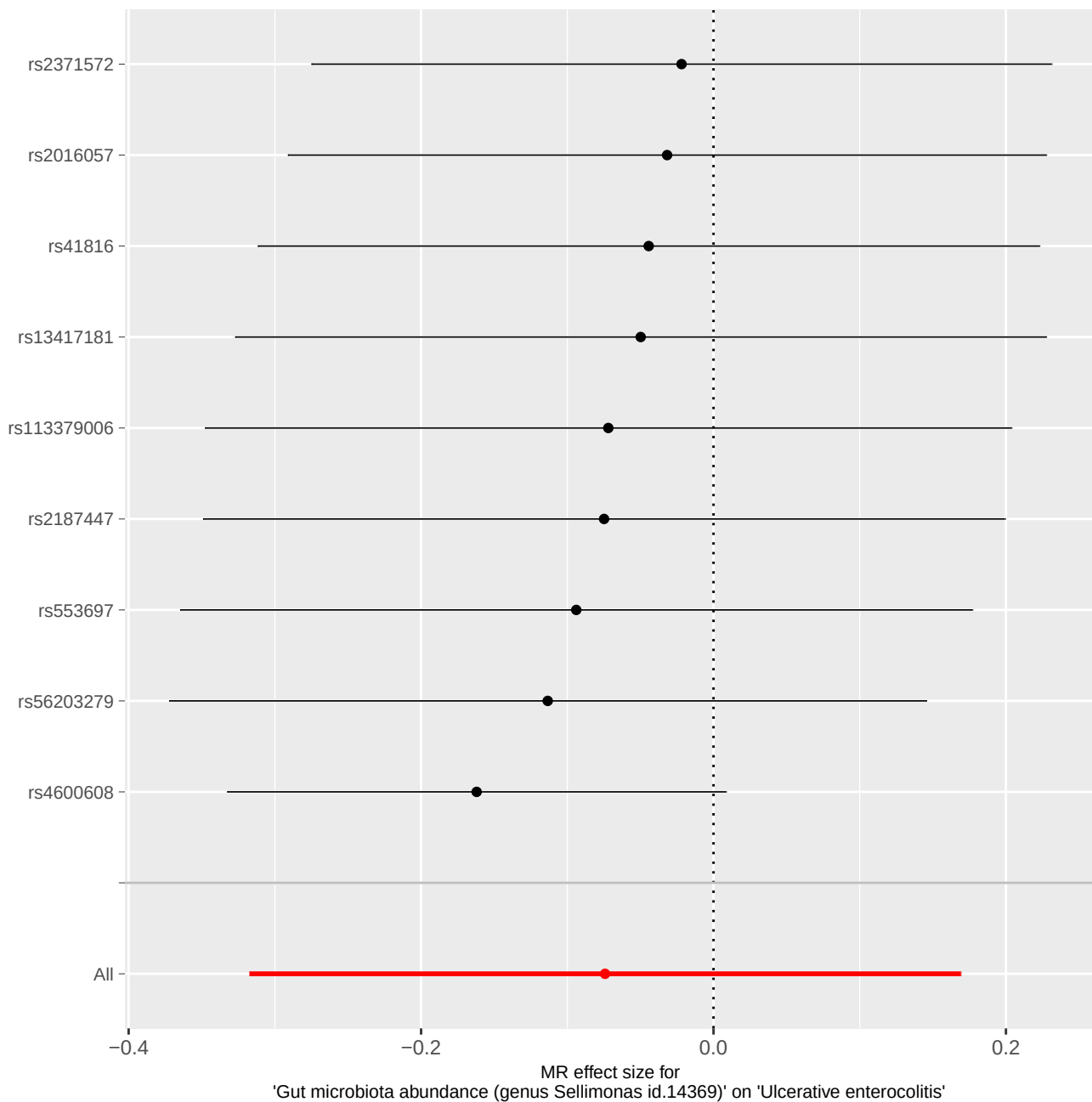


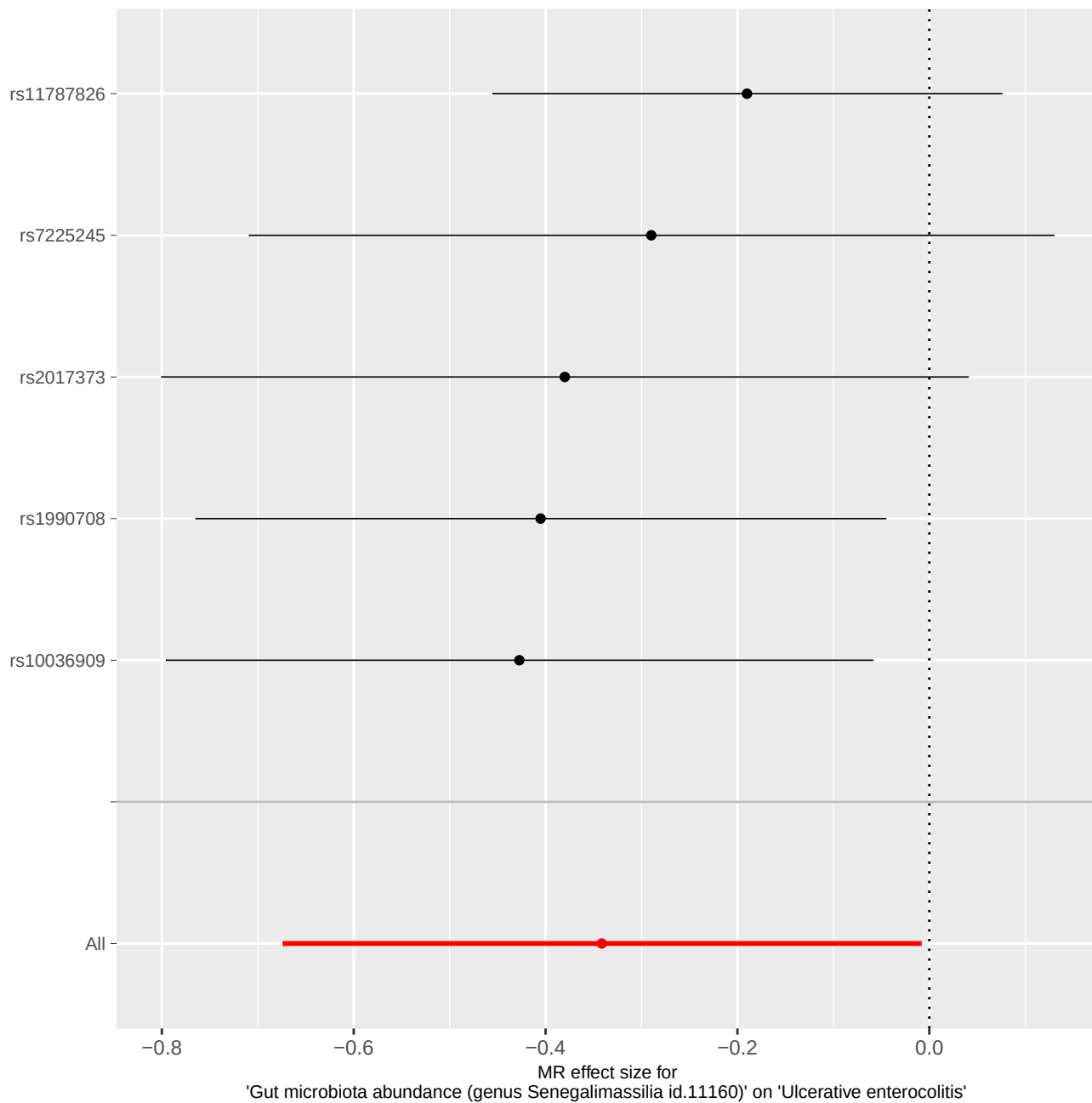


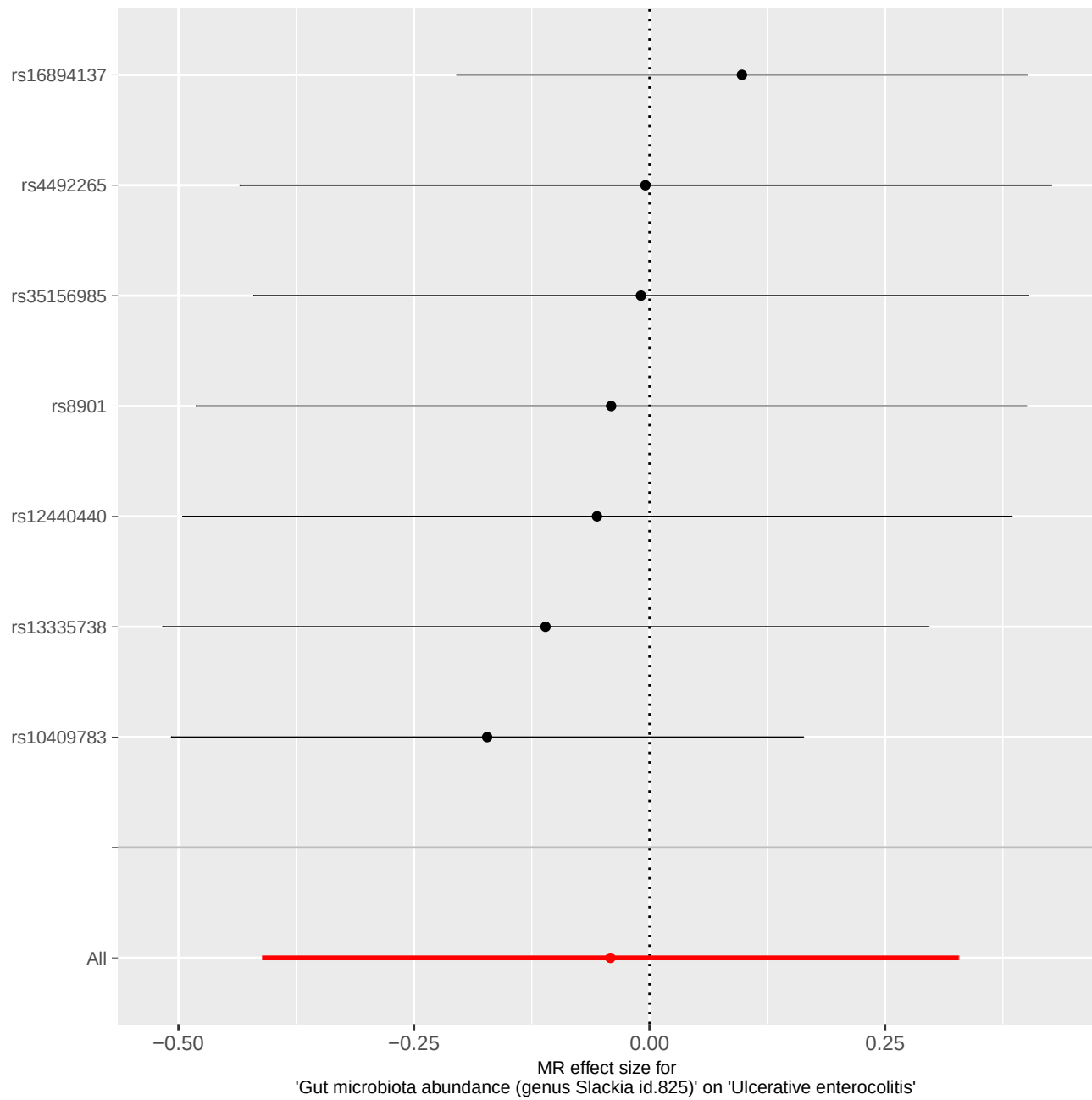


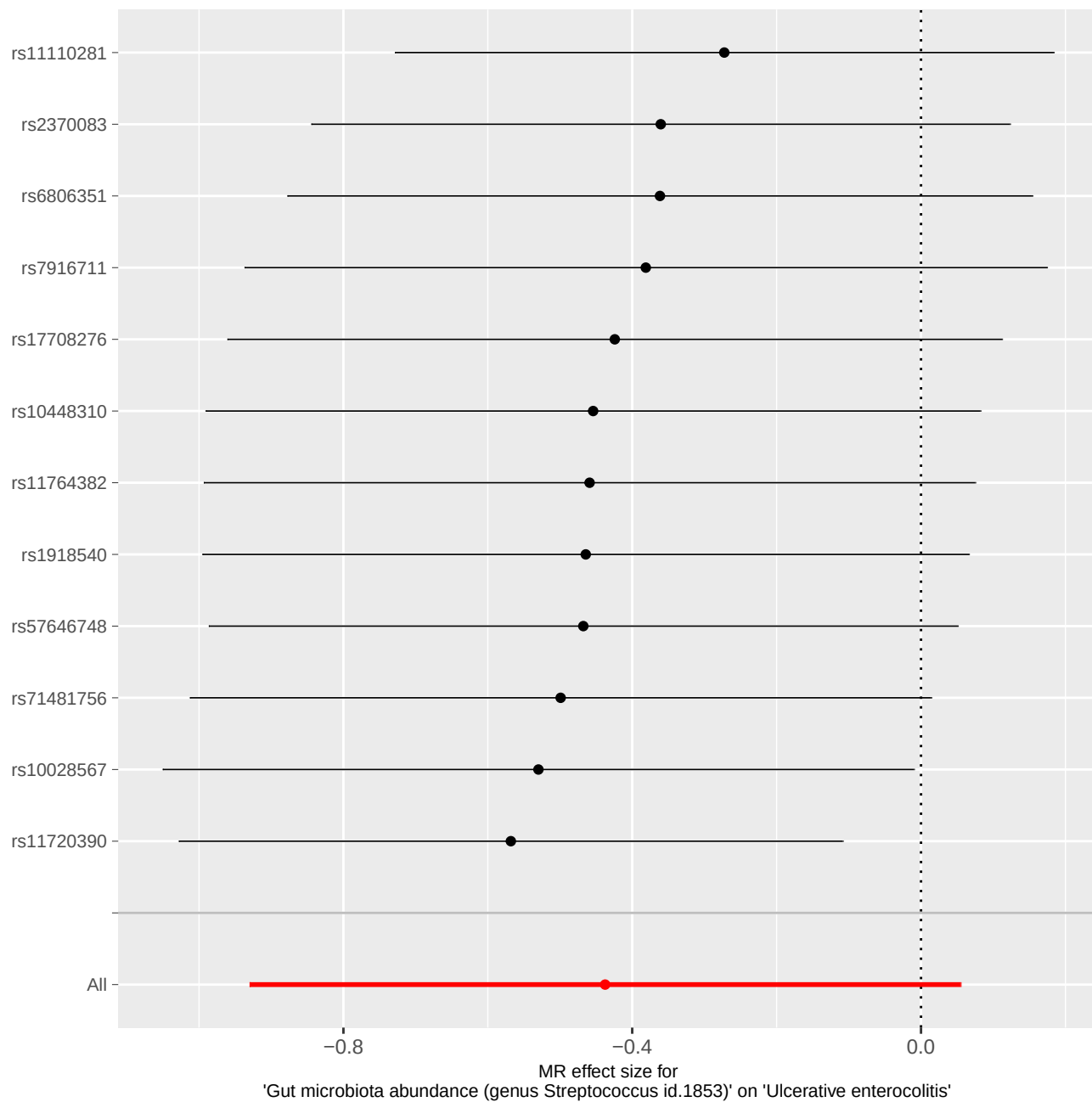


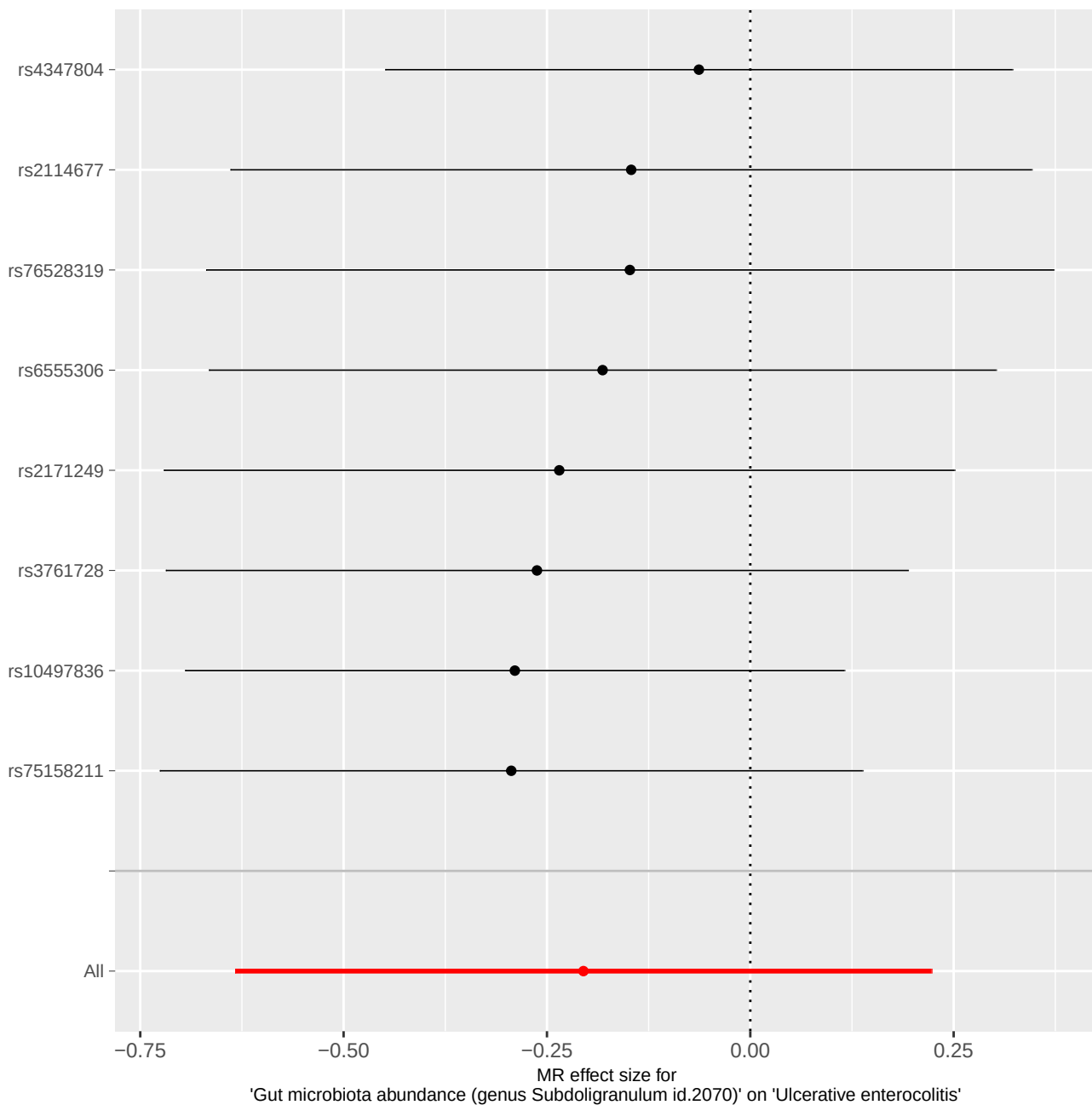
MR effect size for
'Gut microbiota abundance (genus Ruminococcus torques group id.14377)' on 'Ulcerative enterocolitis'

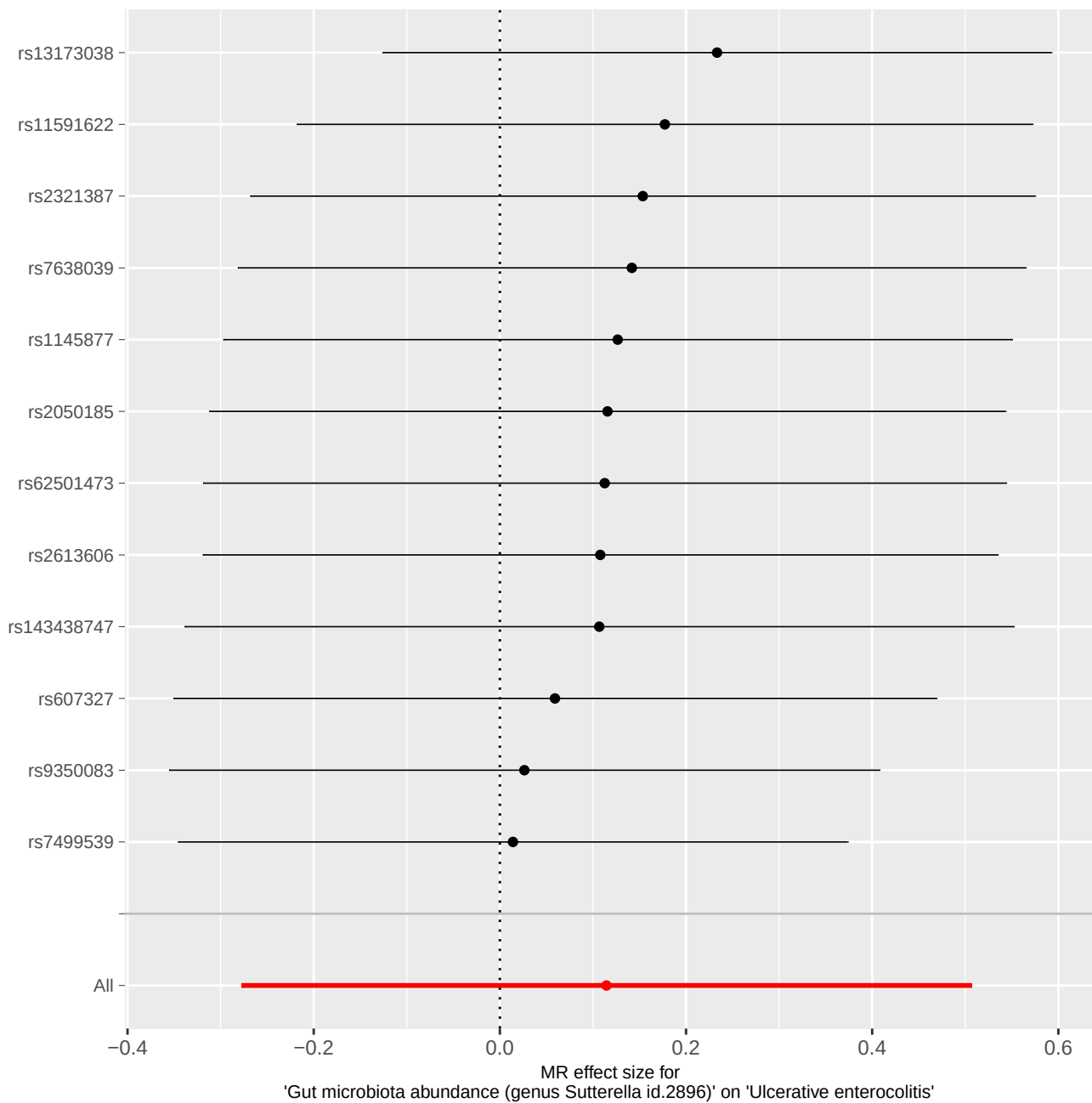


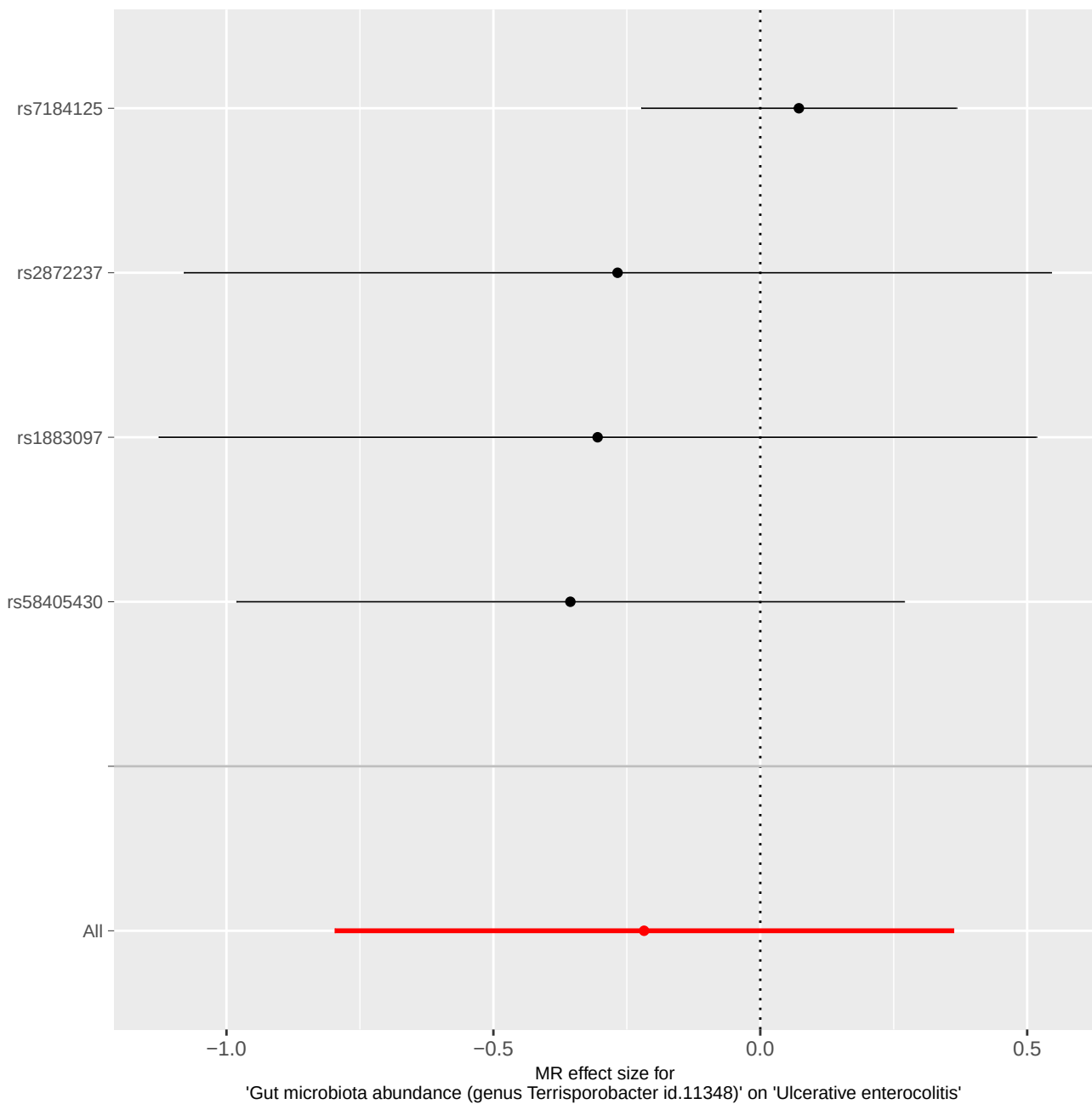


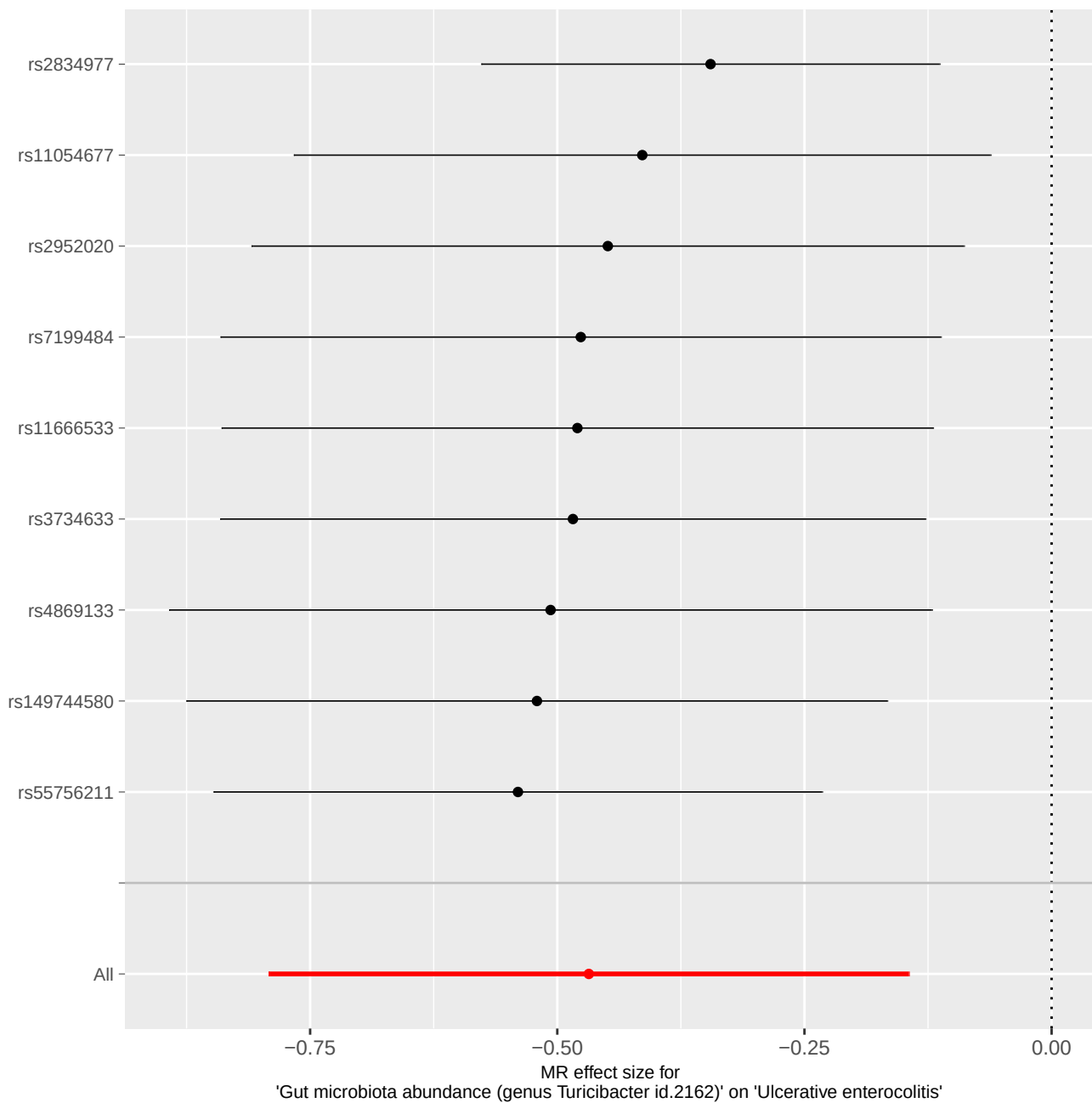


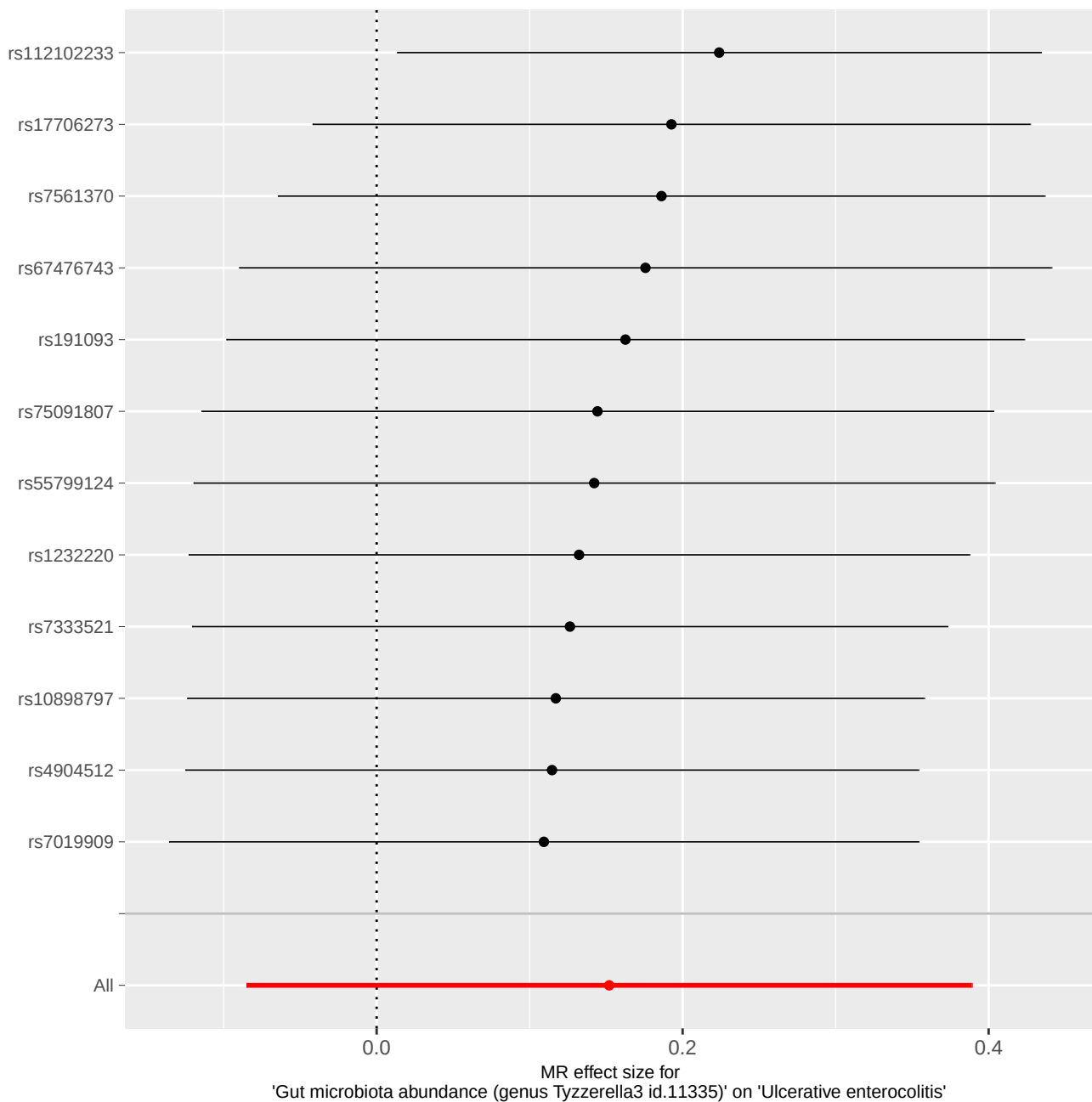


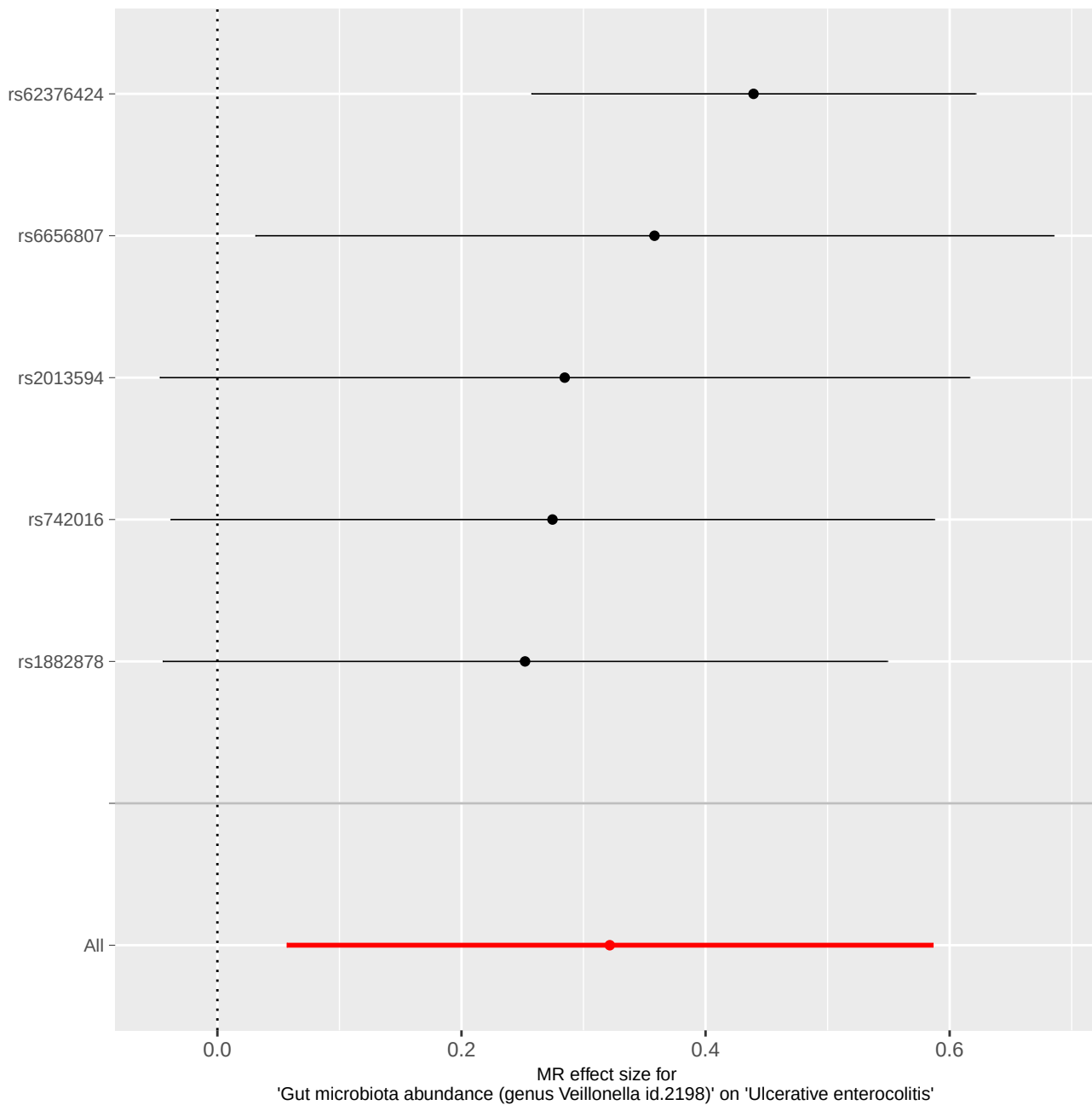


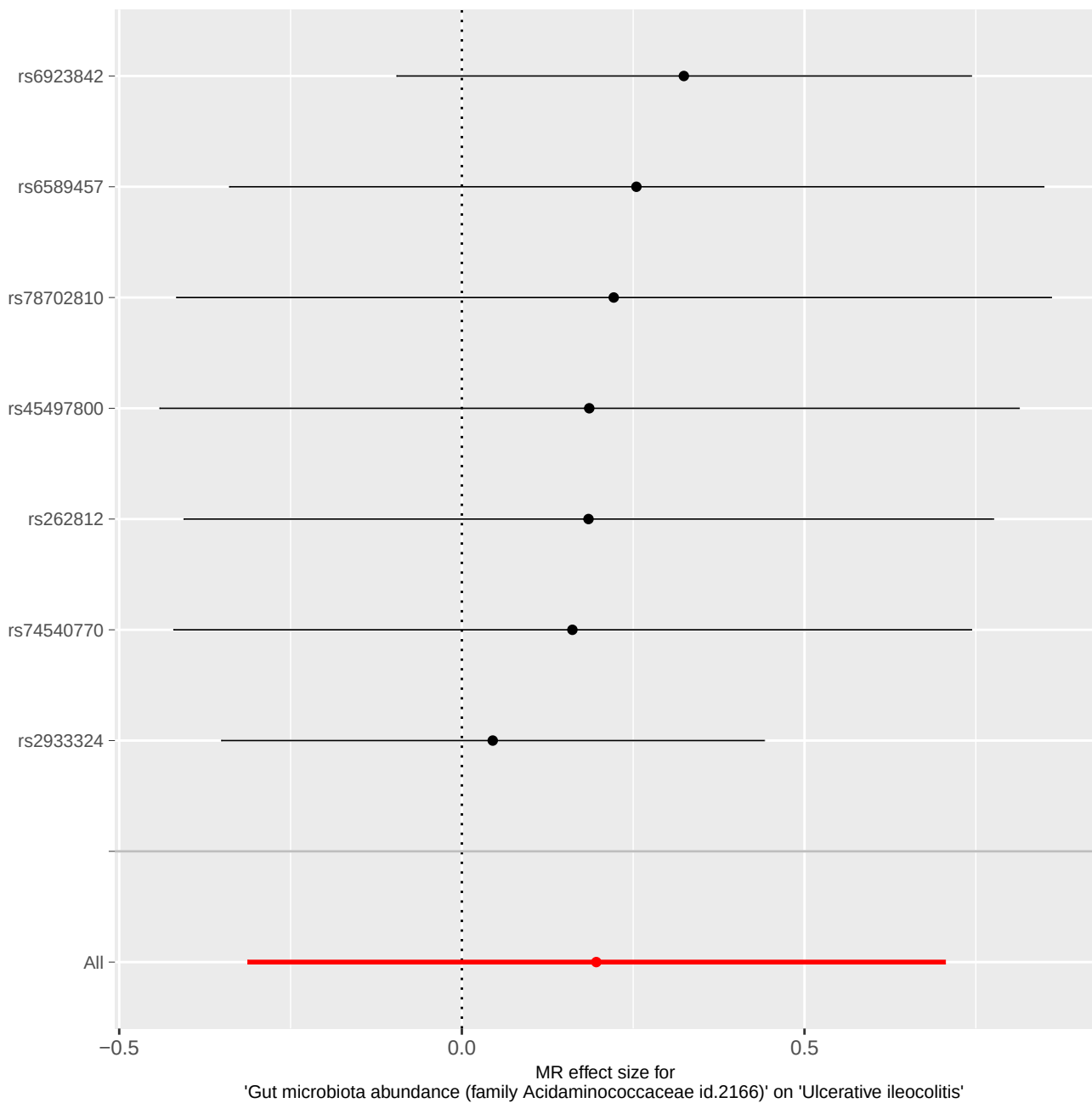


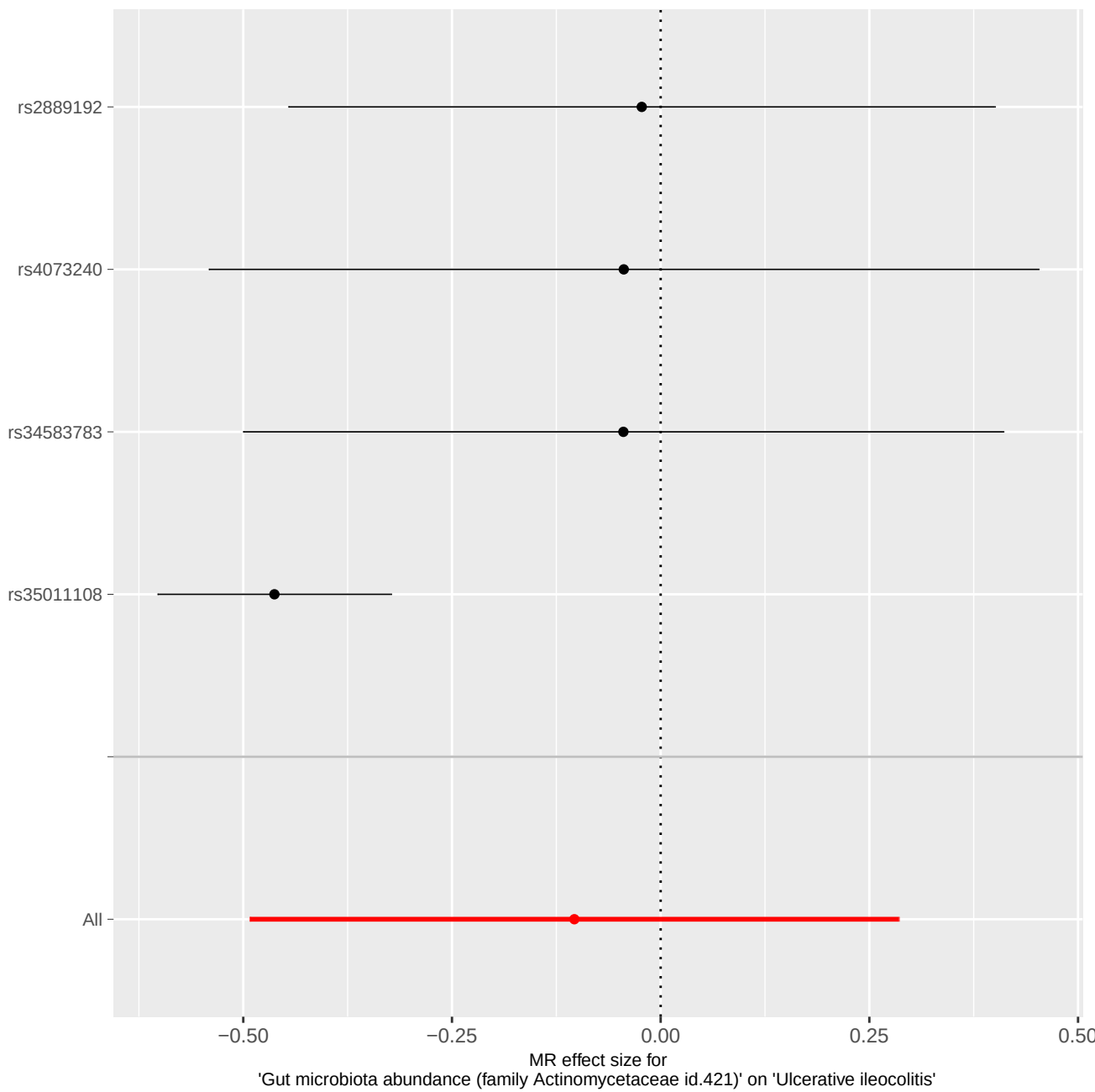


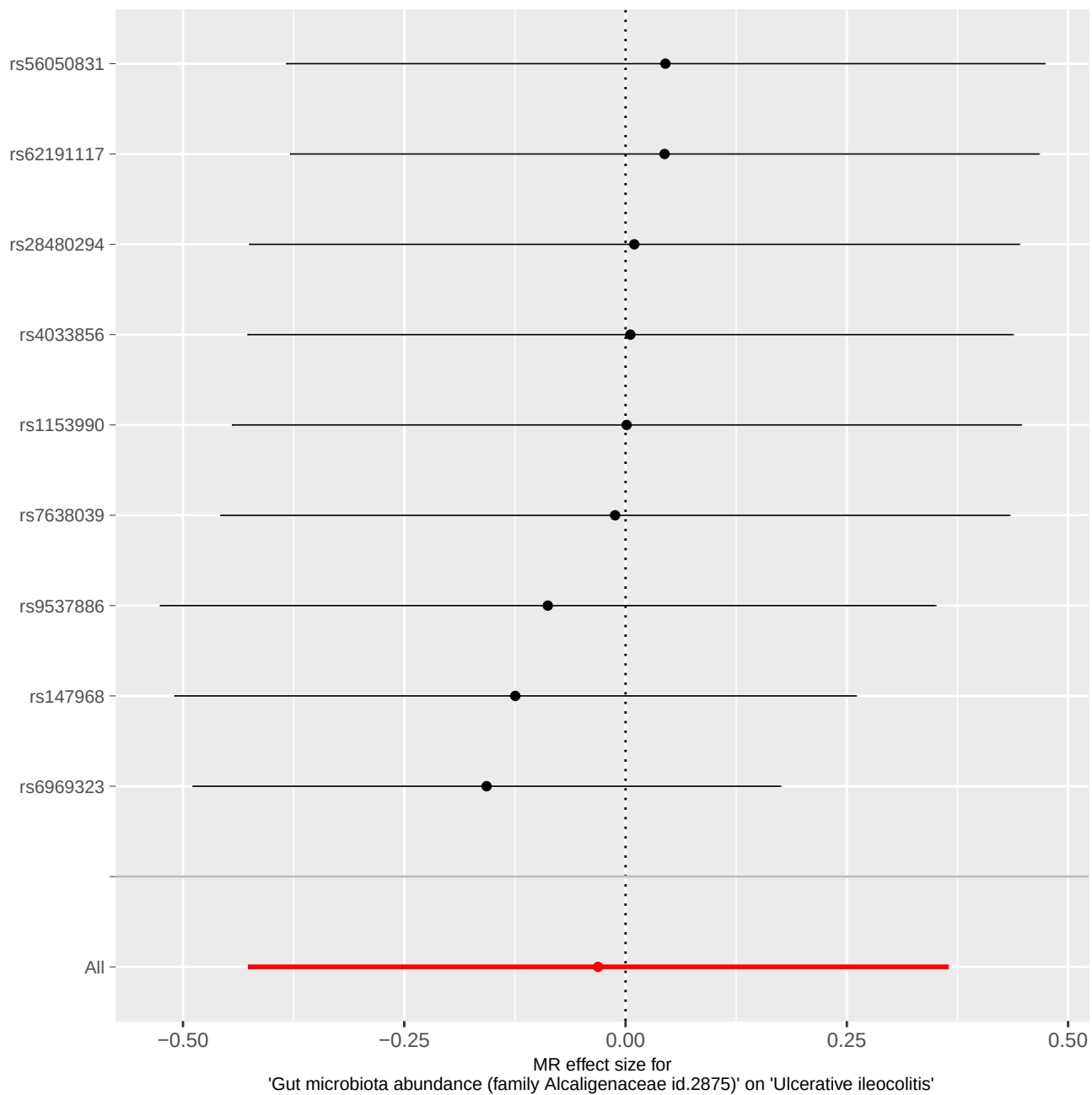


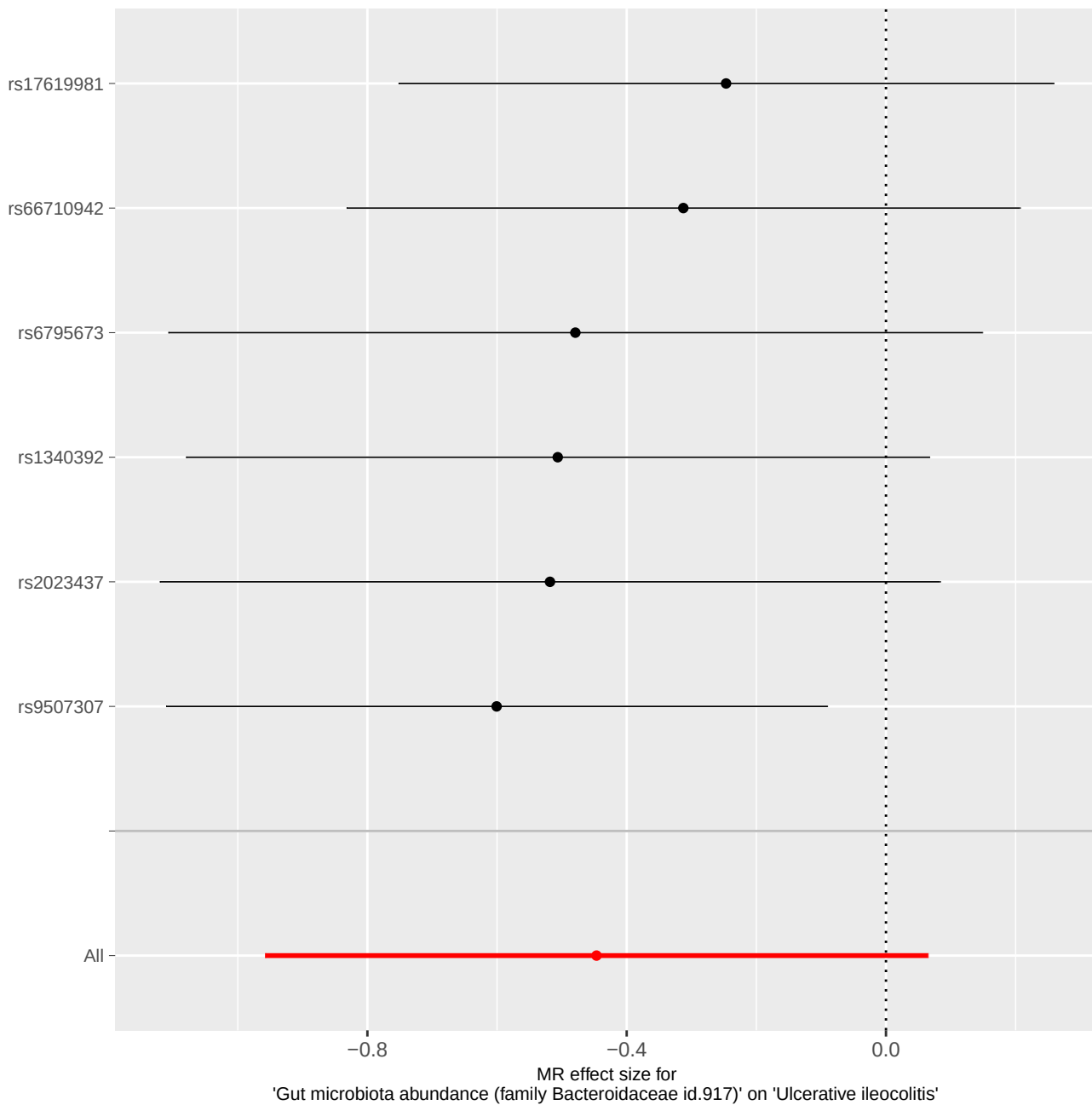


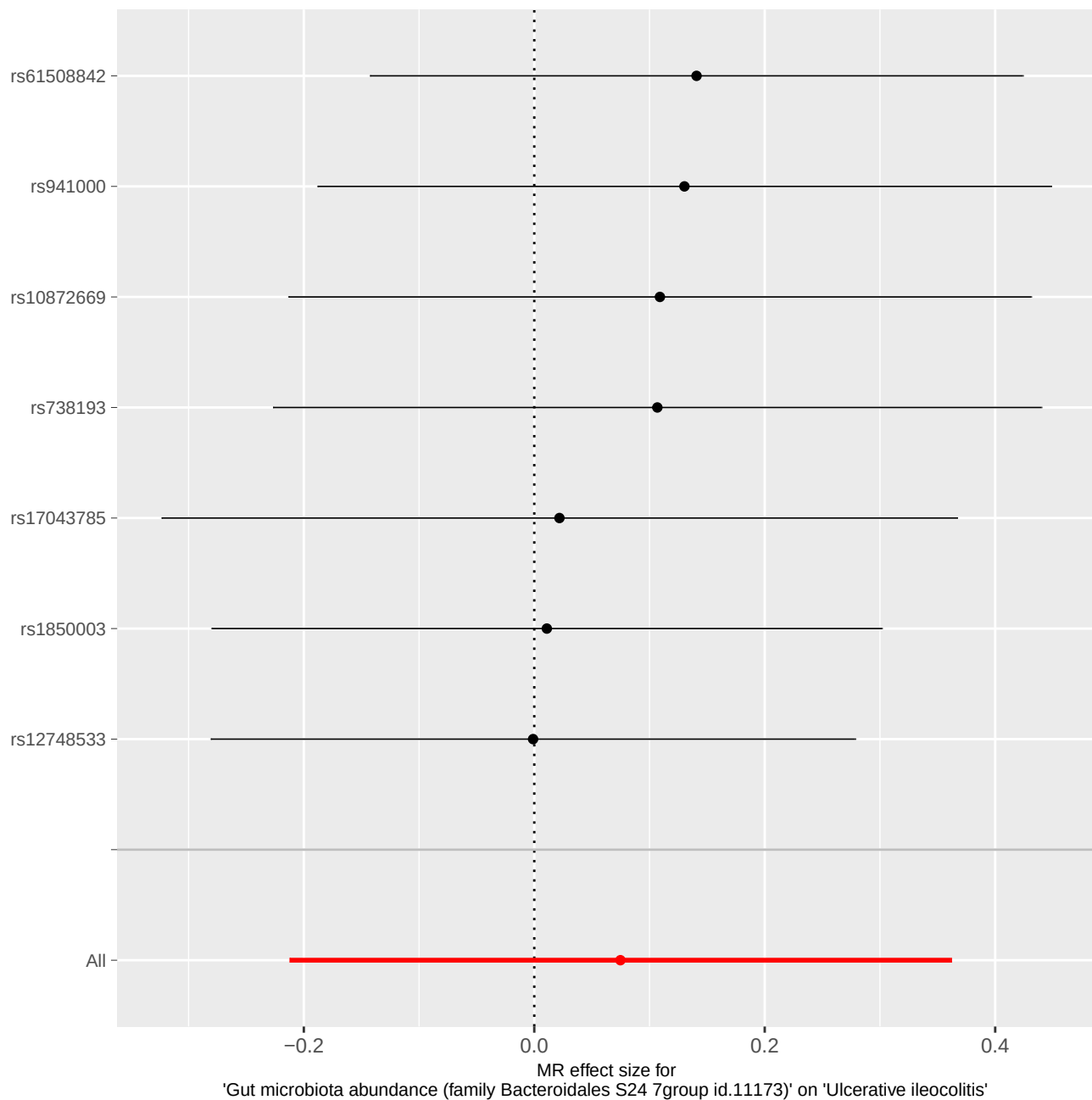


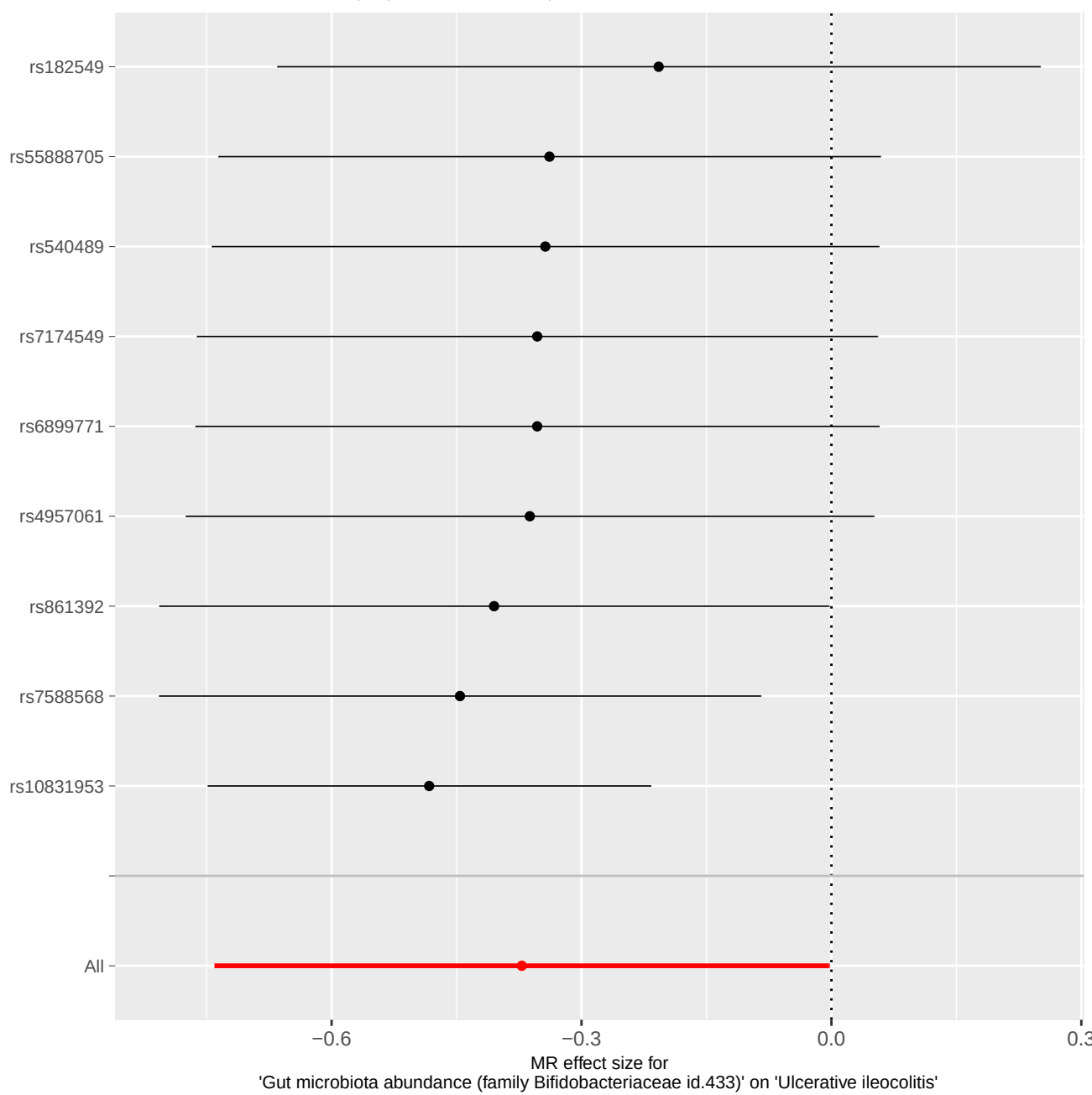


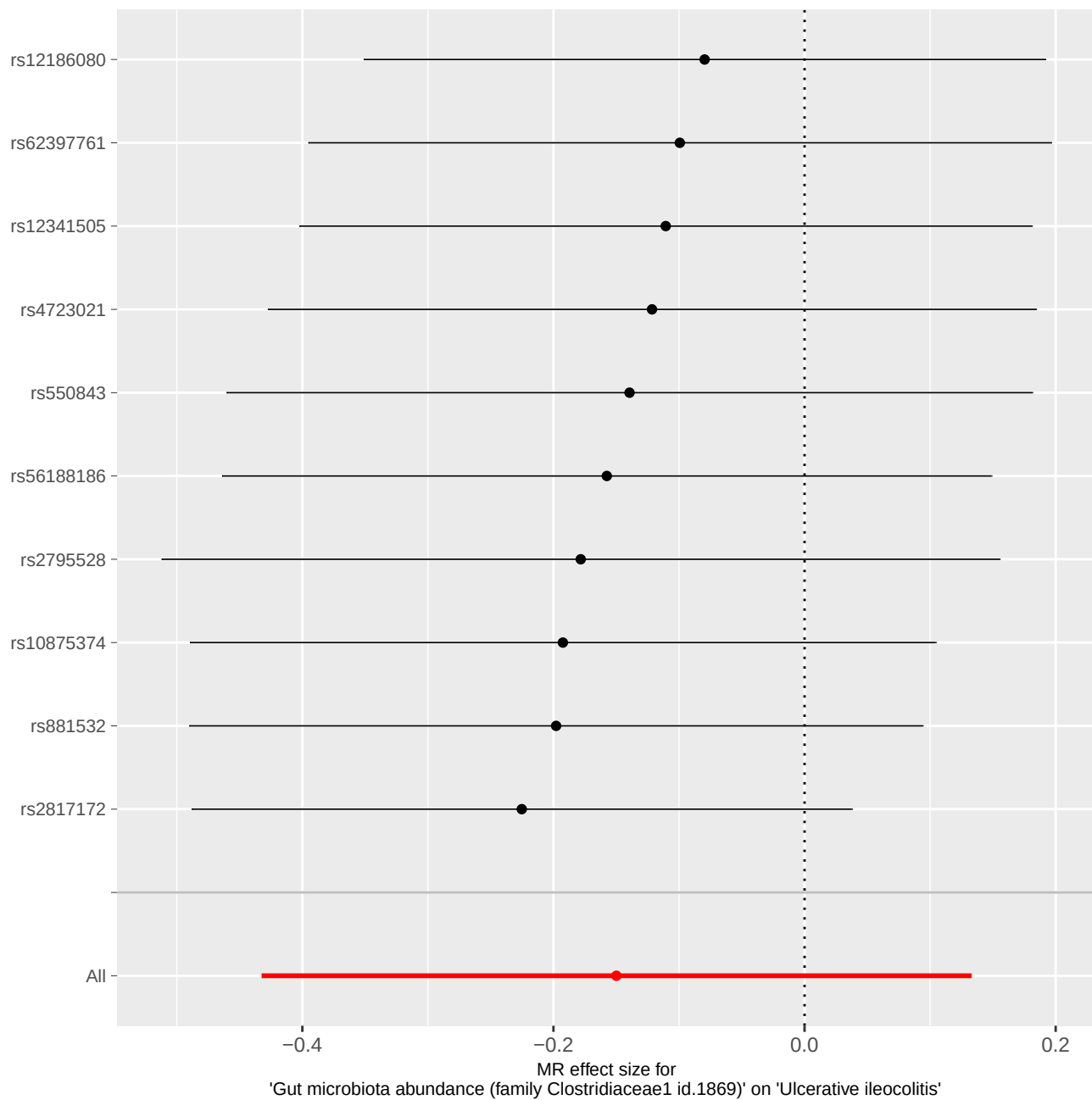


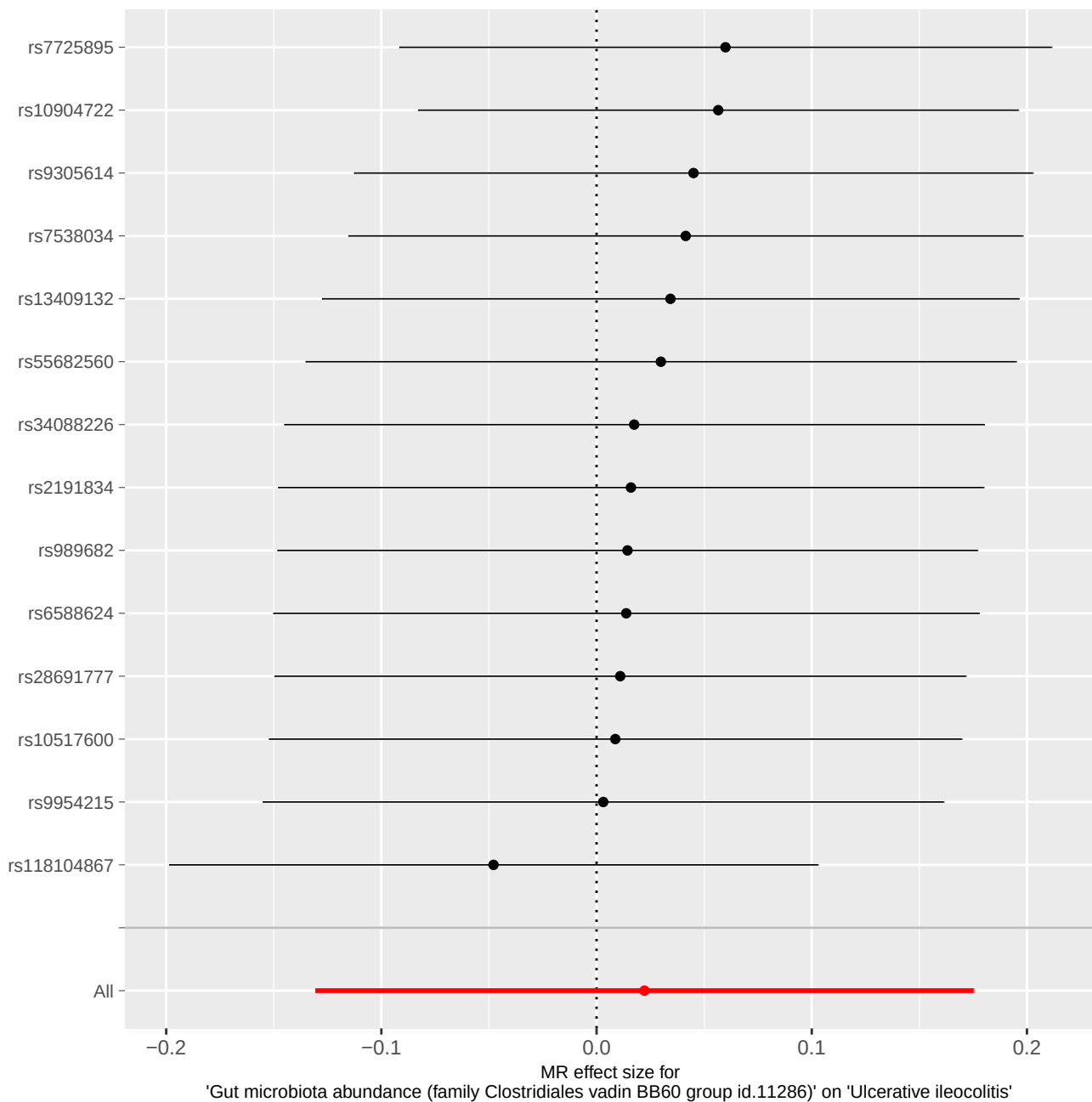


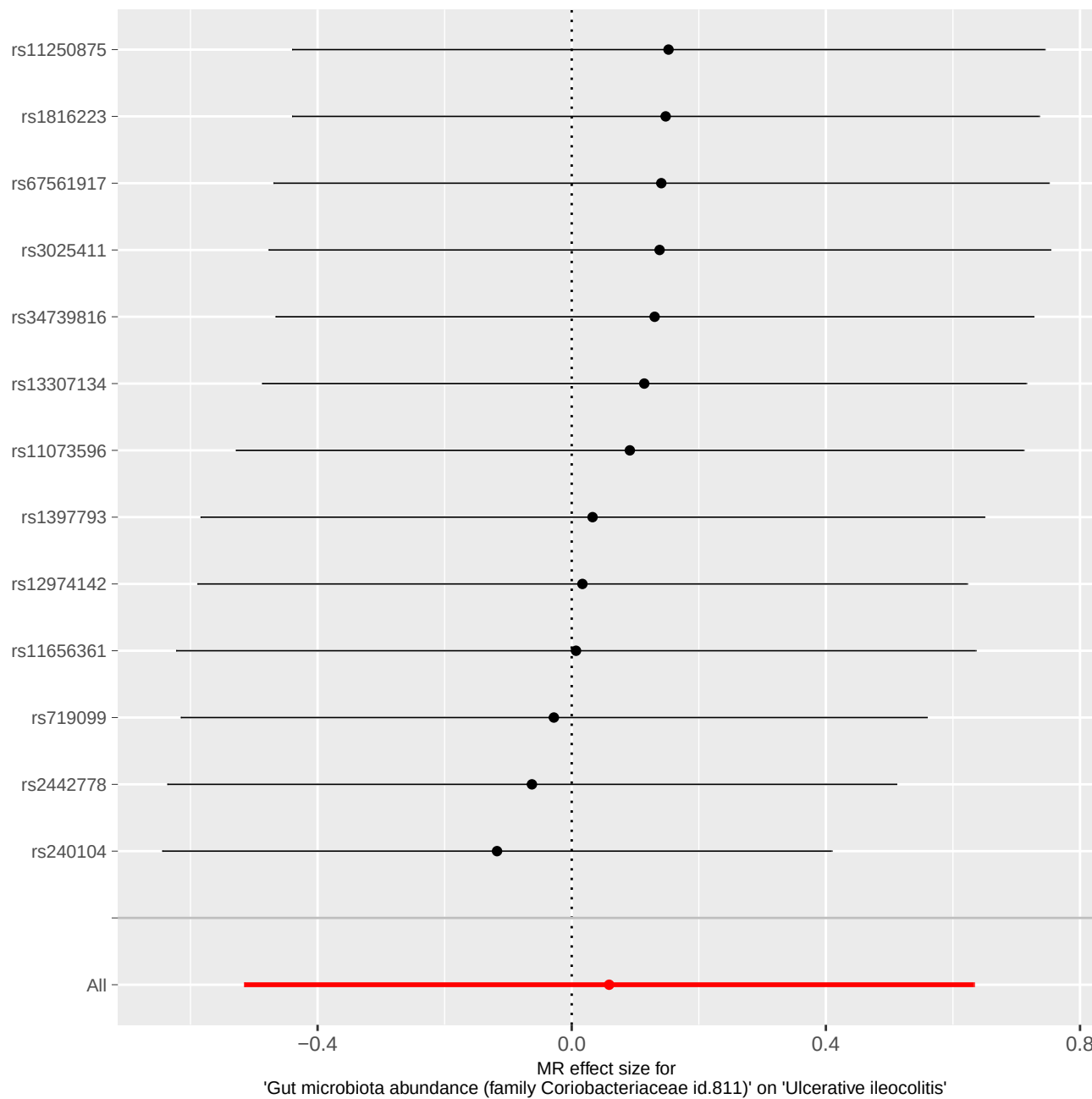


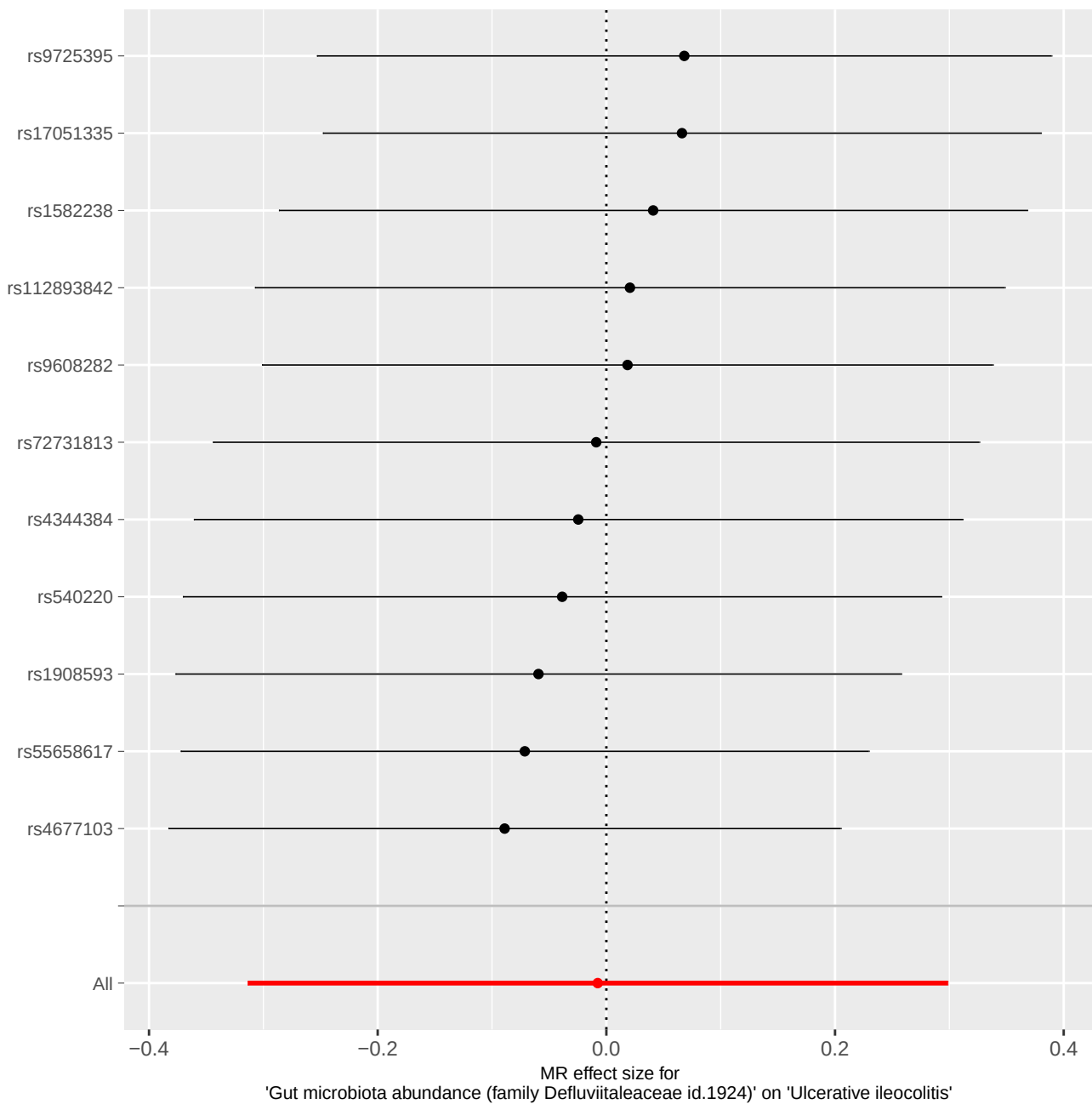


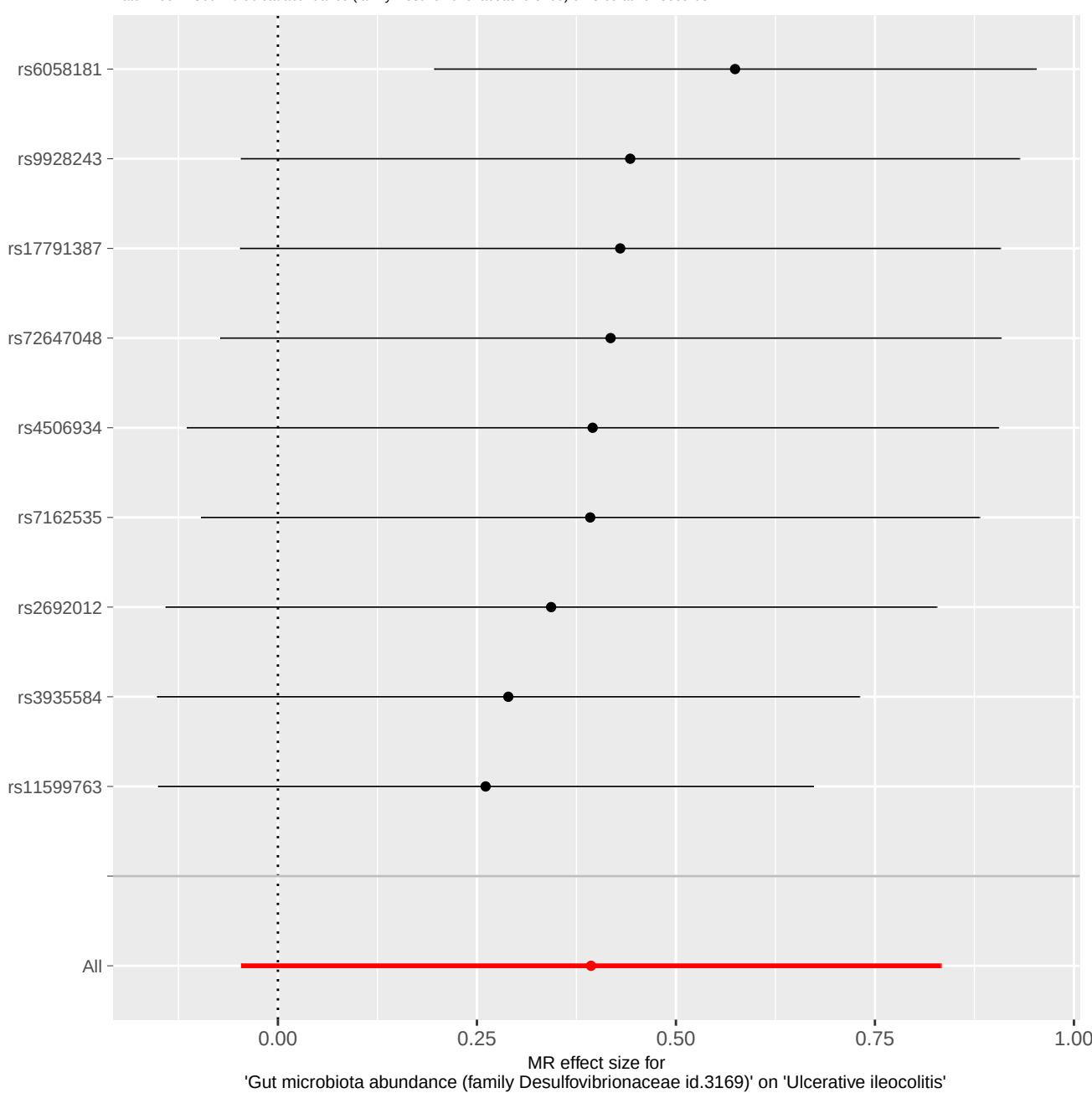


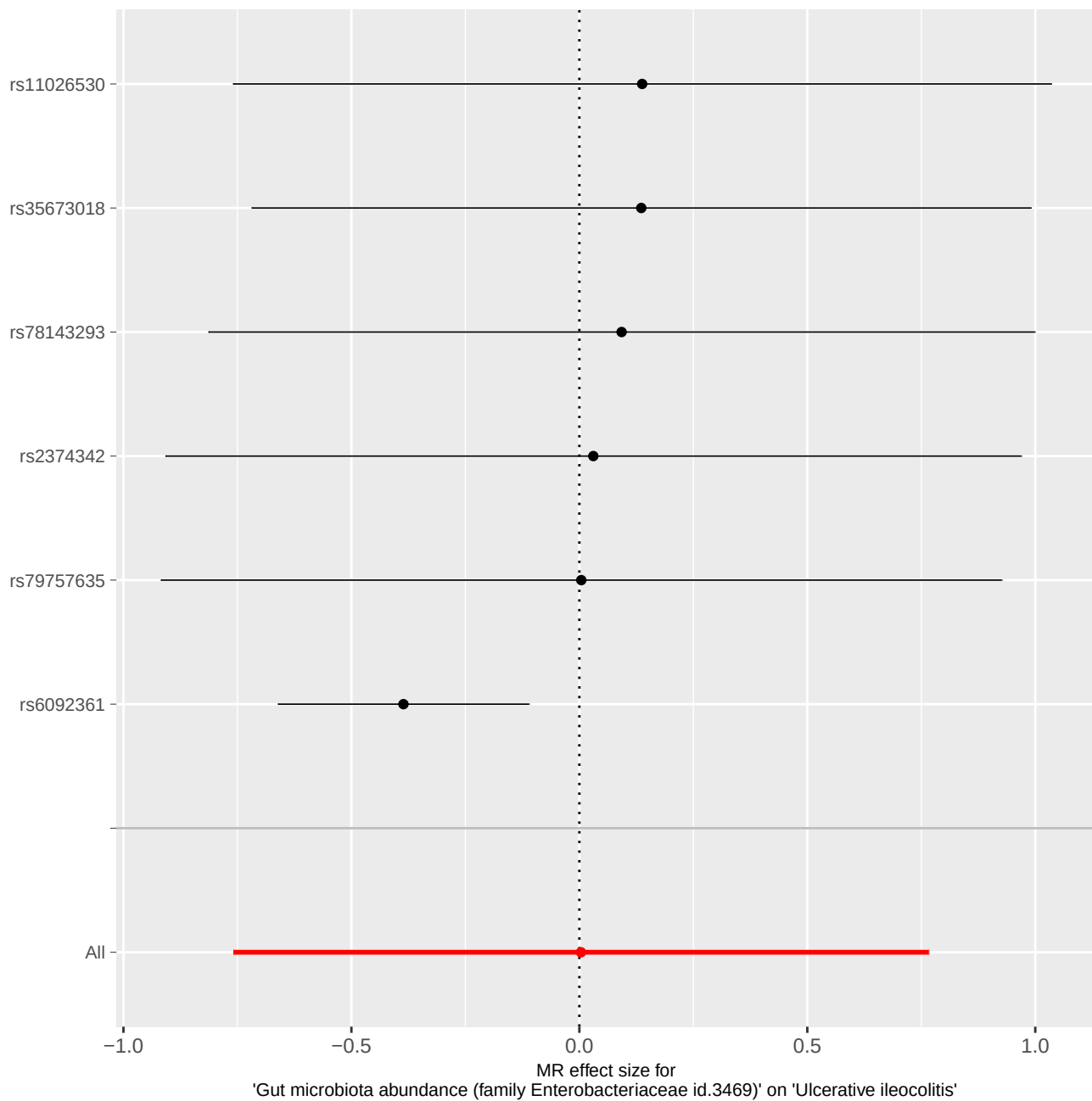


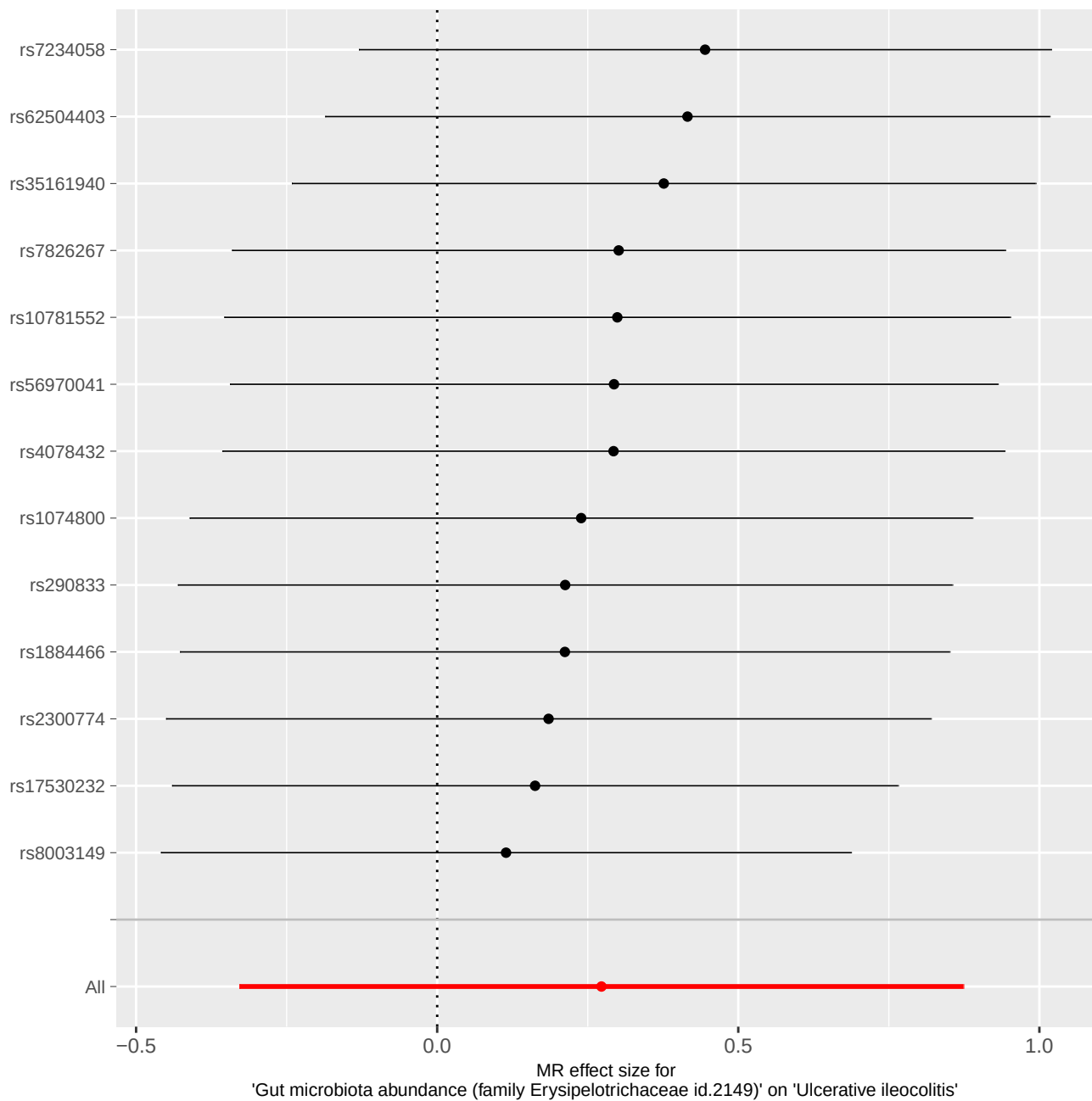


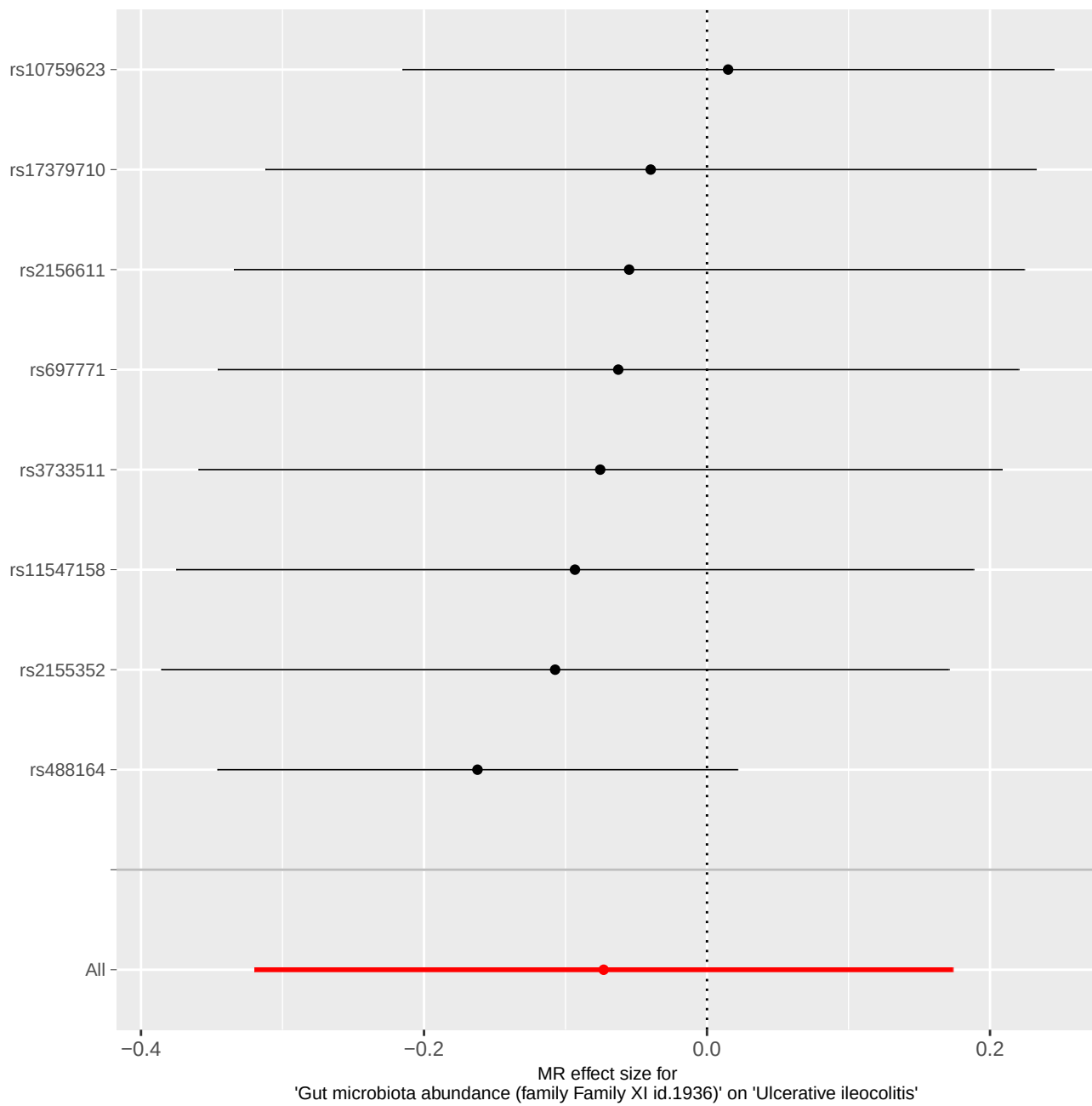


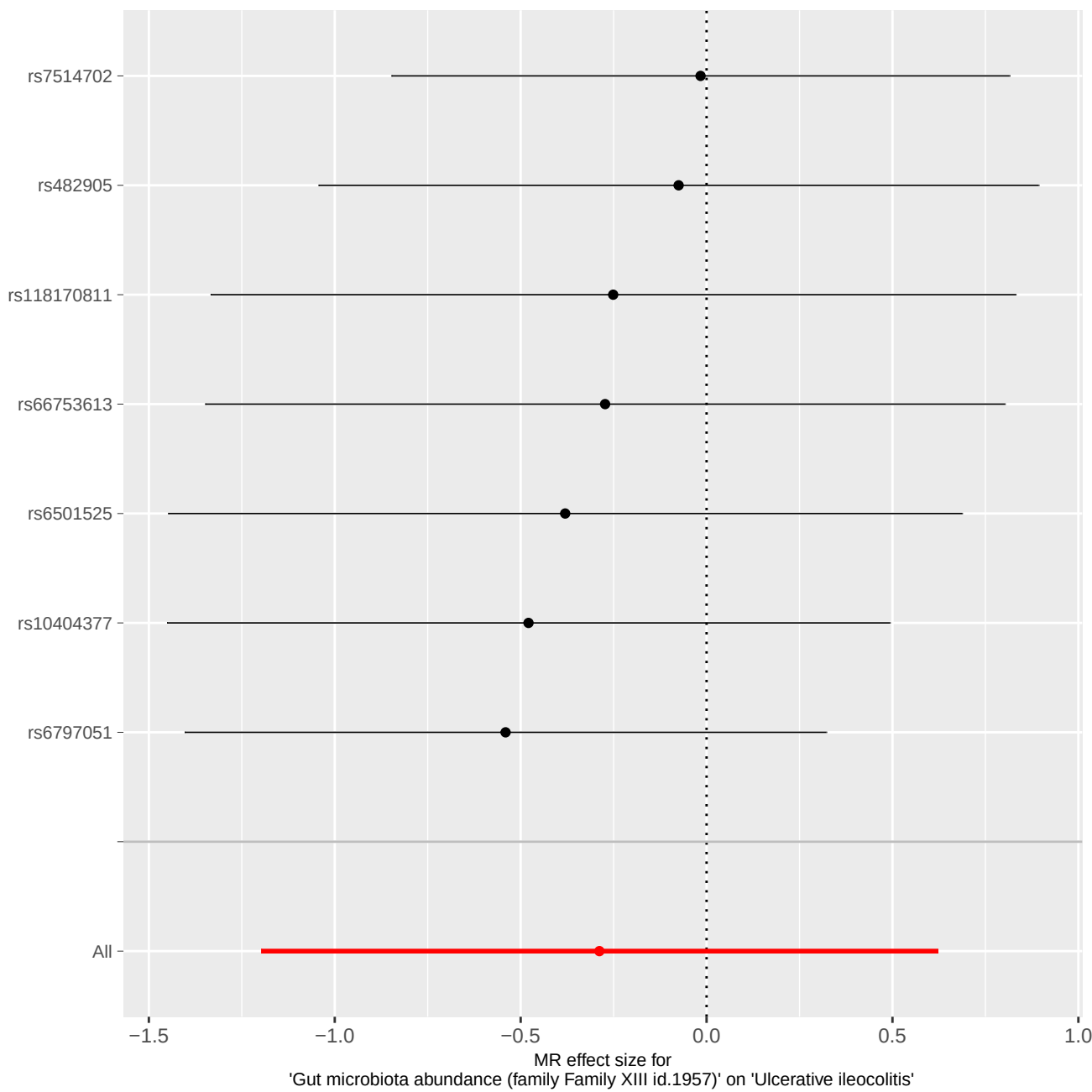


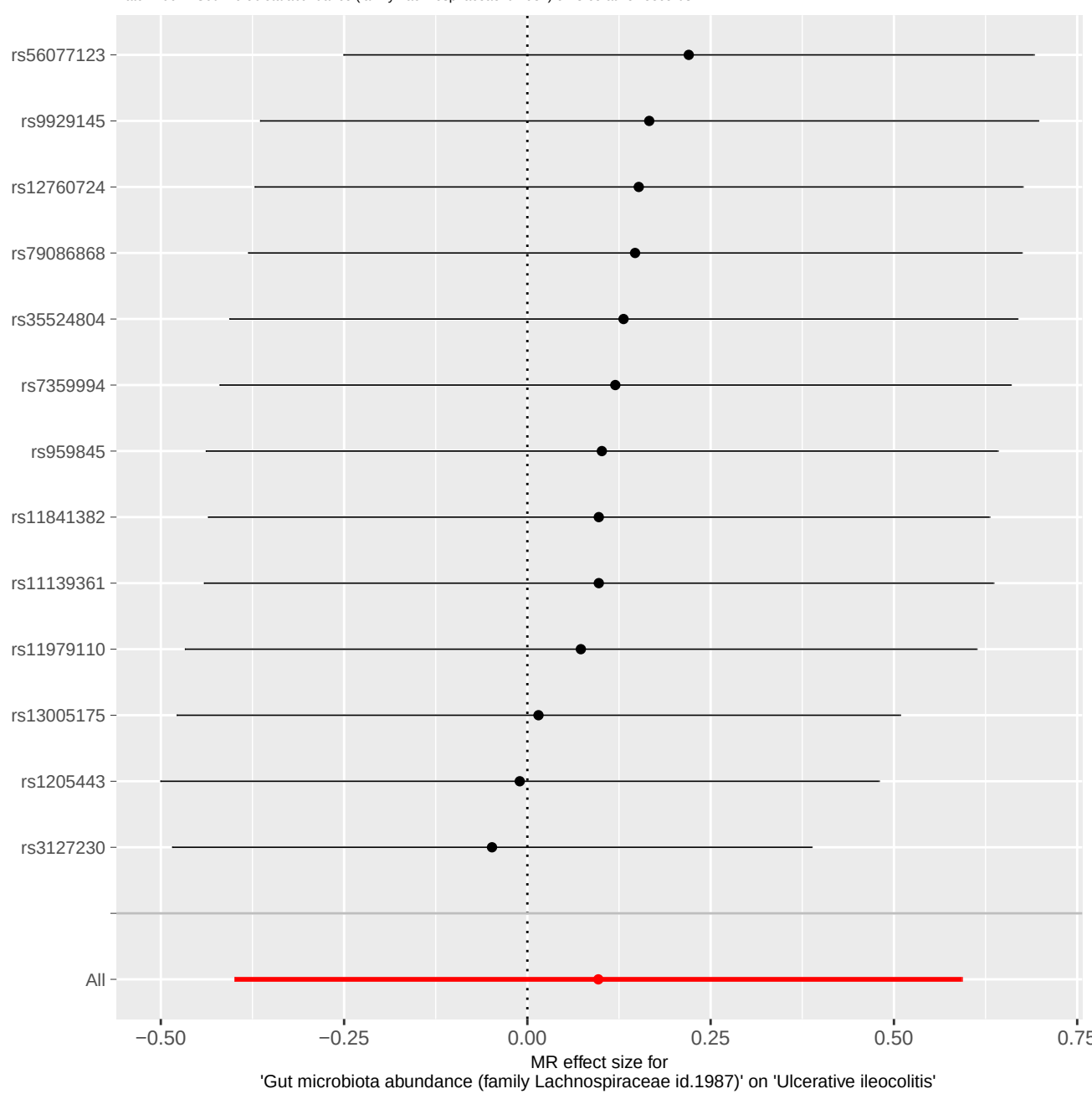


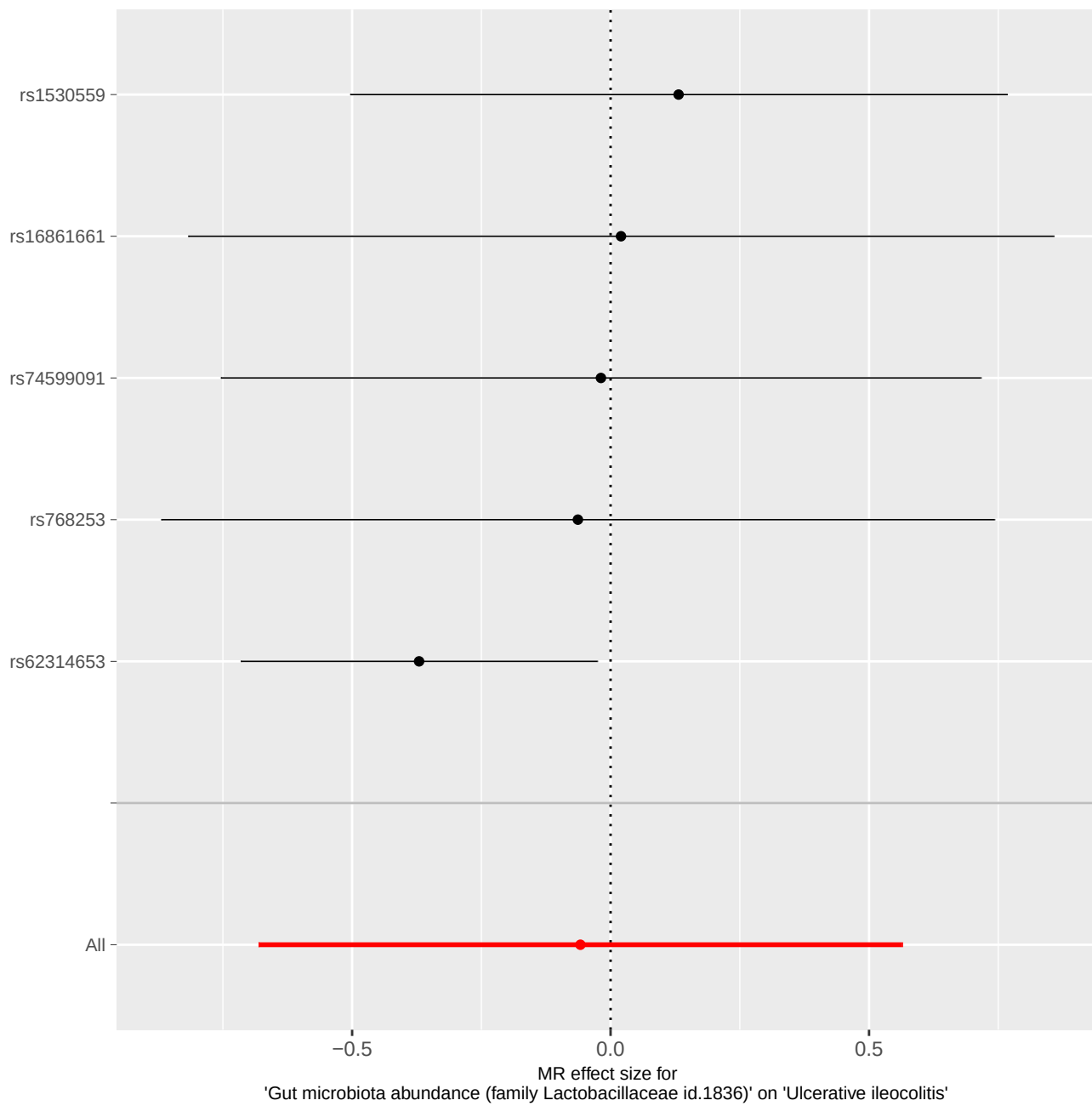


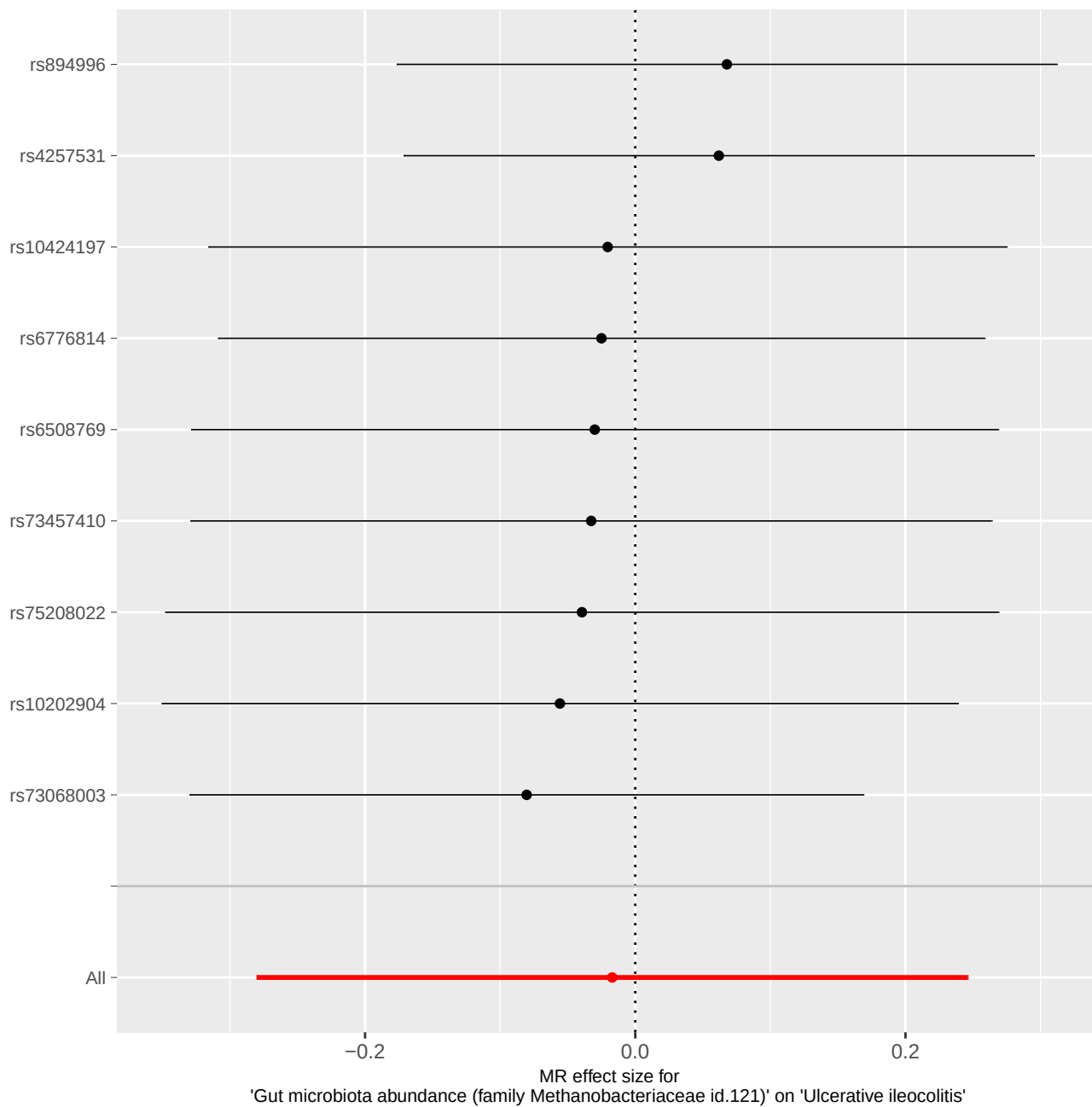


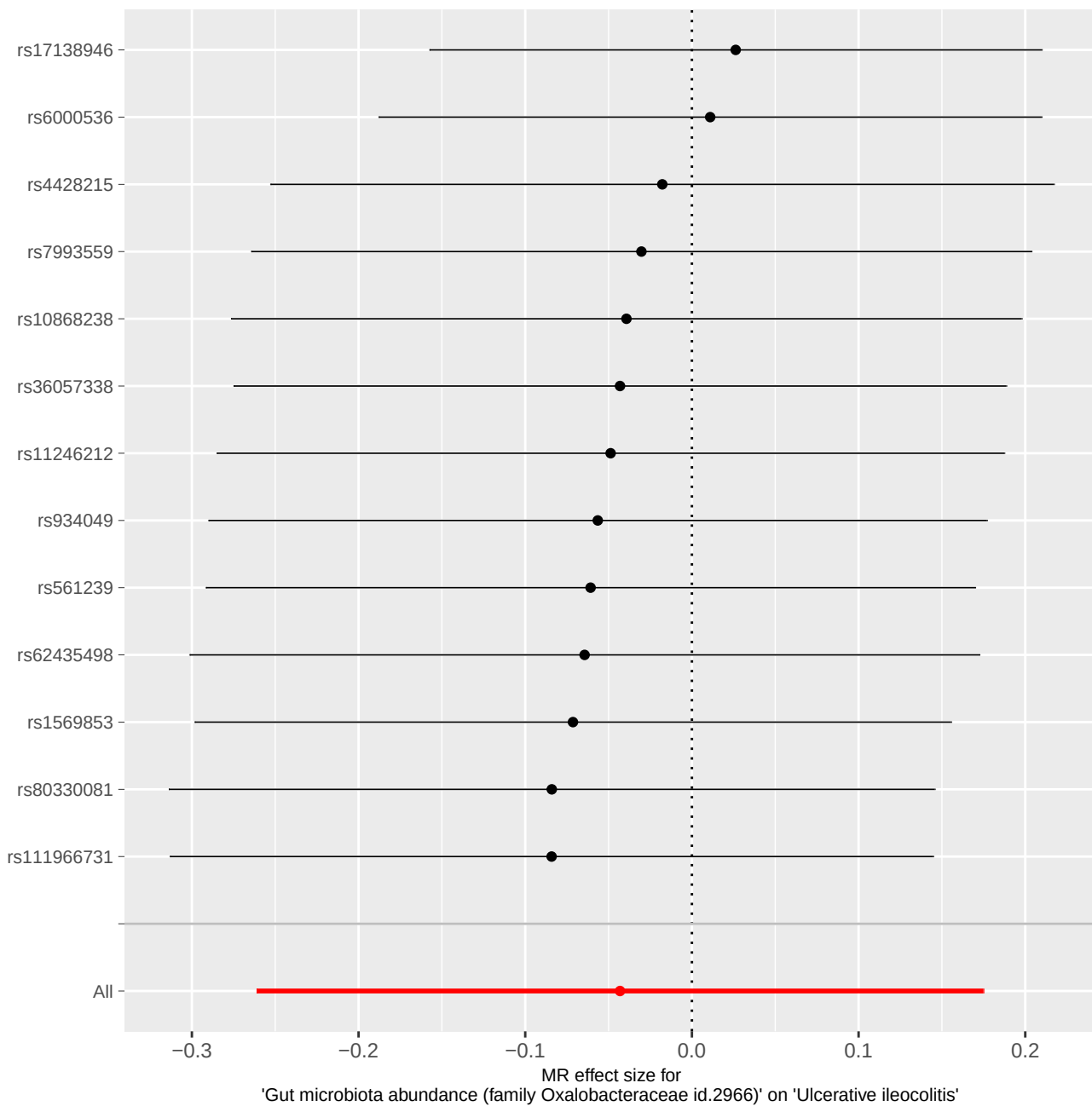


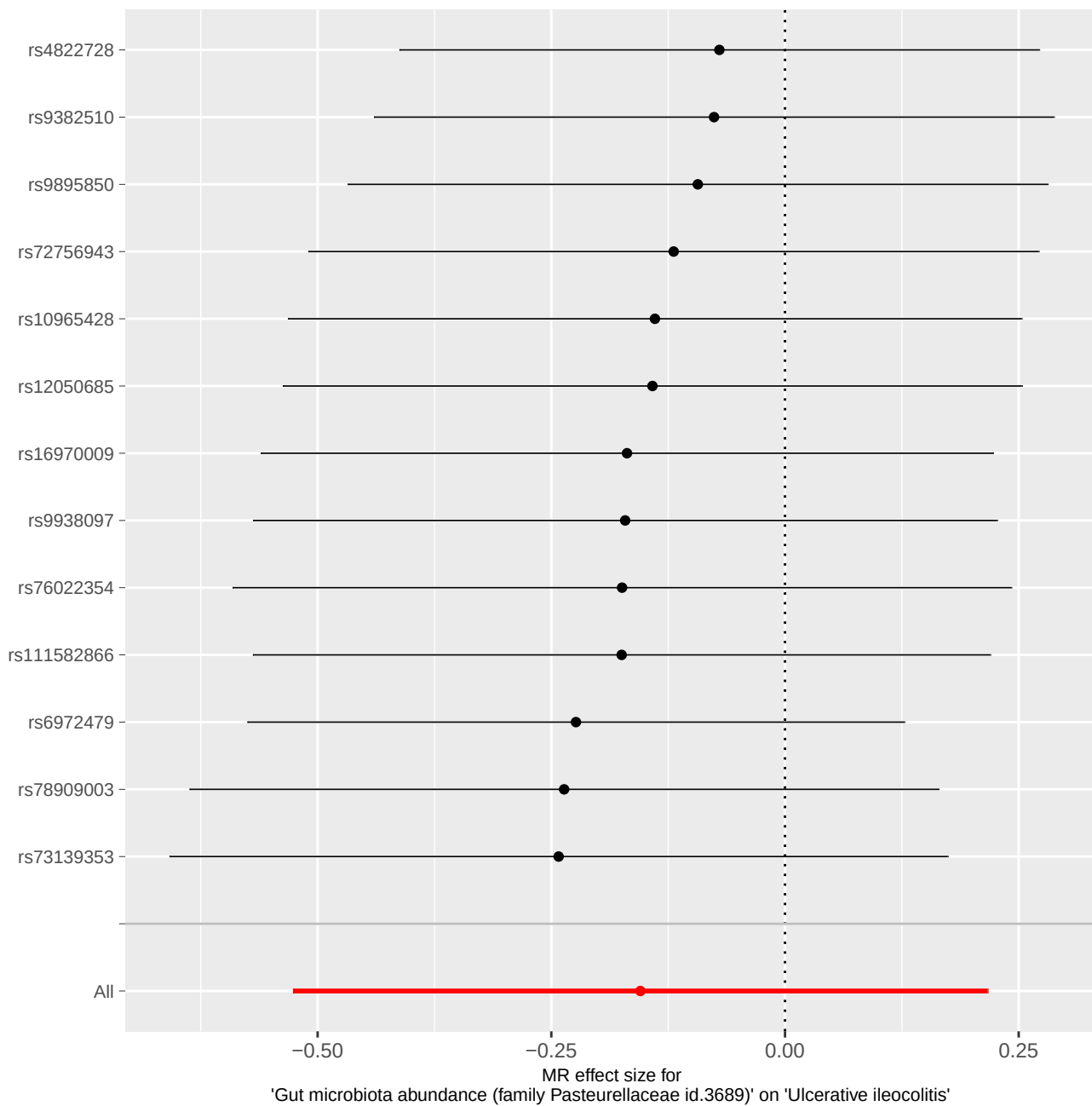


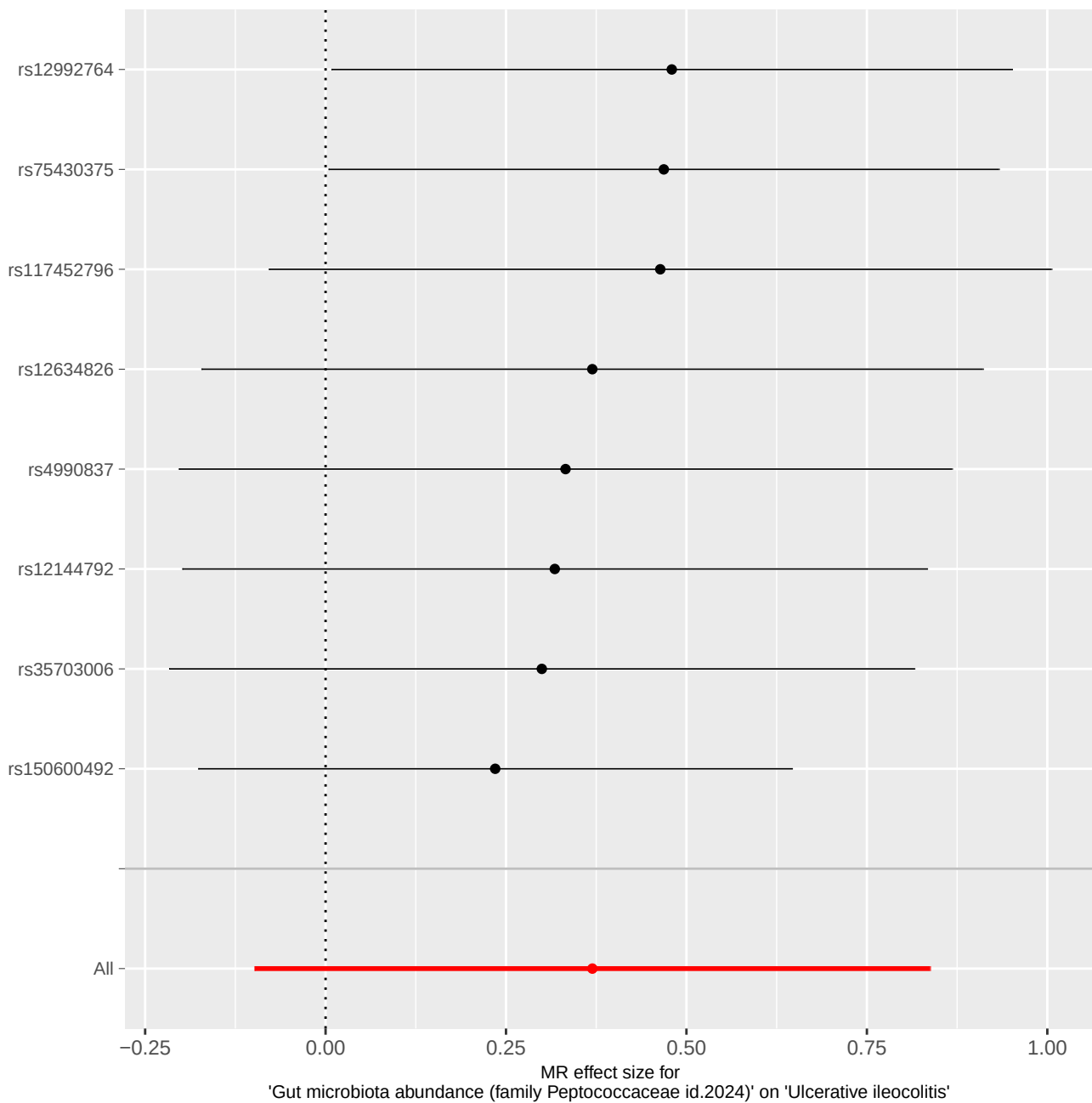


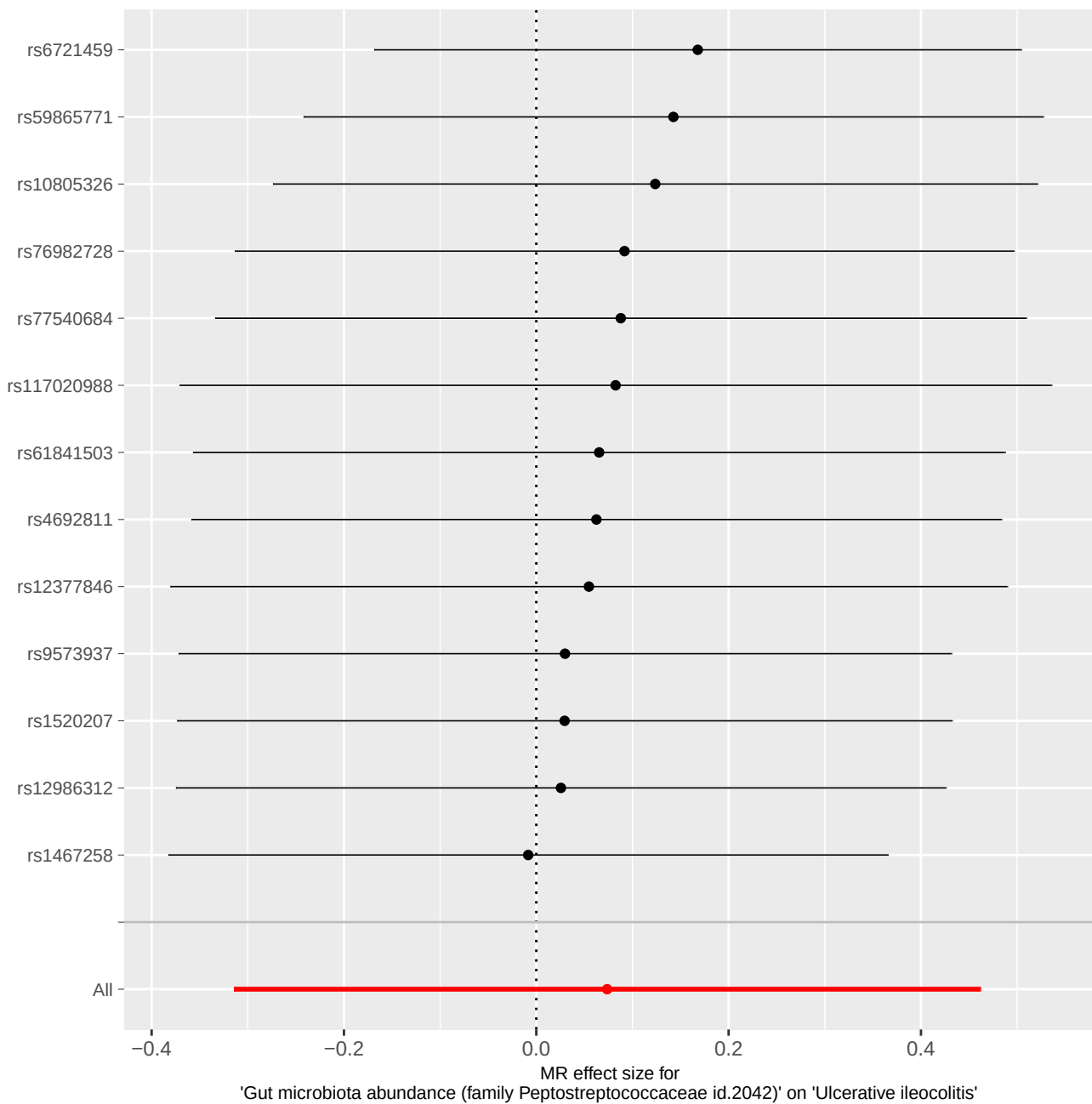


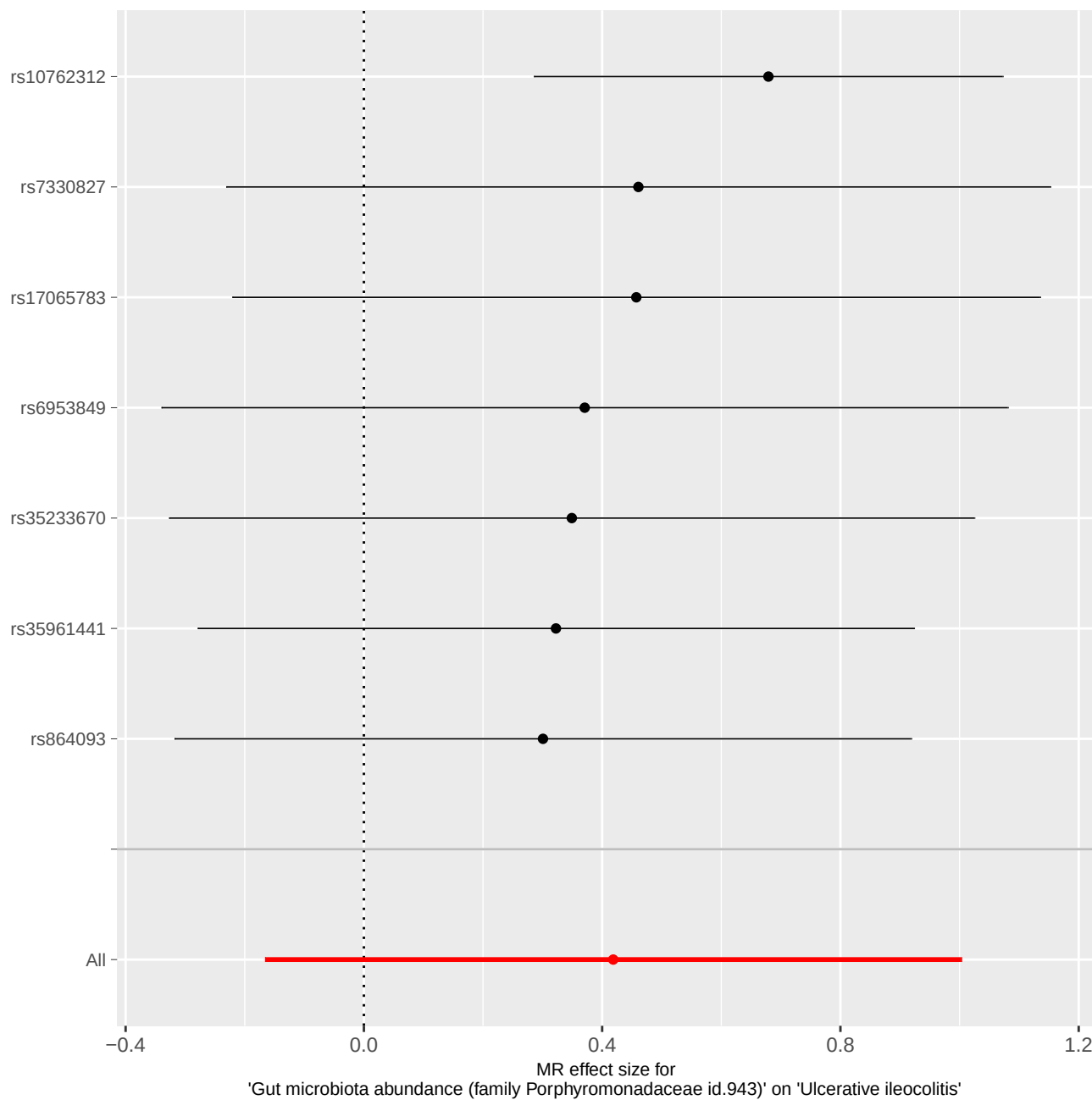


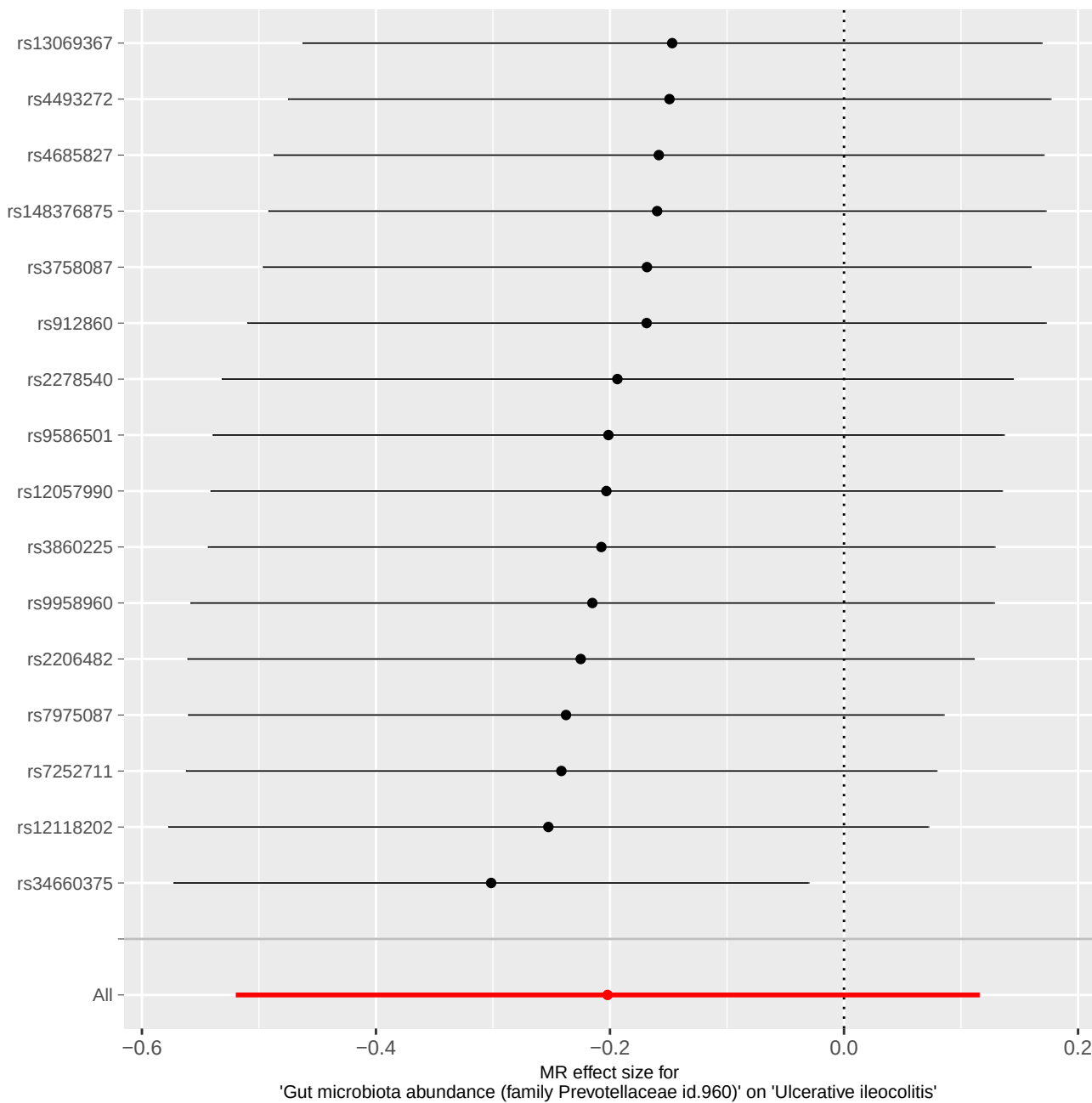


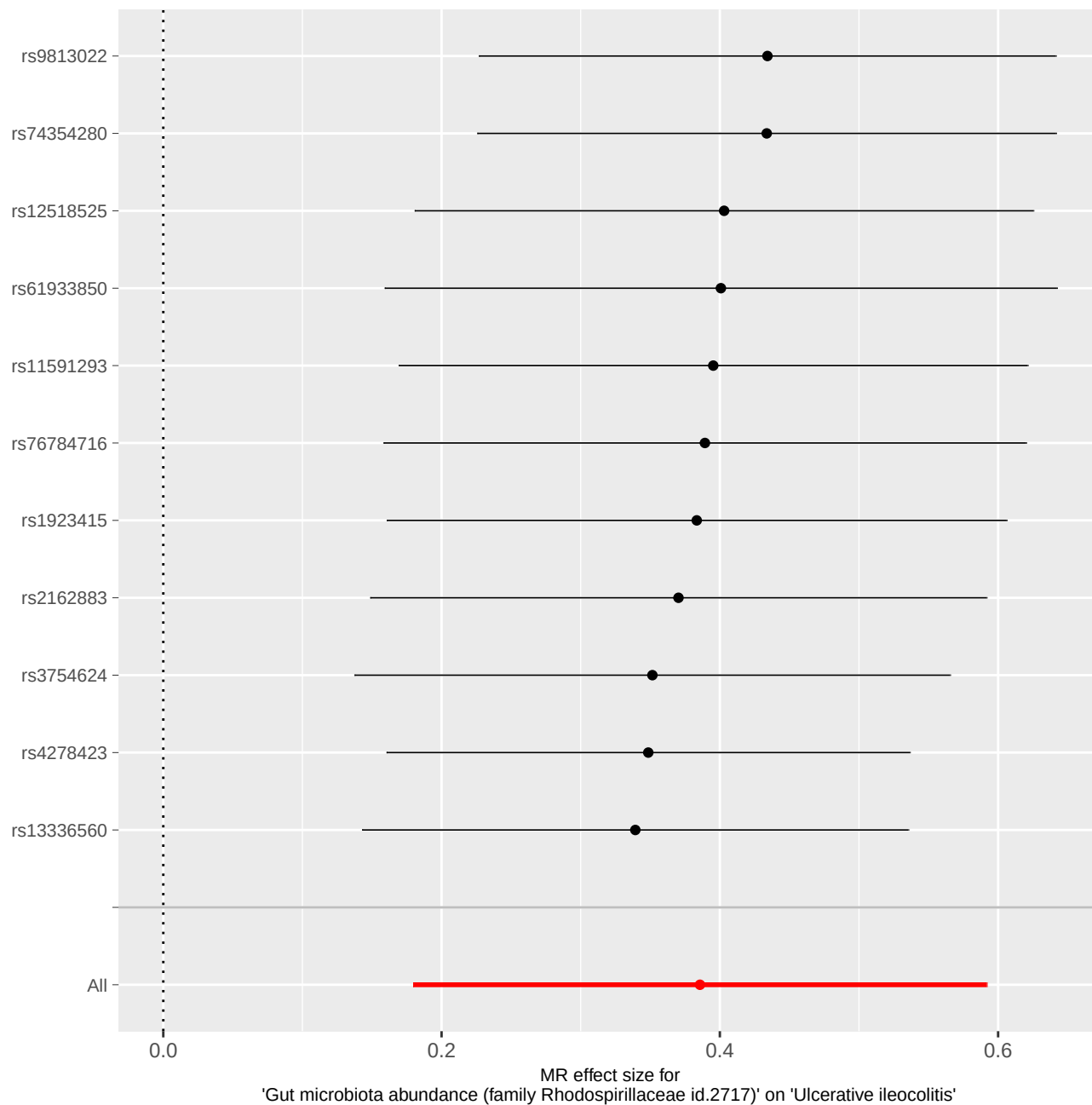




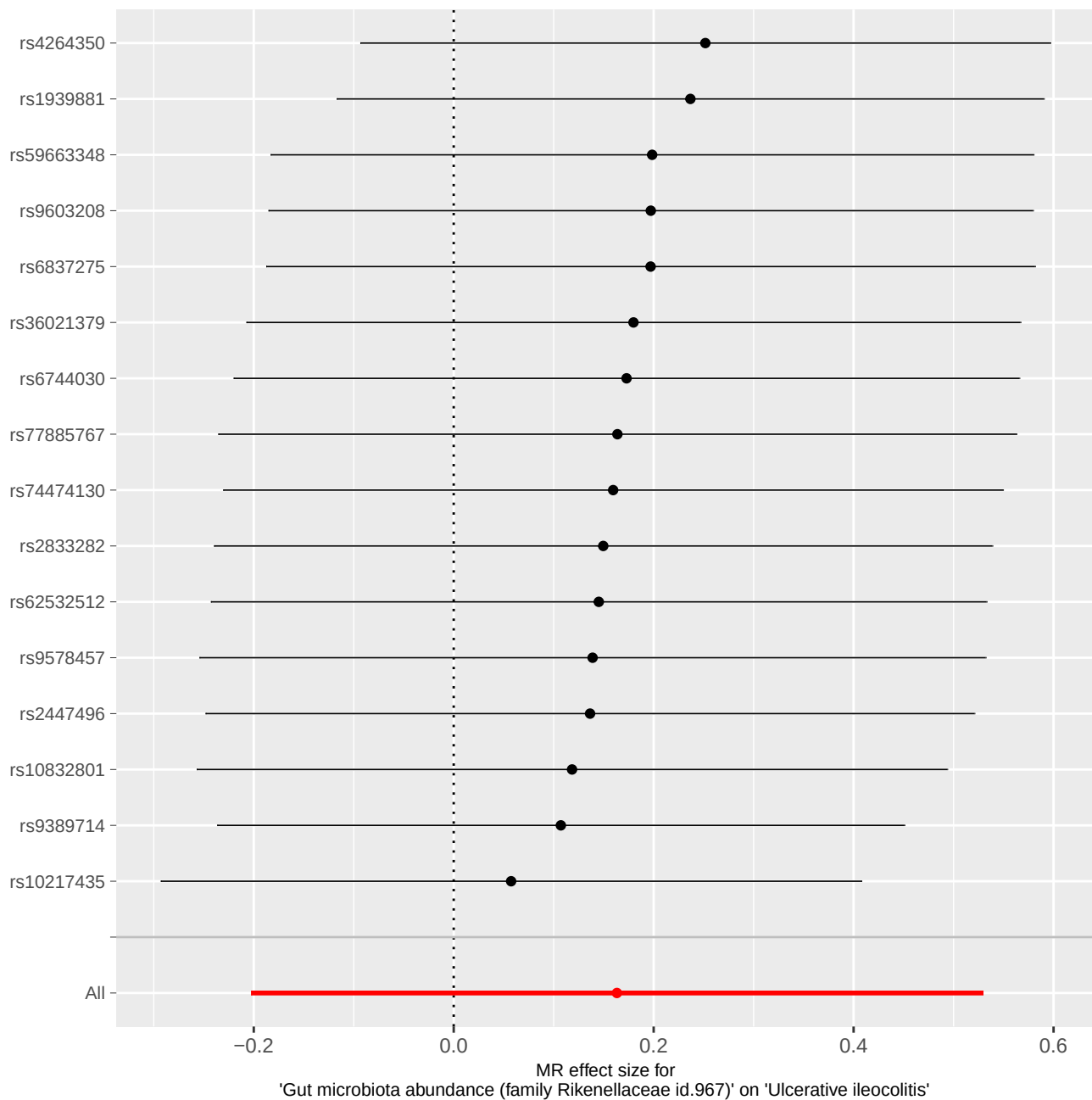




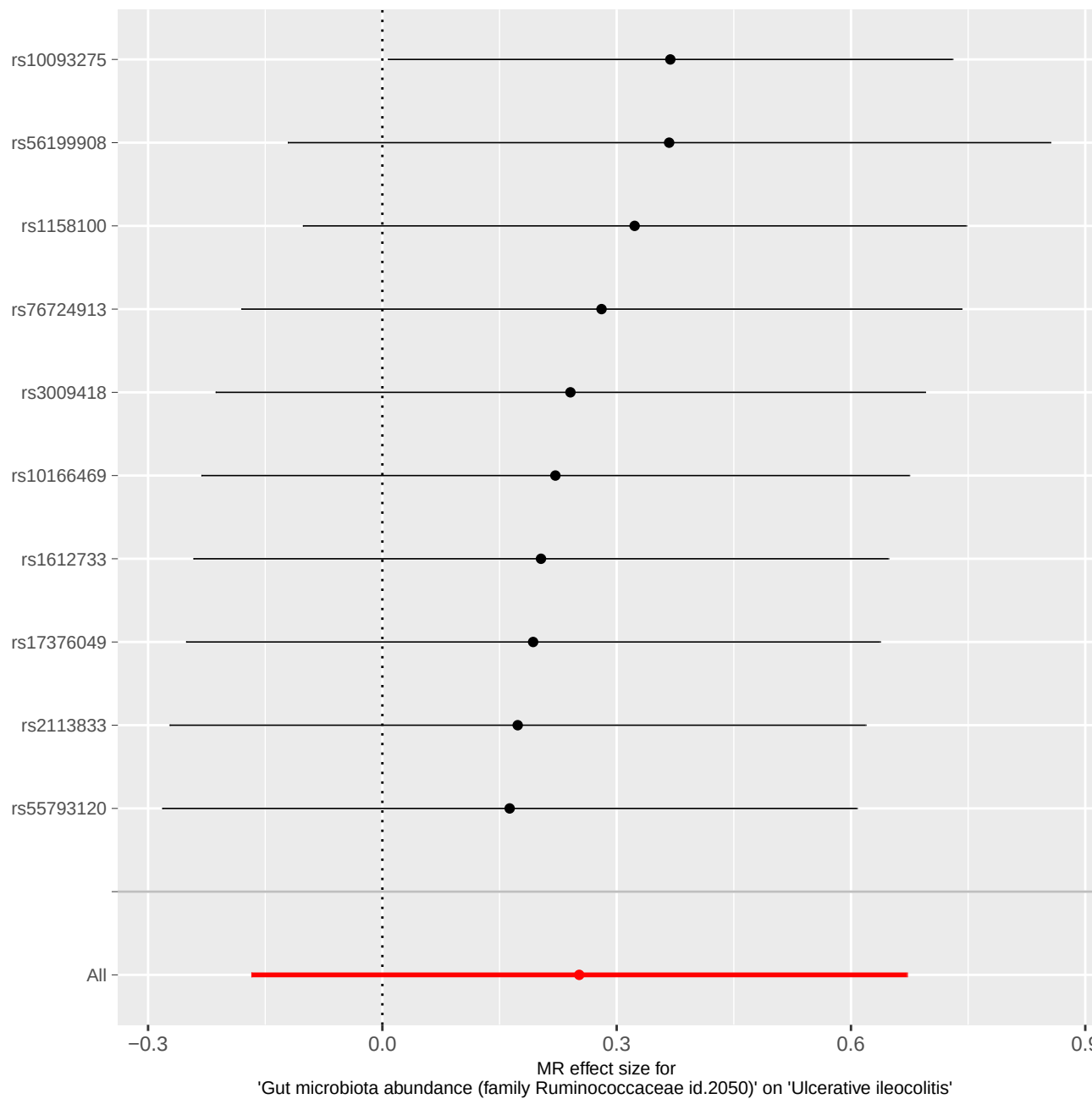


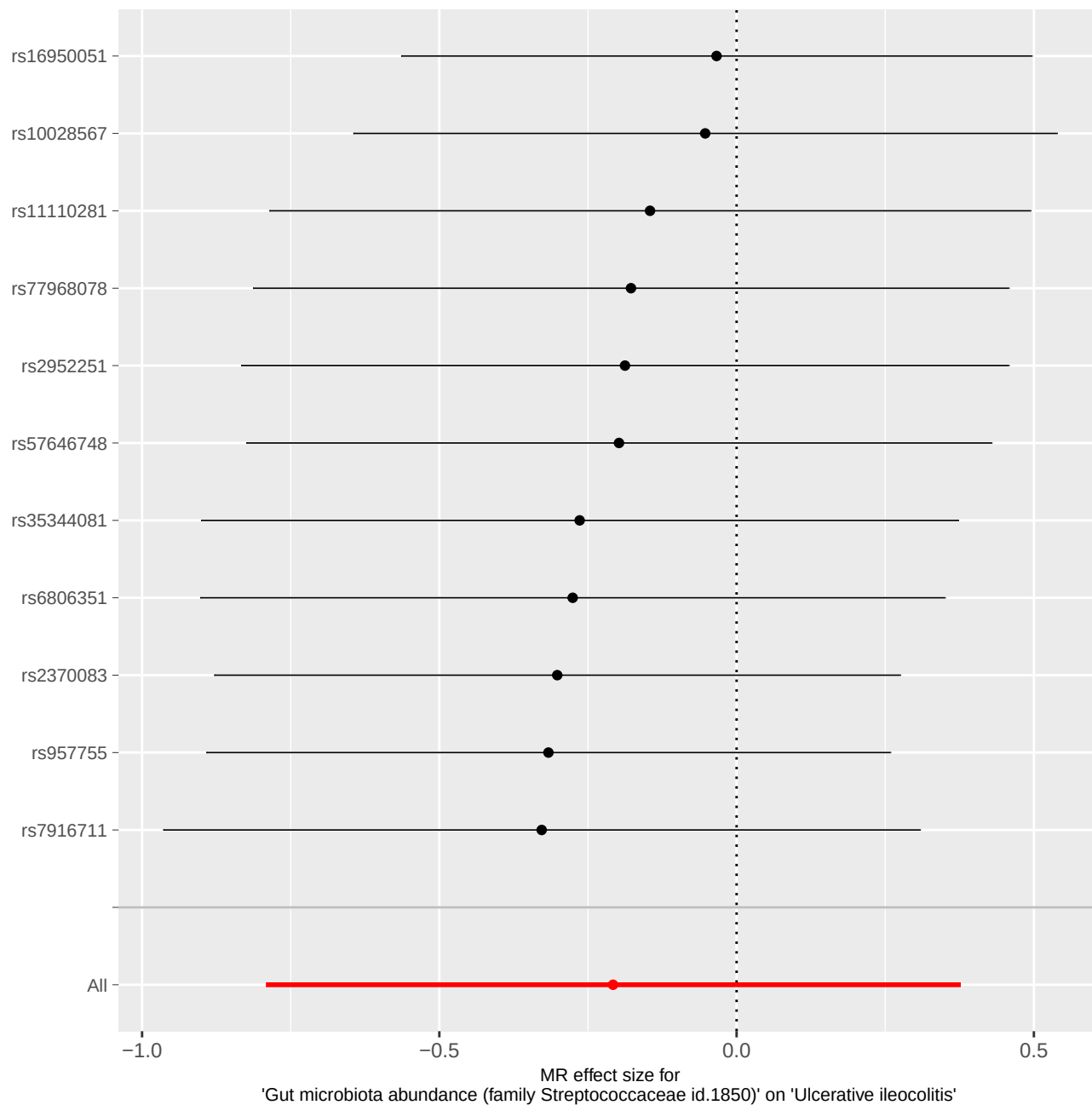


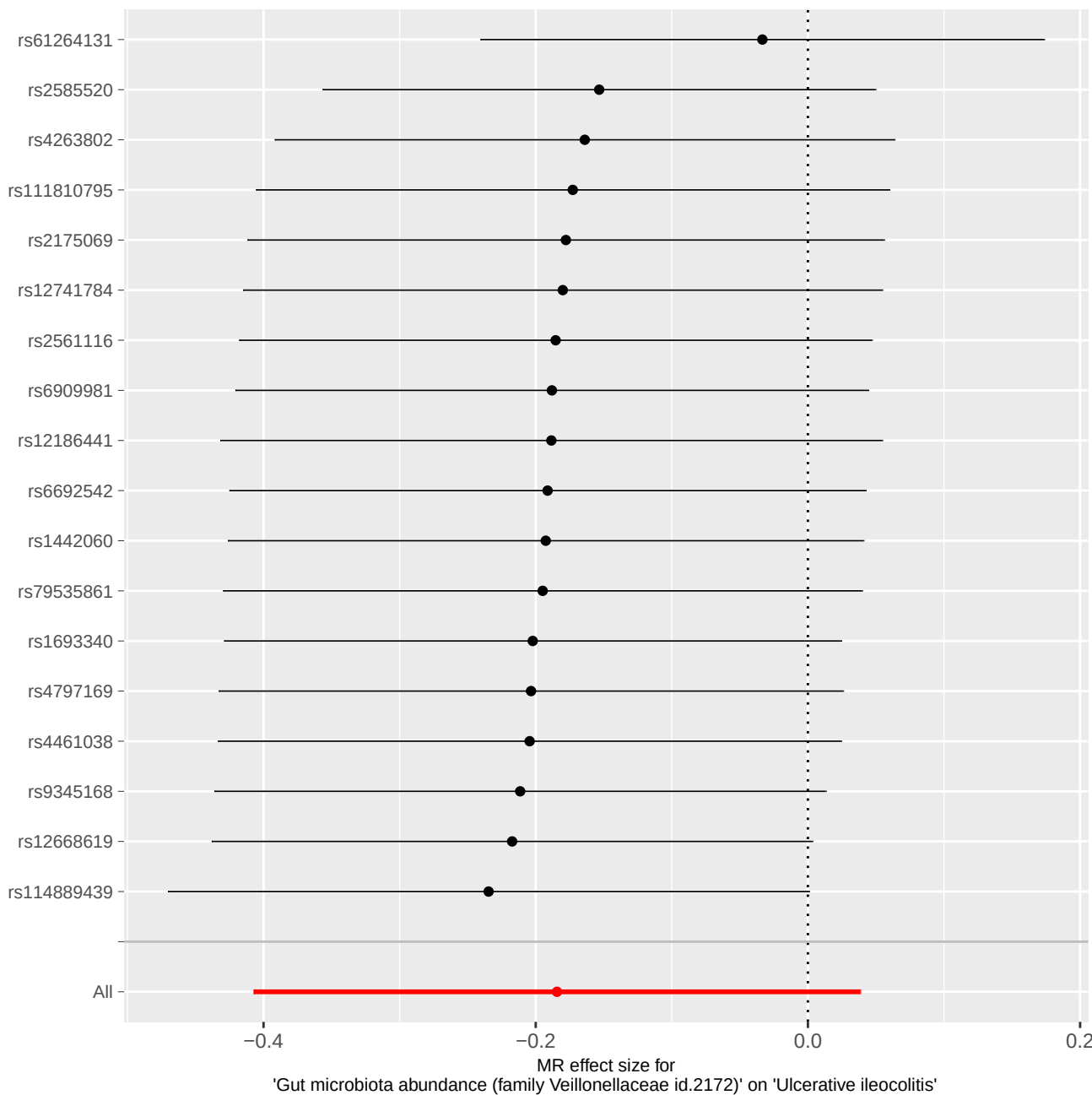
Batch 1077 : Gut microbiota abundance (family Rikenellaceae id.967) on Ulcerative ileocolitis



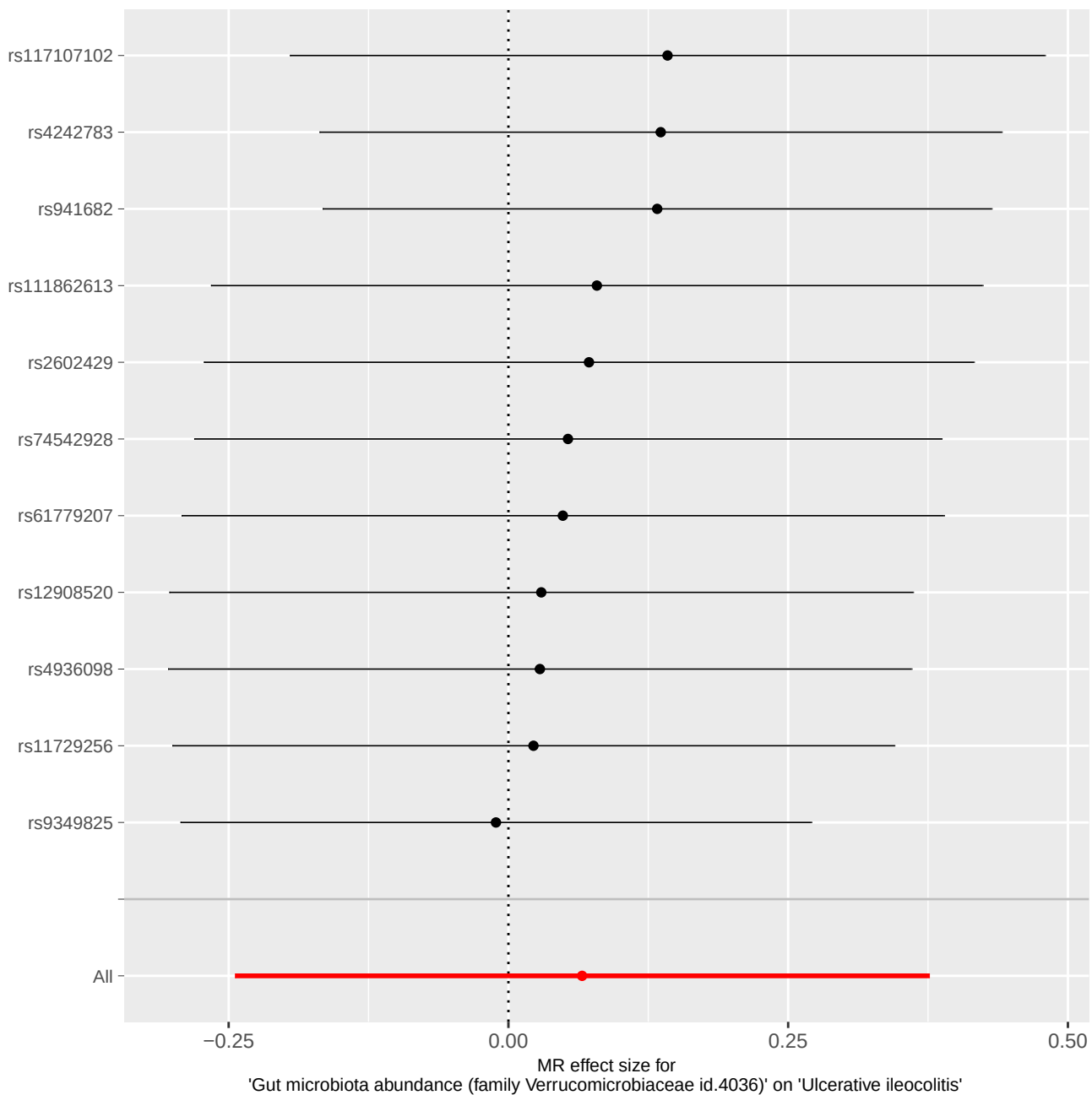
Batch 1078 : Gut microbiota abundance (family Ruminococcaceae id.2050) on Ulcerative ileocolitis

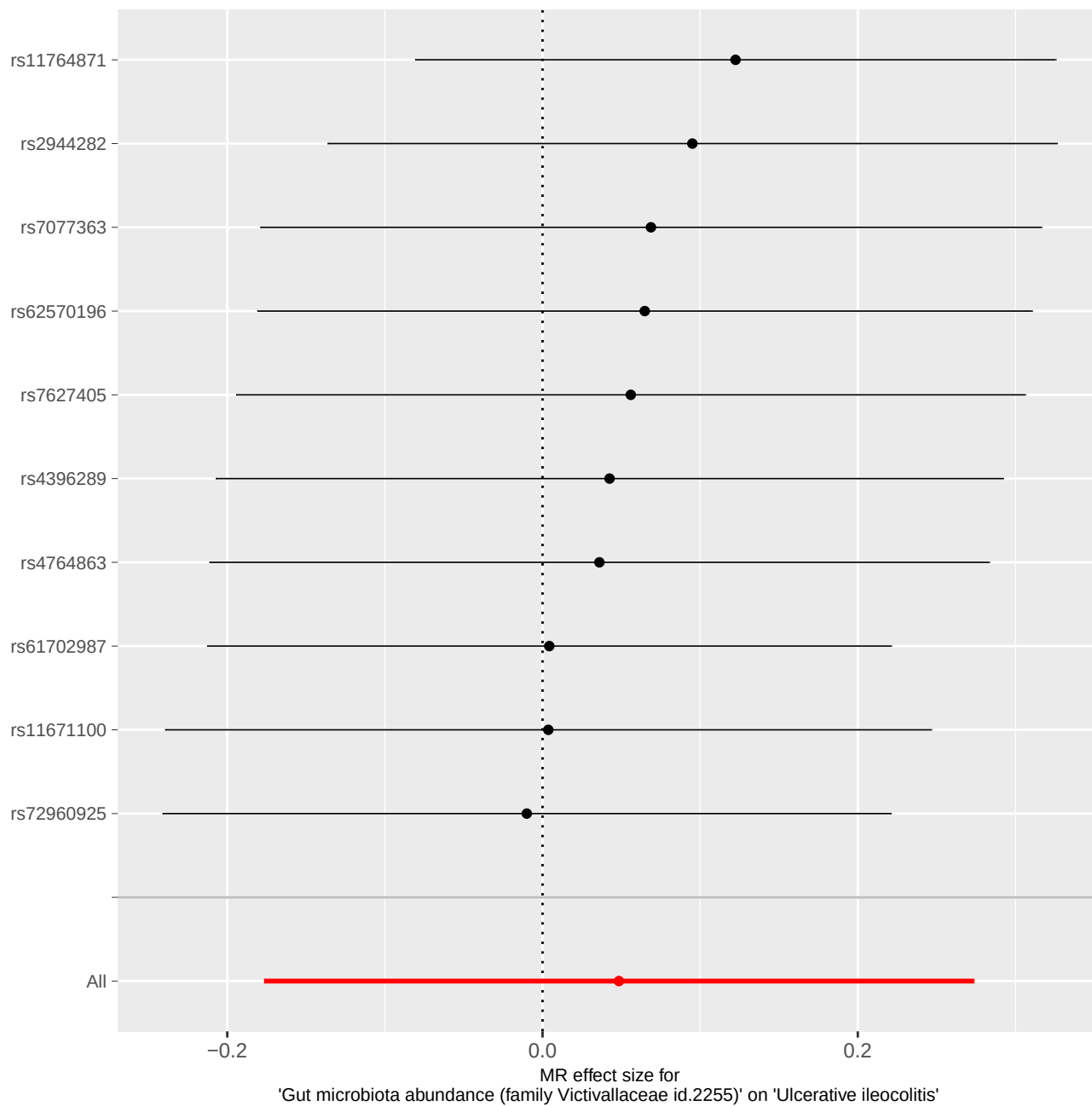


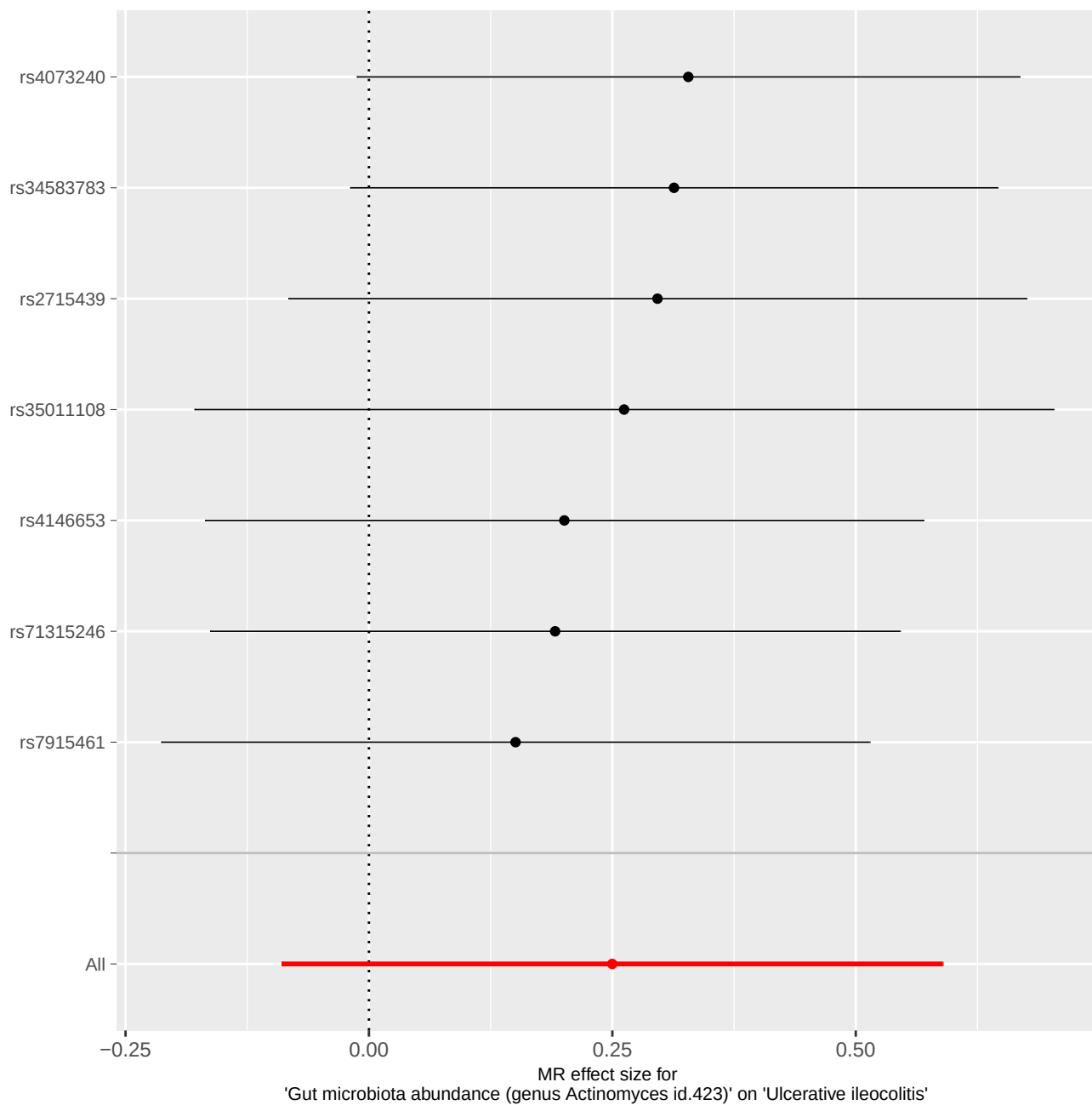


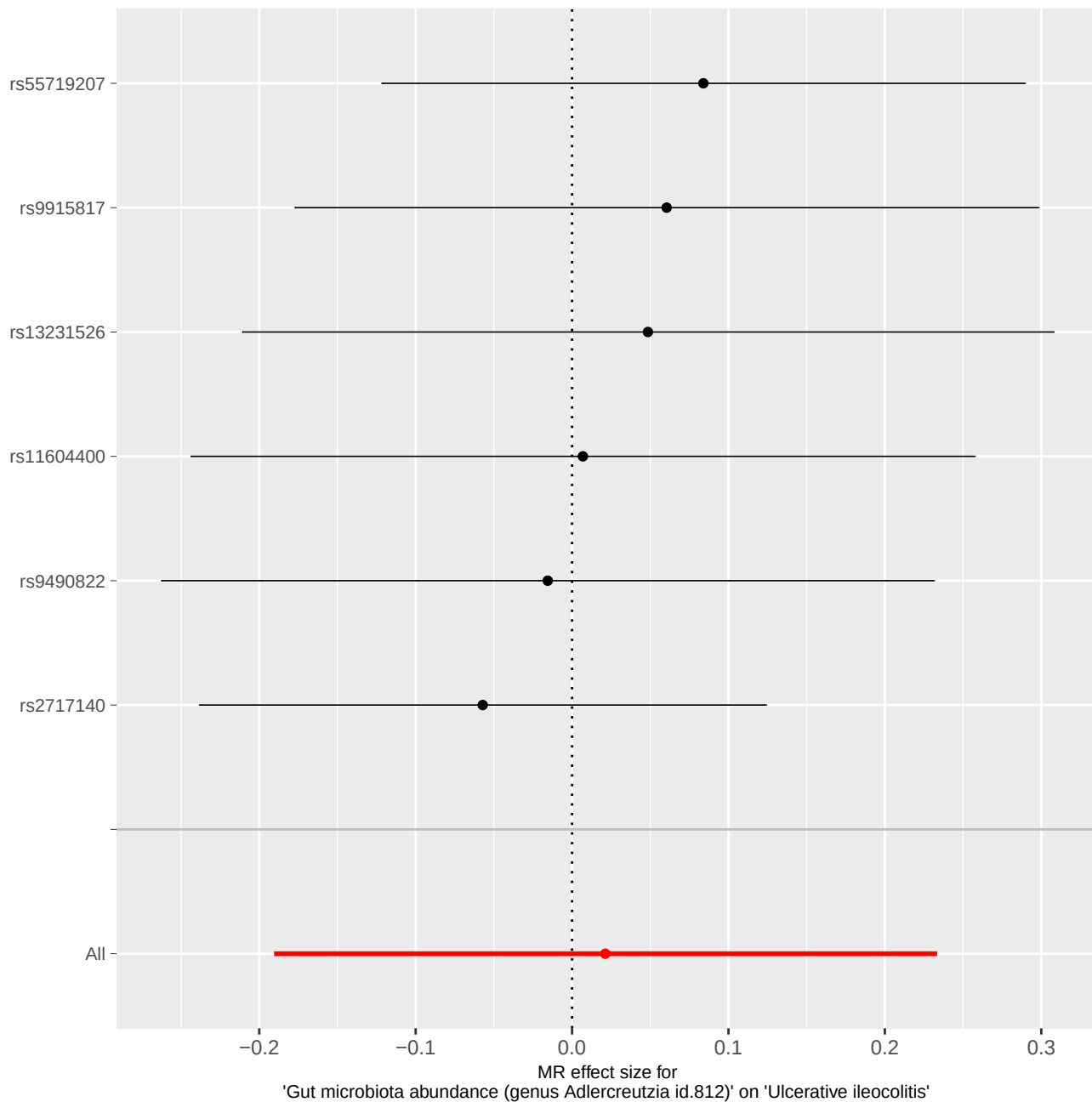


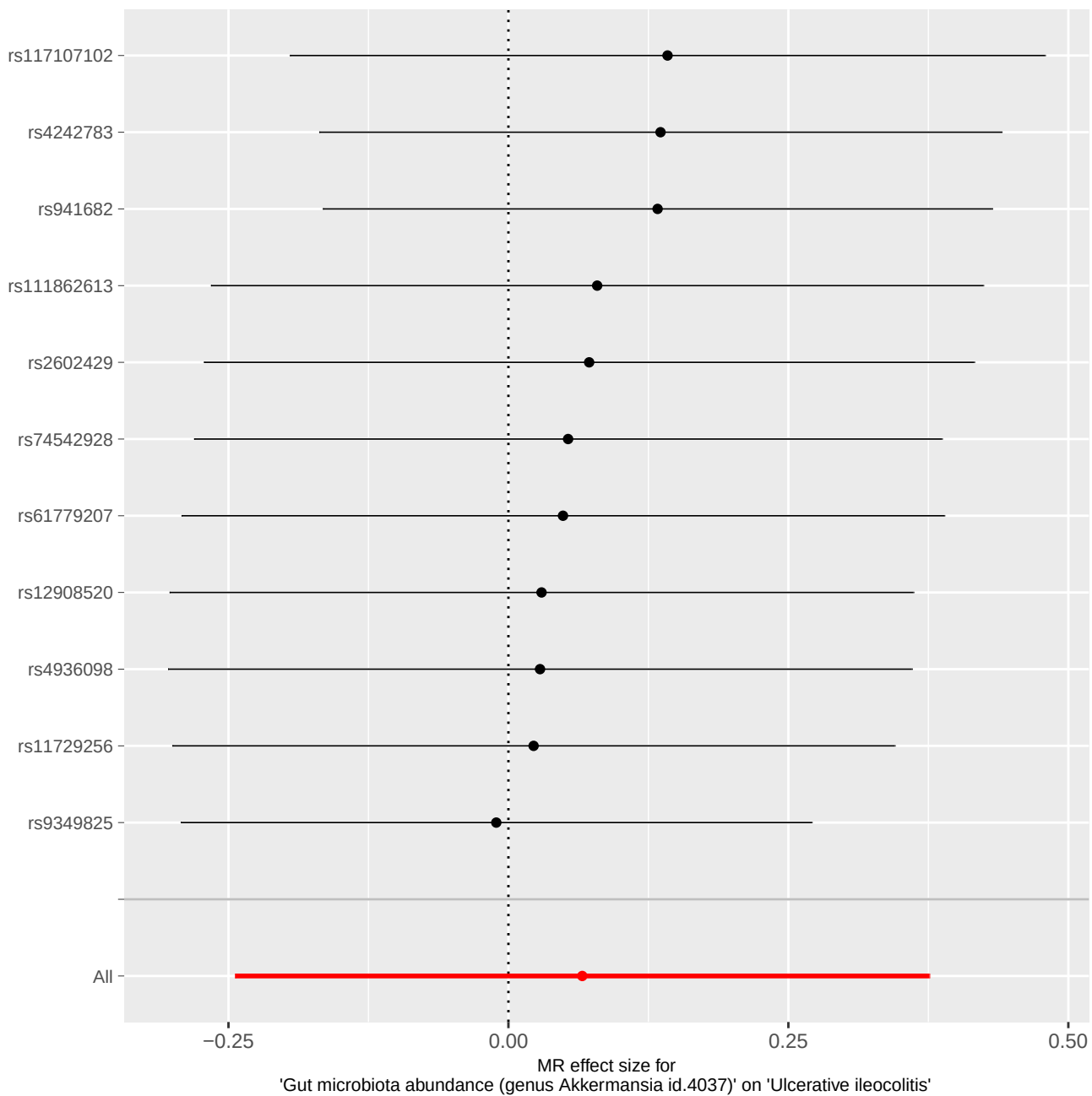
MR effect size for
'Gut microbiota abundance (family Veillonellaceae id.2172)' on 'Ulcerative ileocolitis'

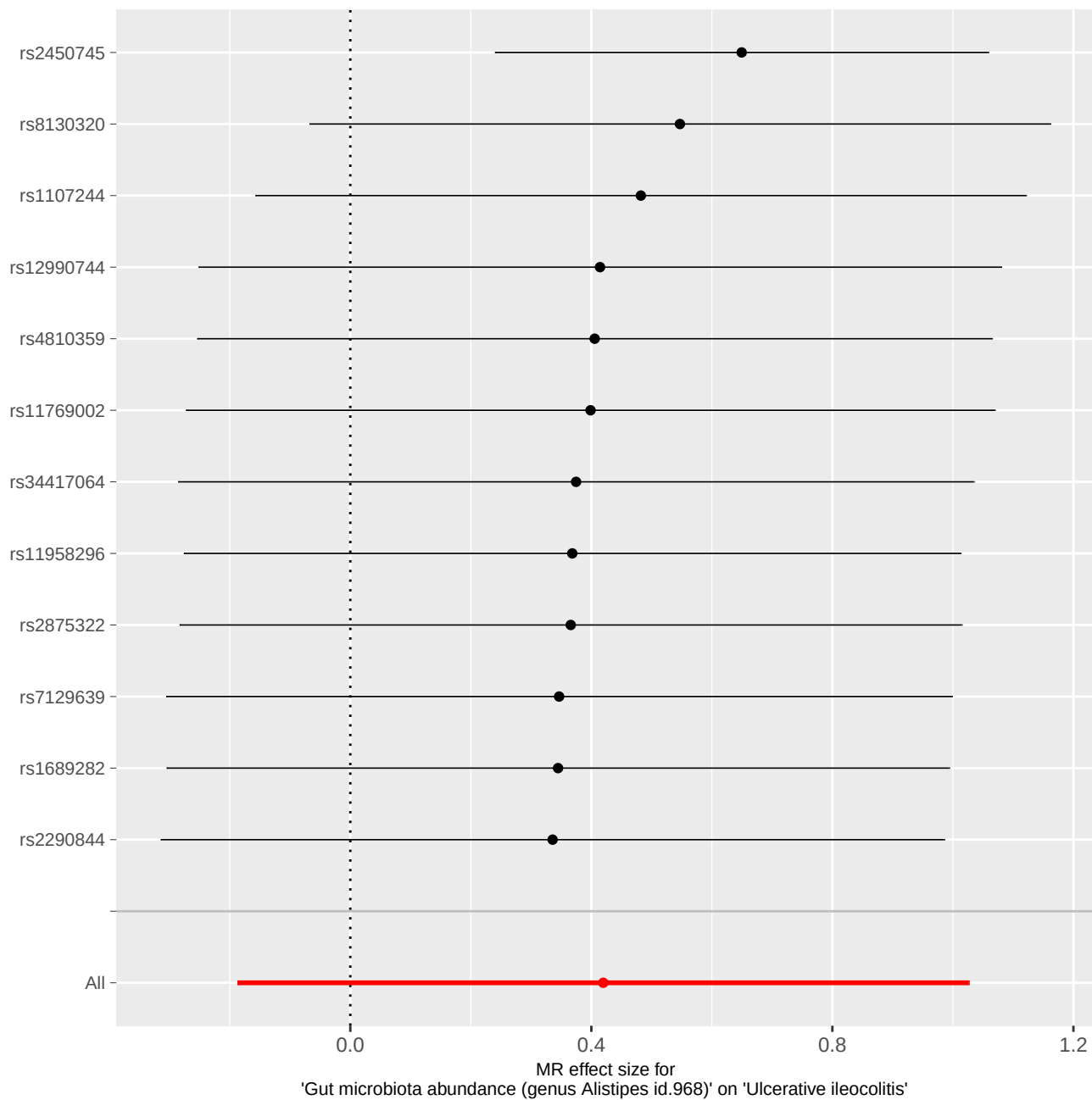


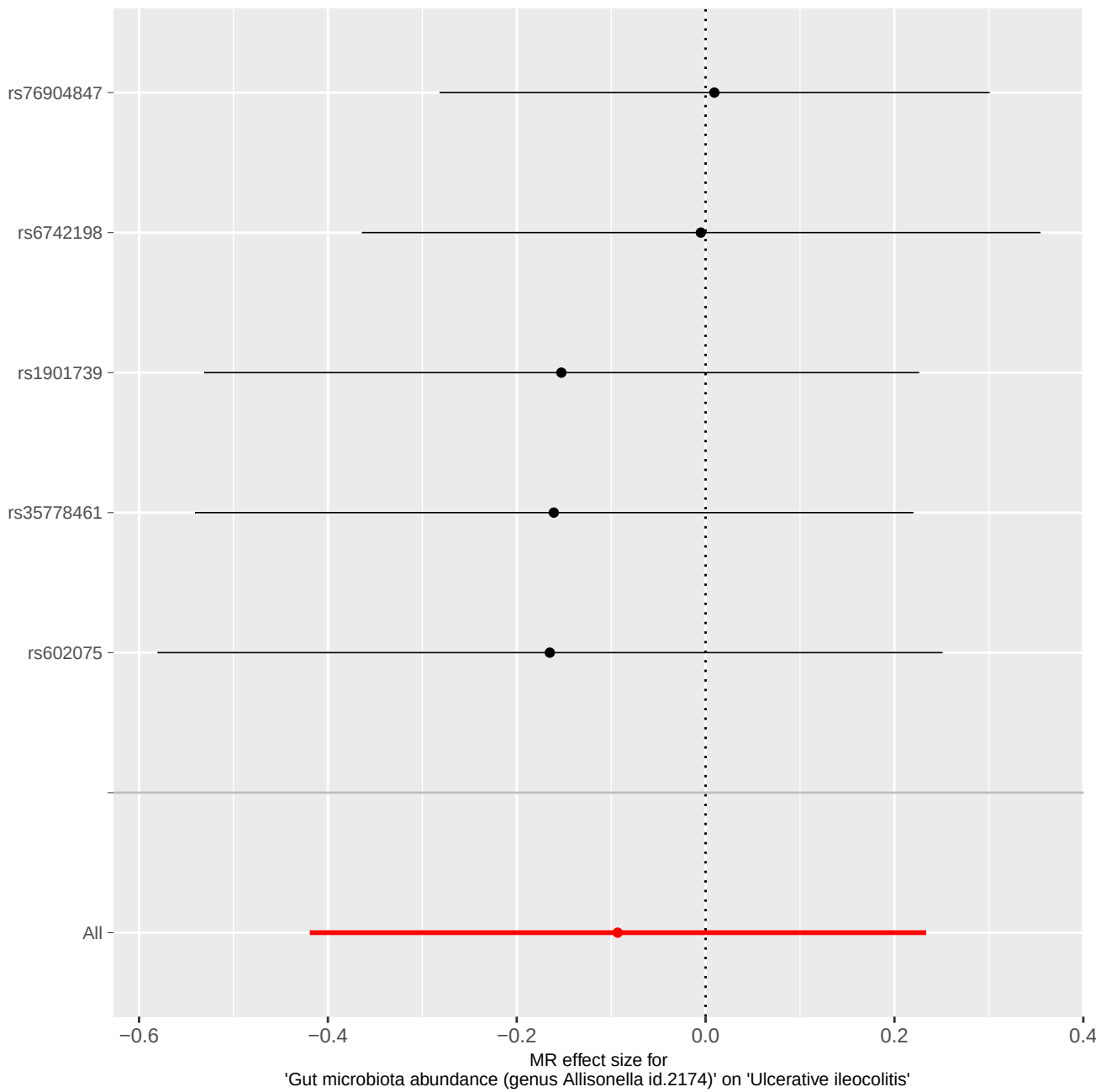


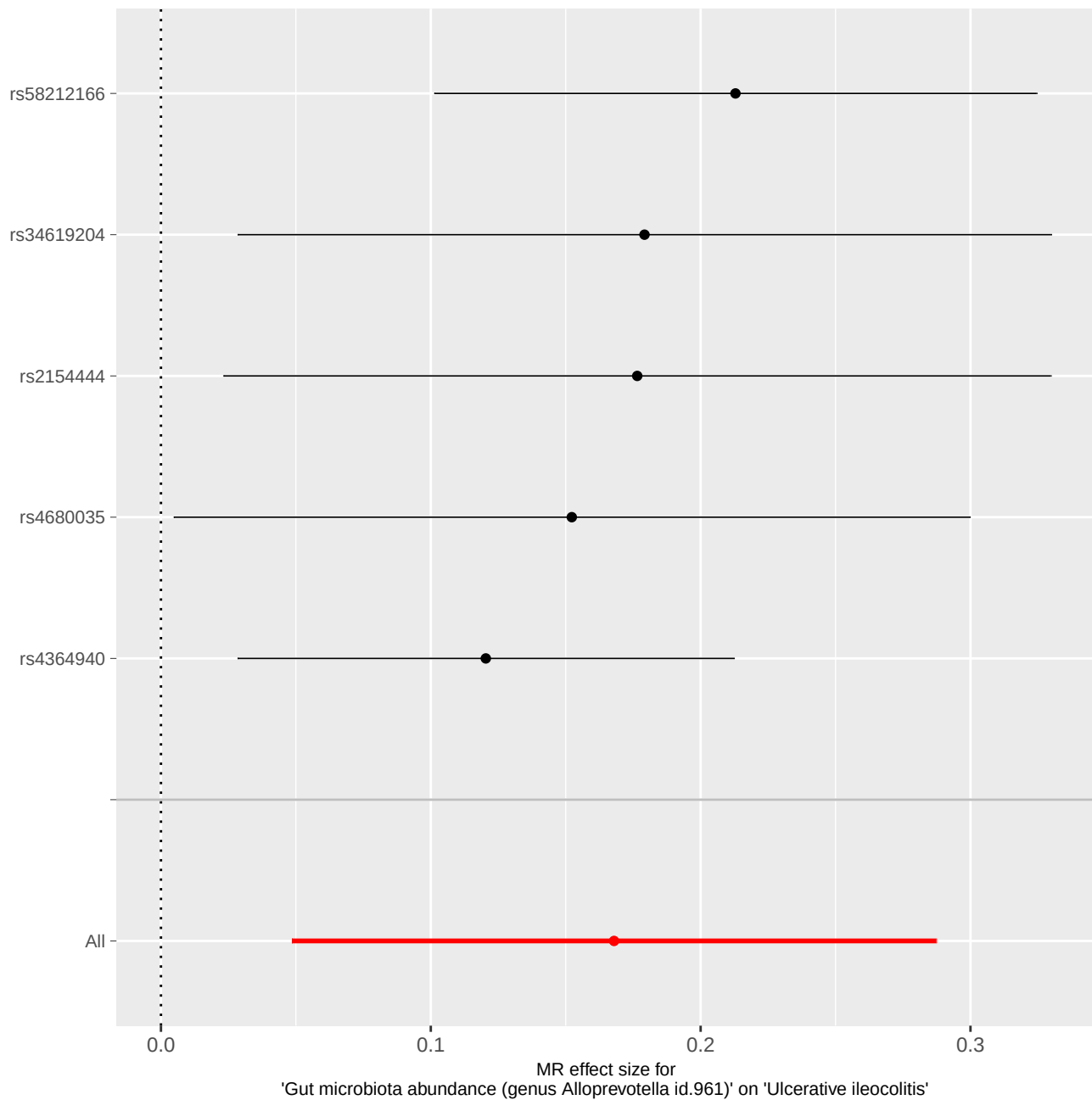


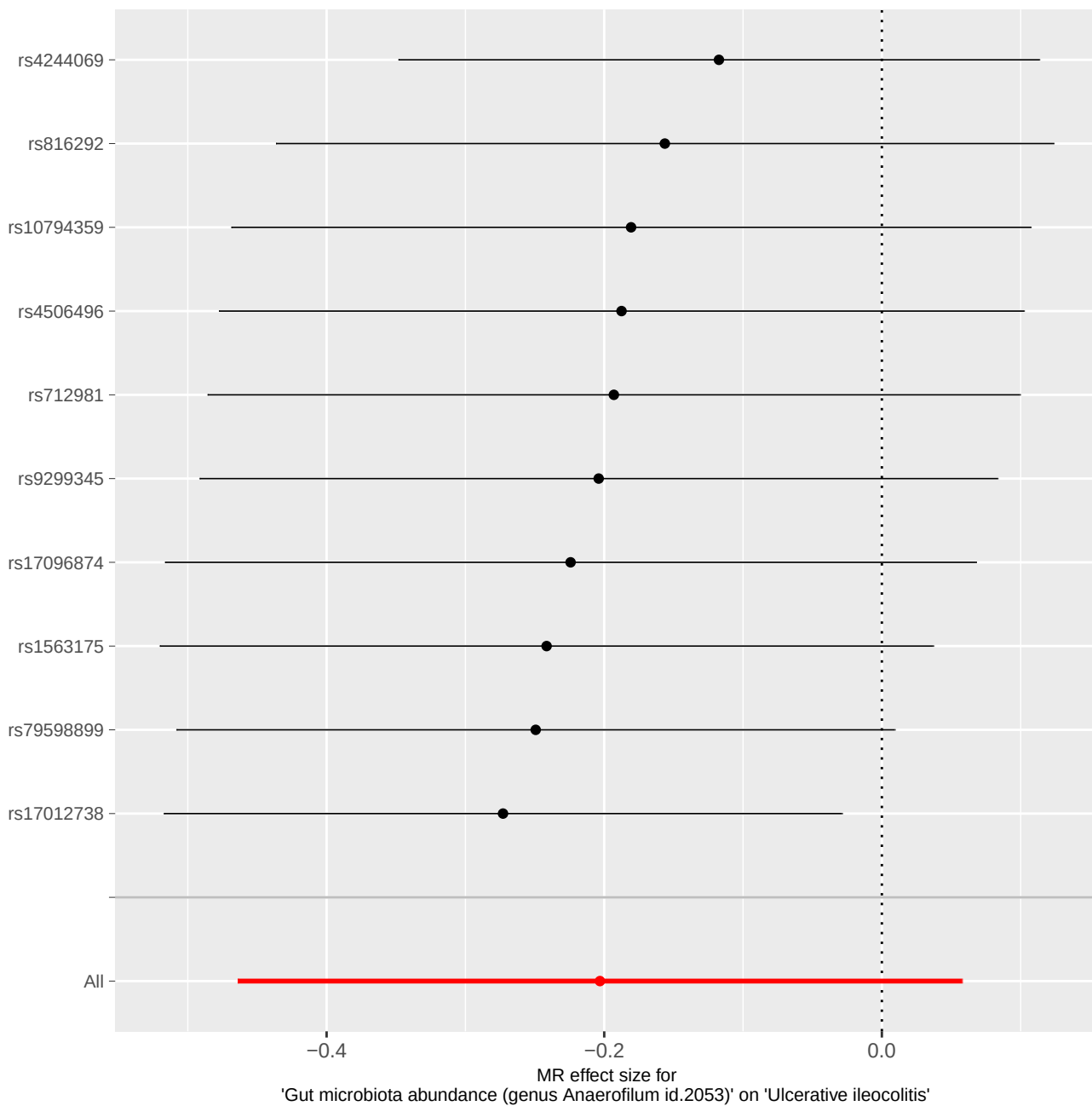




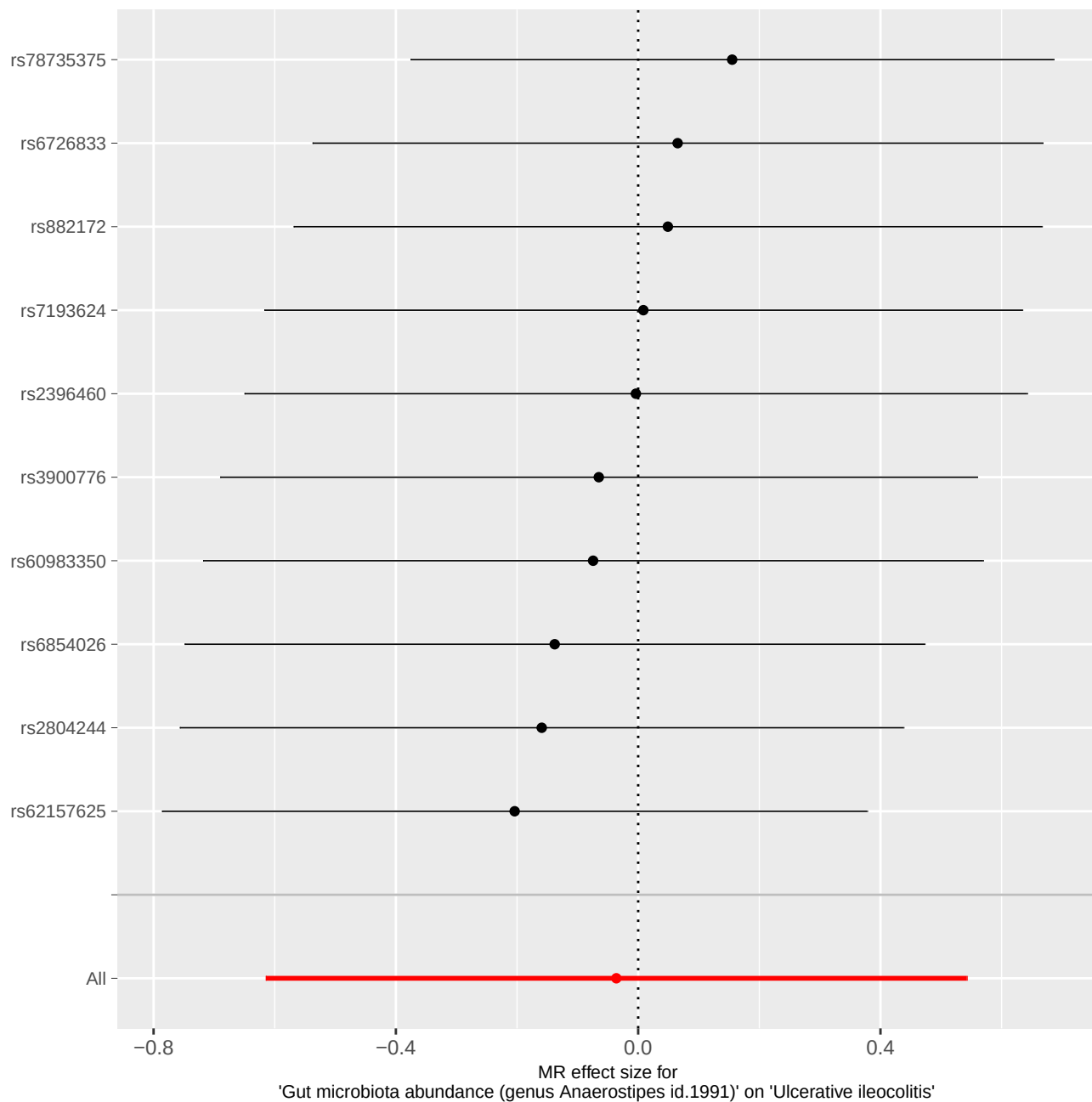


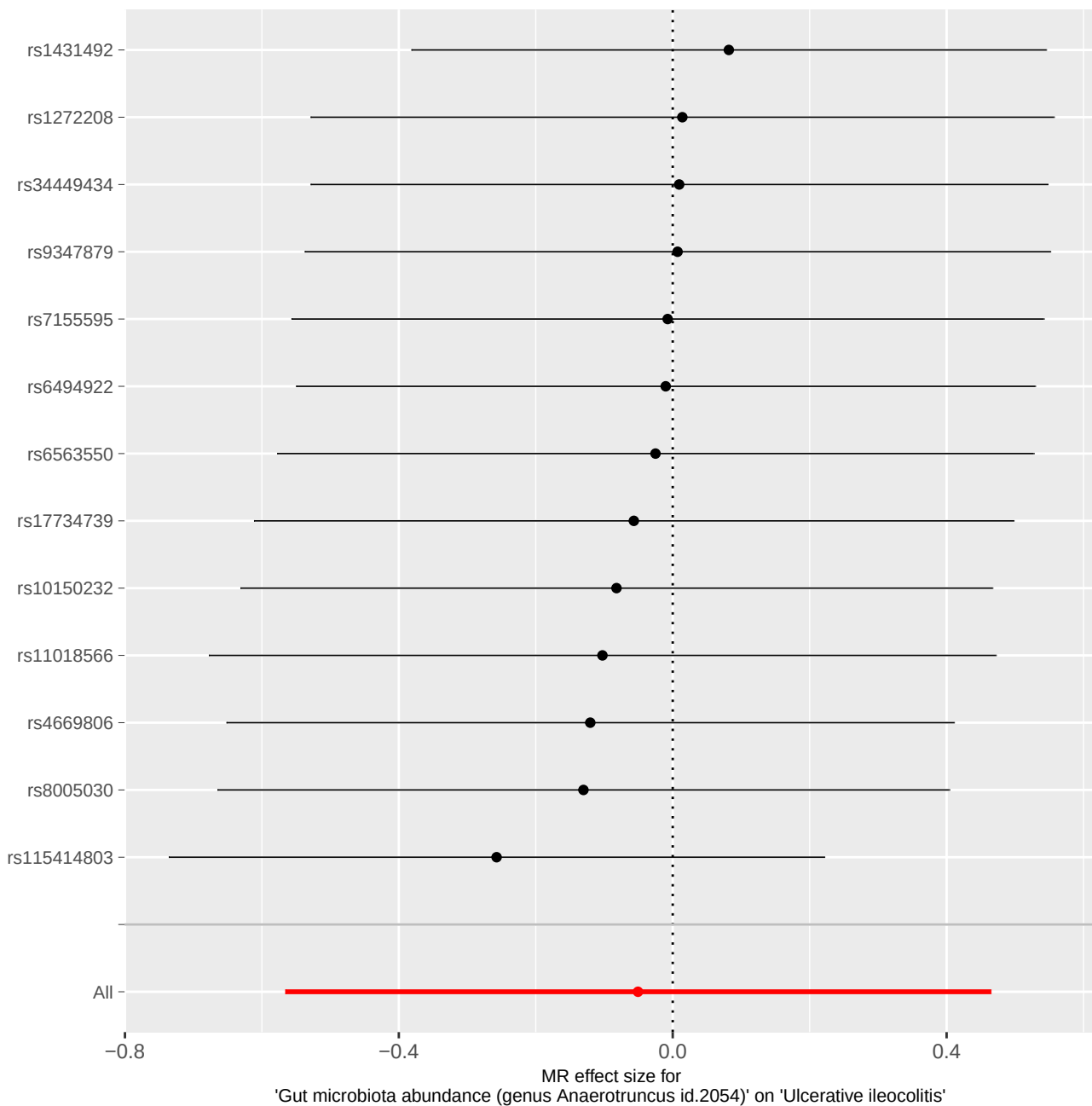


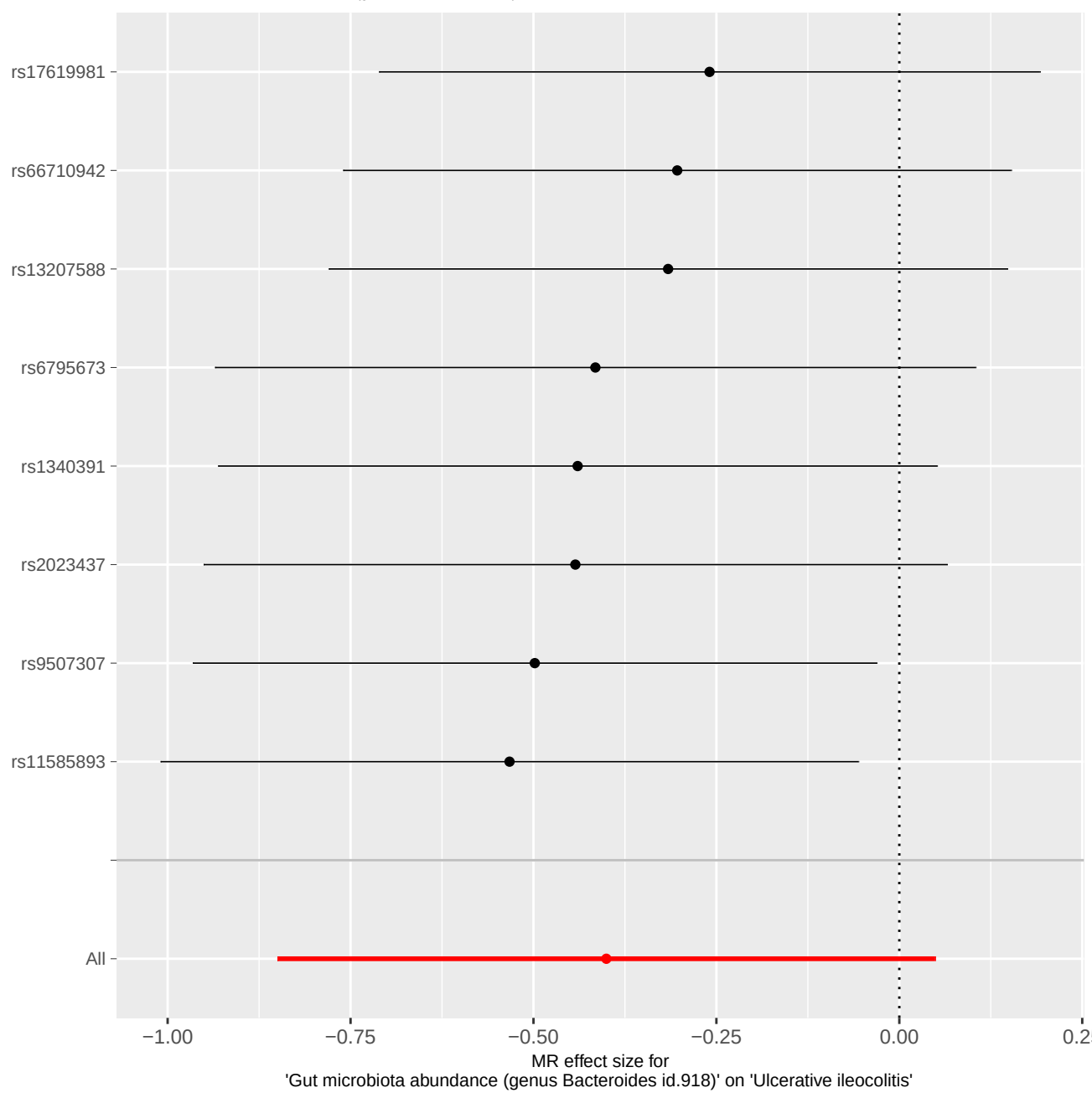


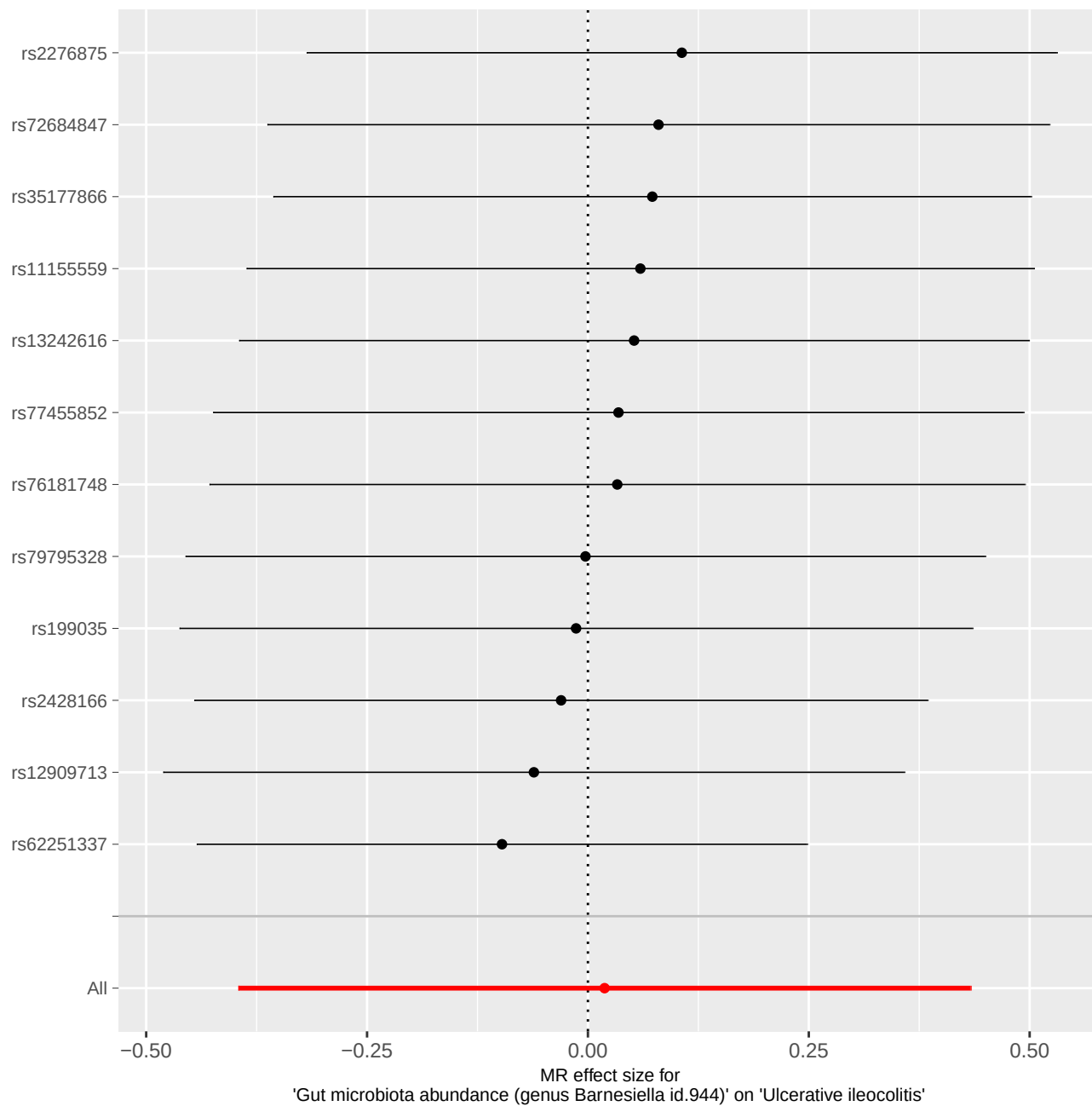


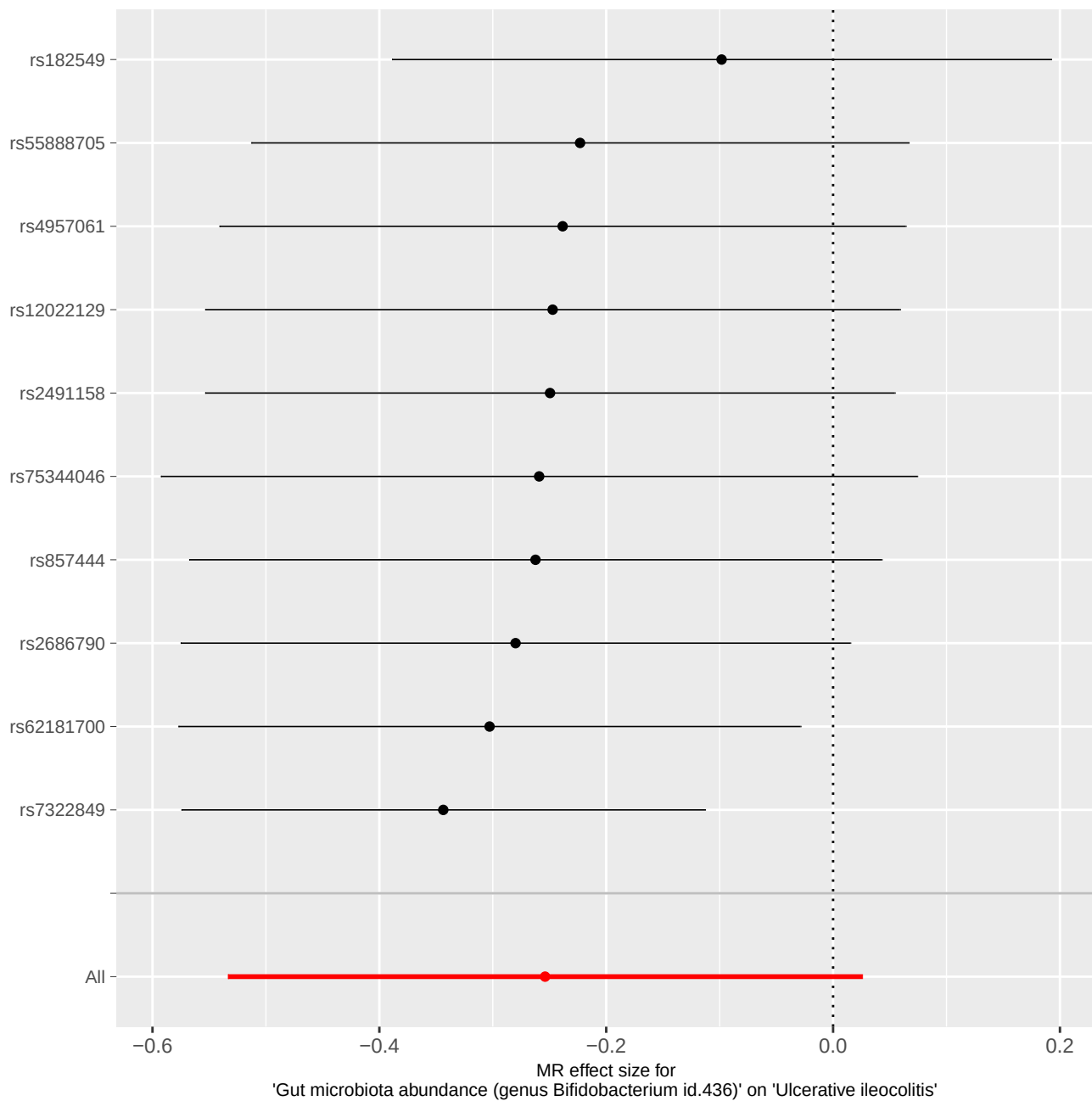
Batch 1090 : Gut microbiota abundance (genus Anaerostipes id.1991) on Ulcerative ileocolitis

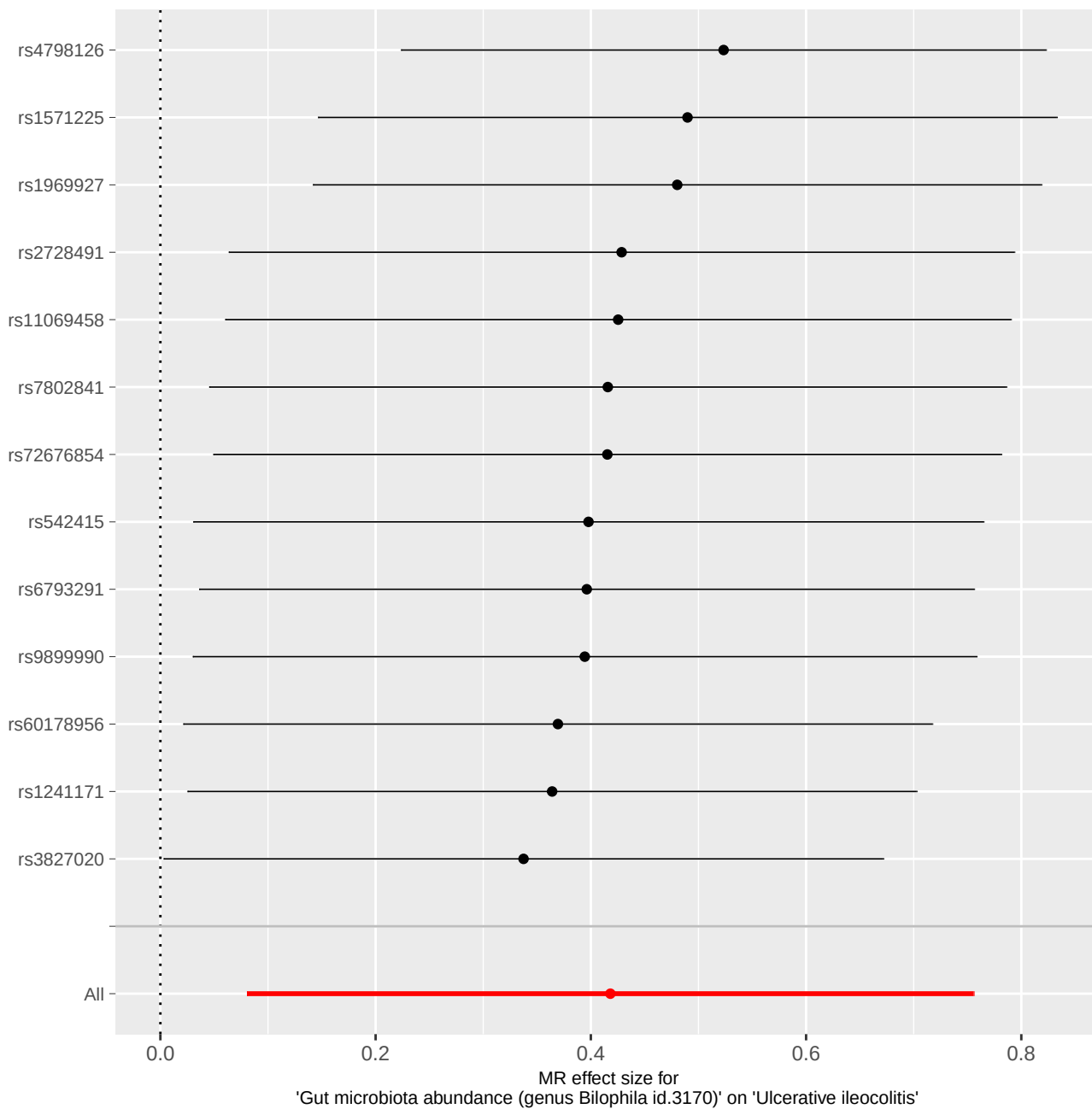


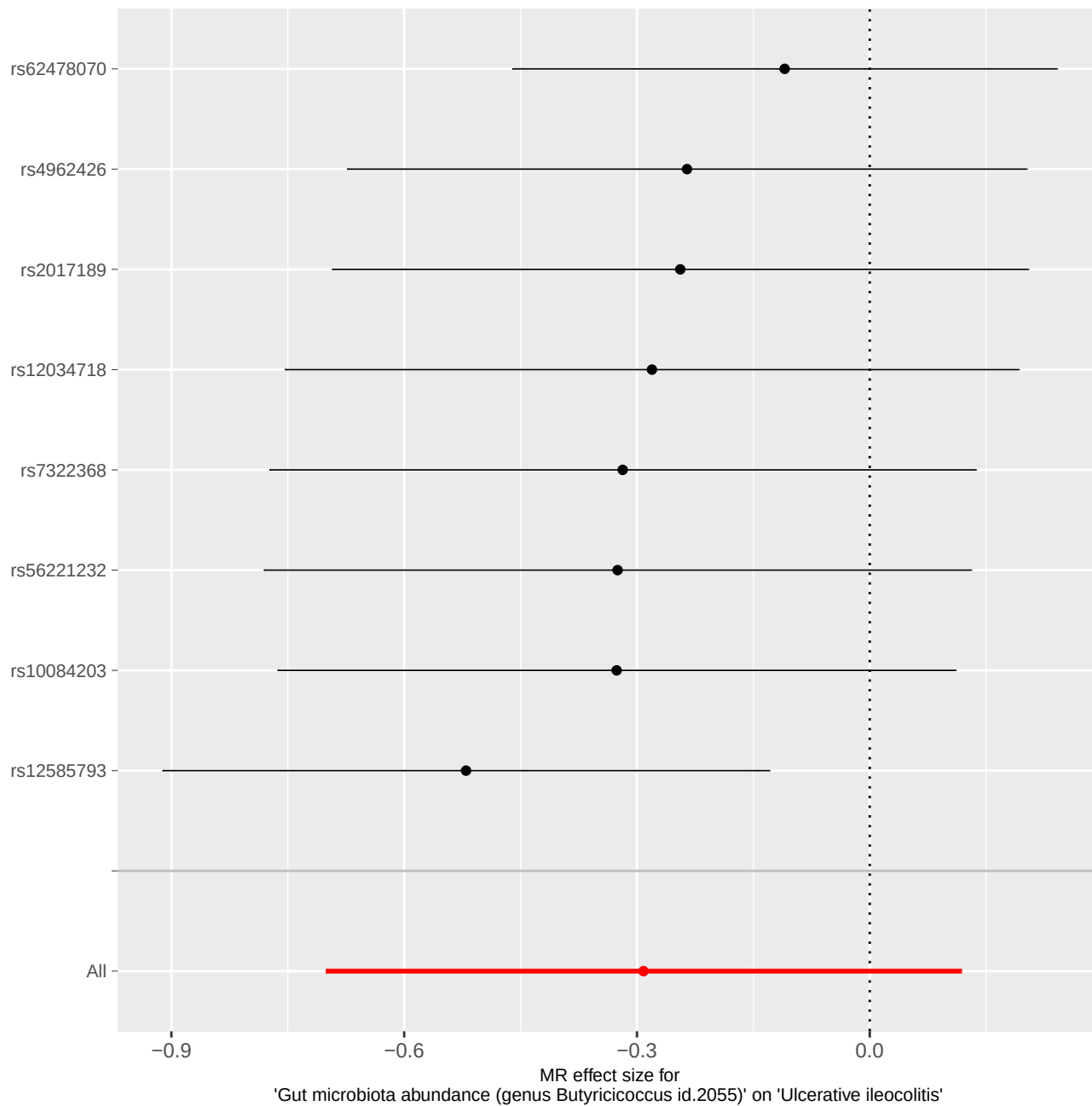


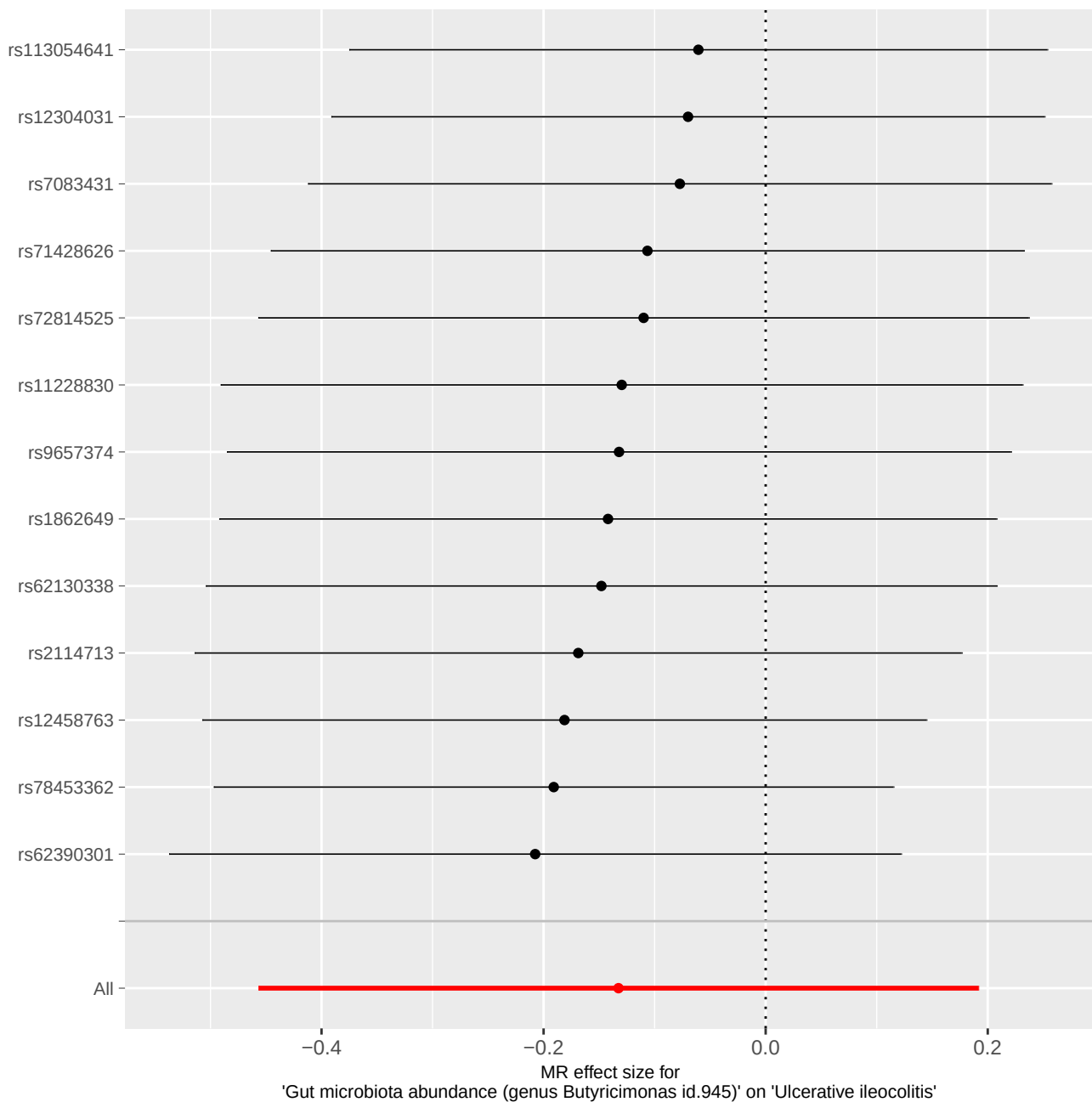


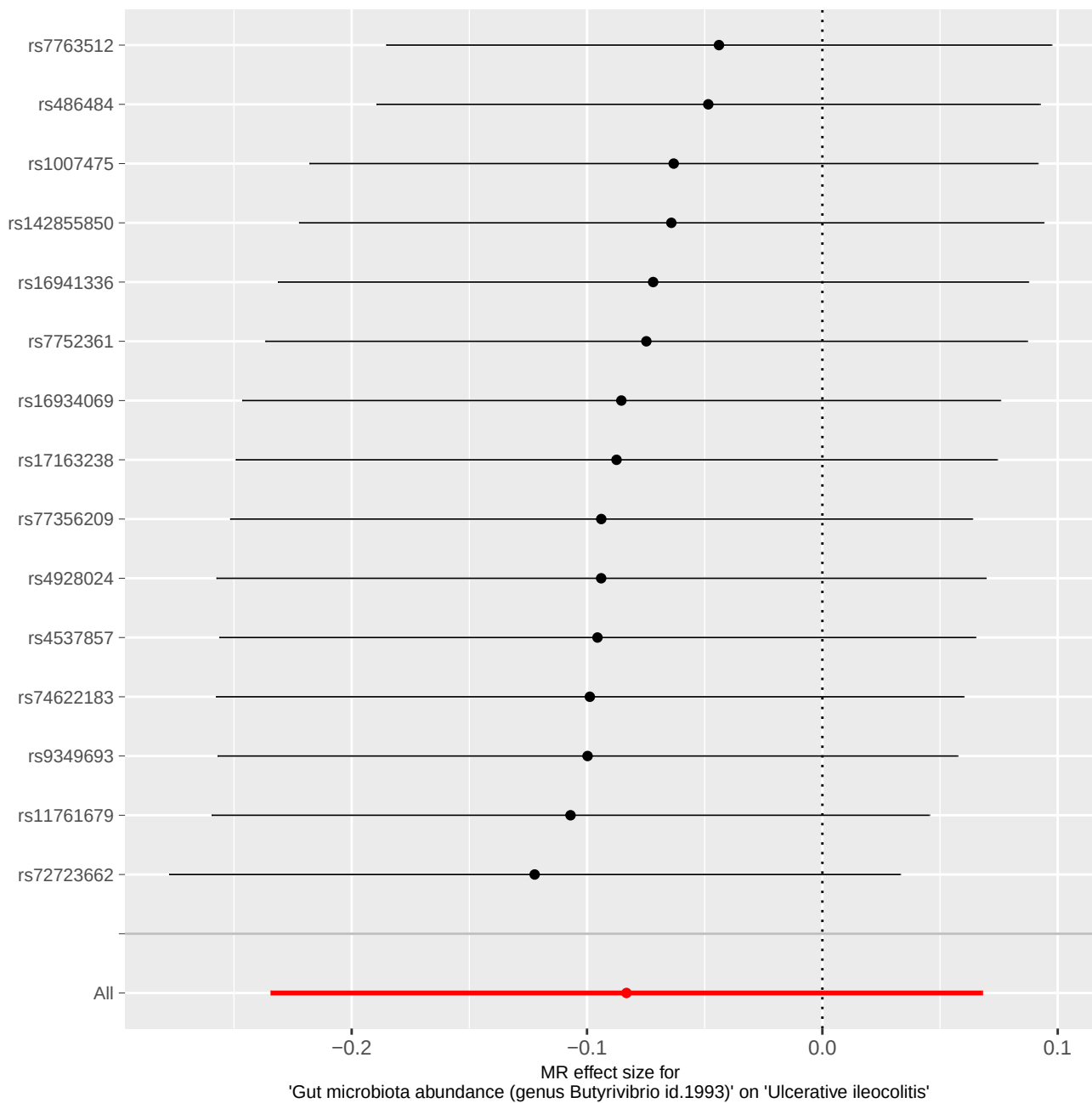


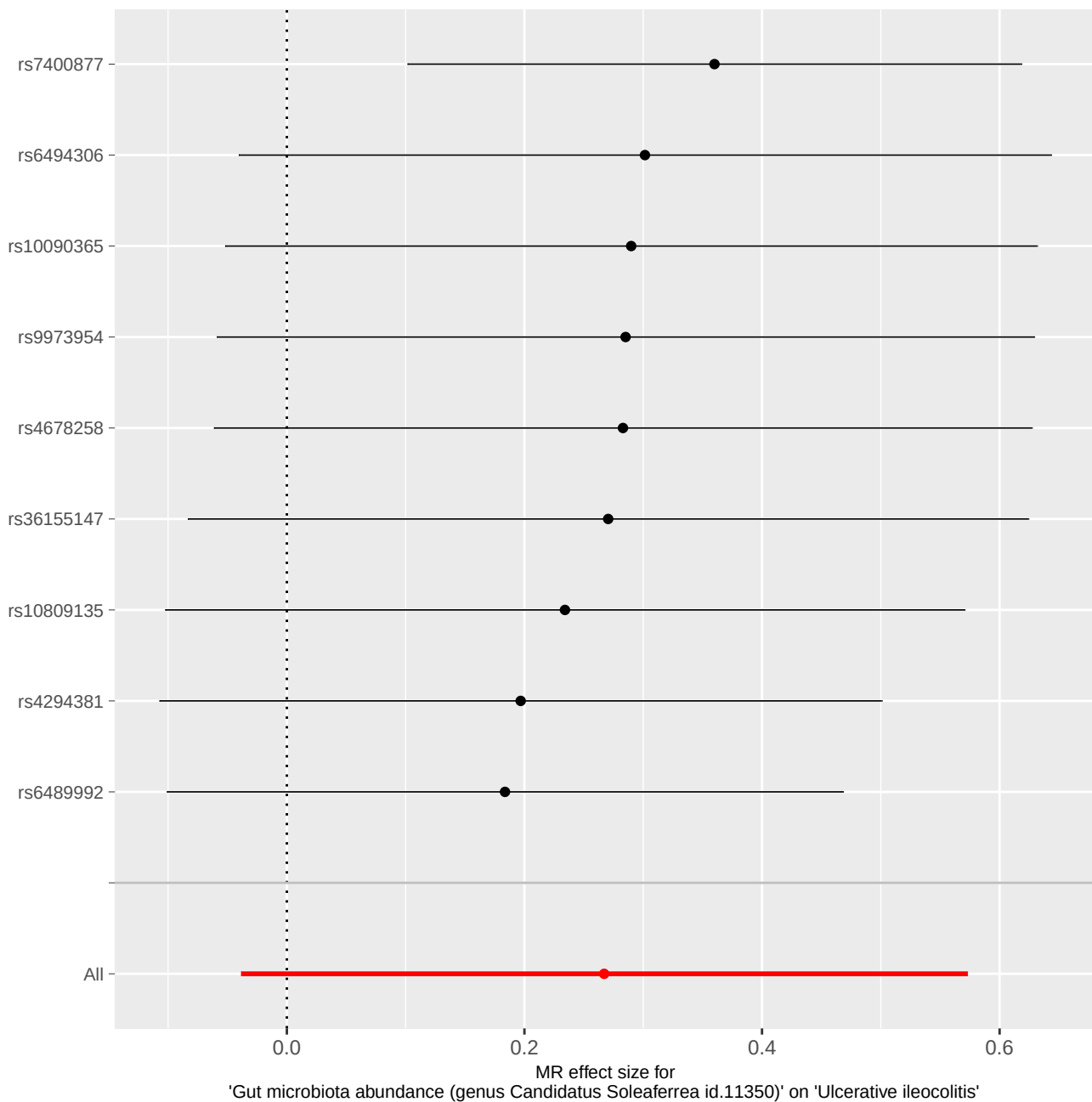


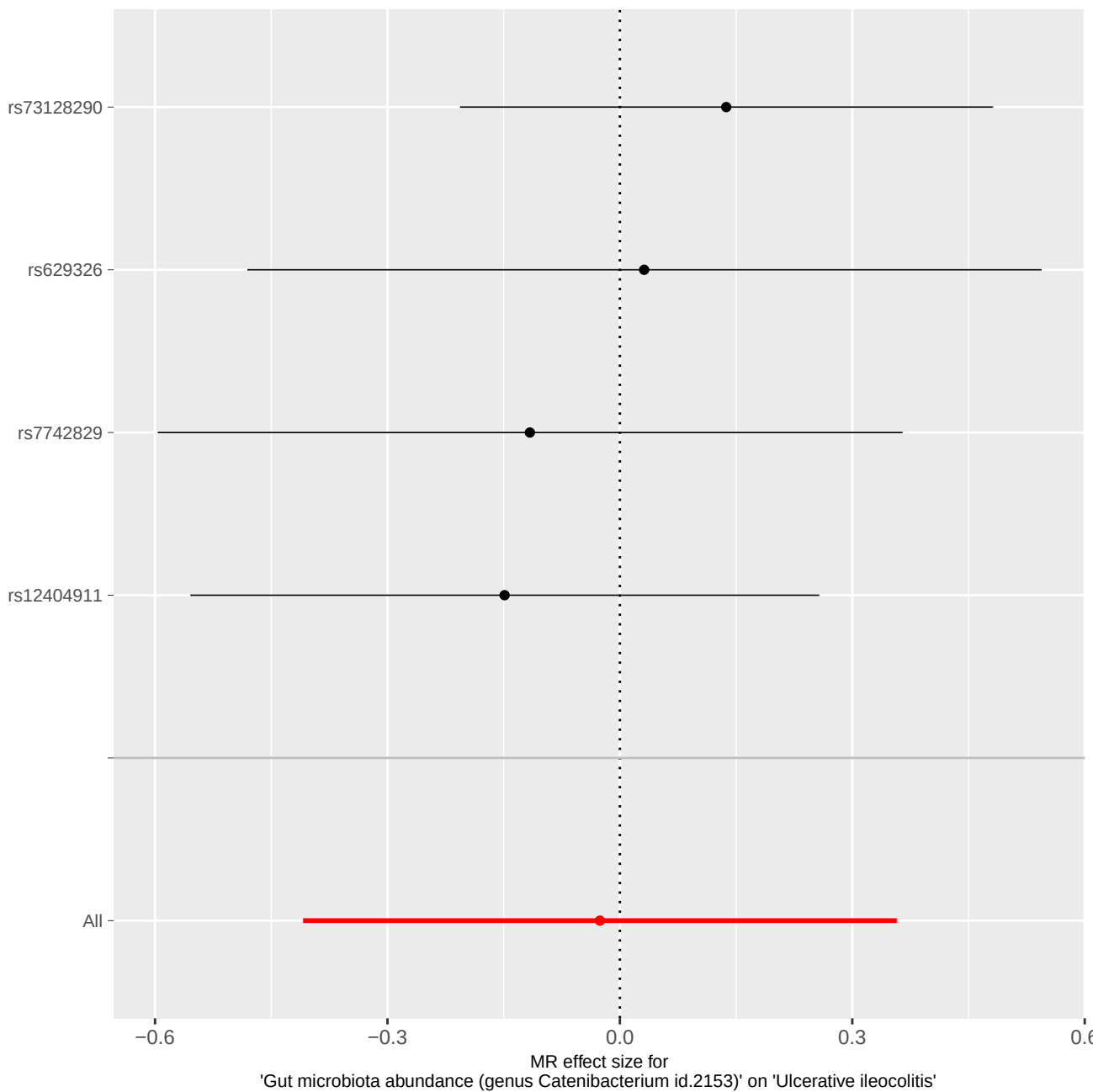




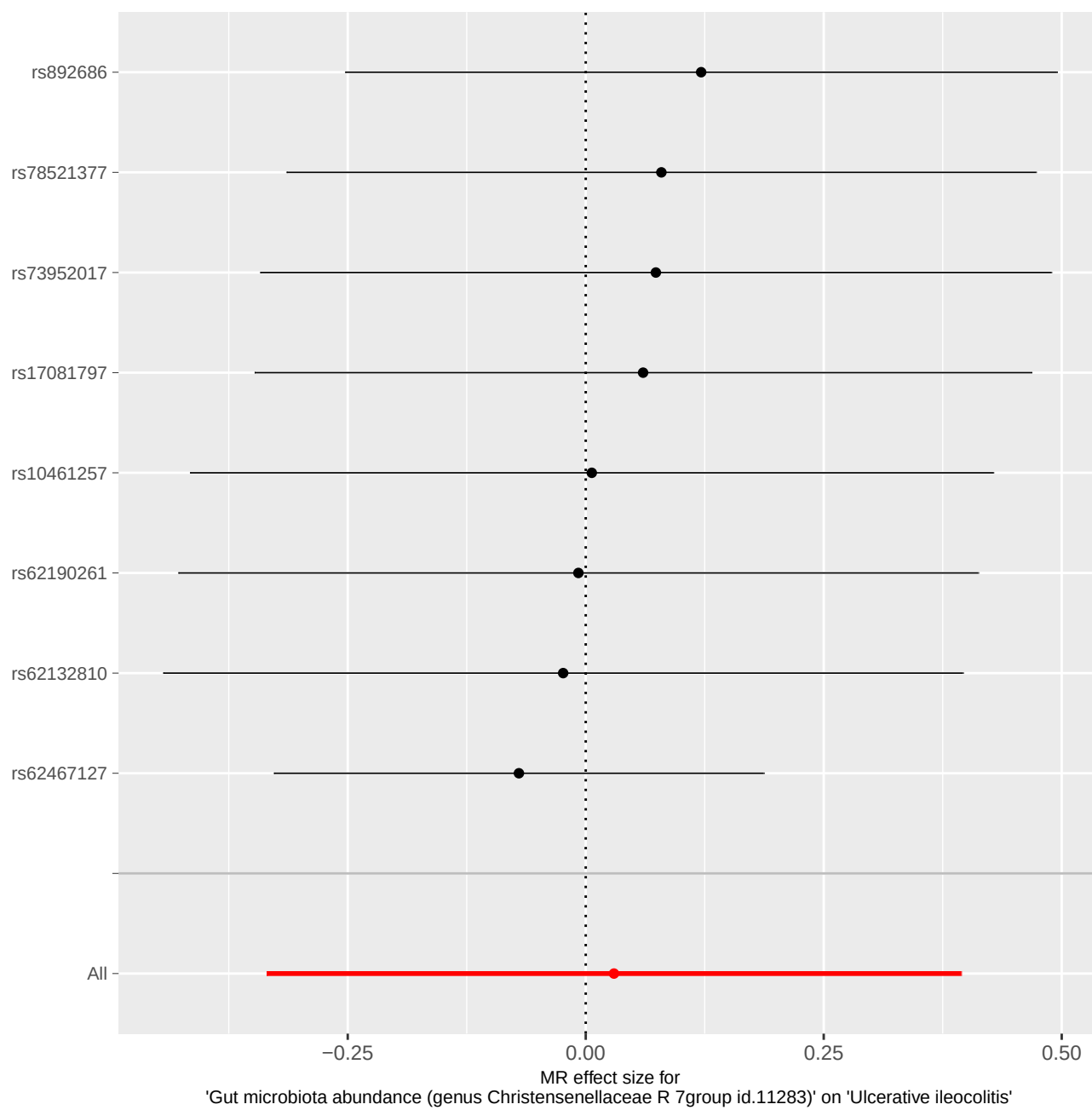


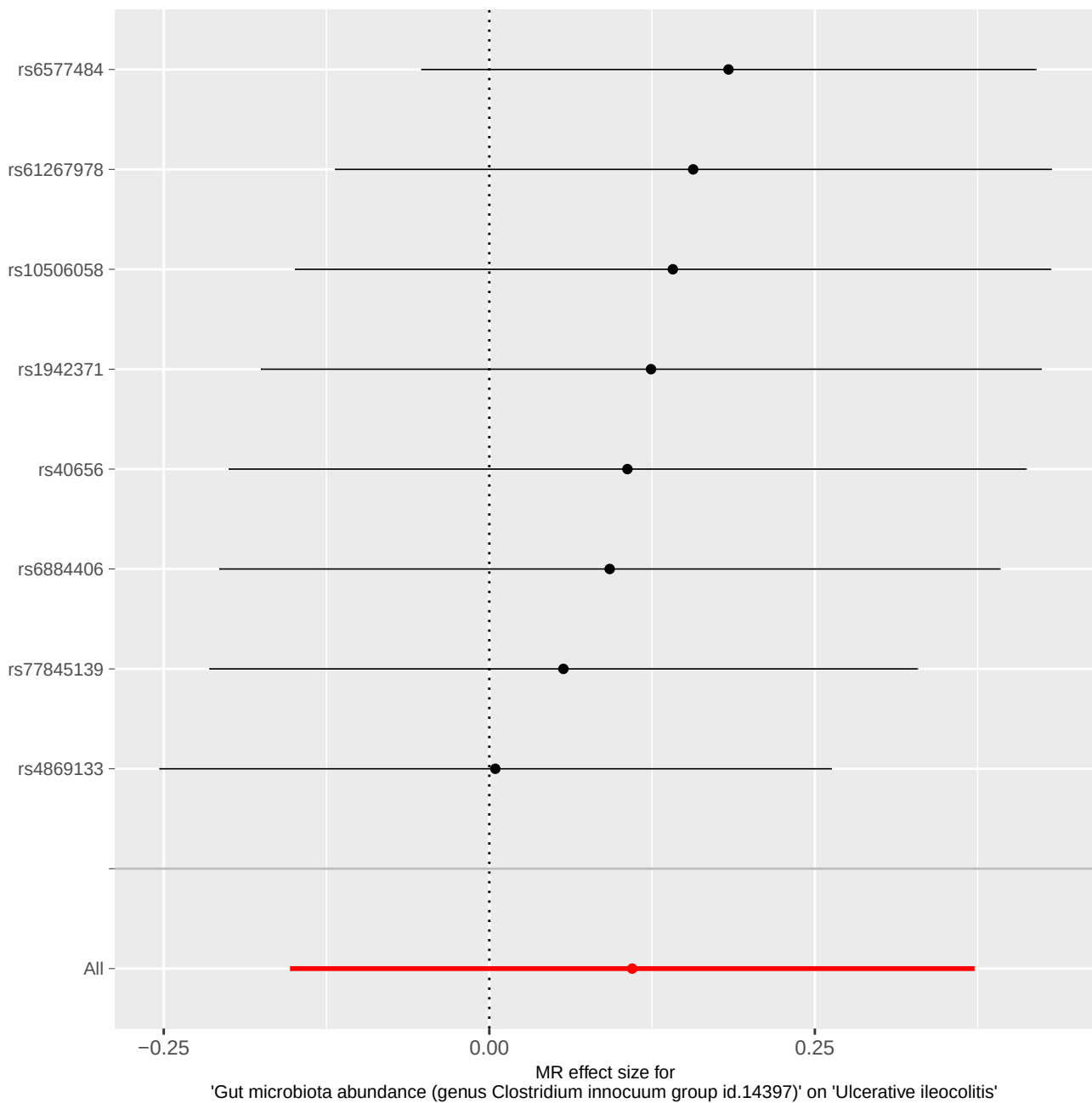


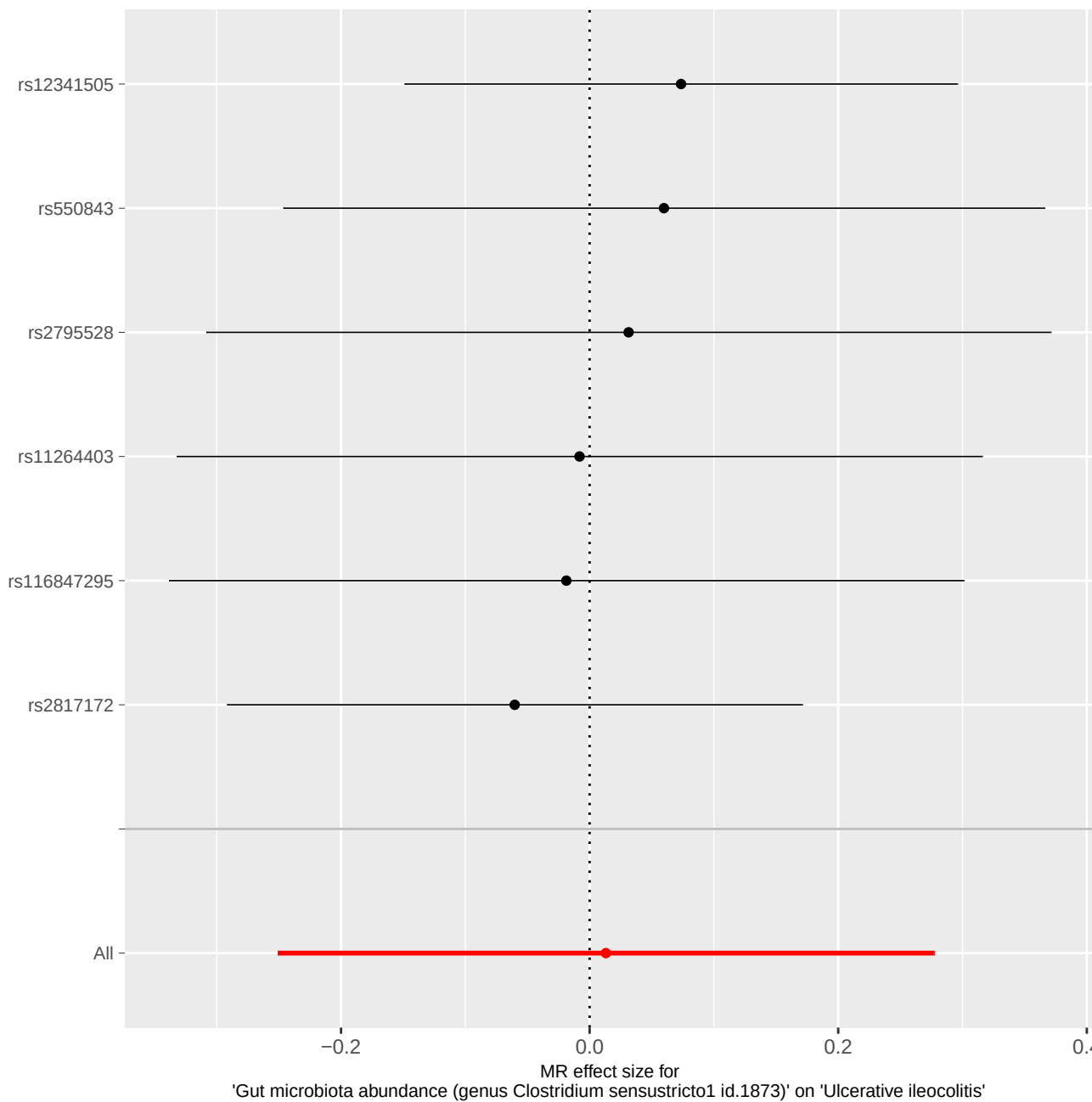


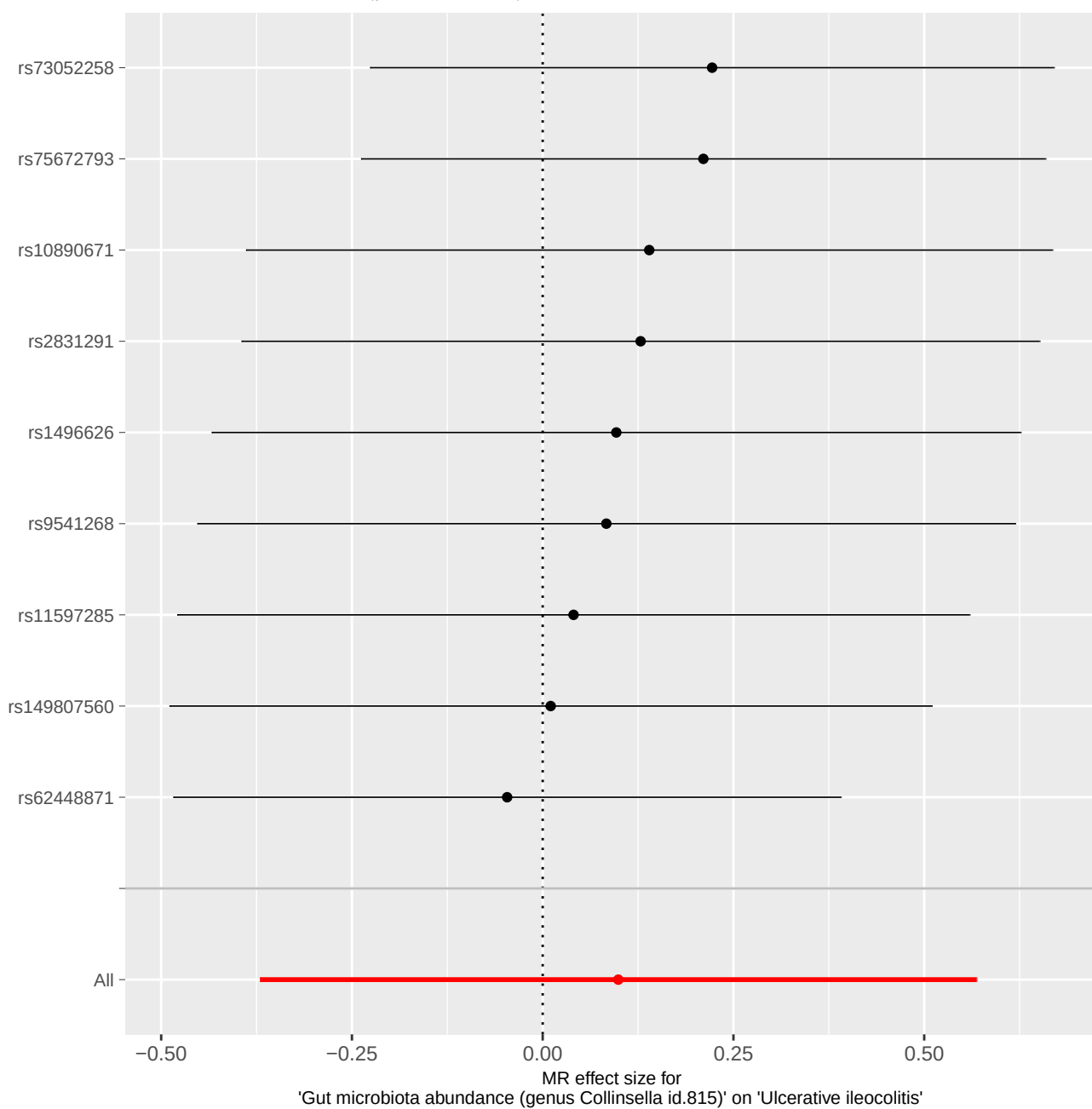


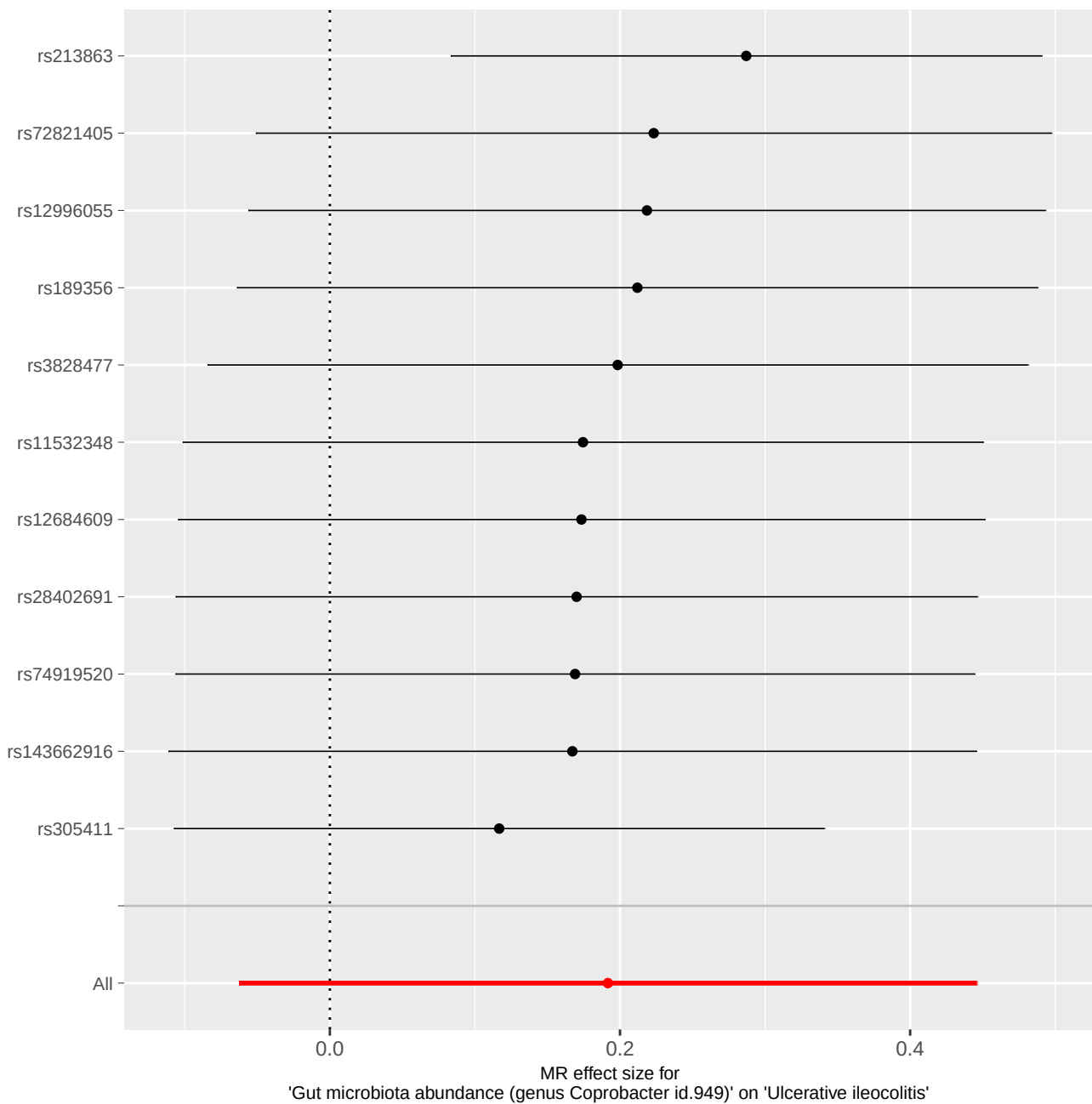
MR effect size for
'Gut microbiota abundance (genus Catenibacterium id.2153)' on 'Ulcerative ileocolitis'

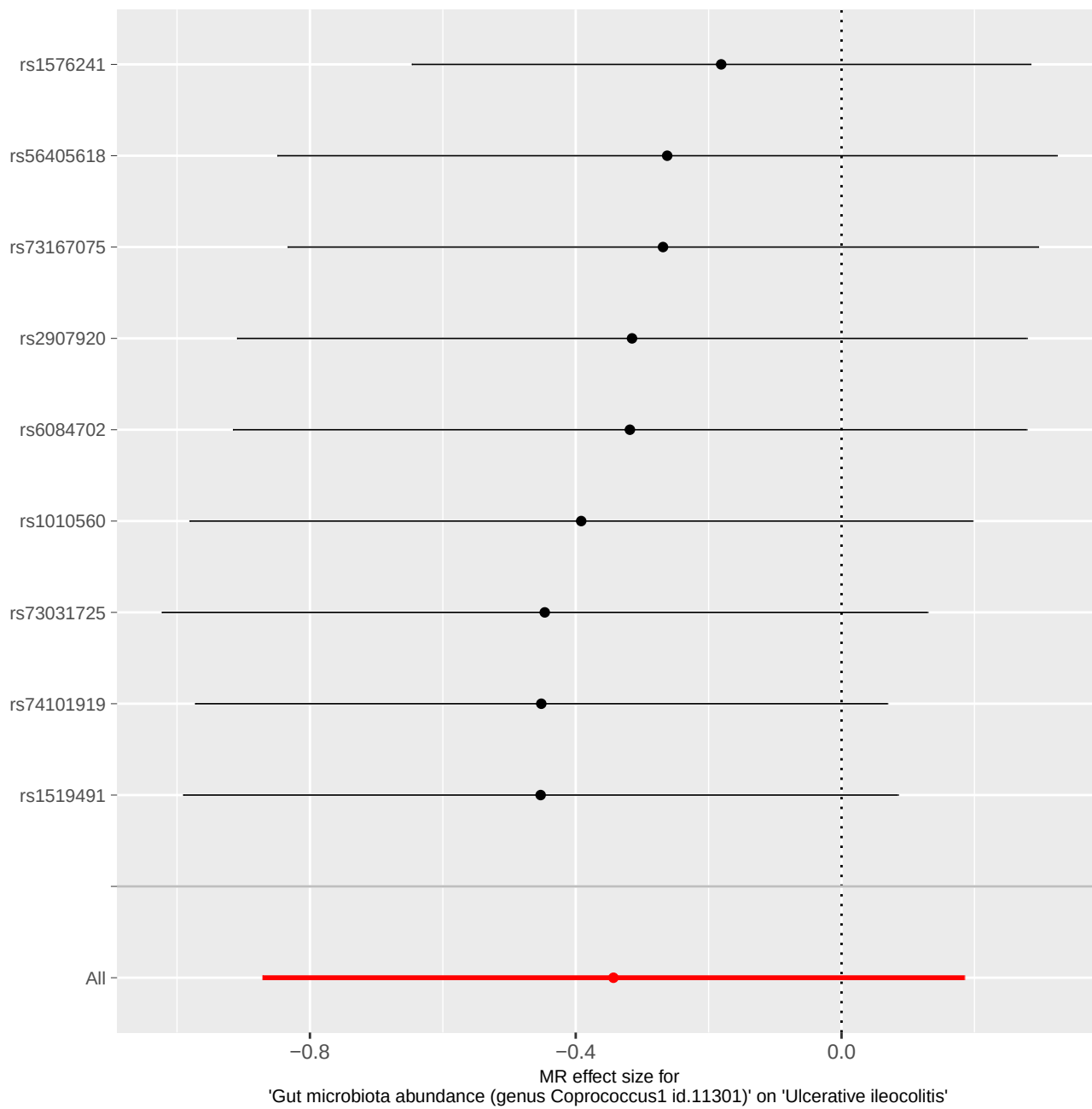


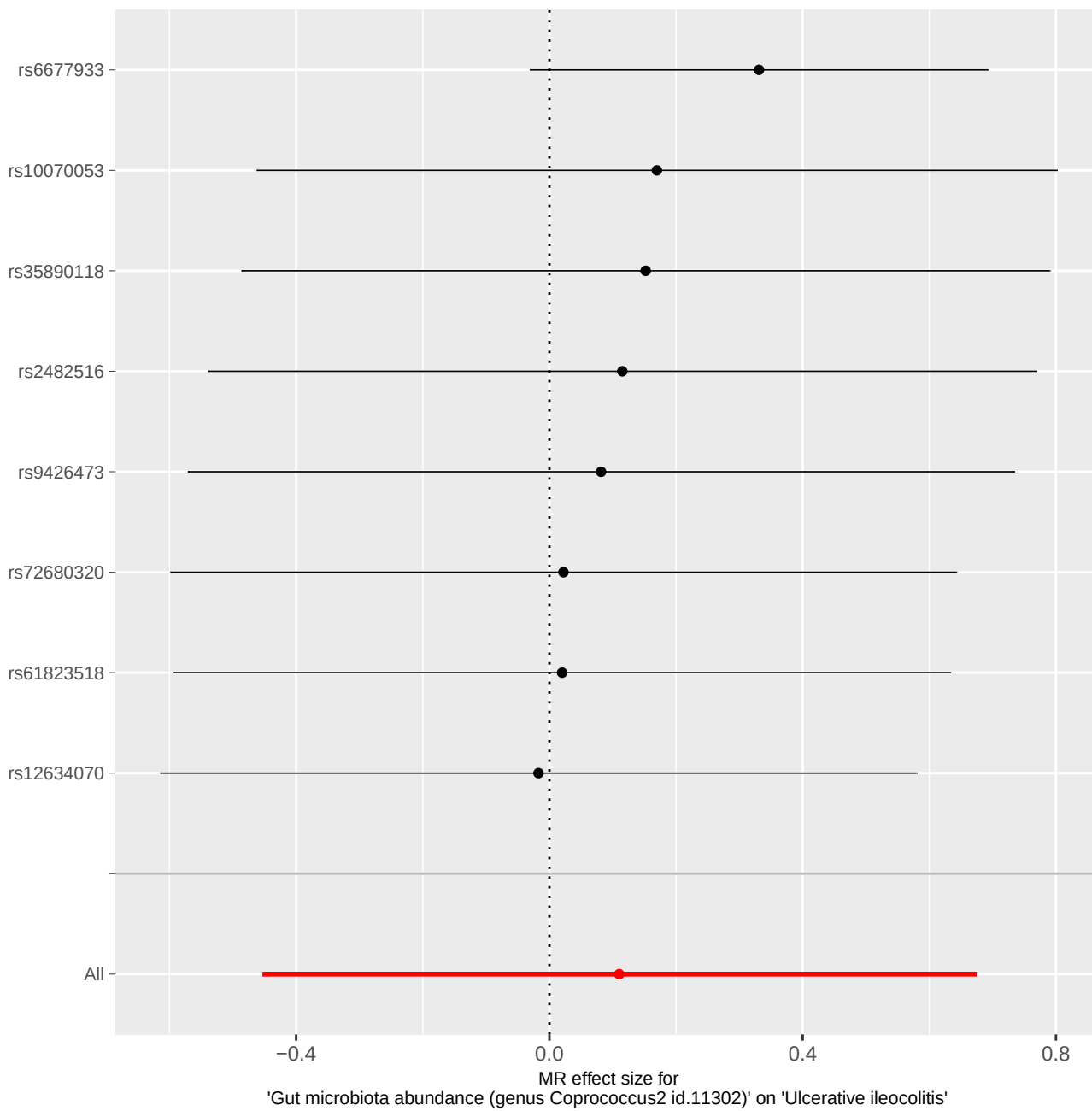


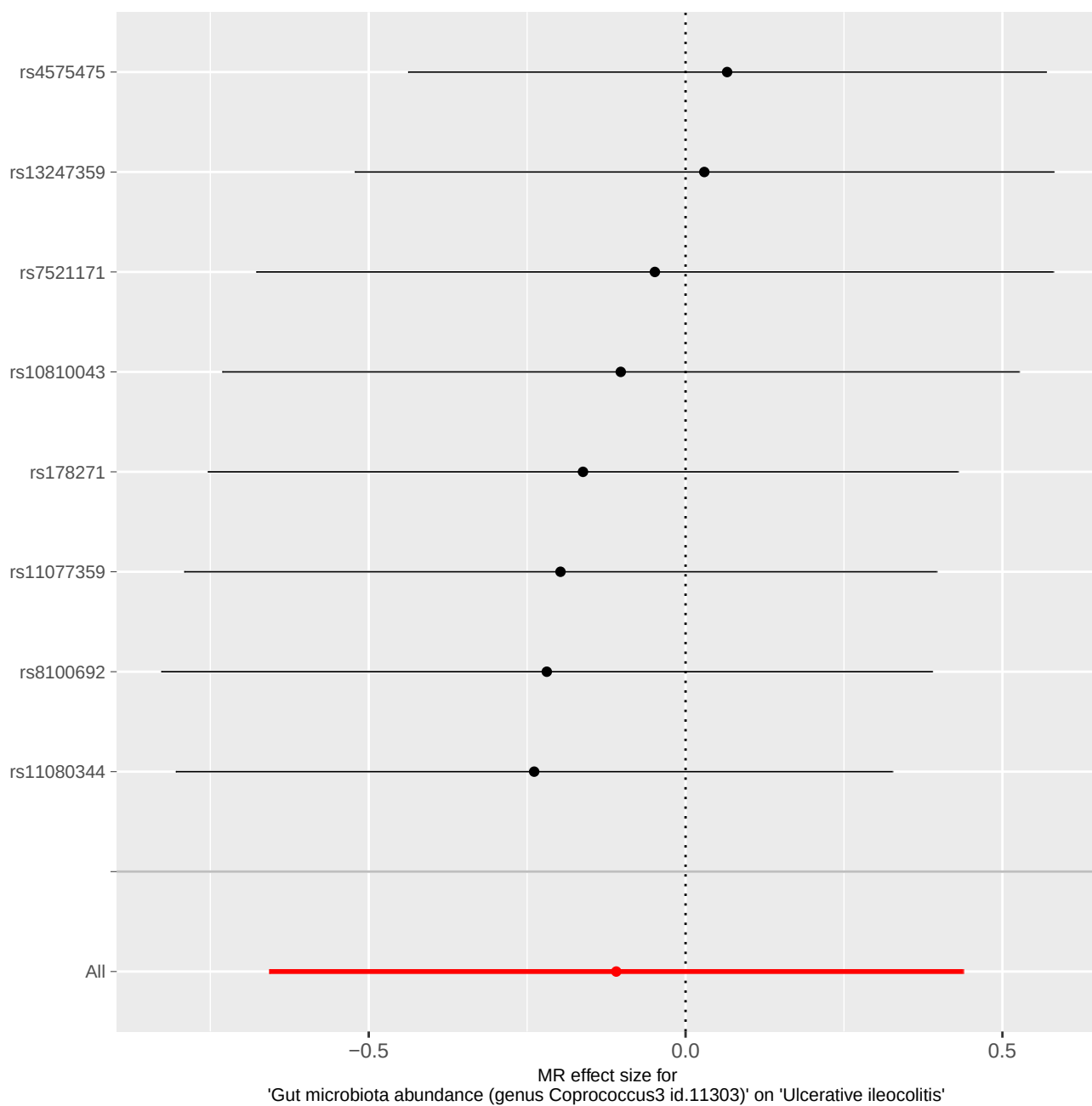


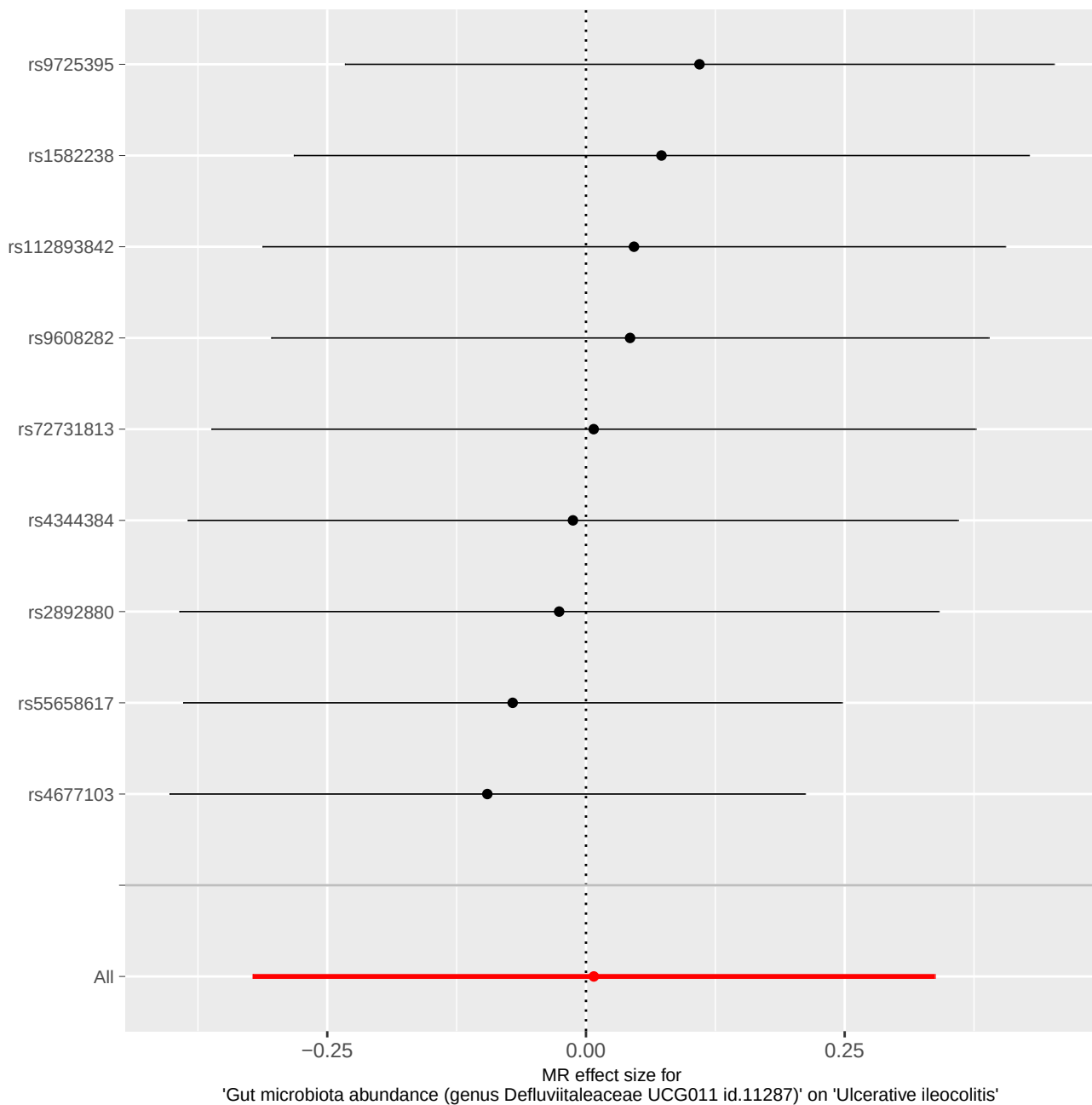


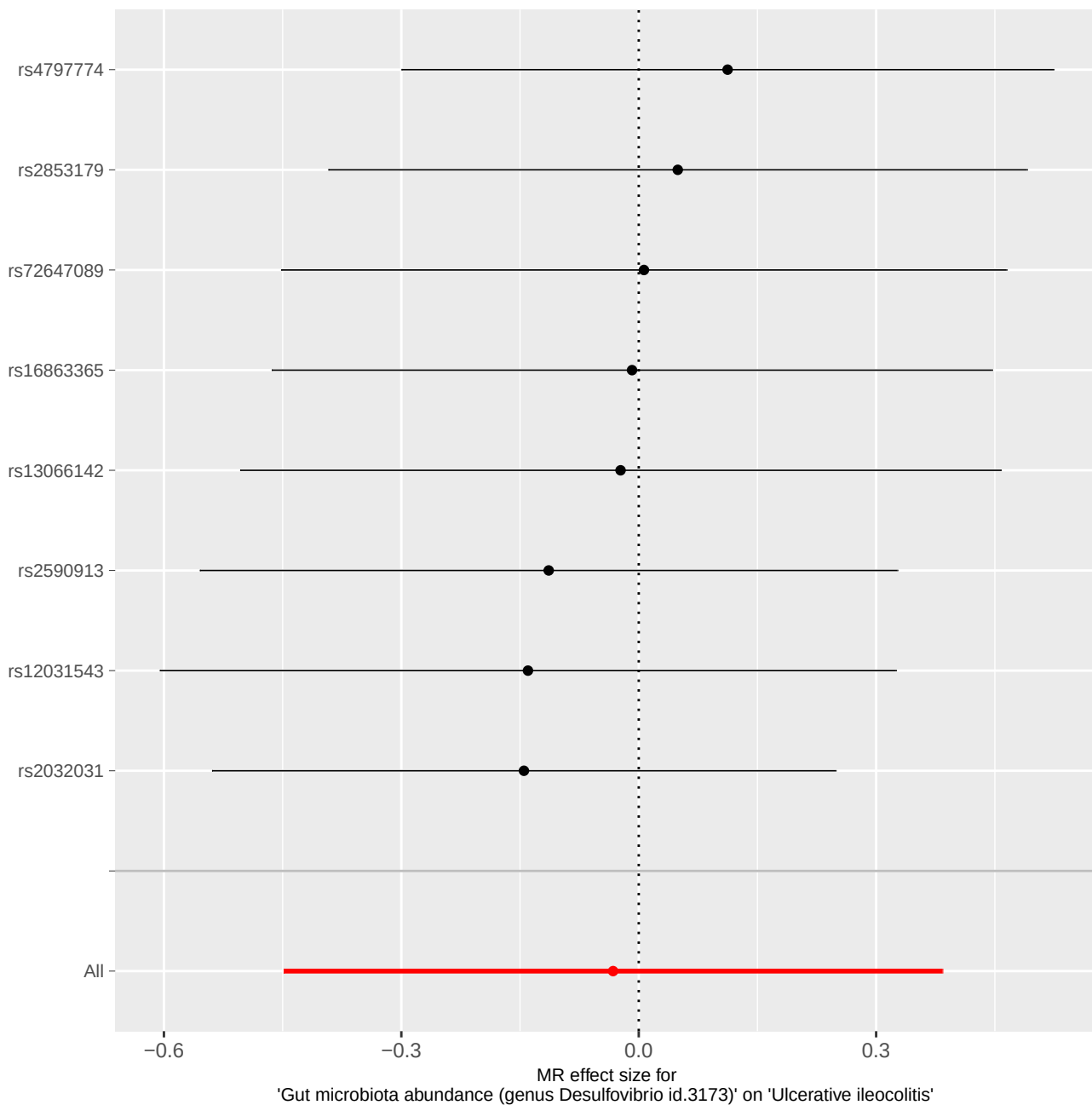


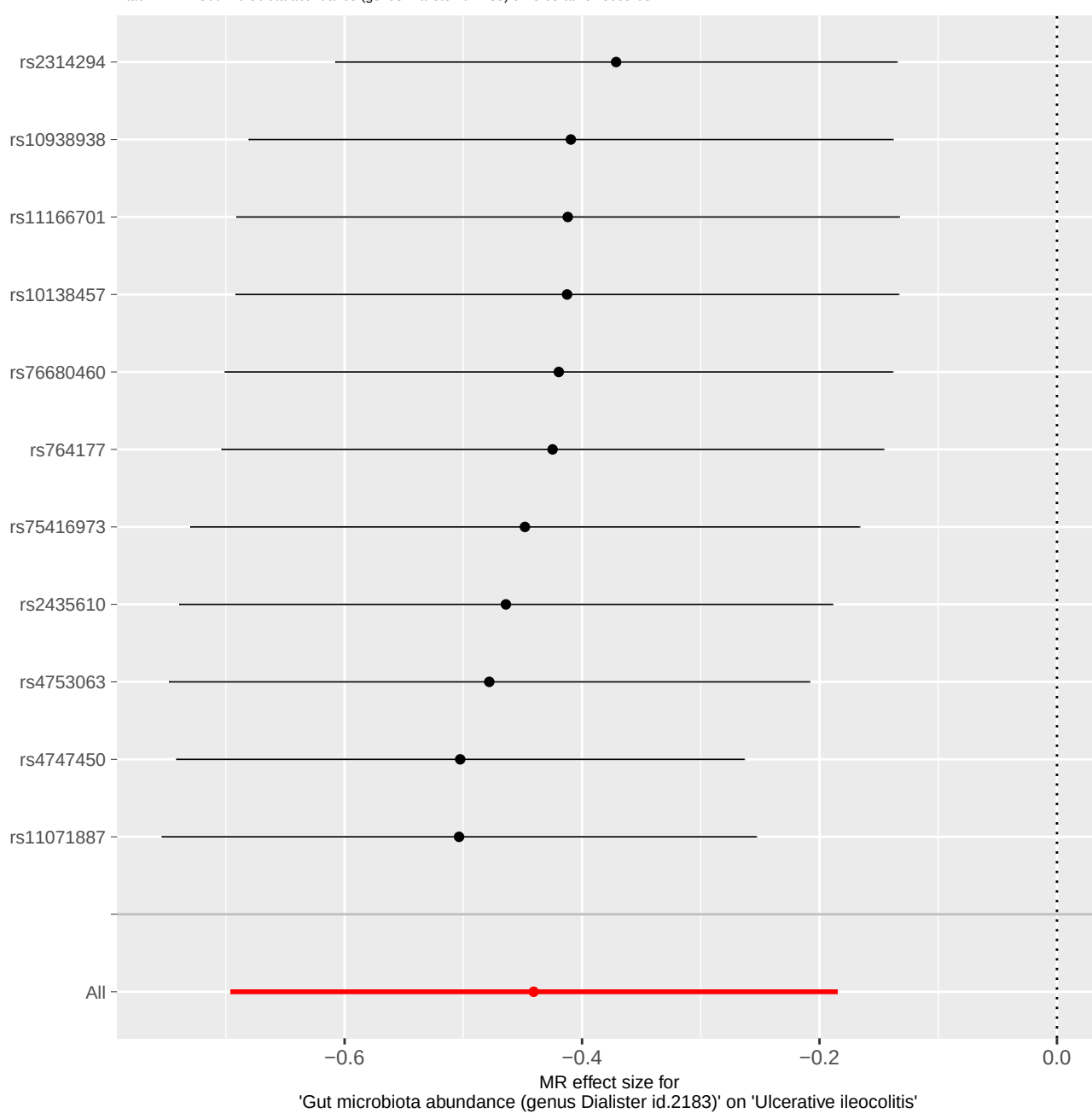


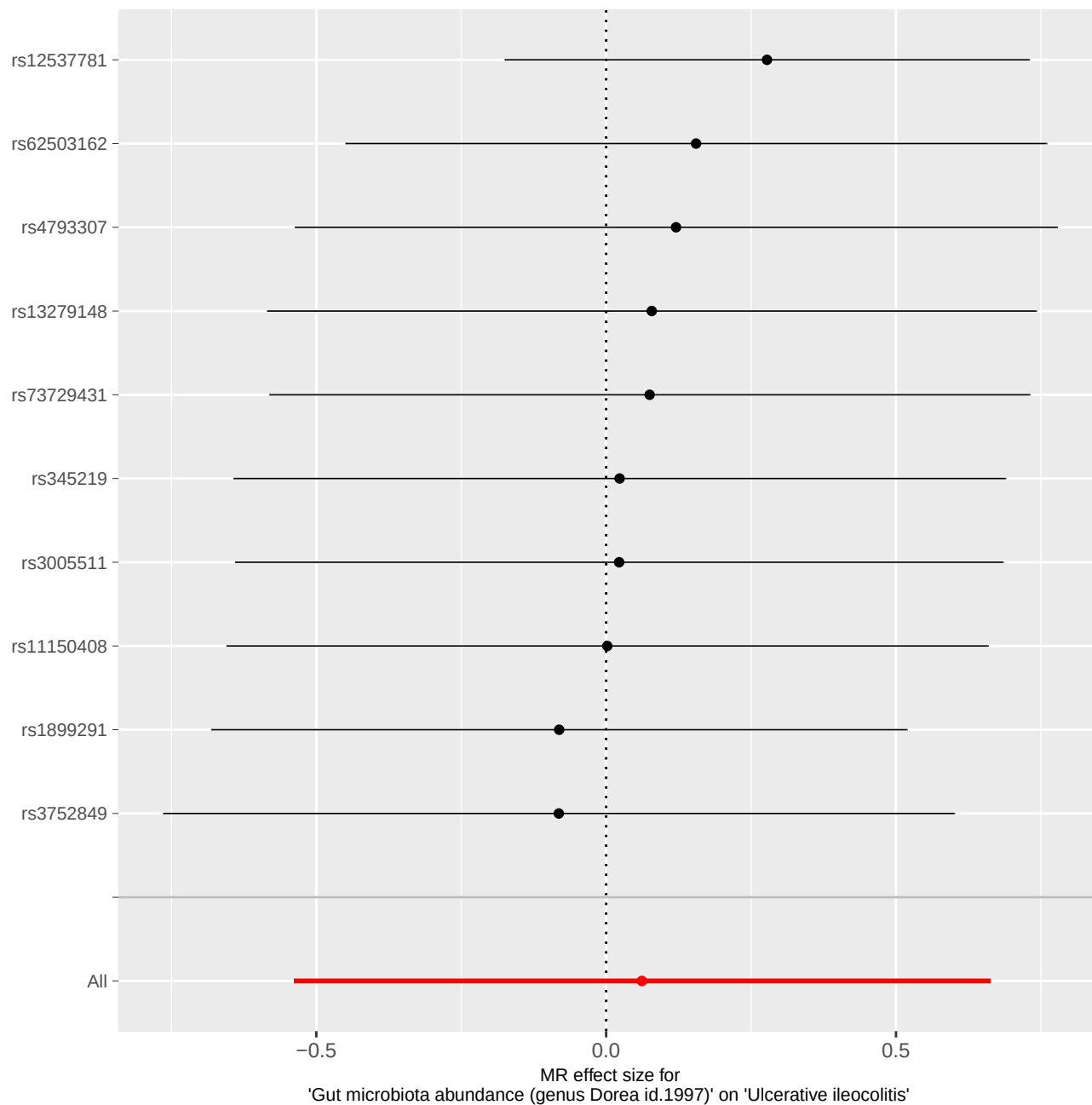


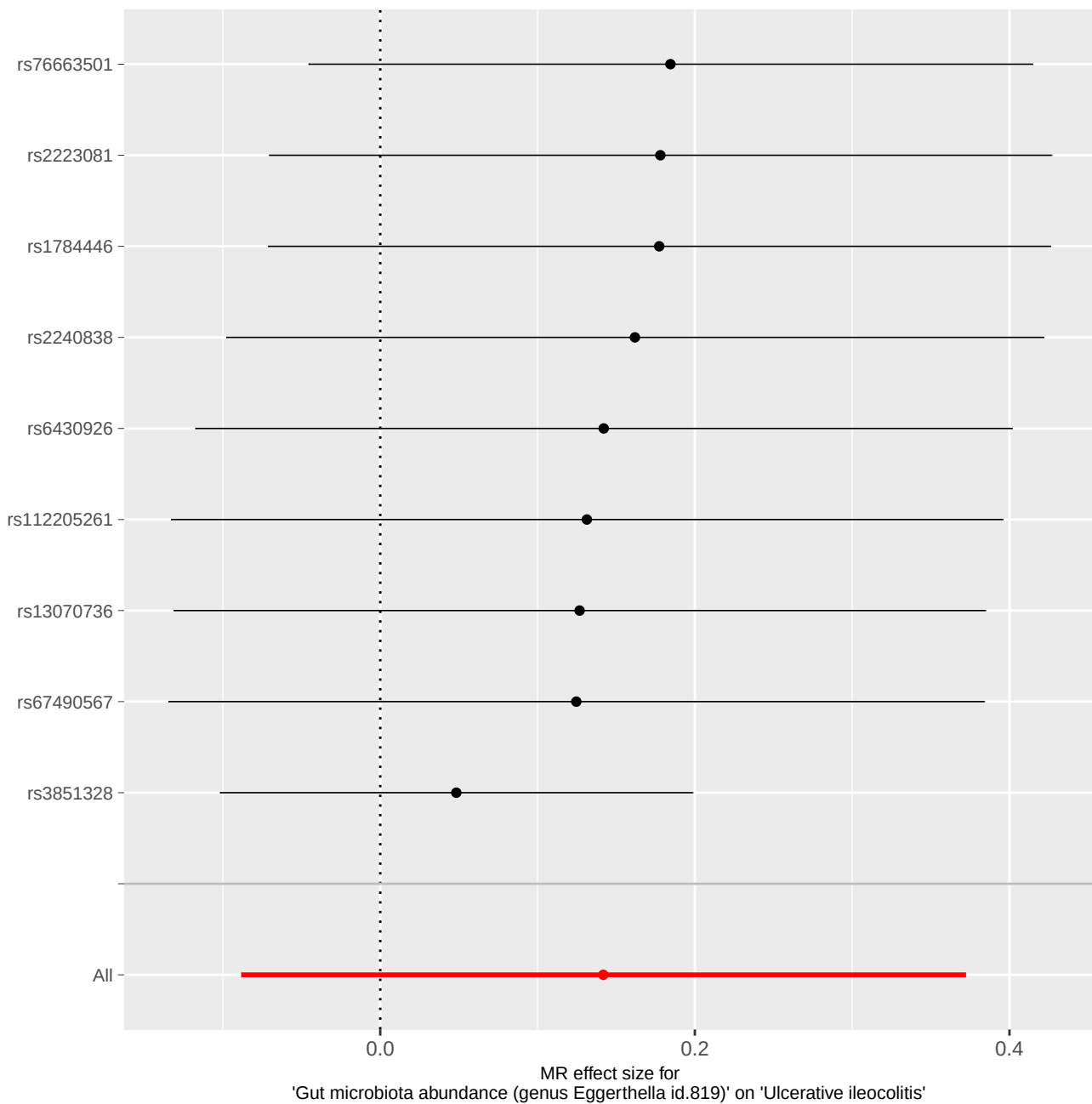


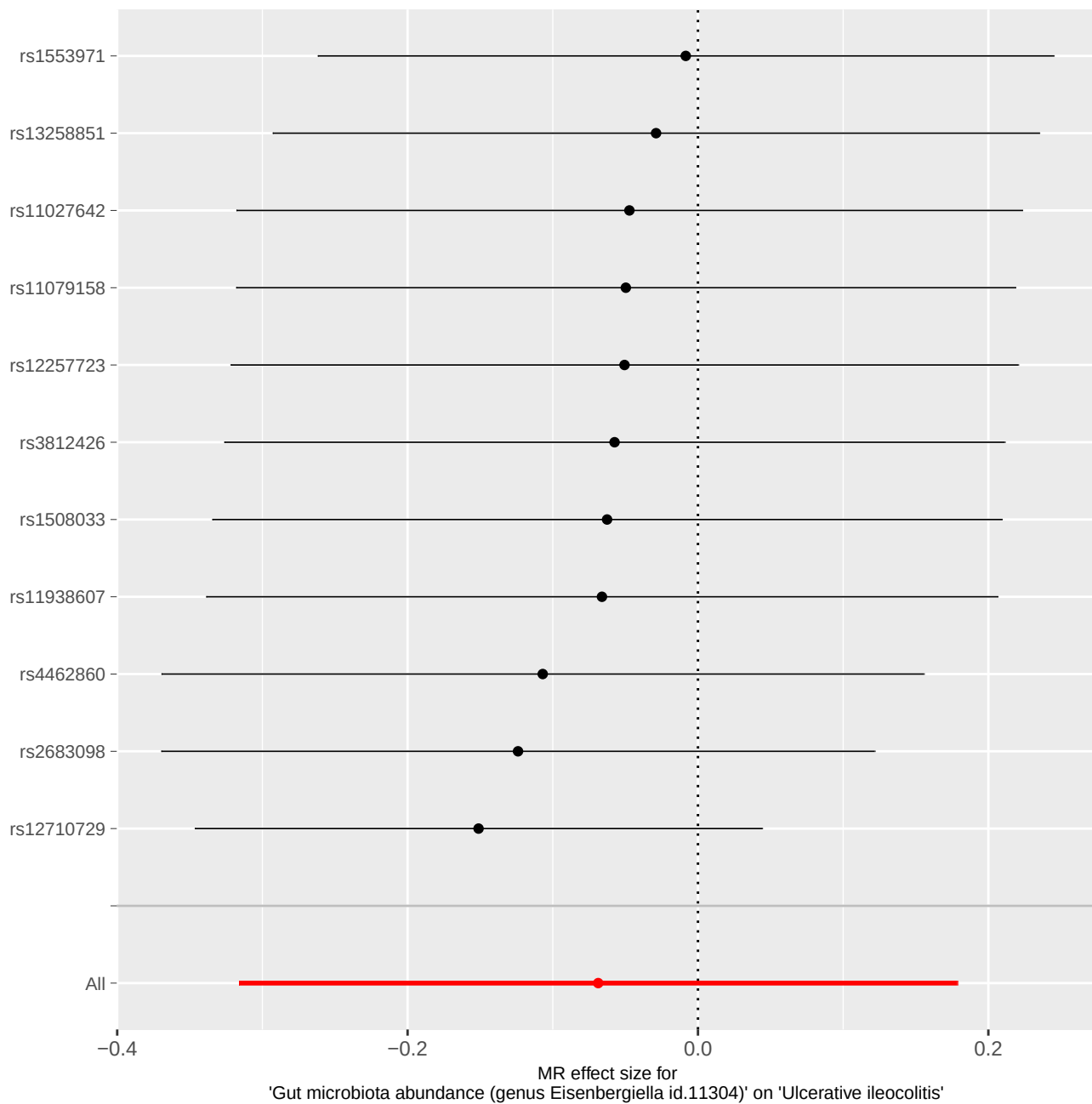


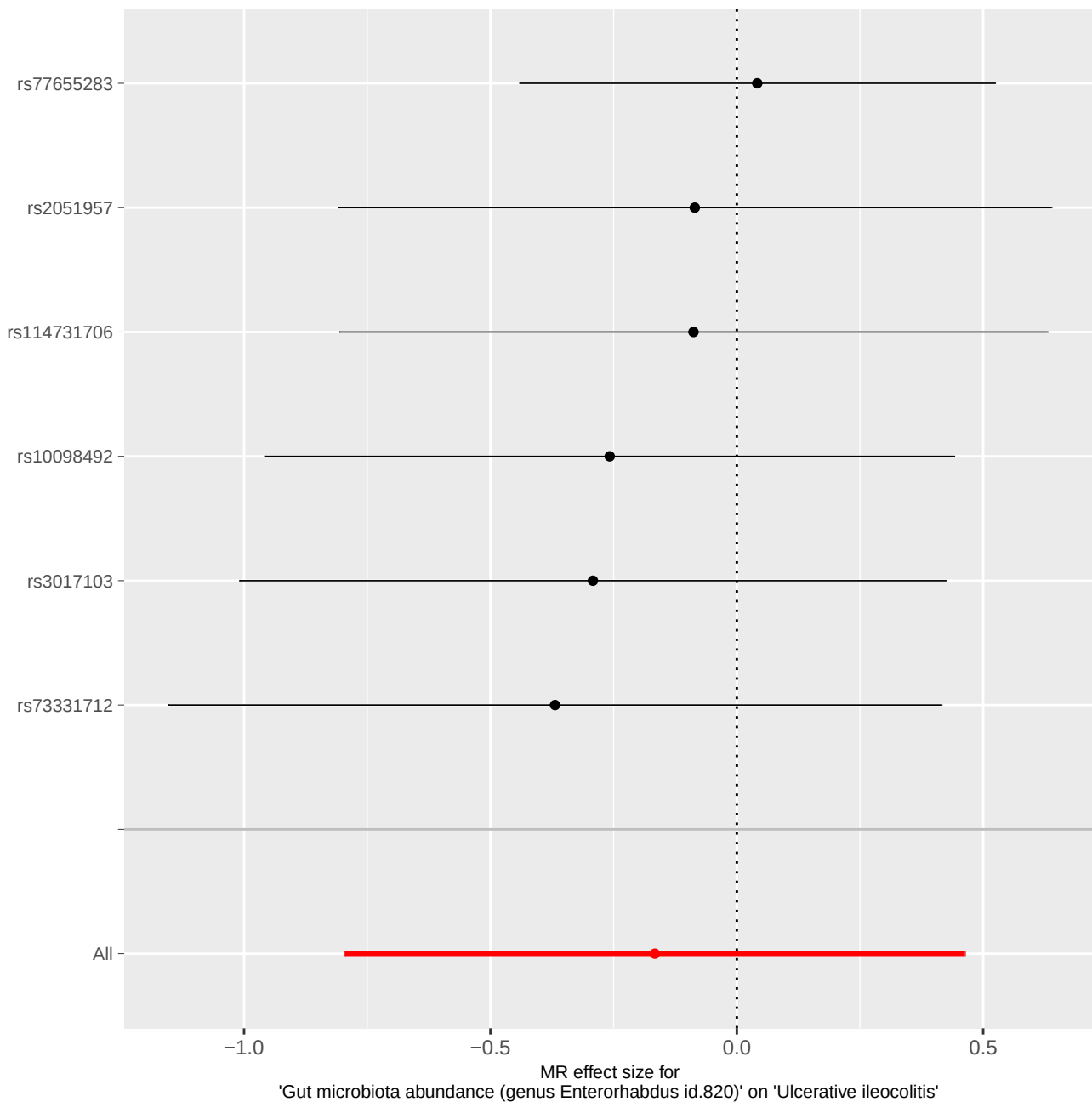


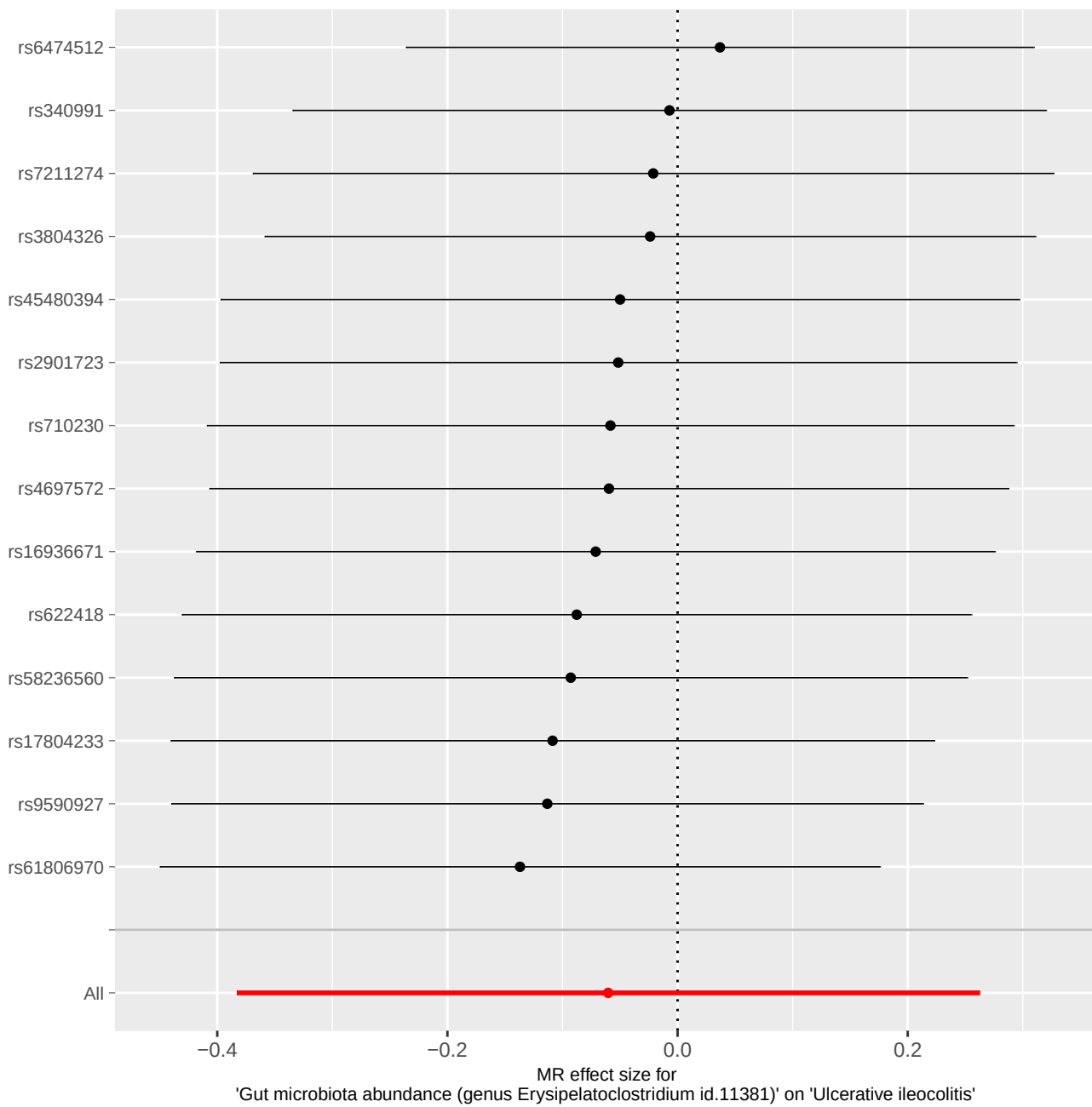


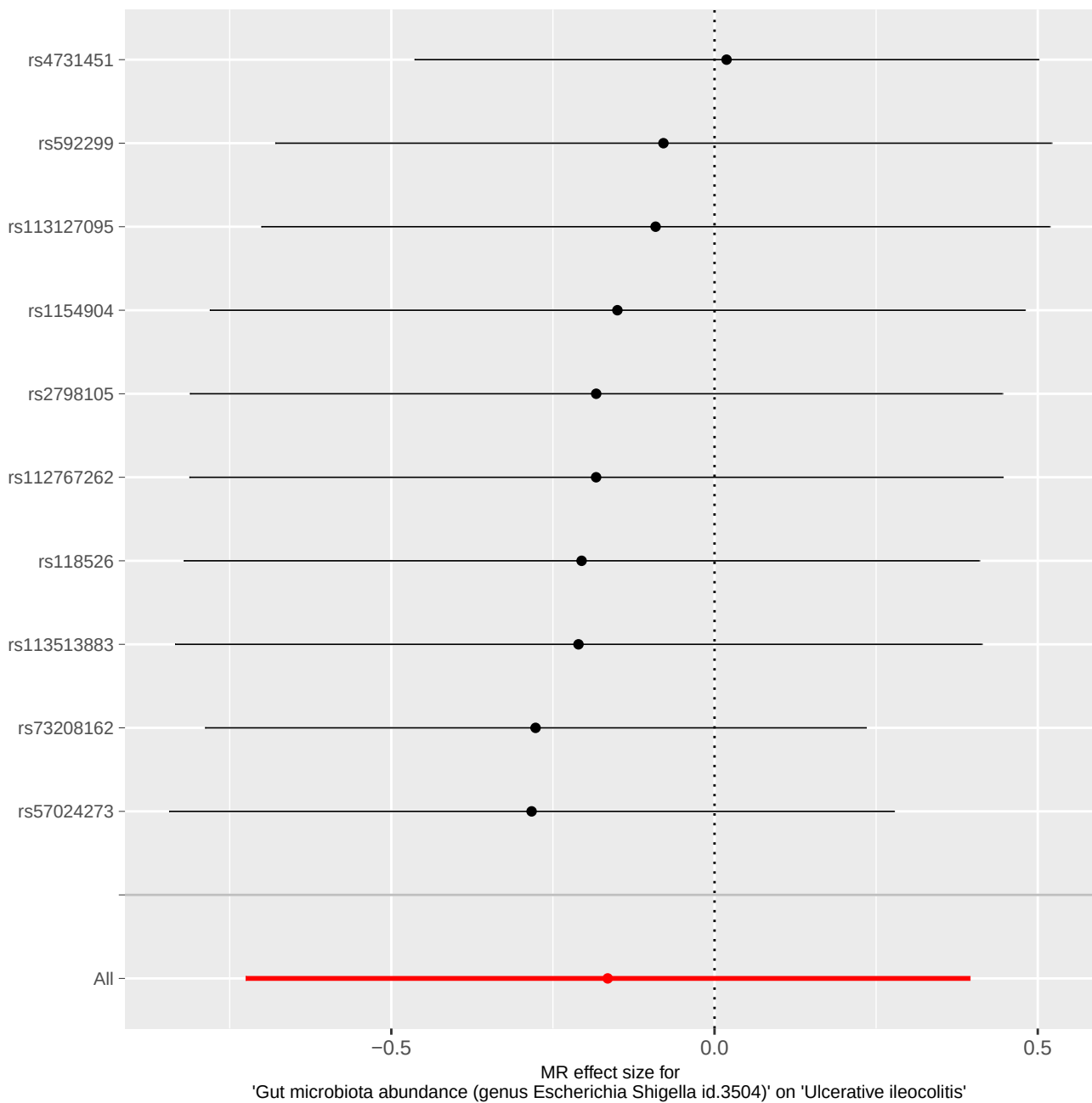


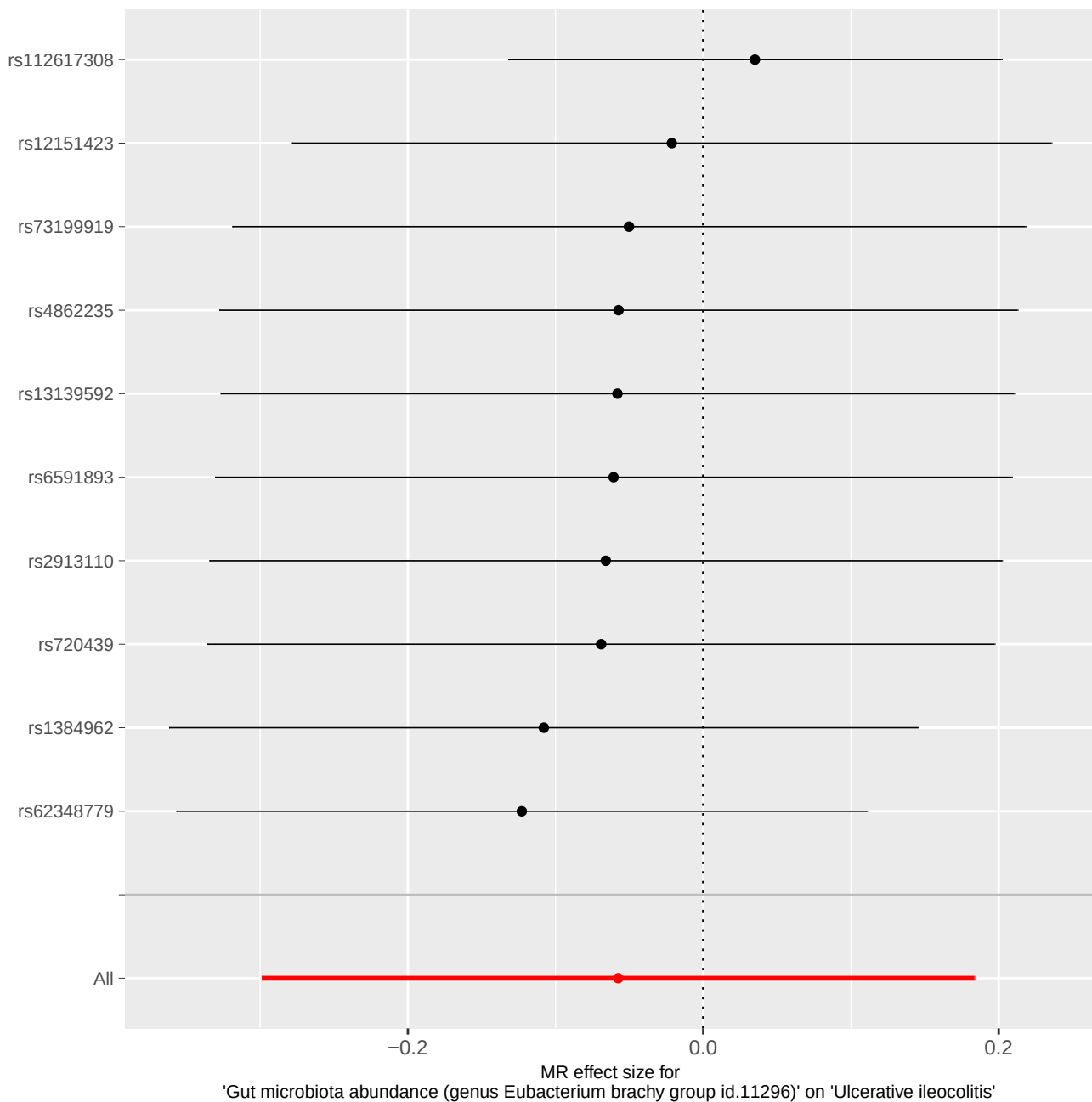


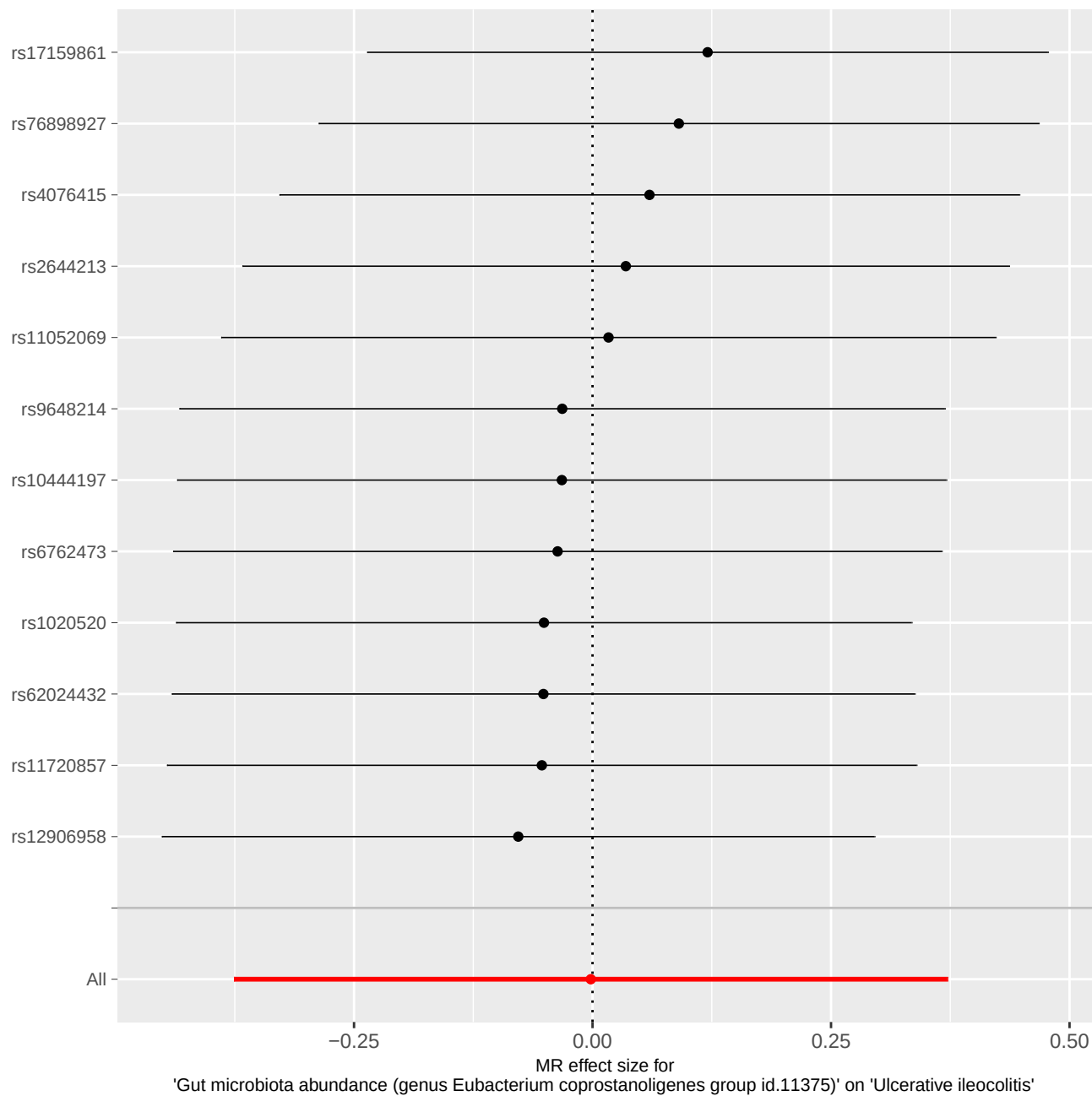


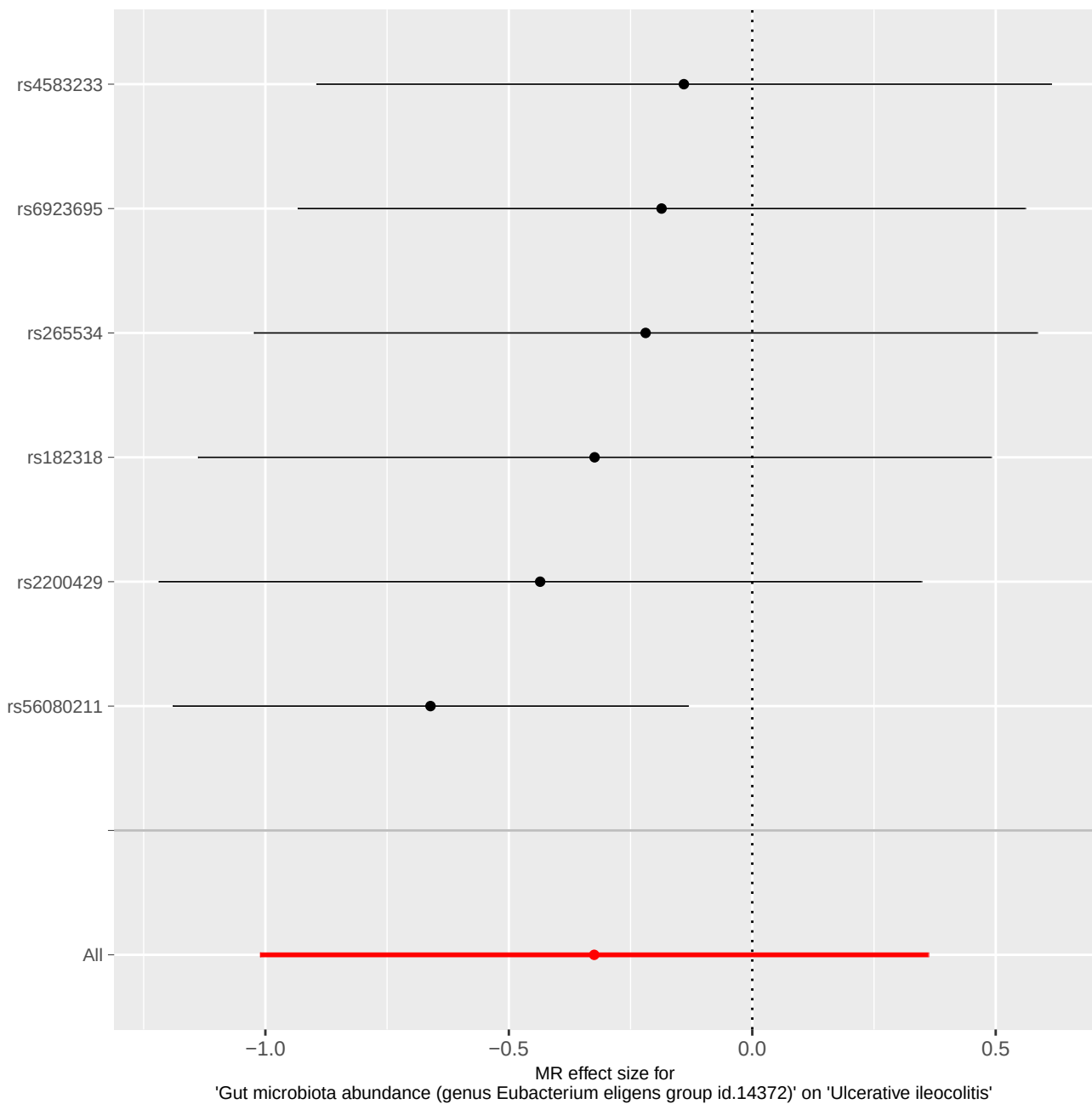


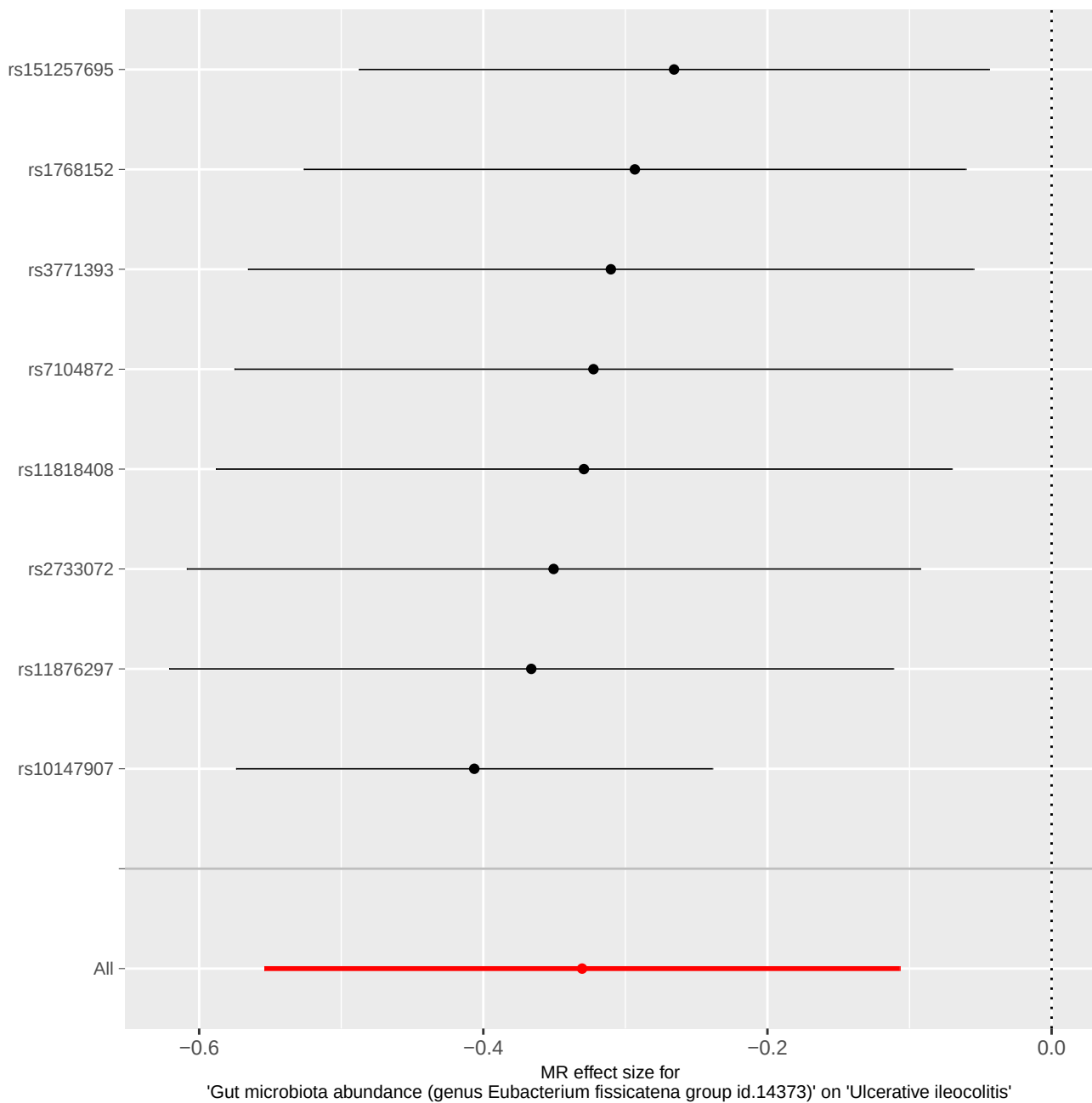


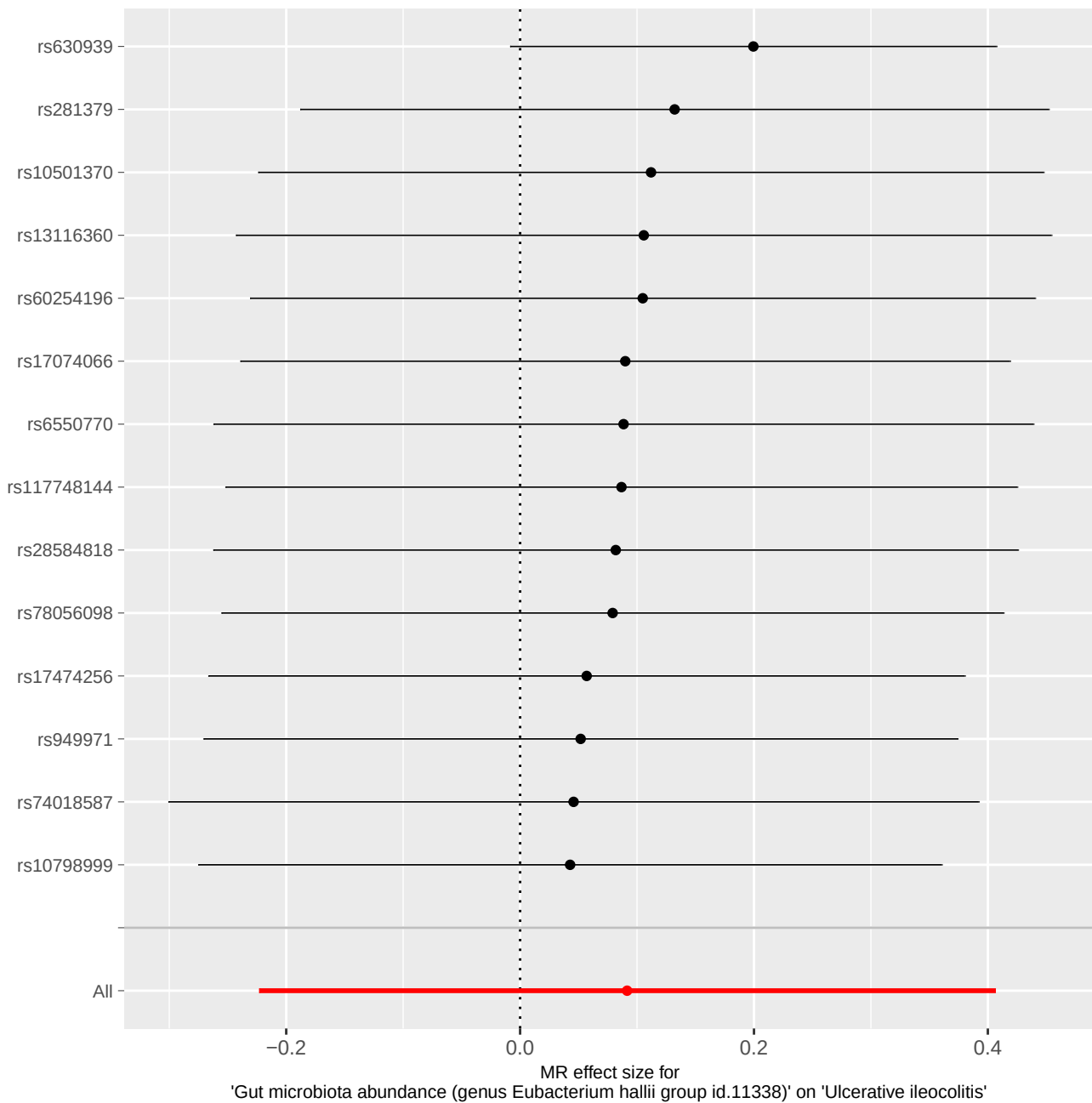




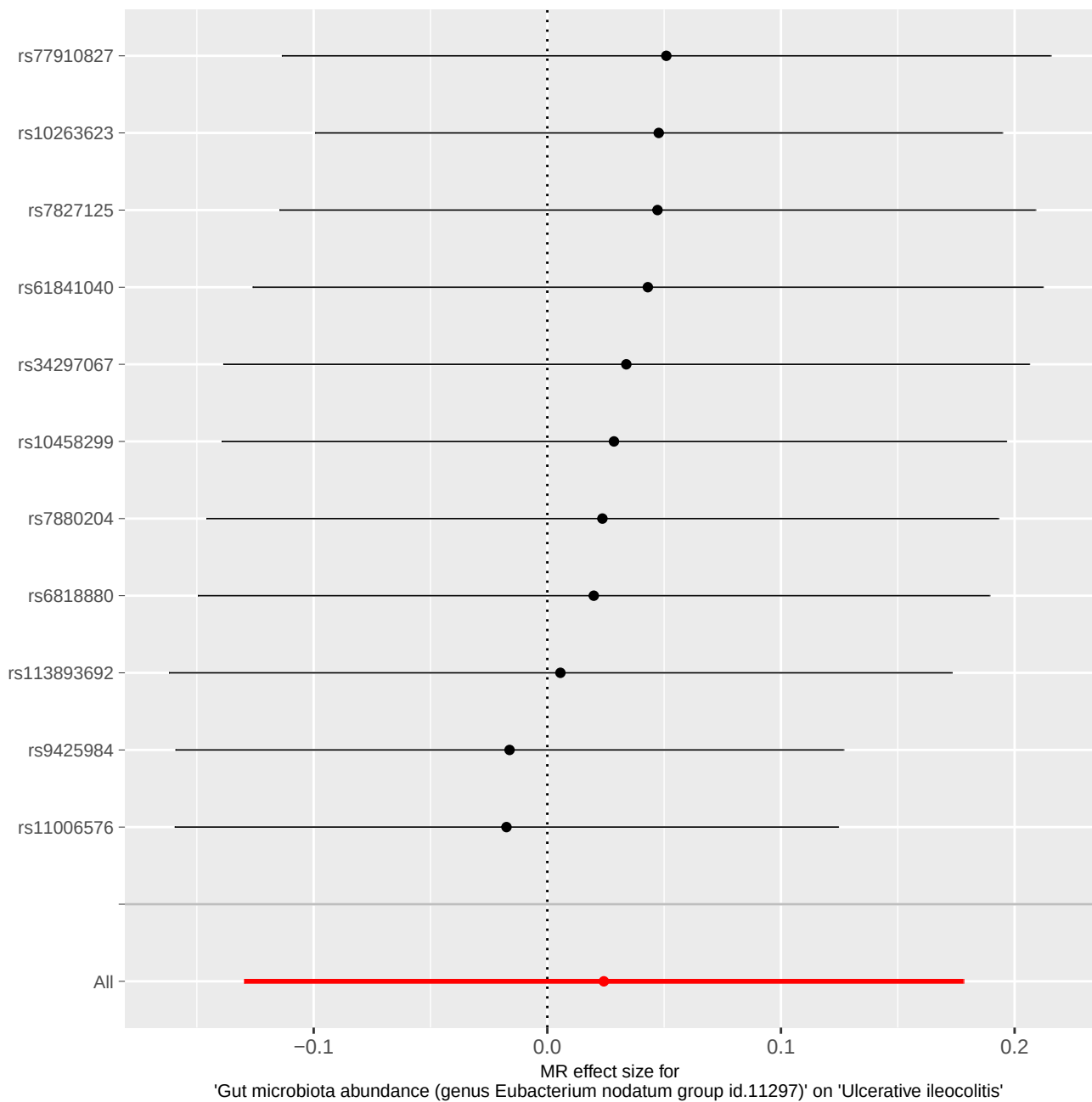


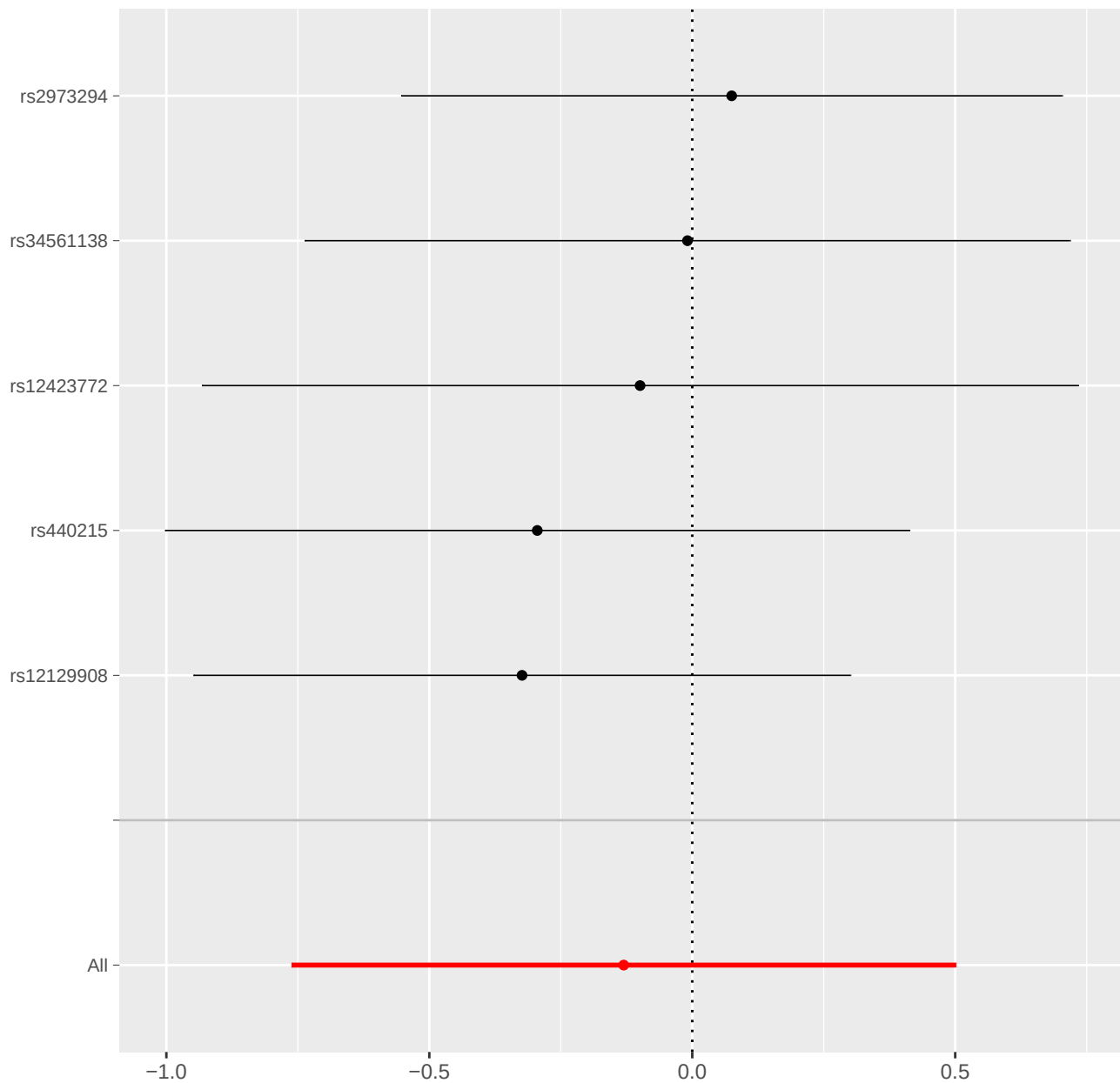




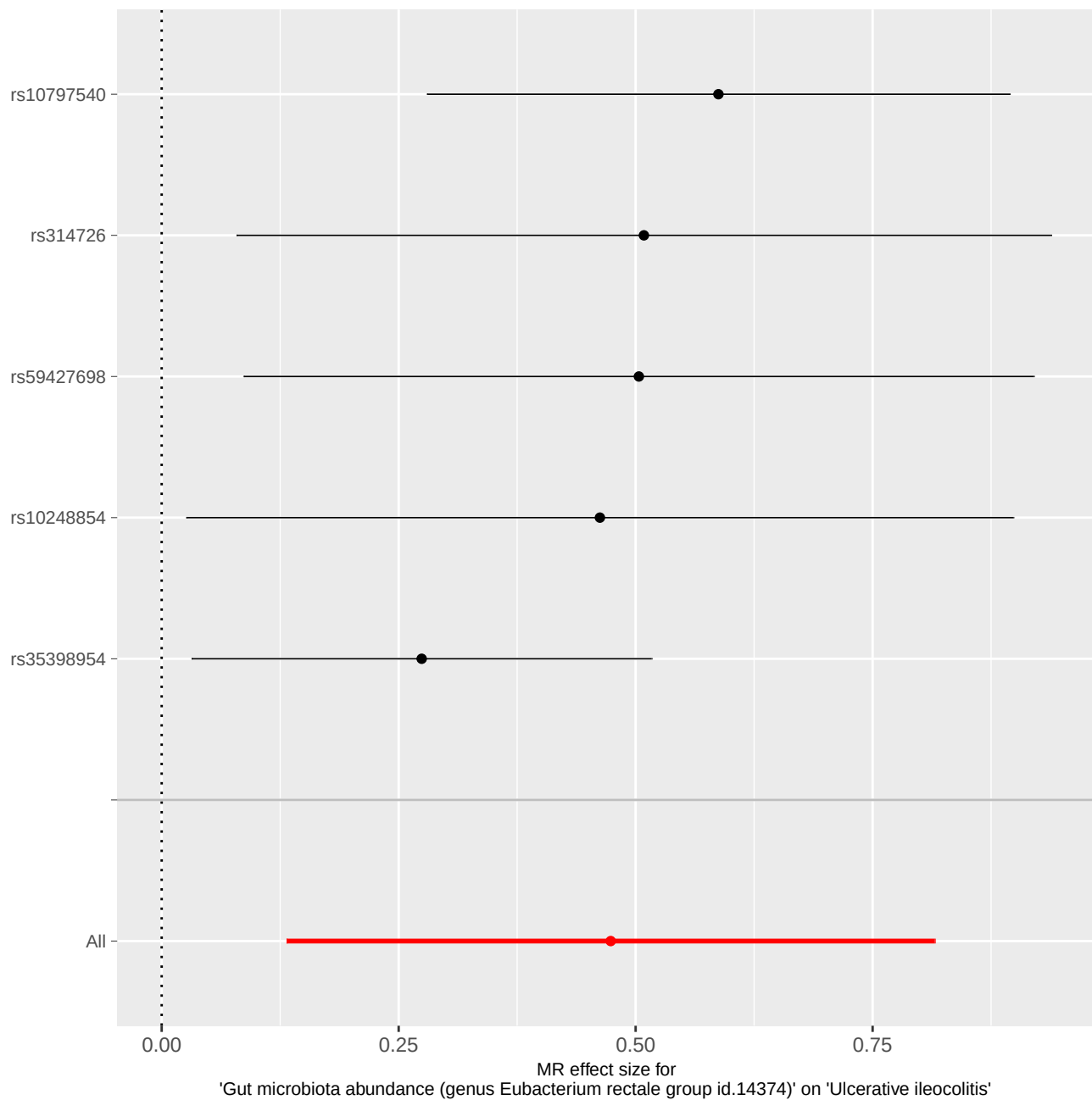


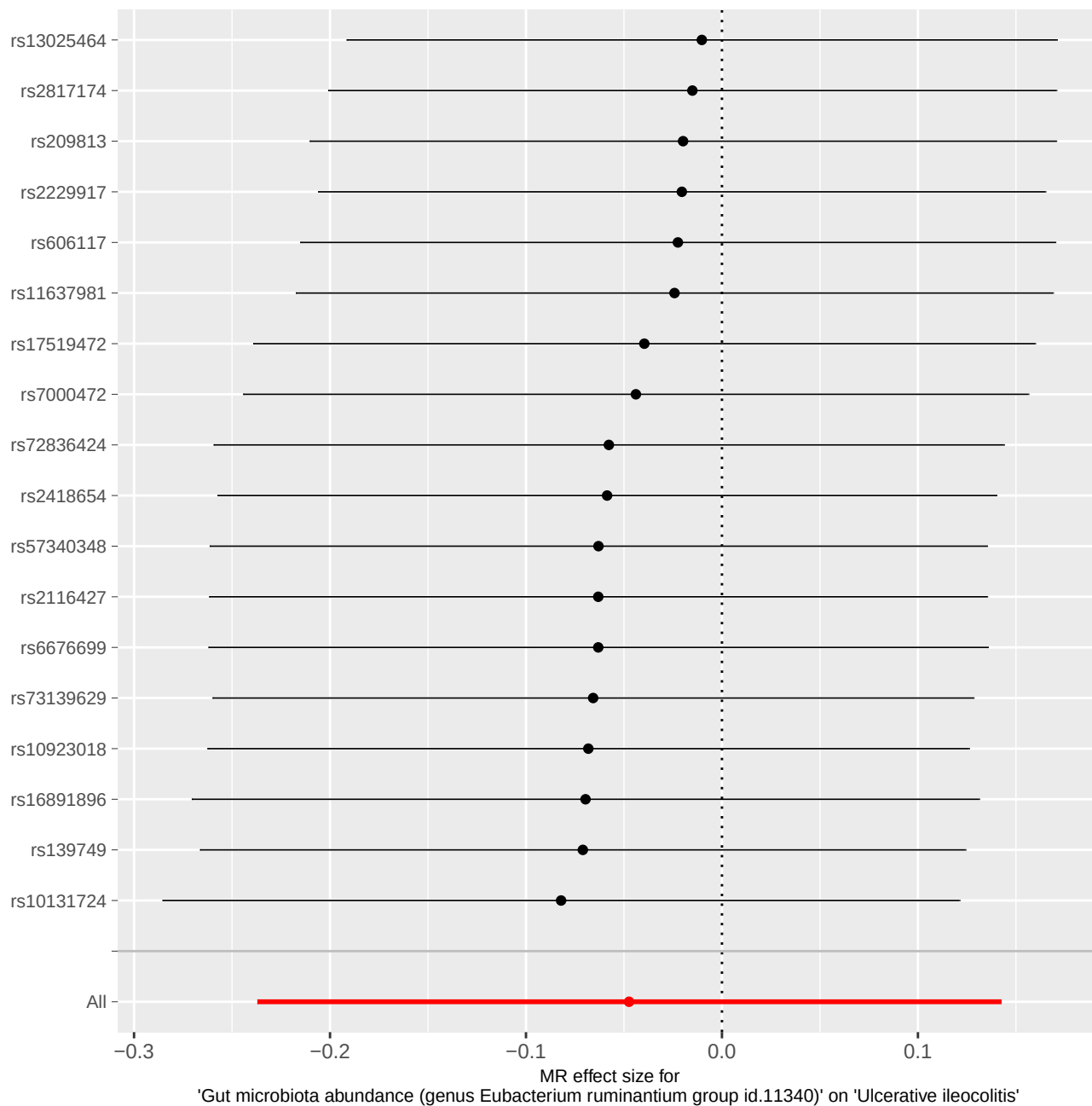
Batch 1125 : Gut microbiota abundance (genus Eubacterium nodatum group id.11297) on Ulcerative ileocolitis



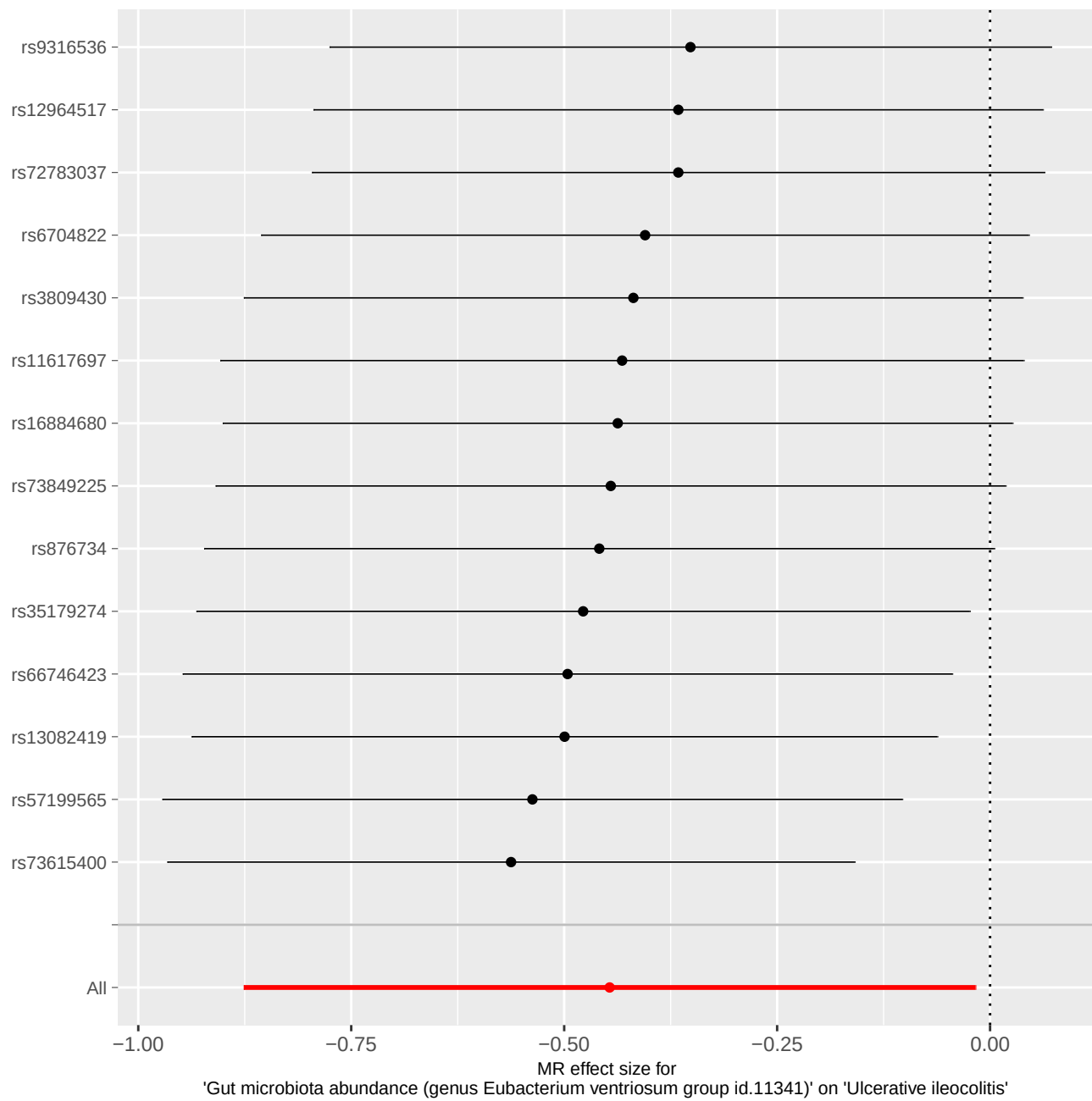


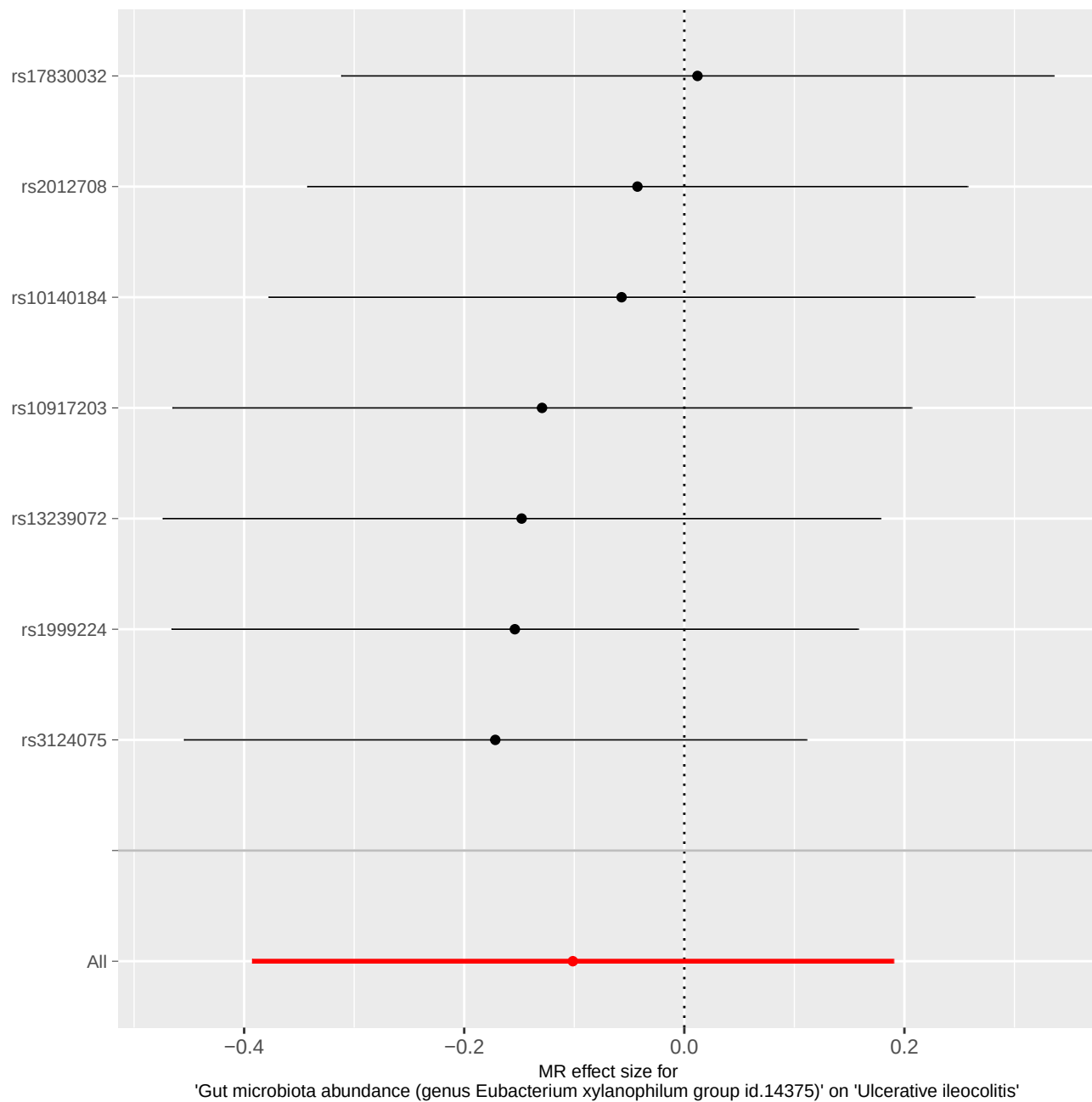
MR effect size for
'Gut microbiota abundance (genus Eubacterium oxidoreducens group id.11339)' on 'Ulcerative ileocolitis'

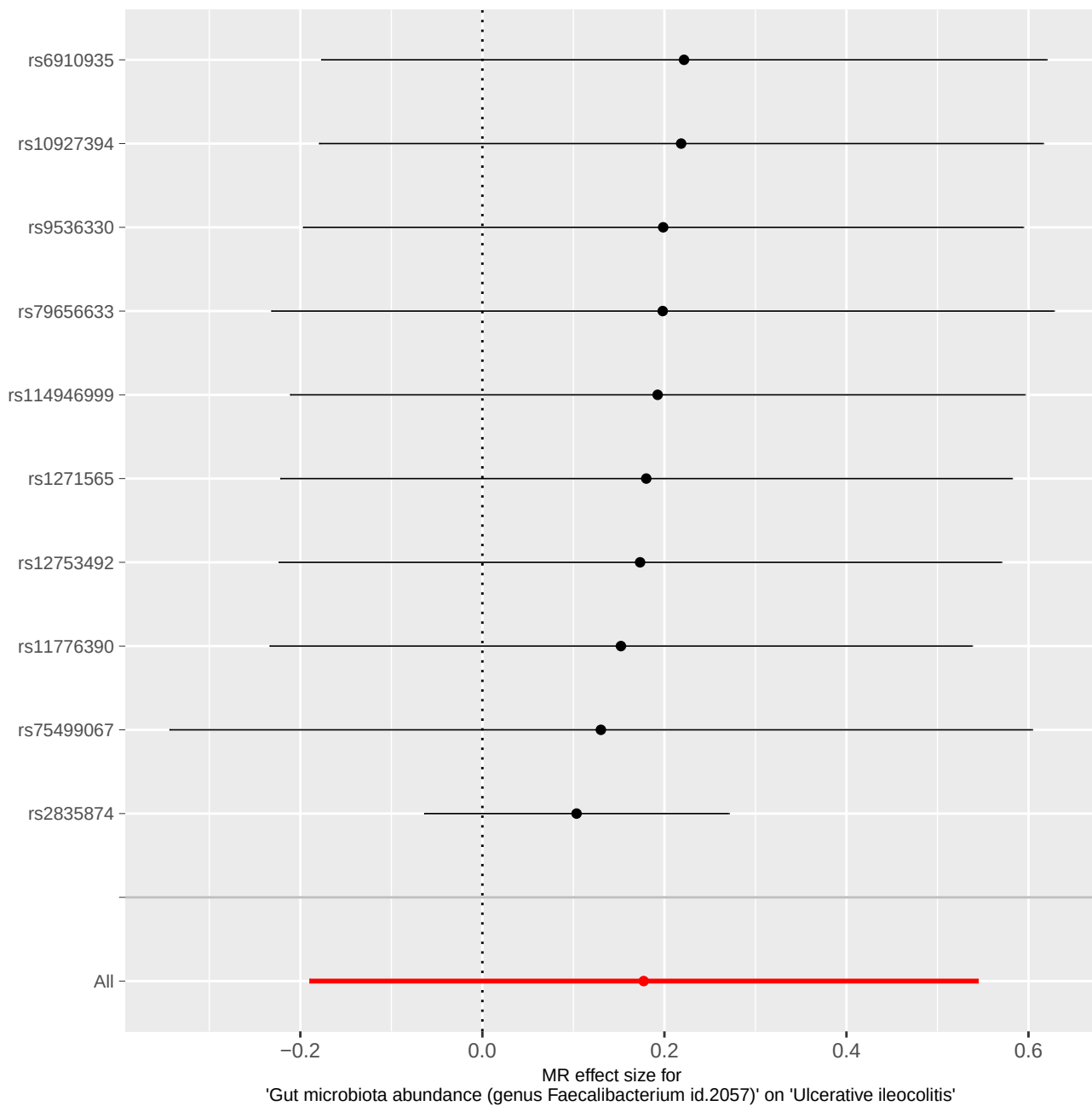


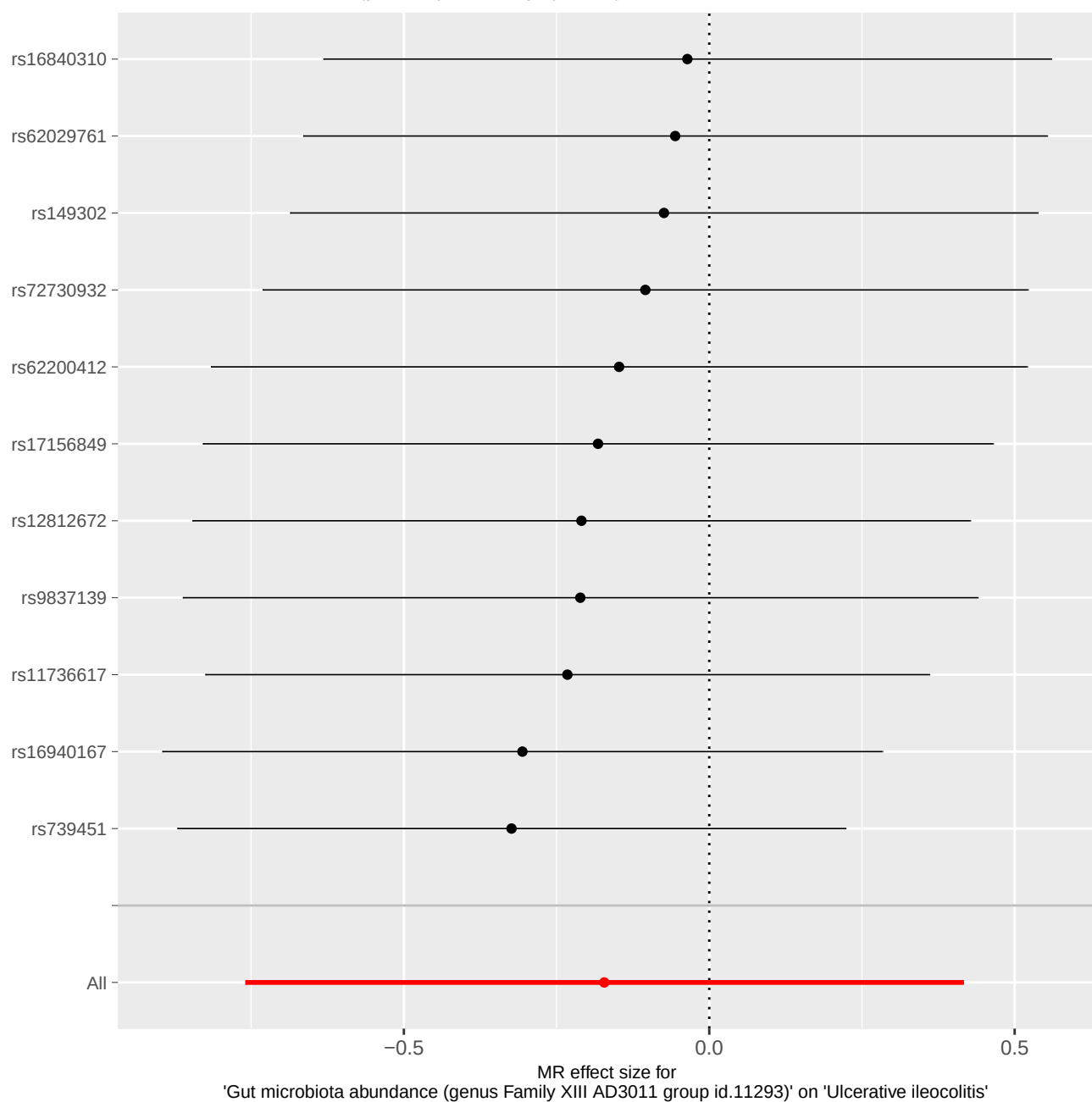


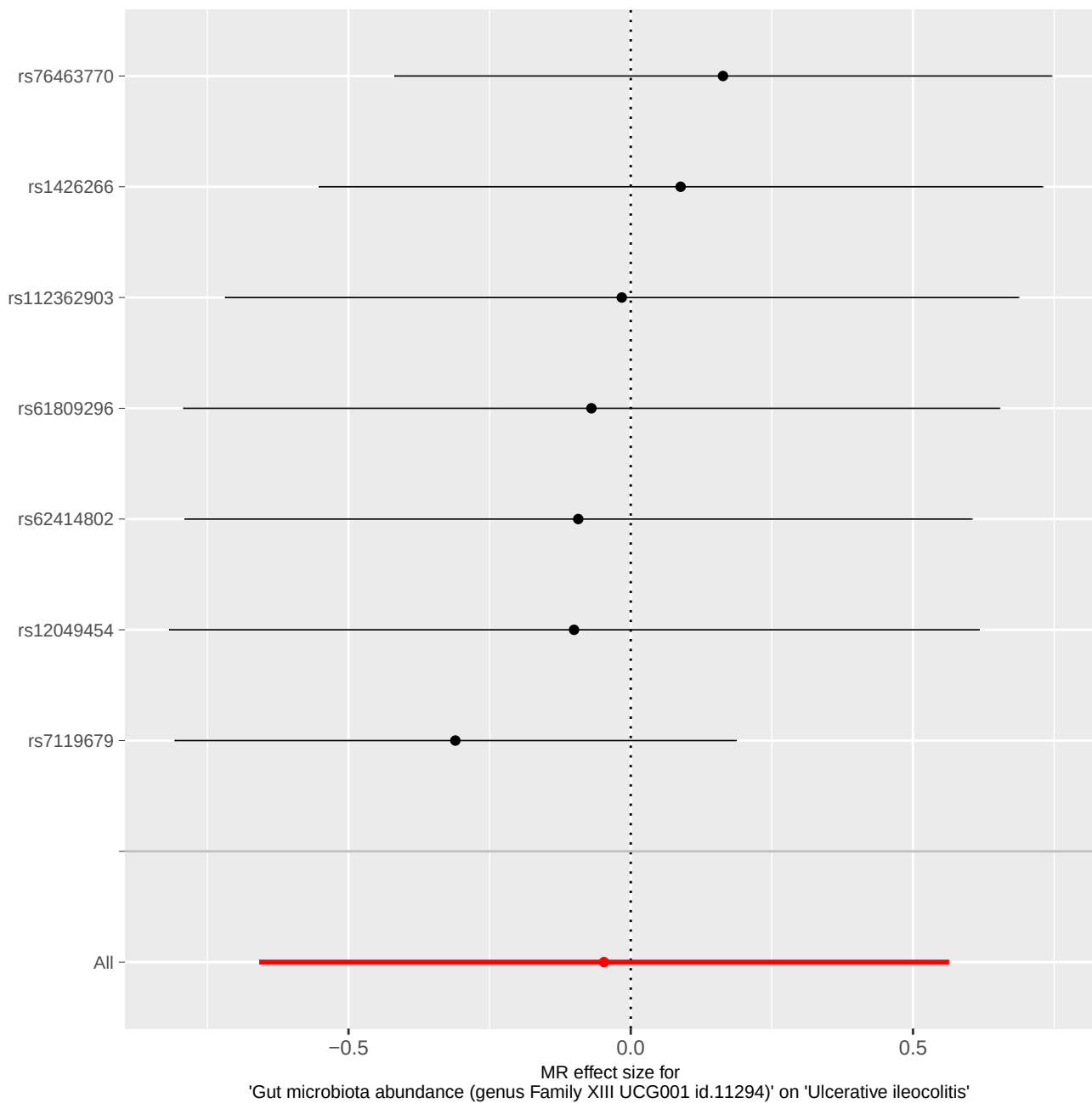
MR effect size for
'Gut microbiota abundance (genus Eubacterium ruminantium group id.11340)' on 'Ulcerative ileocolitis'

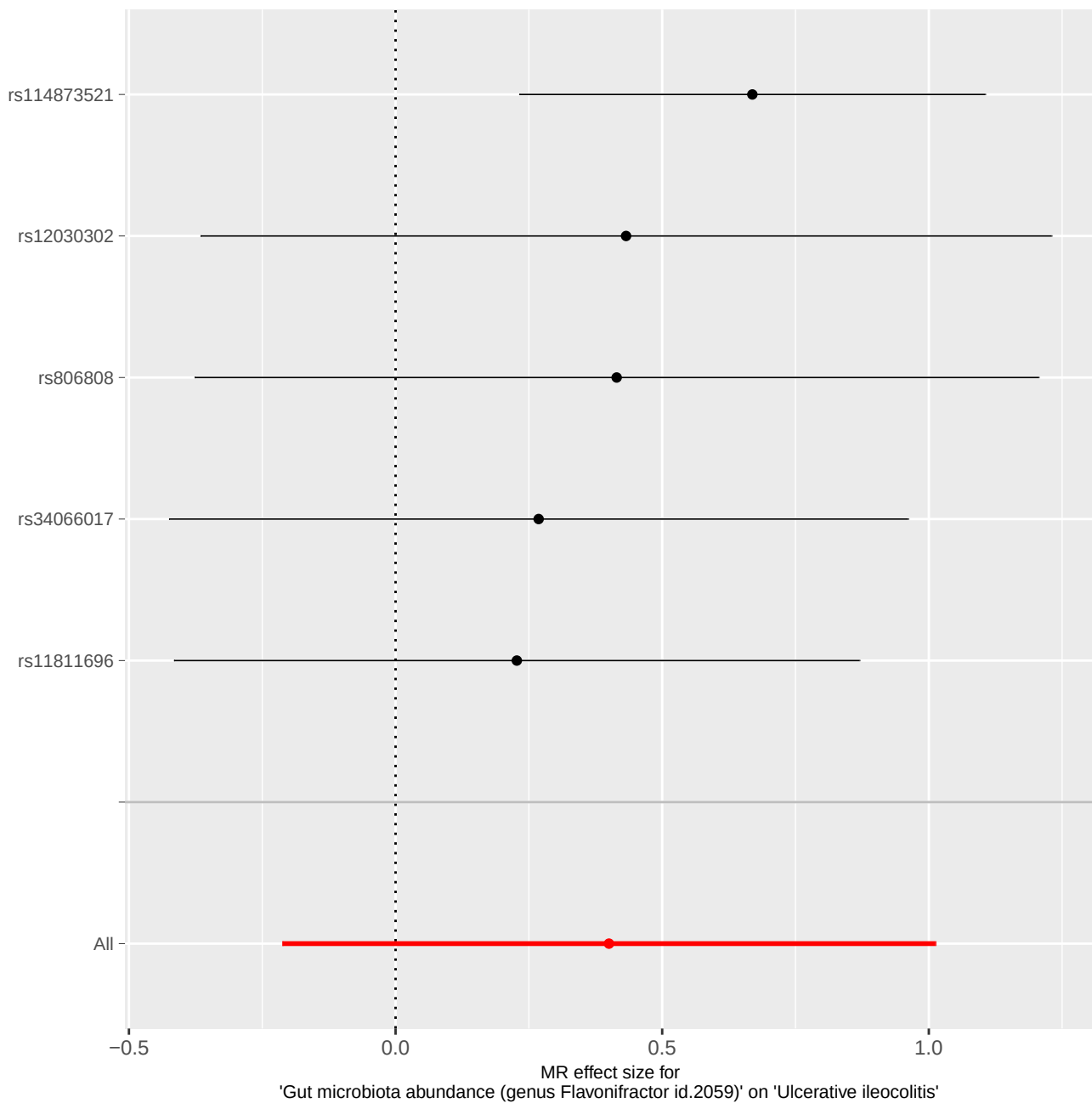




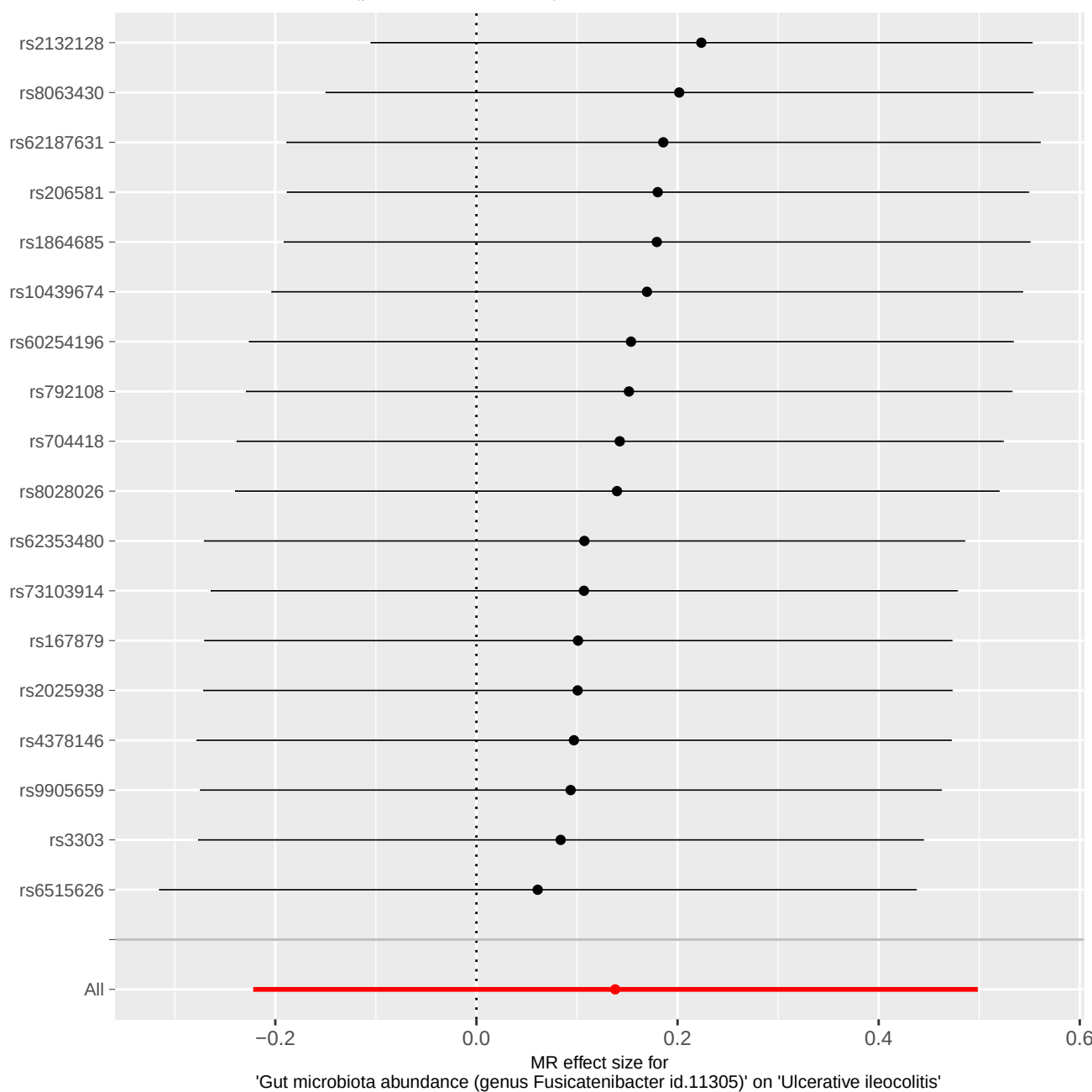


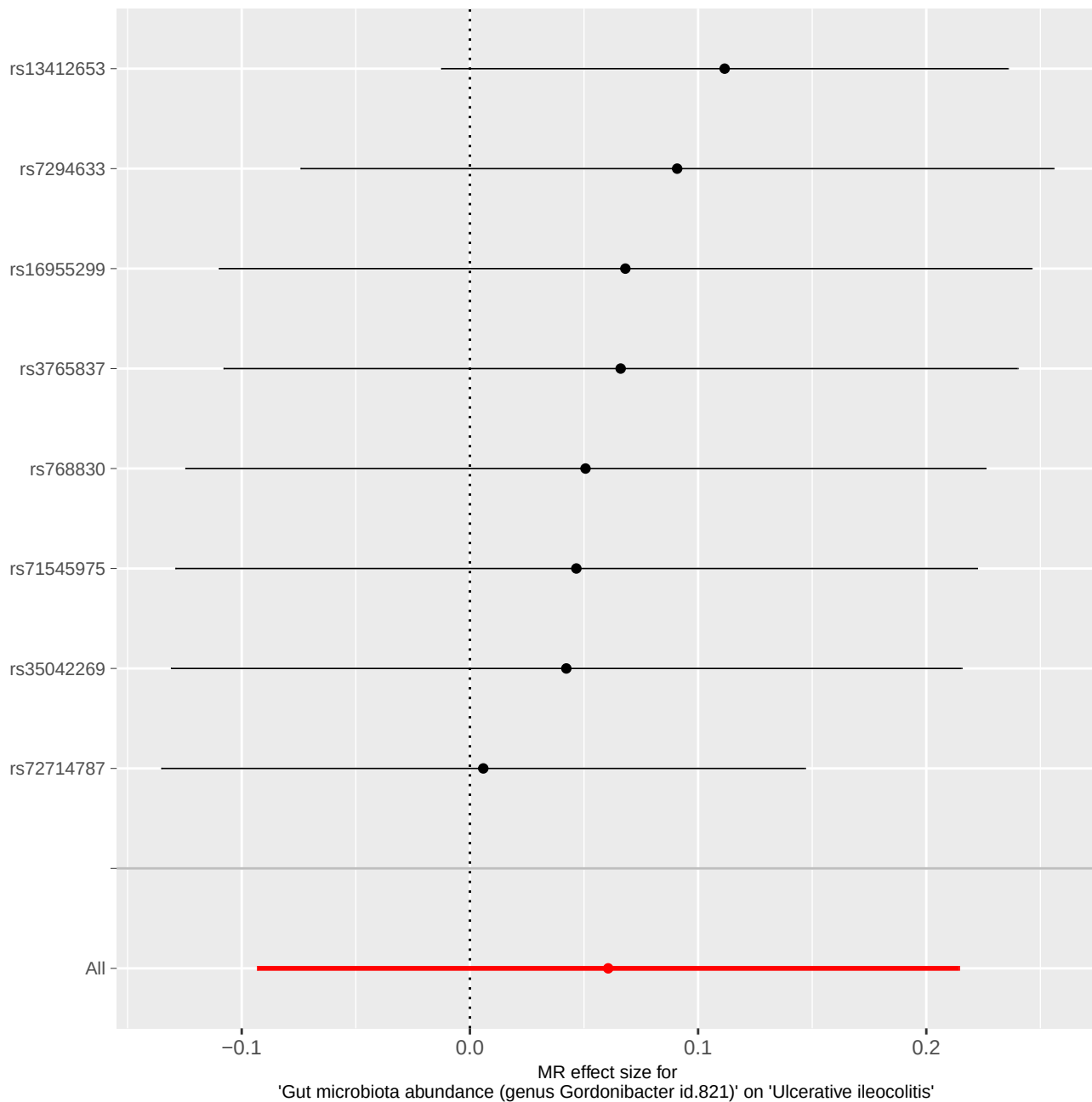


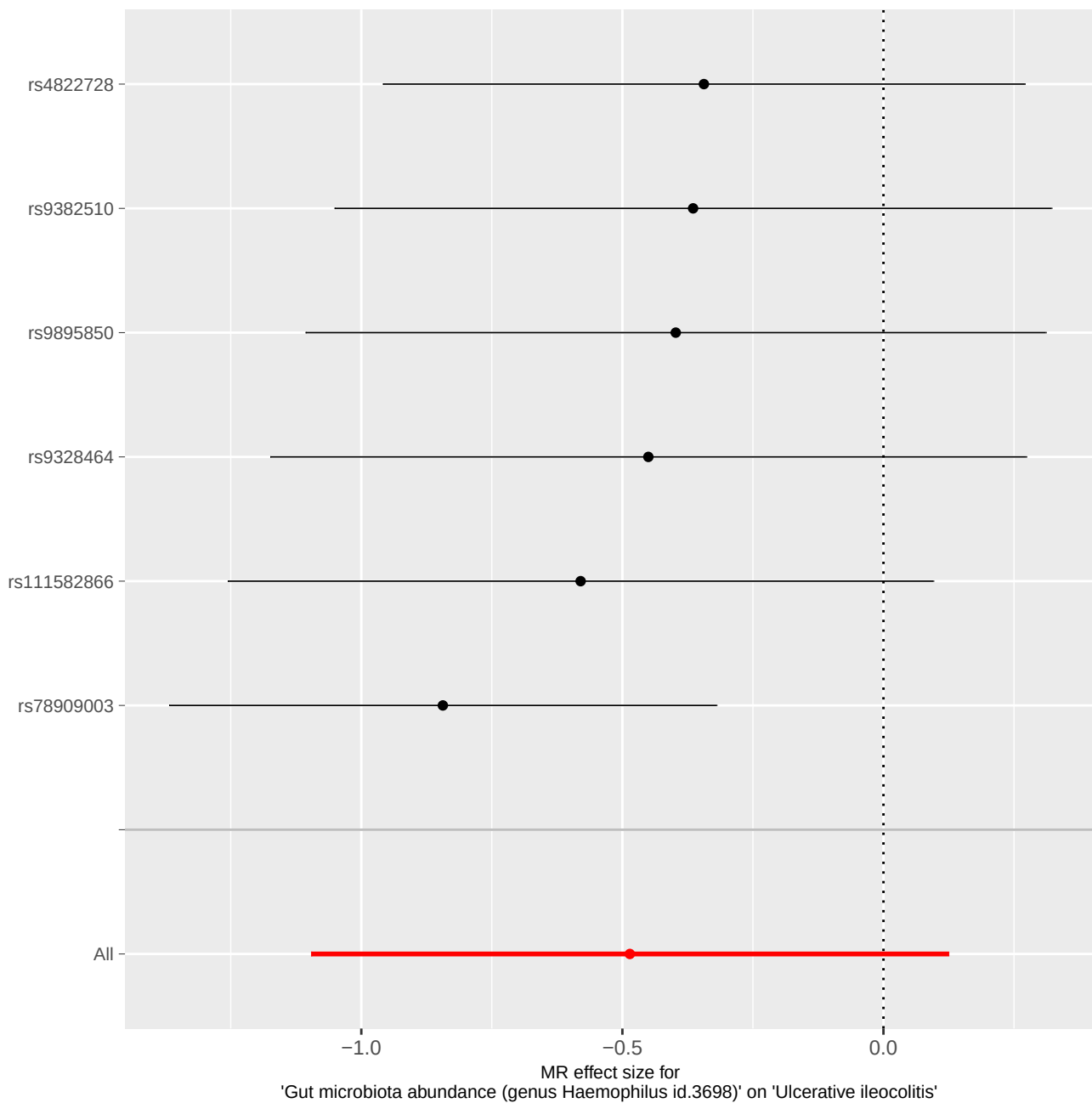


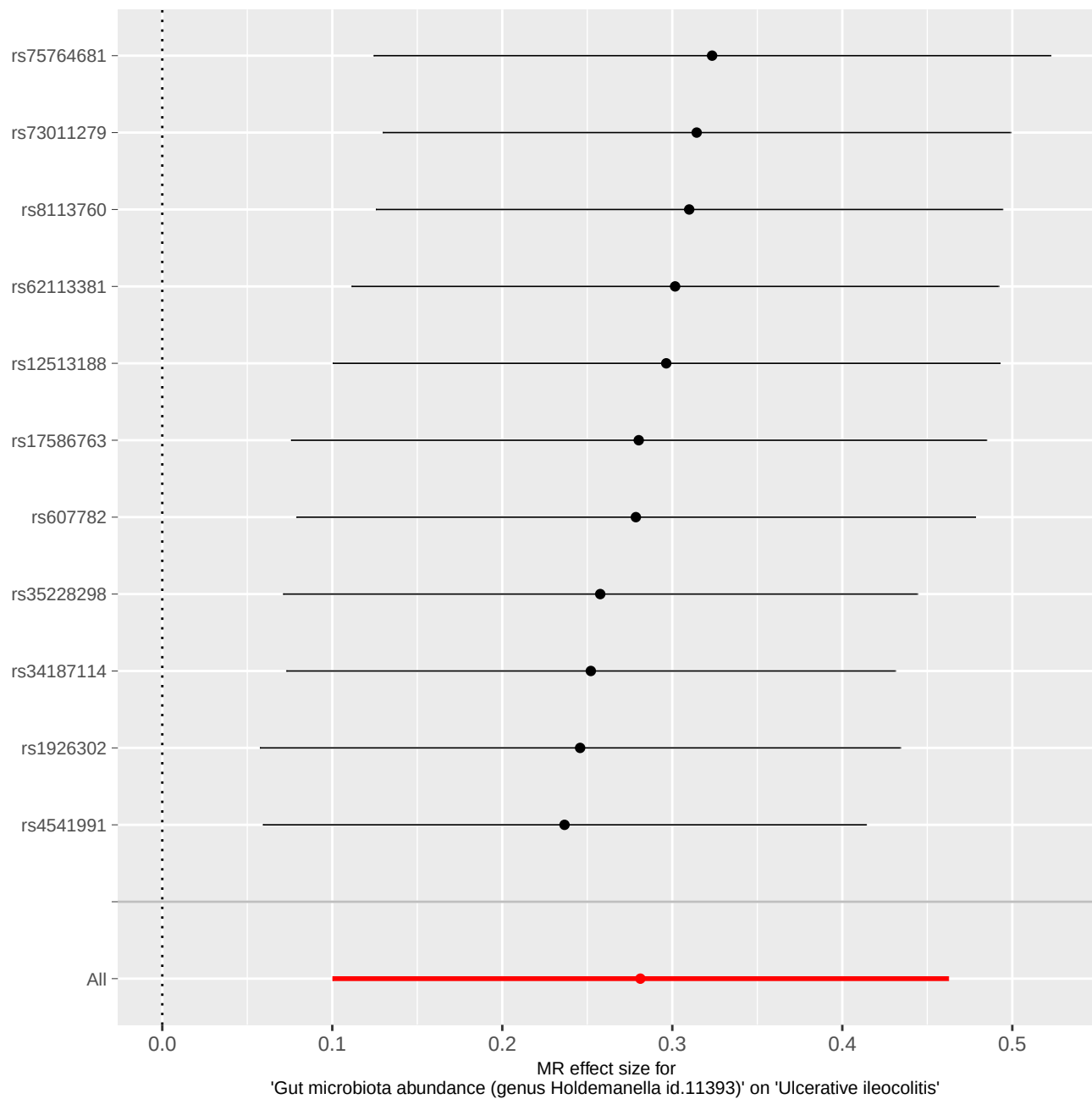


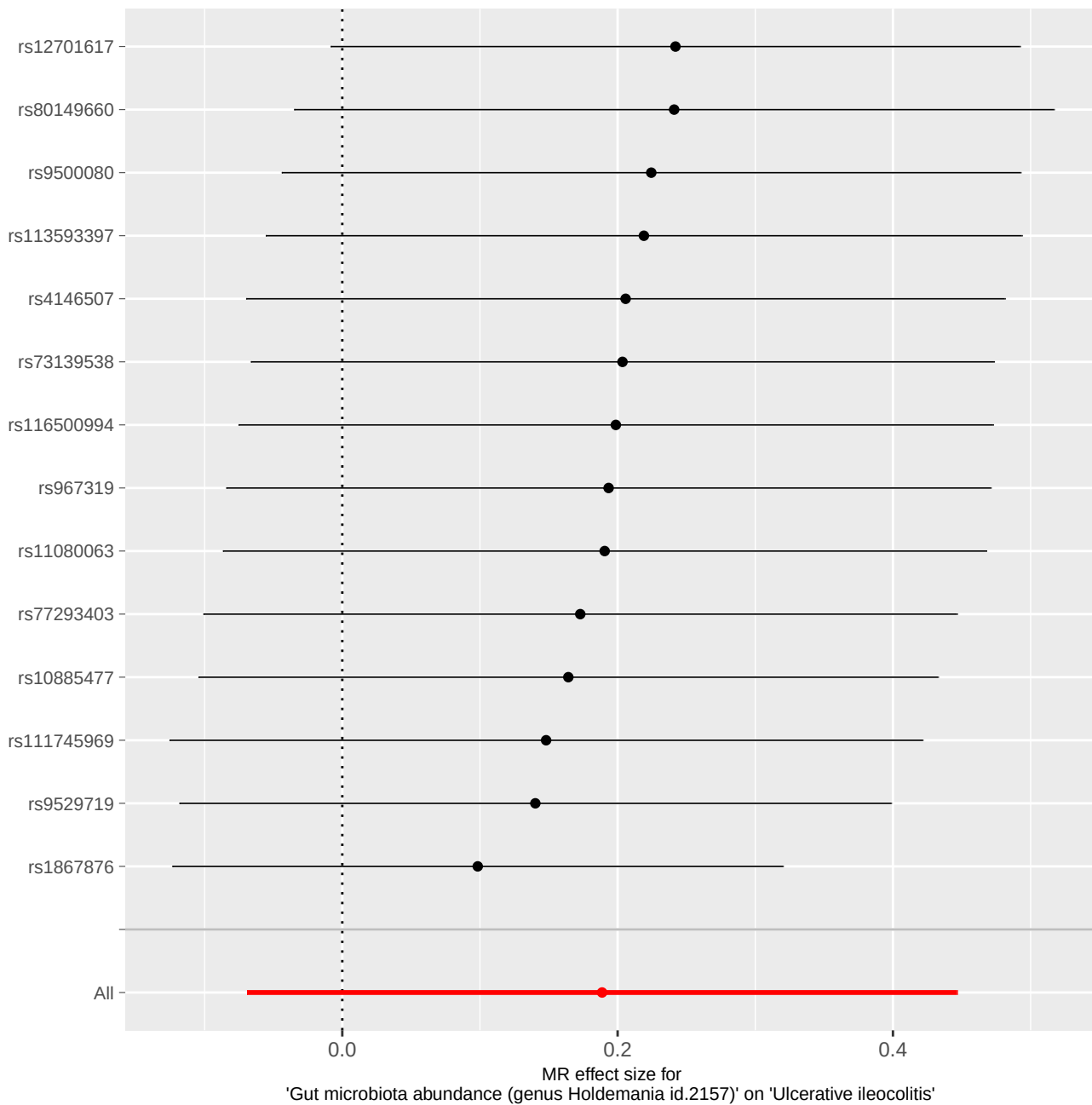
Batch 1135 : Gut microbiota abundance (genus Fusicatenibacter id.11305) on Ulcerative ileocolitis

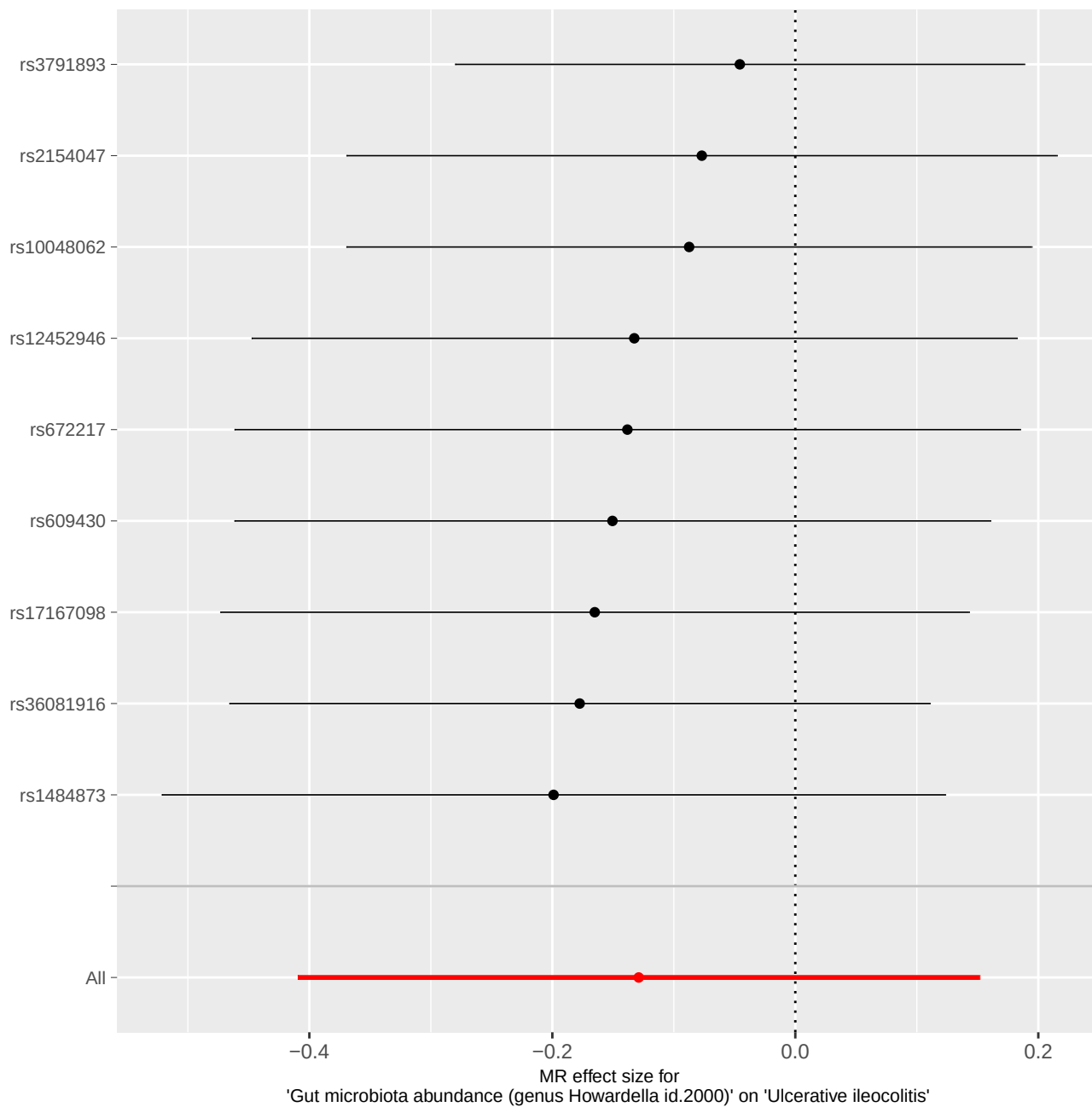


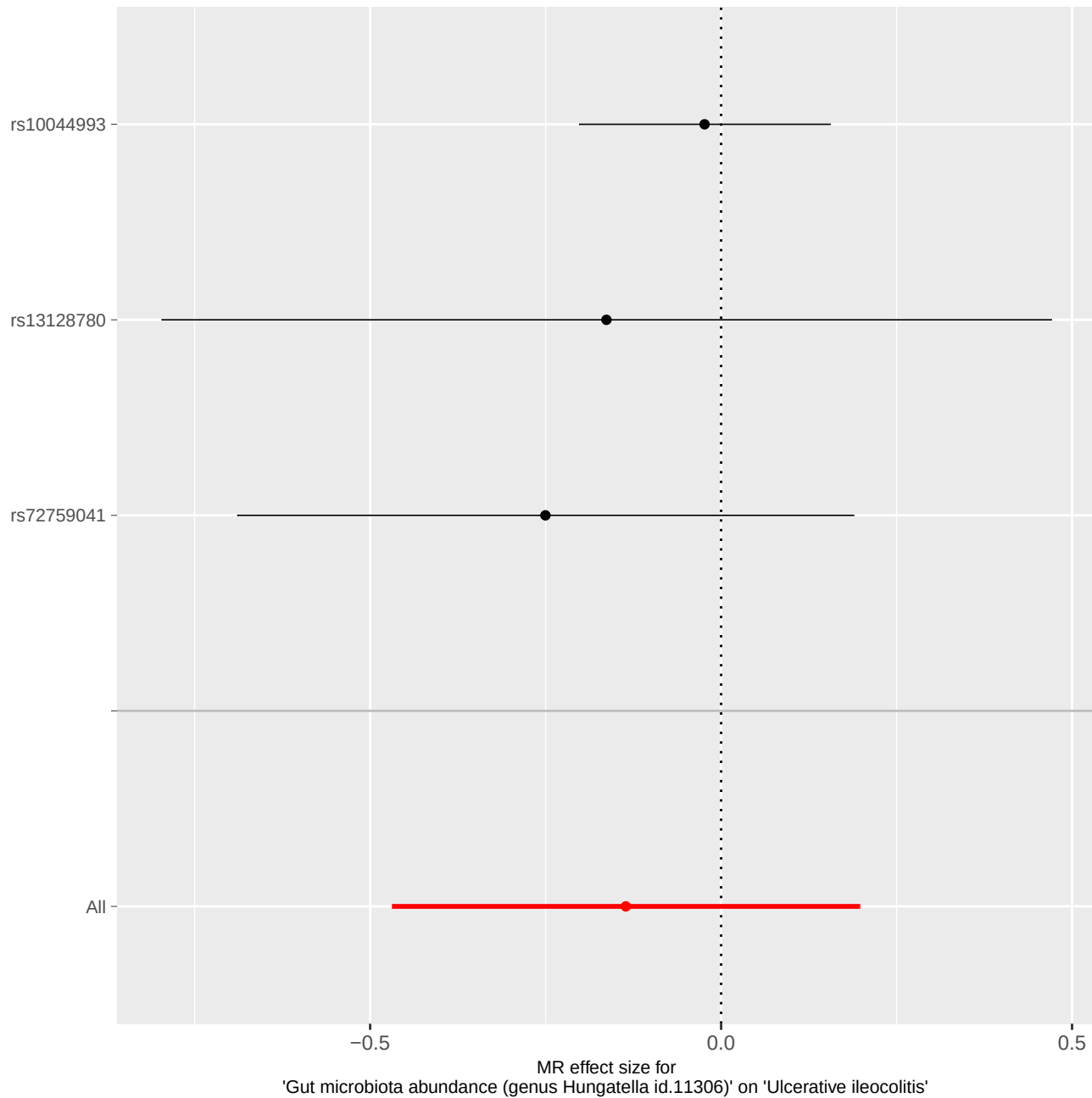


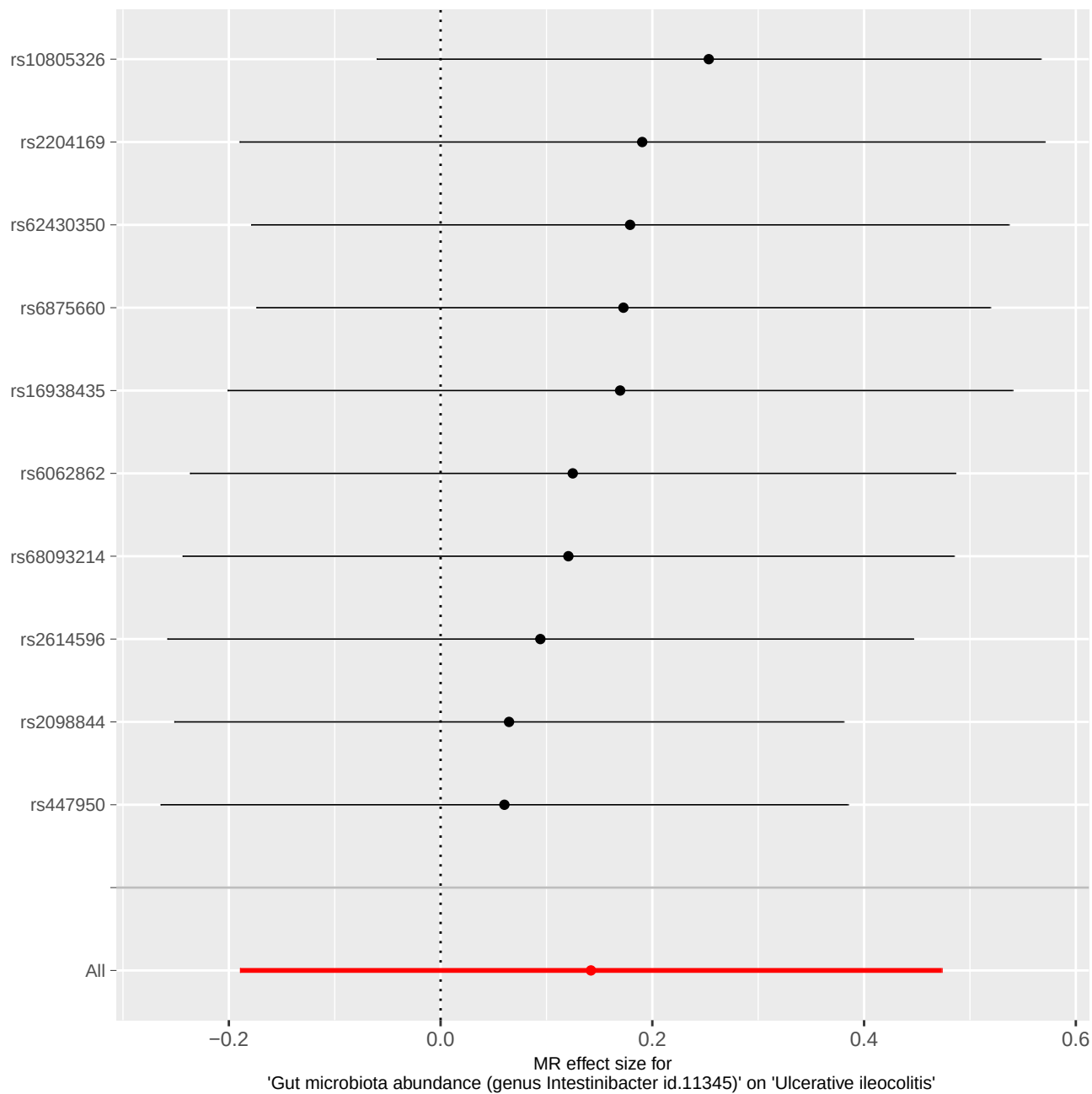


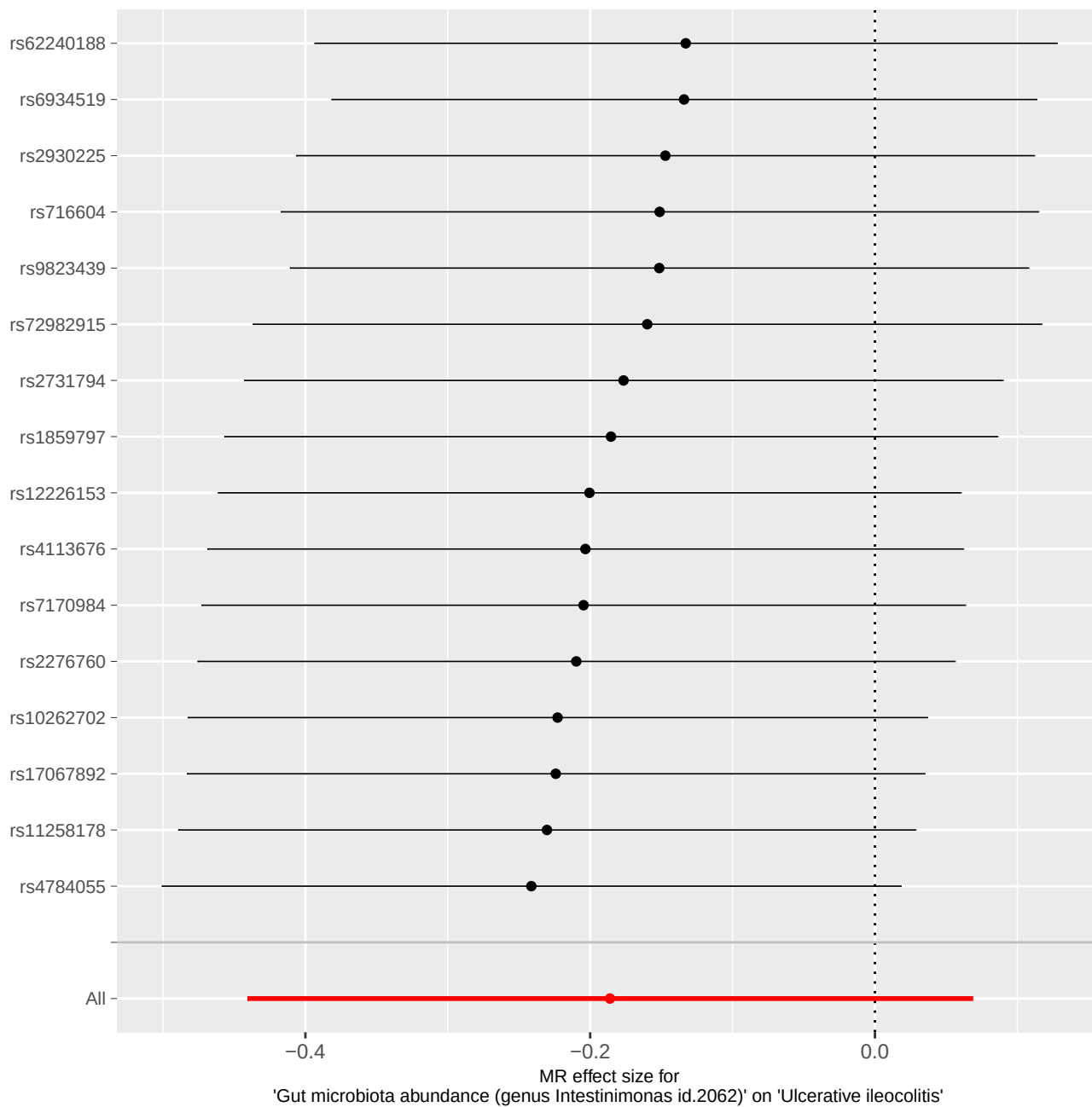




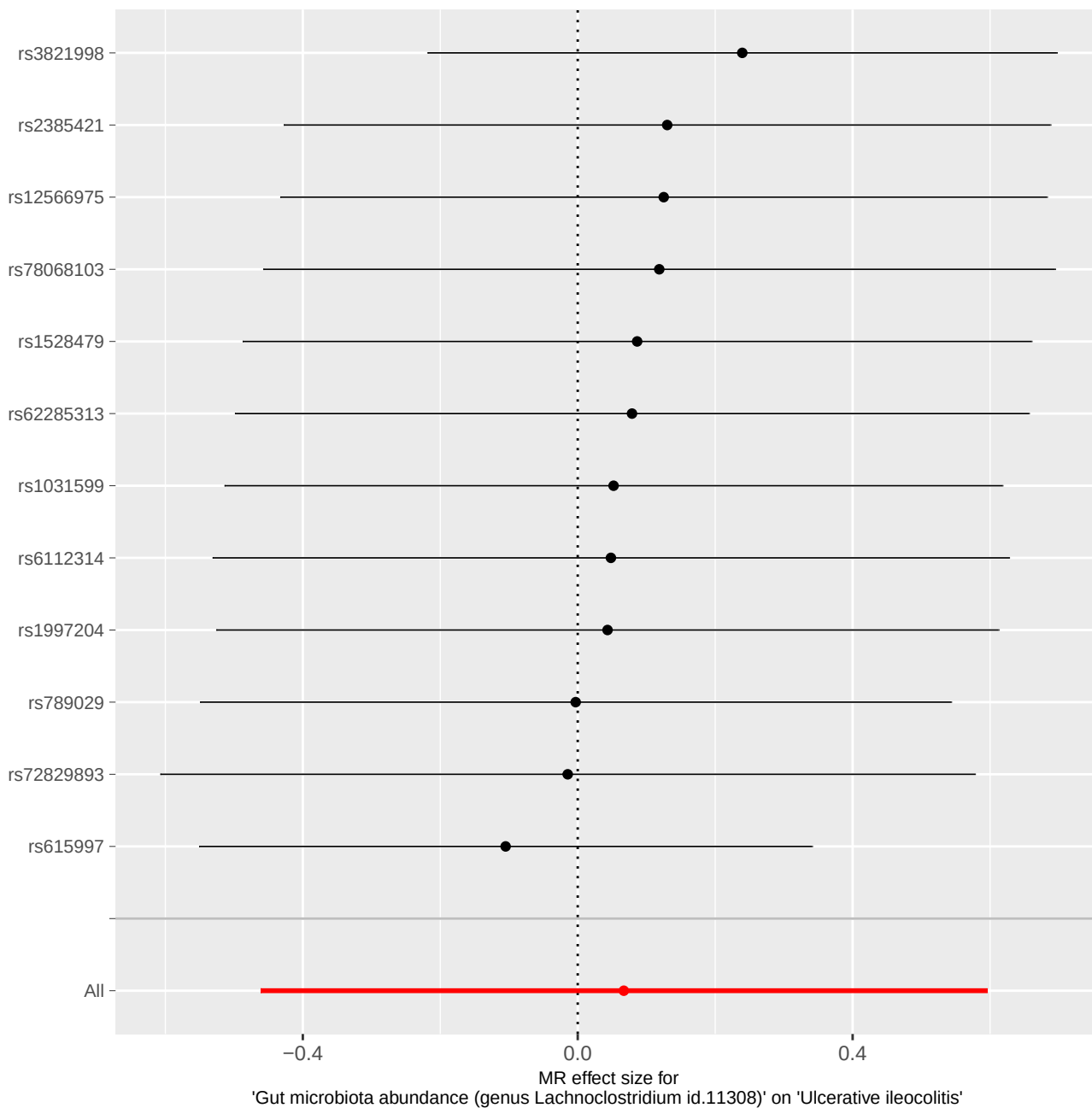


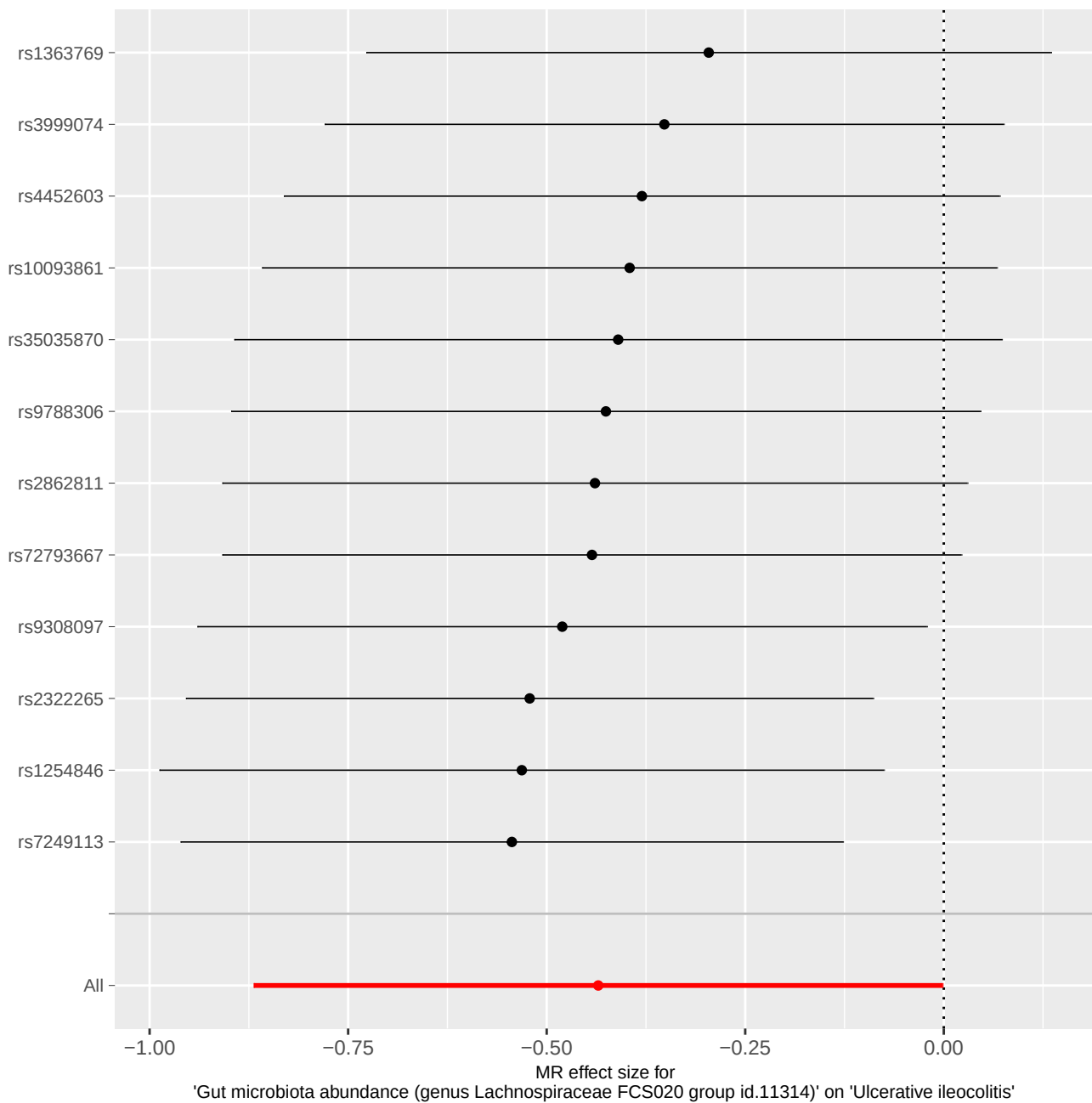


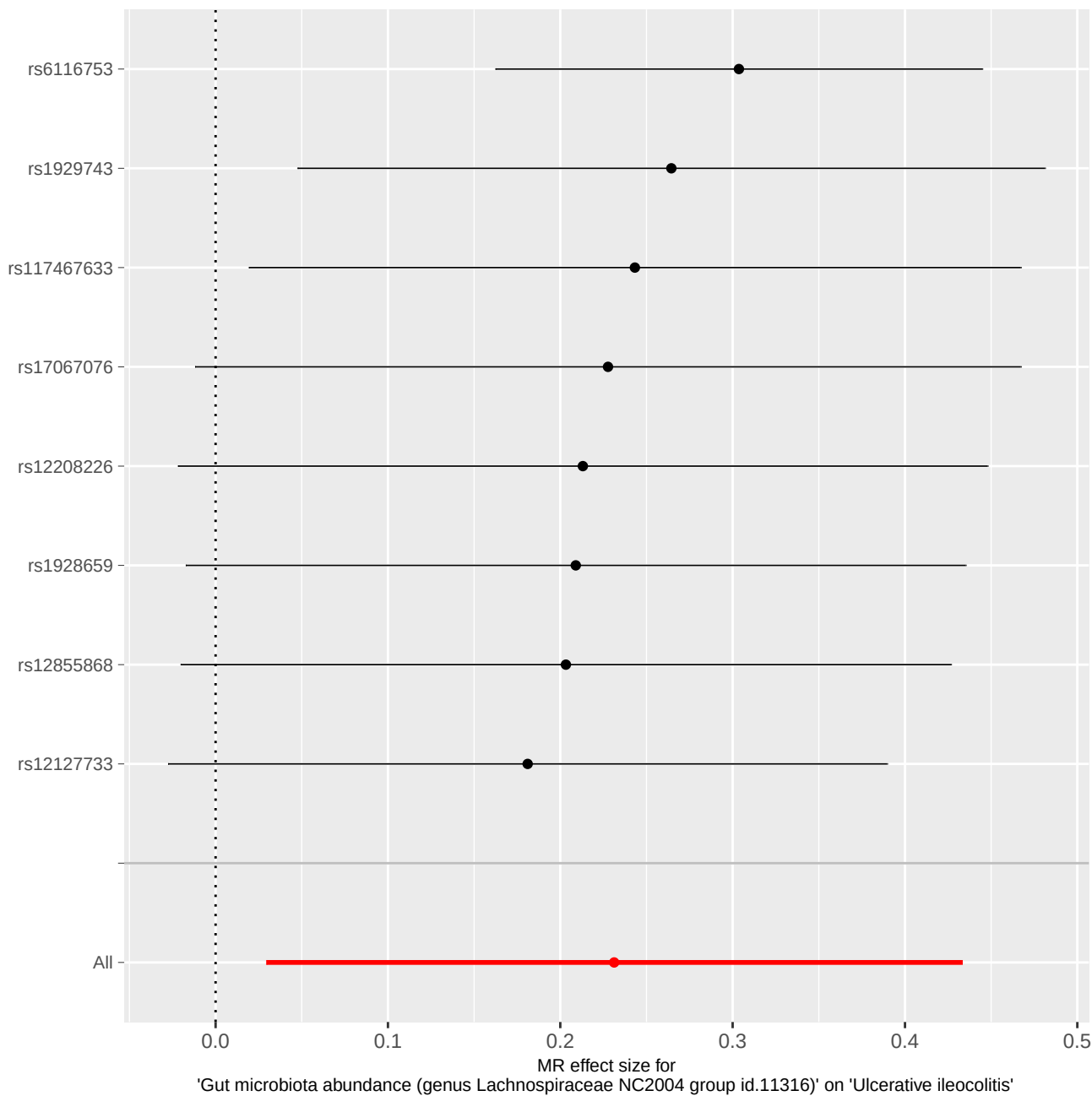




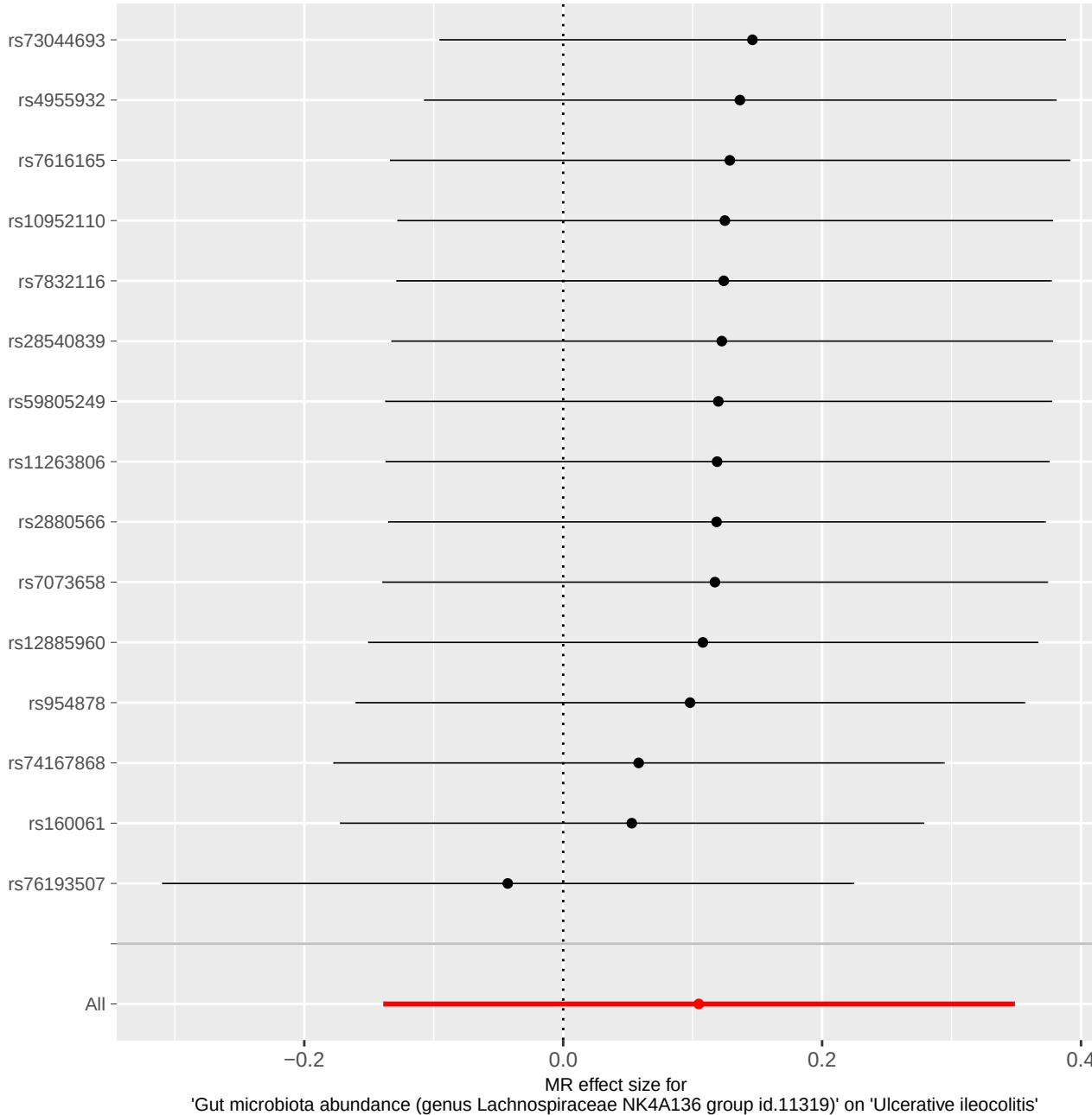
MR effect size for
'Gut microbiota abundance (genus Intestinimonas id.2062)' on 'Ulcerative ileocolitis'

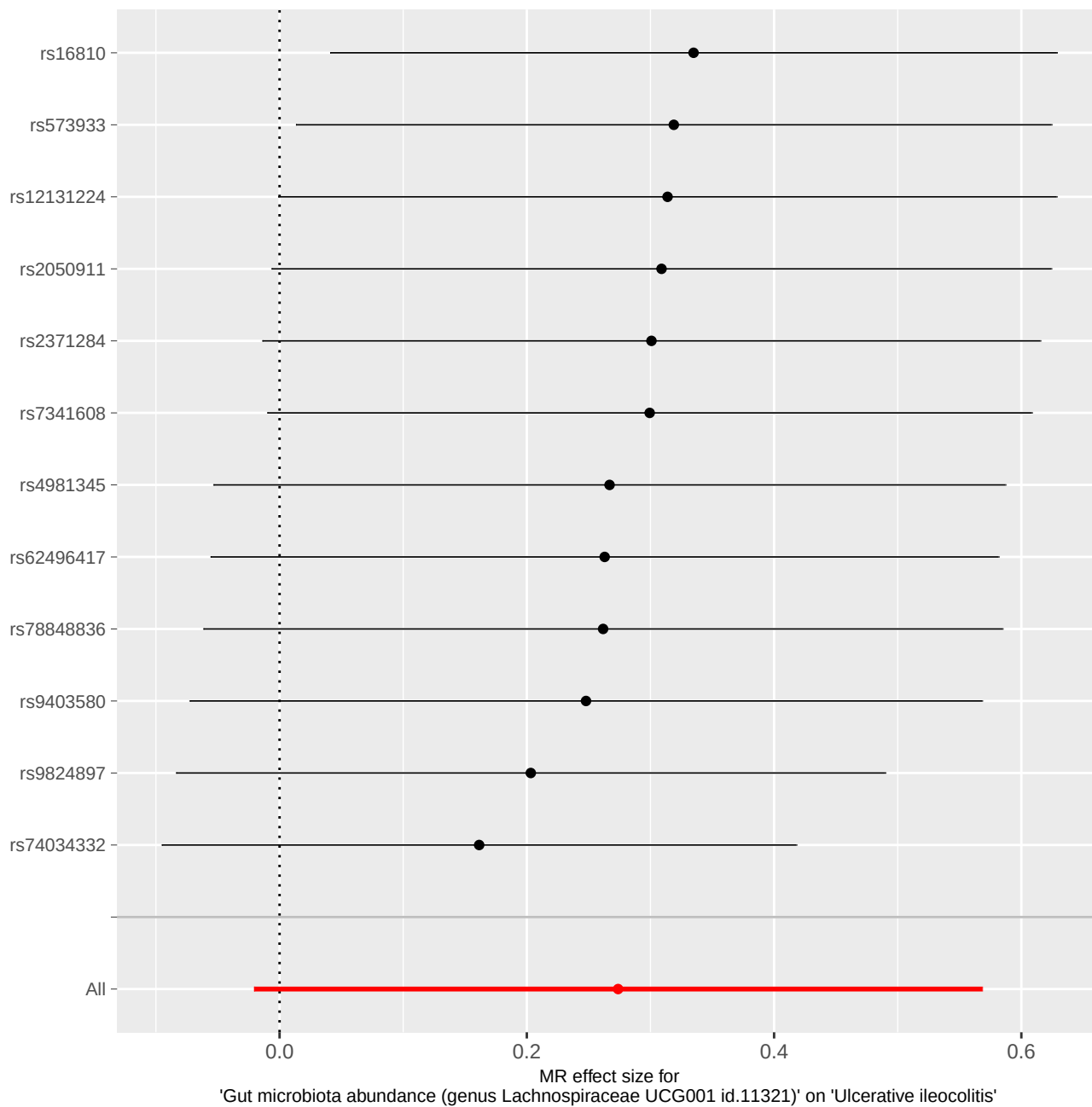


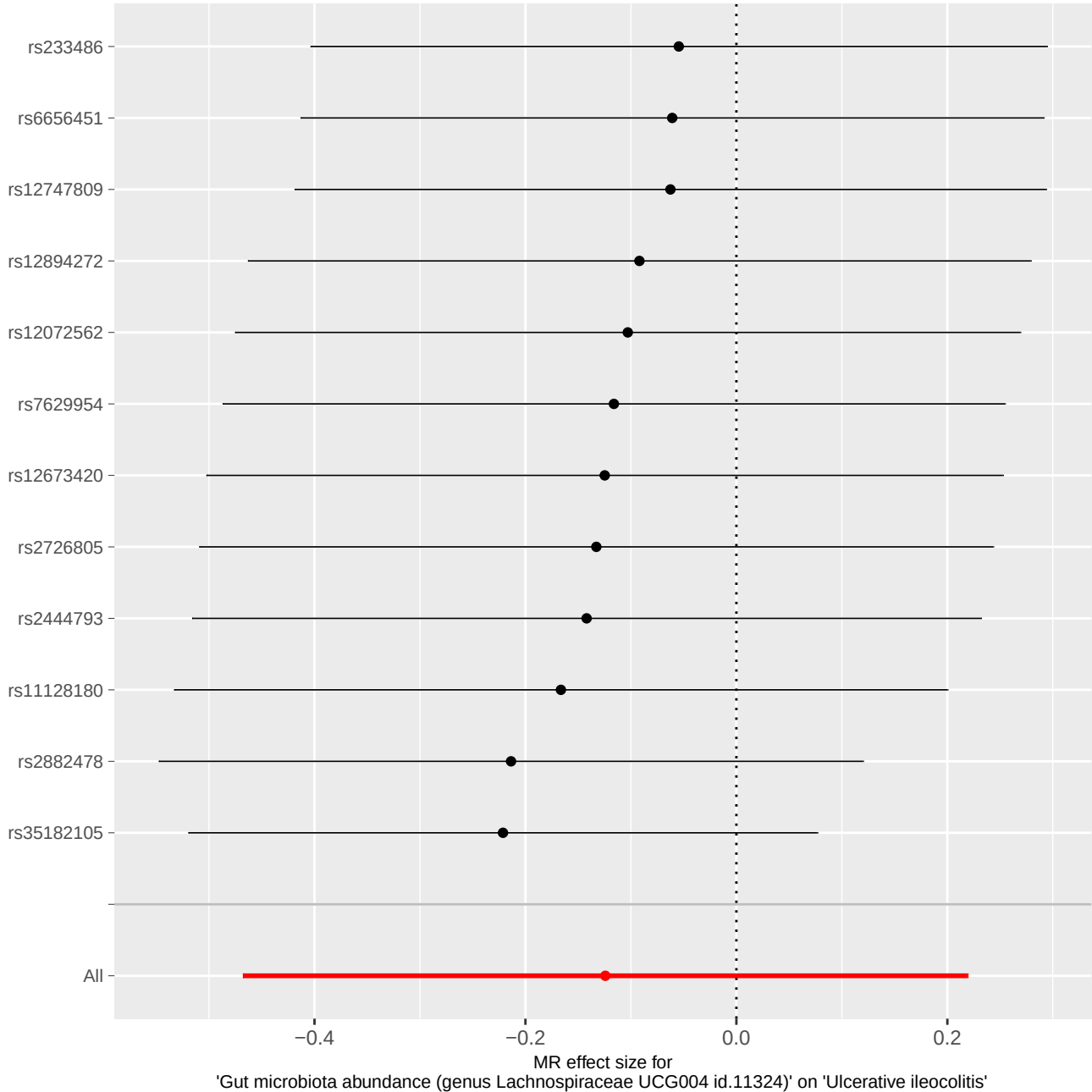


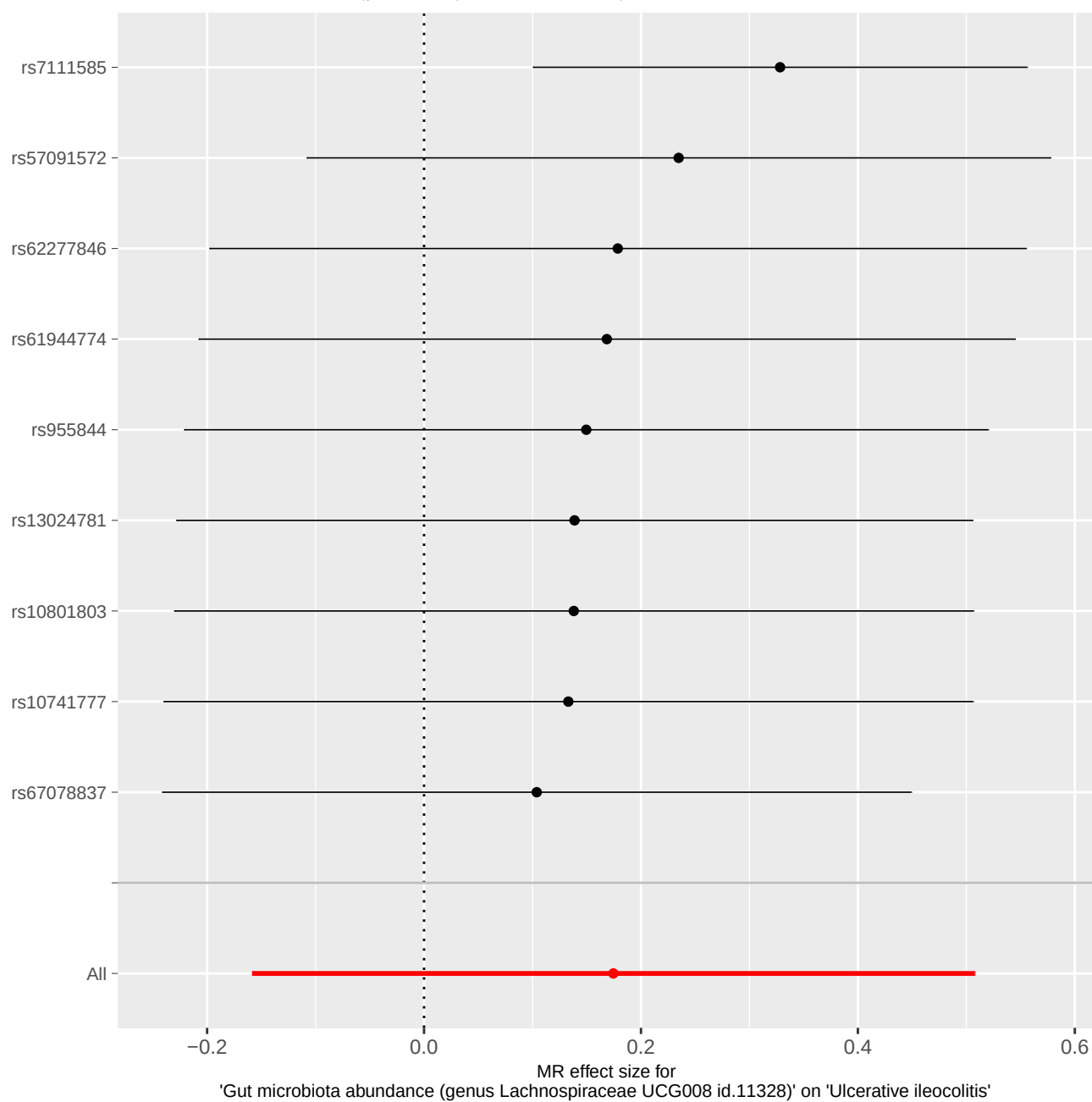


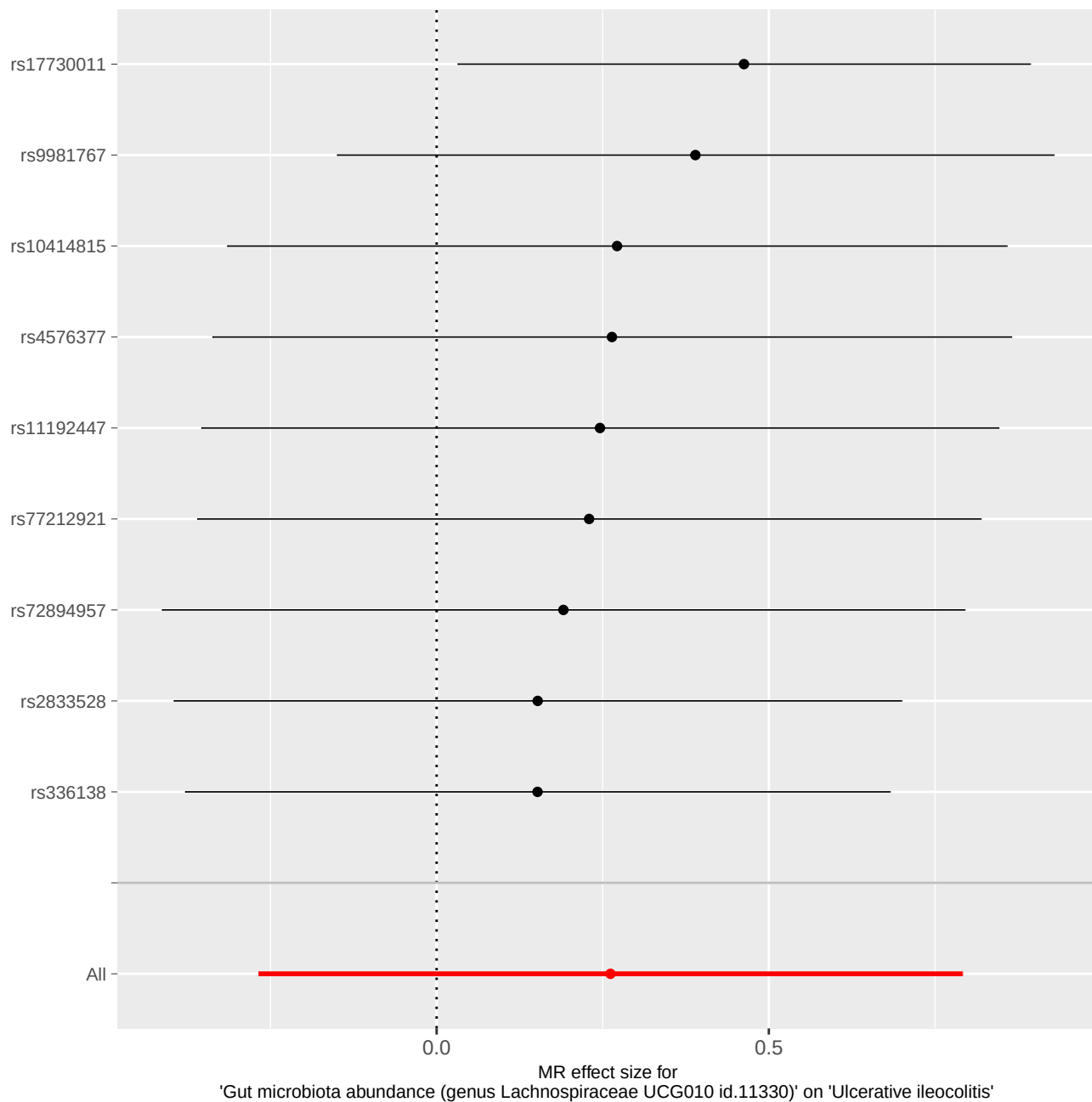
Batch 1148 : Gut microbiota abundance (genus Lachnospiraceae NK4A136 group id.11319) on Ulcerative ileocolitis

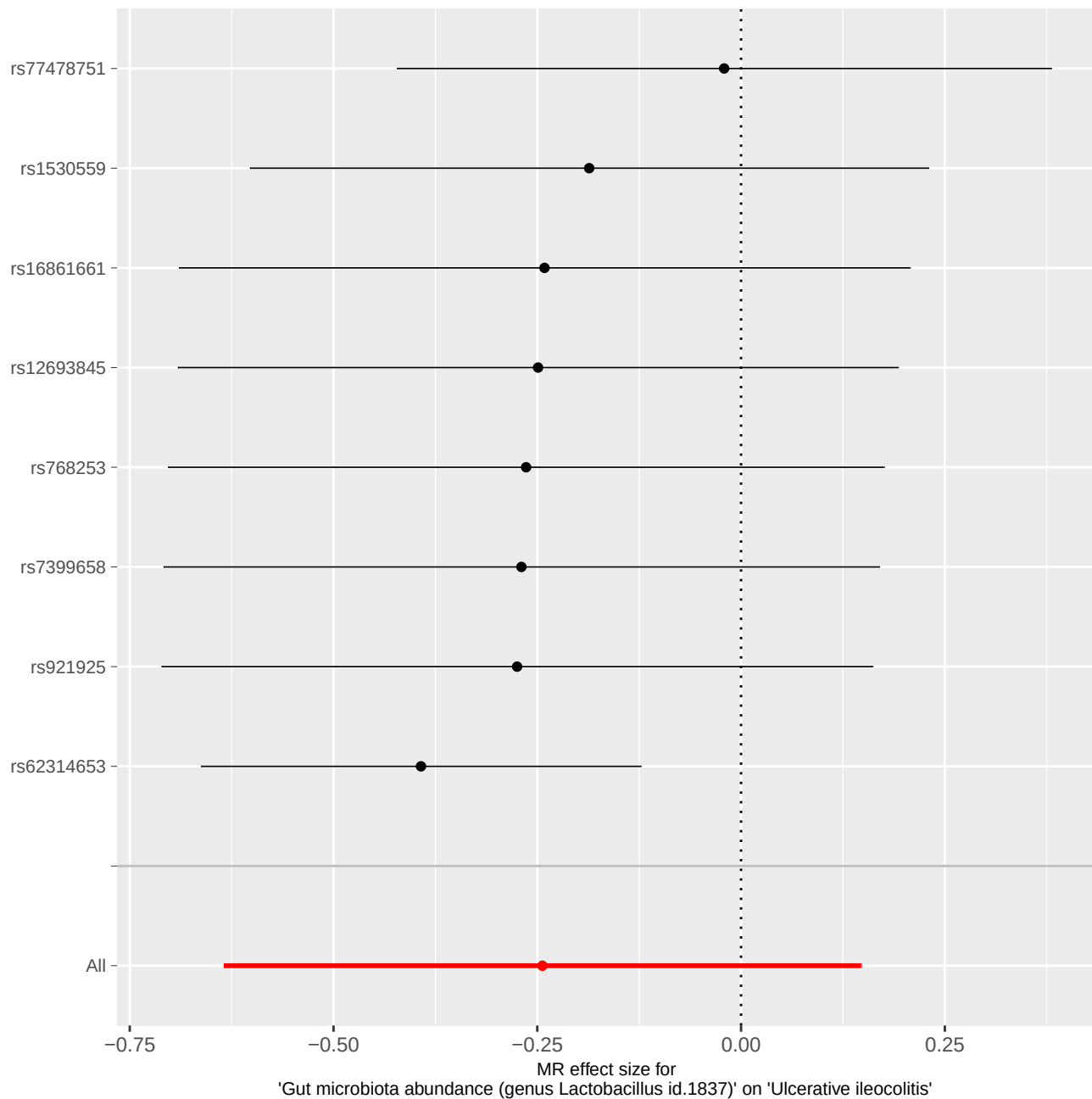


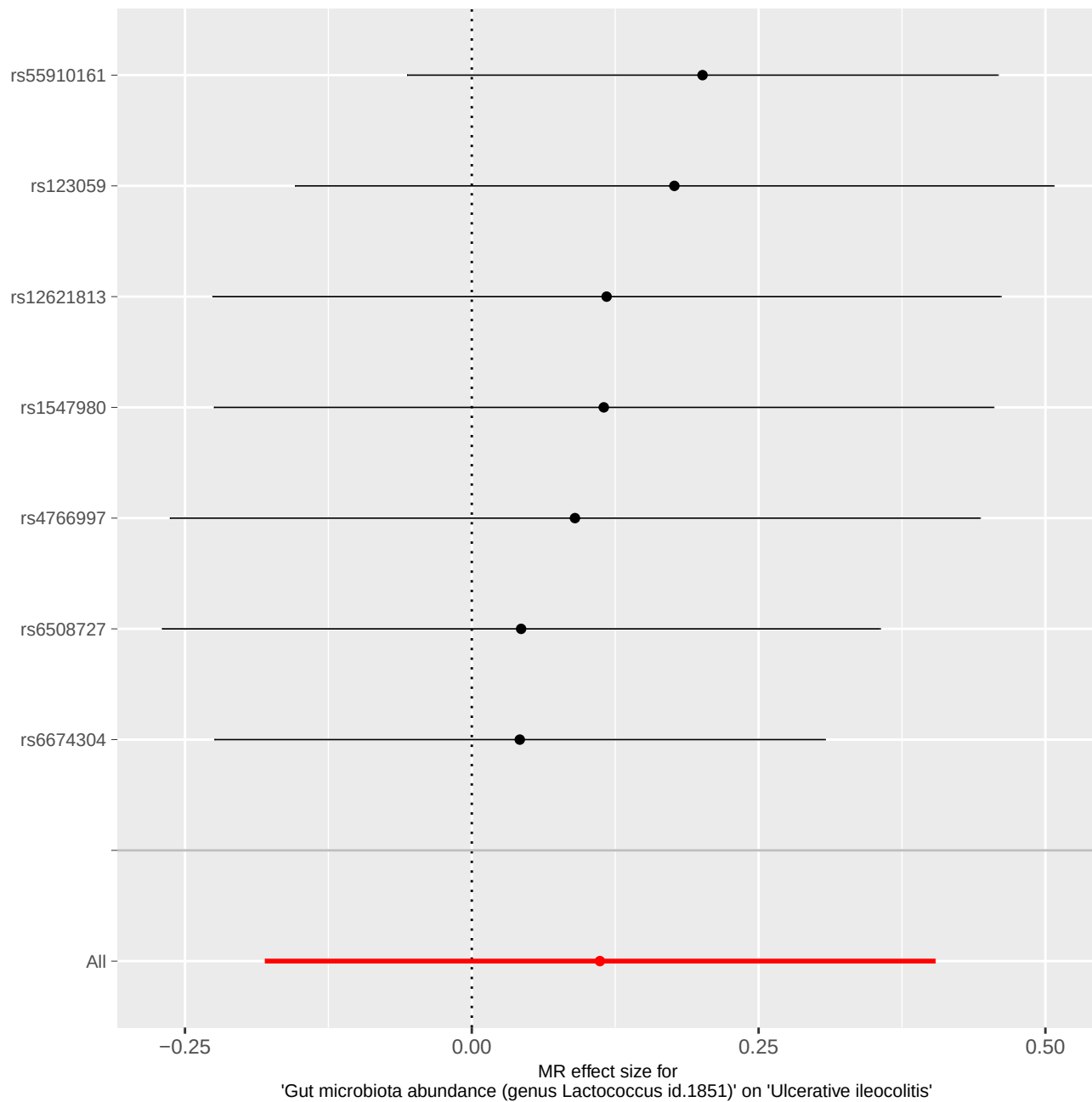


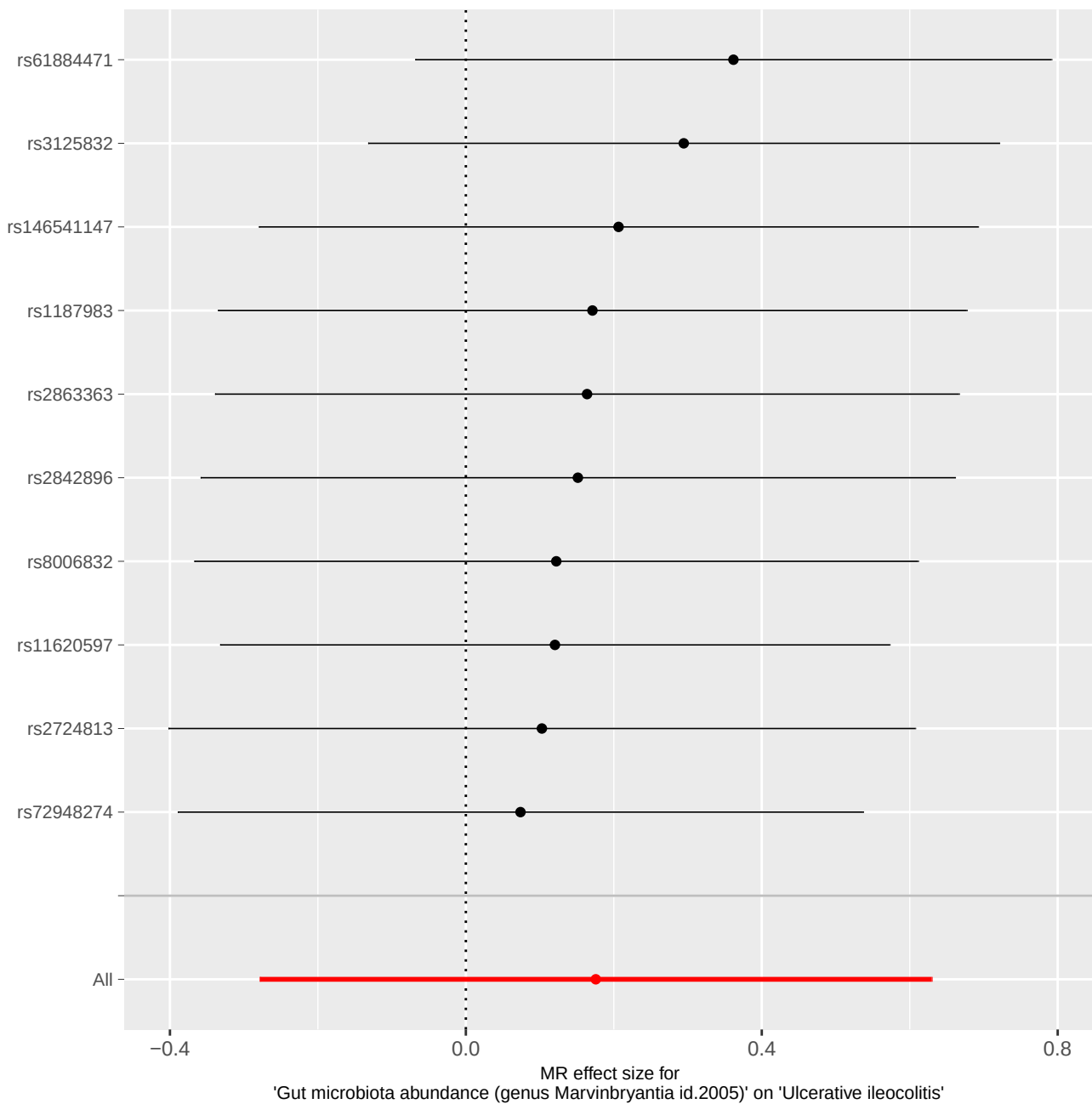


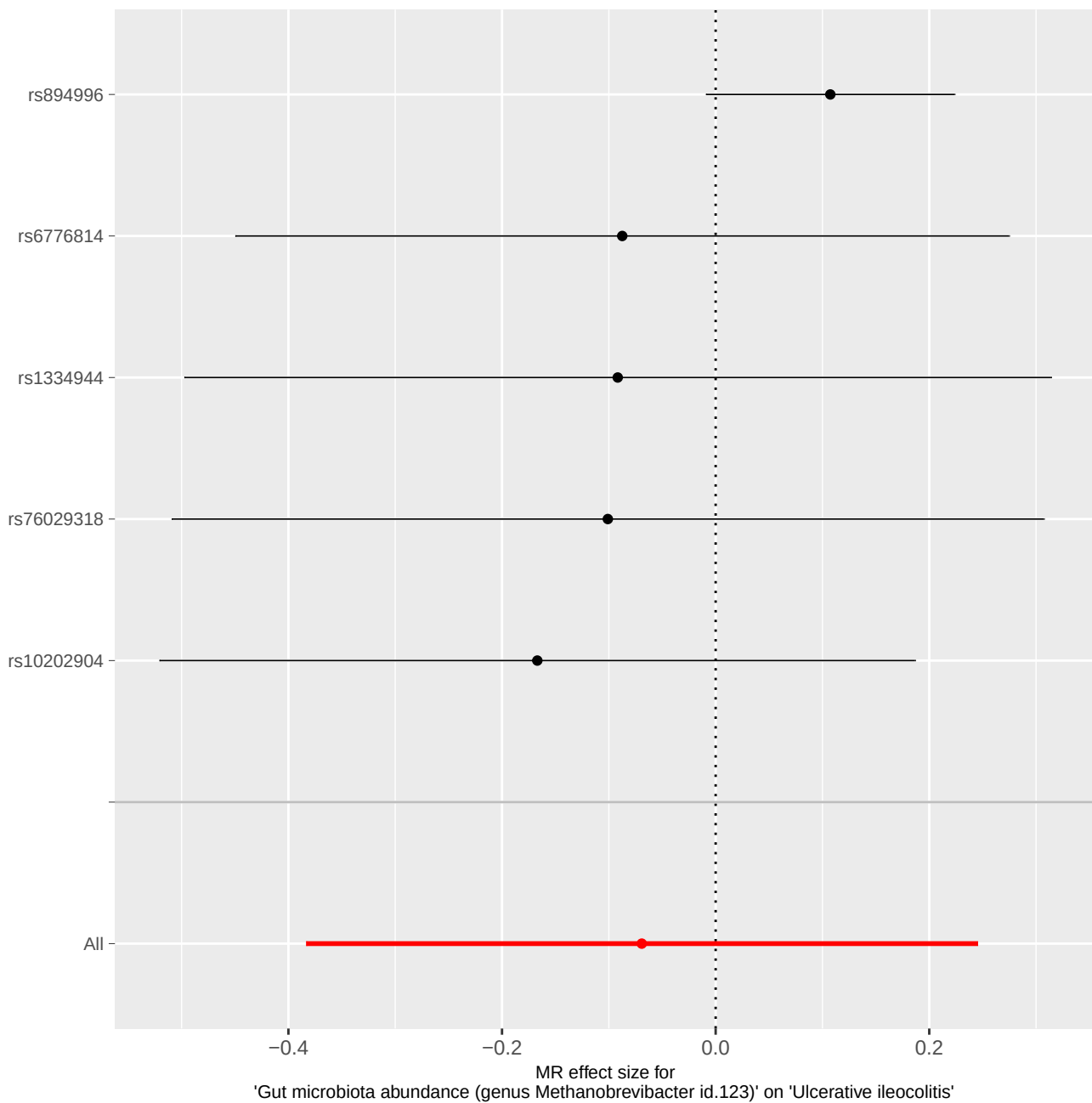


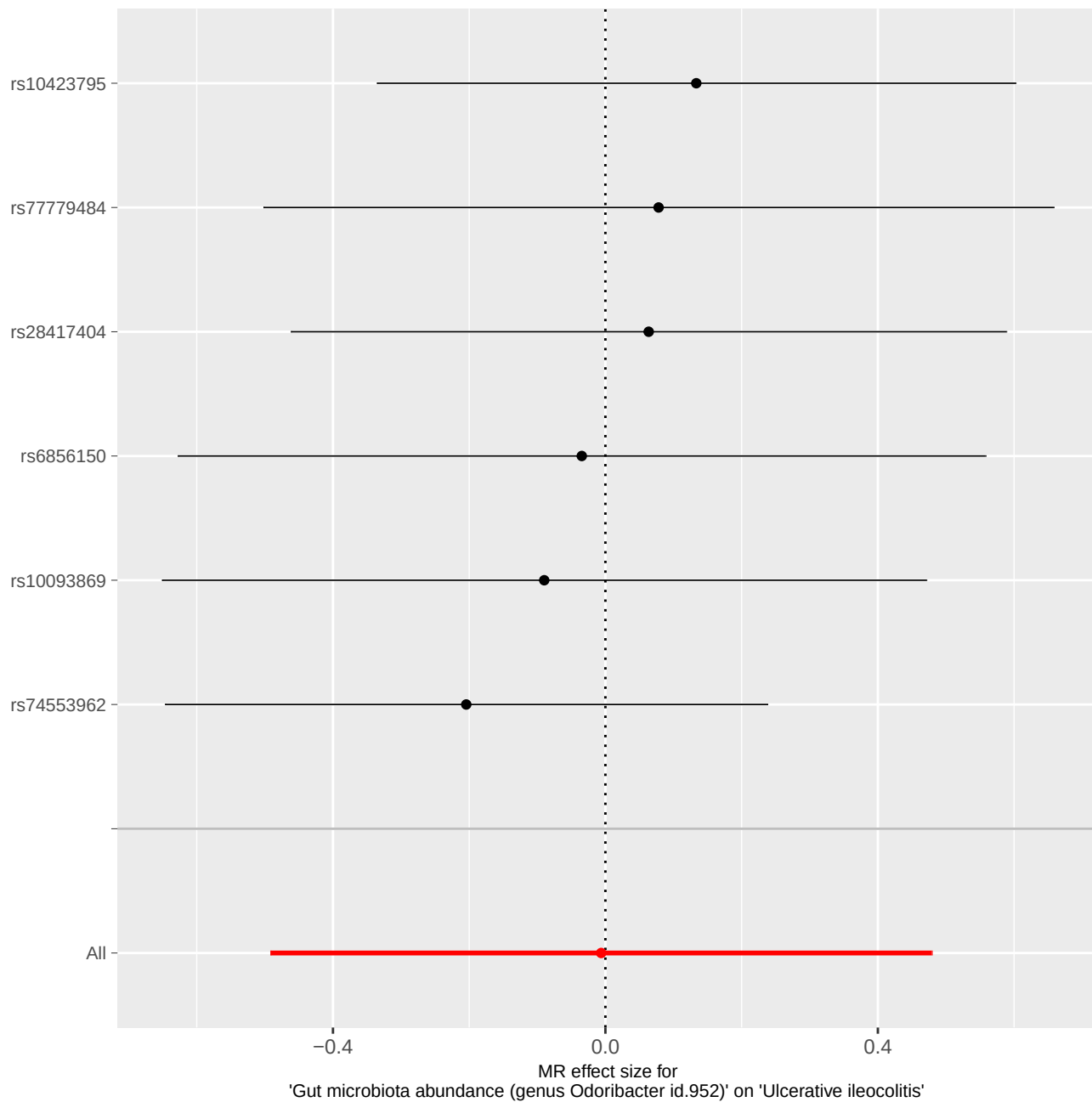


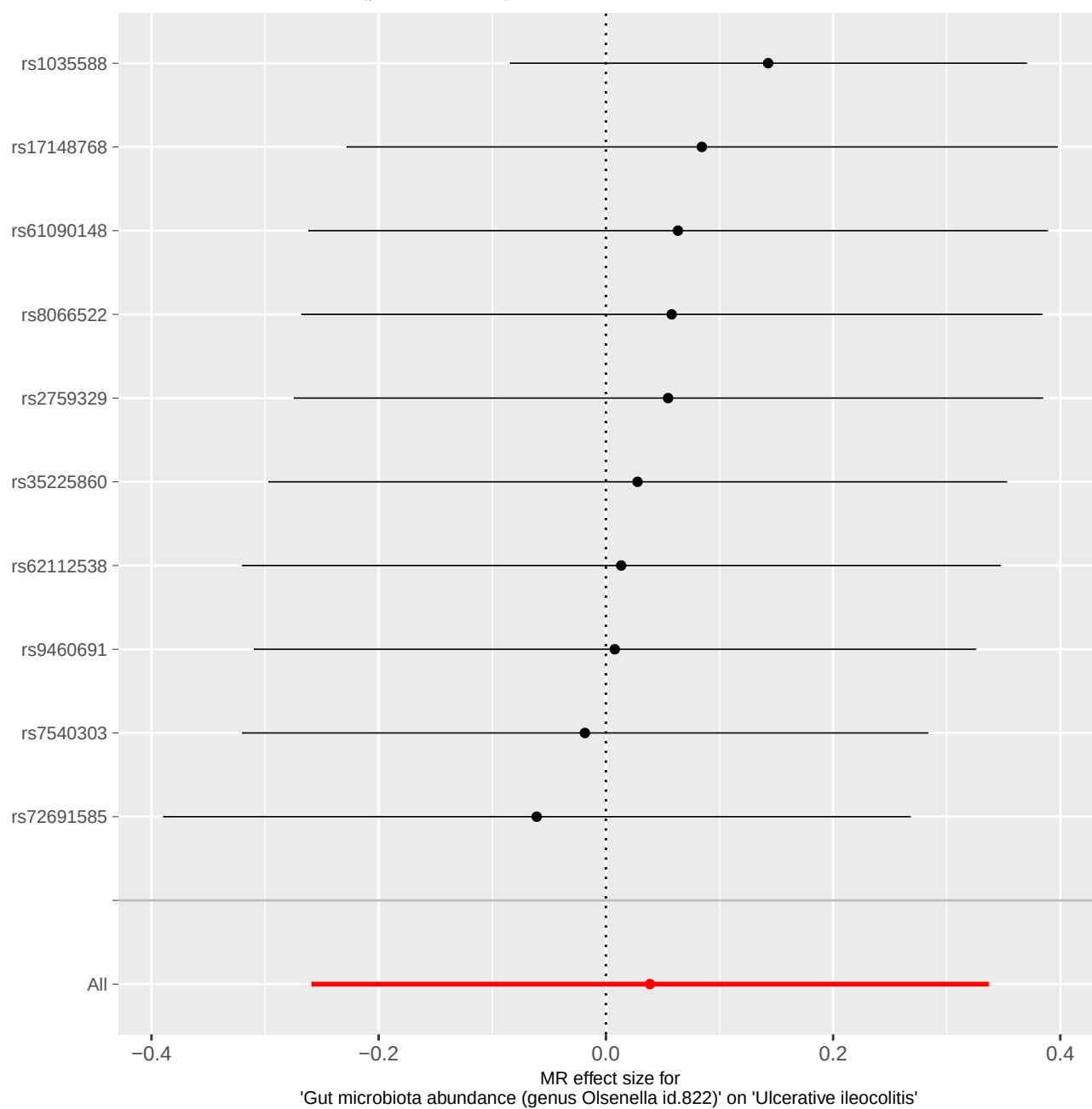


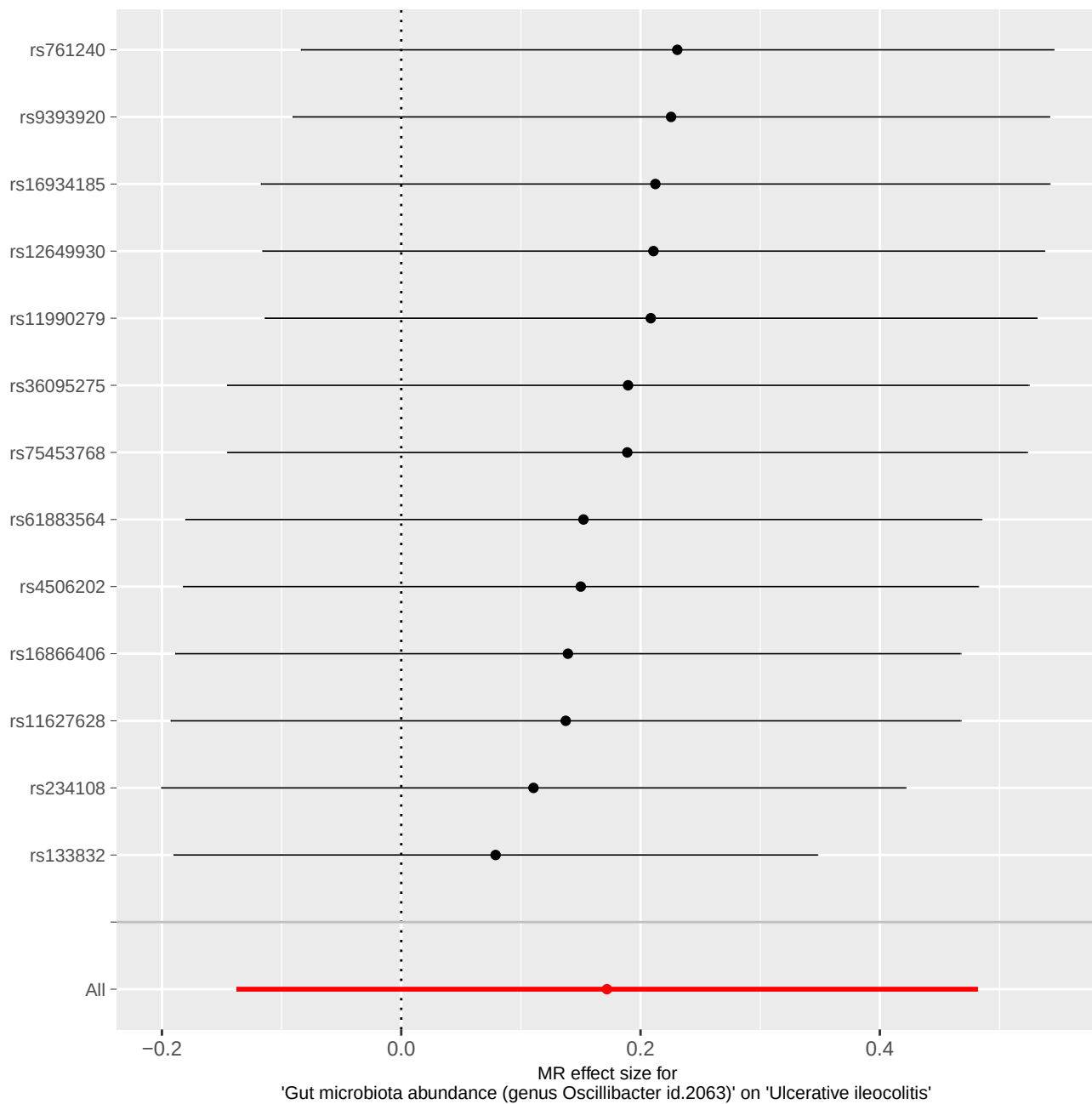


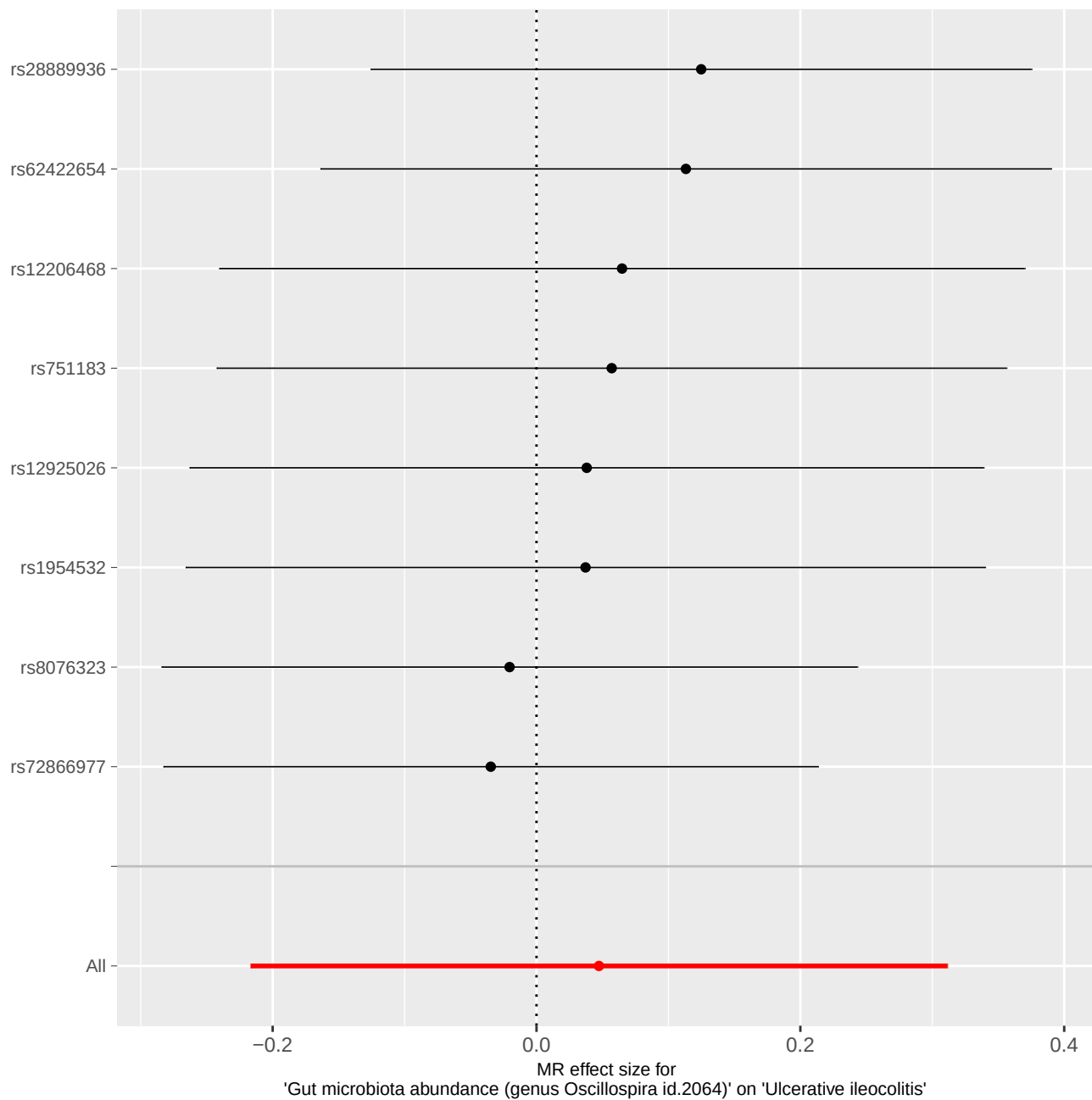


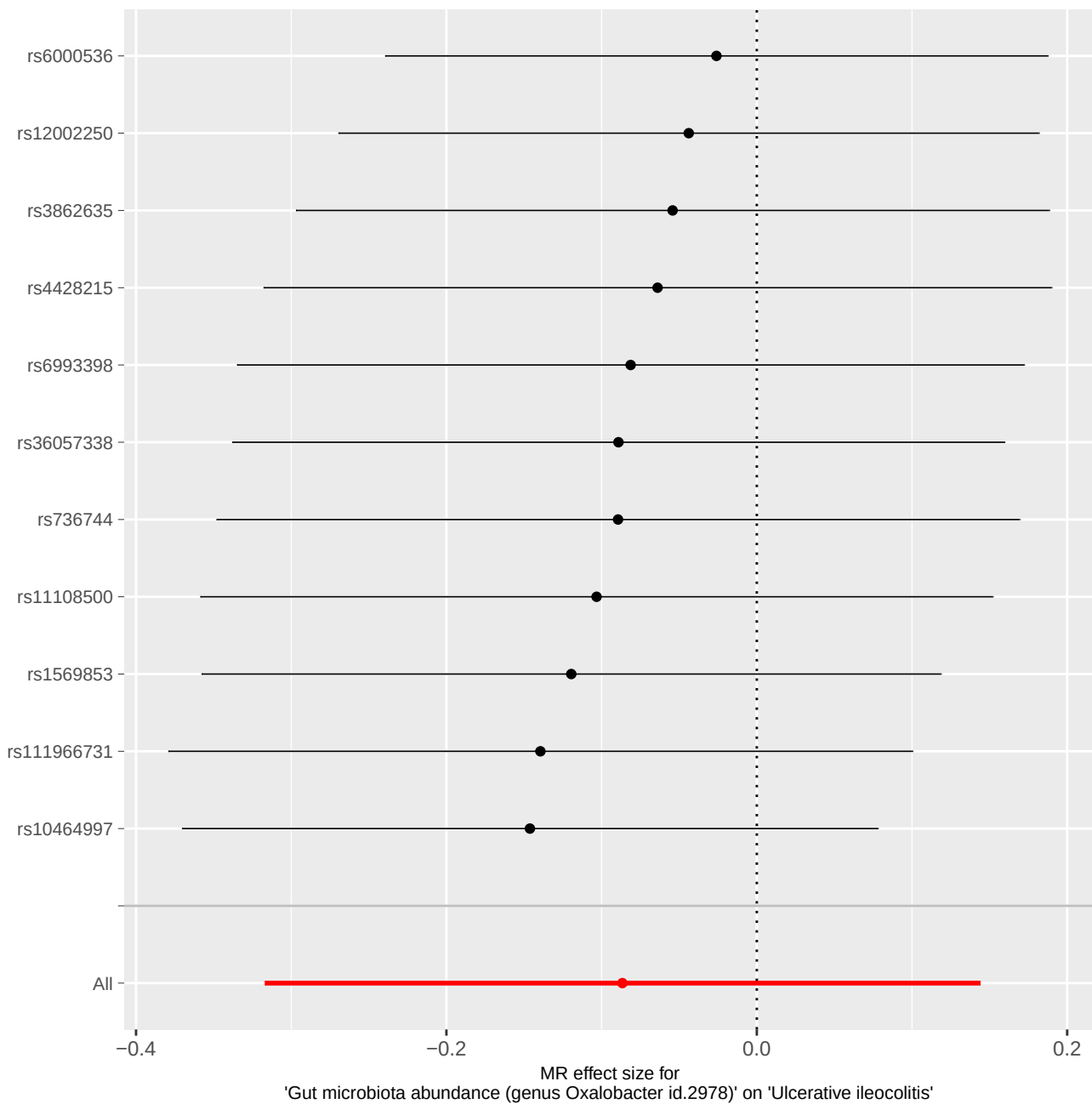


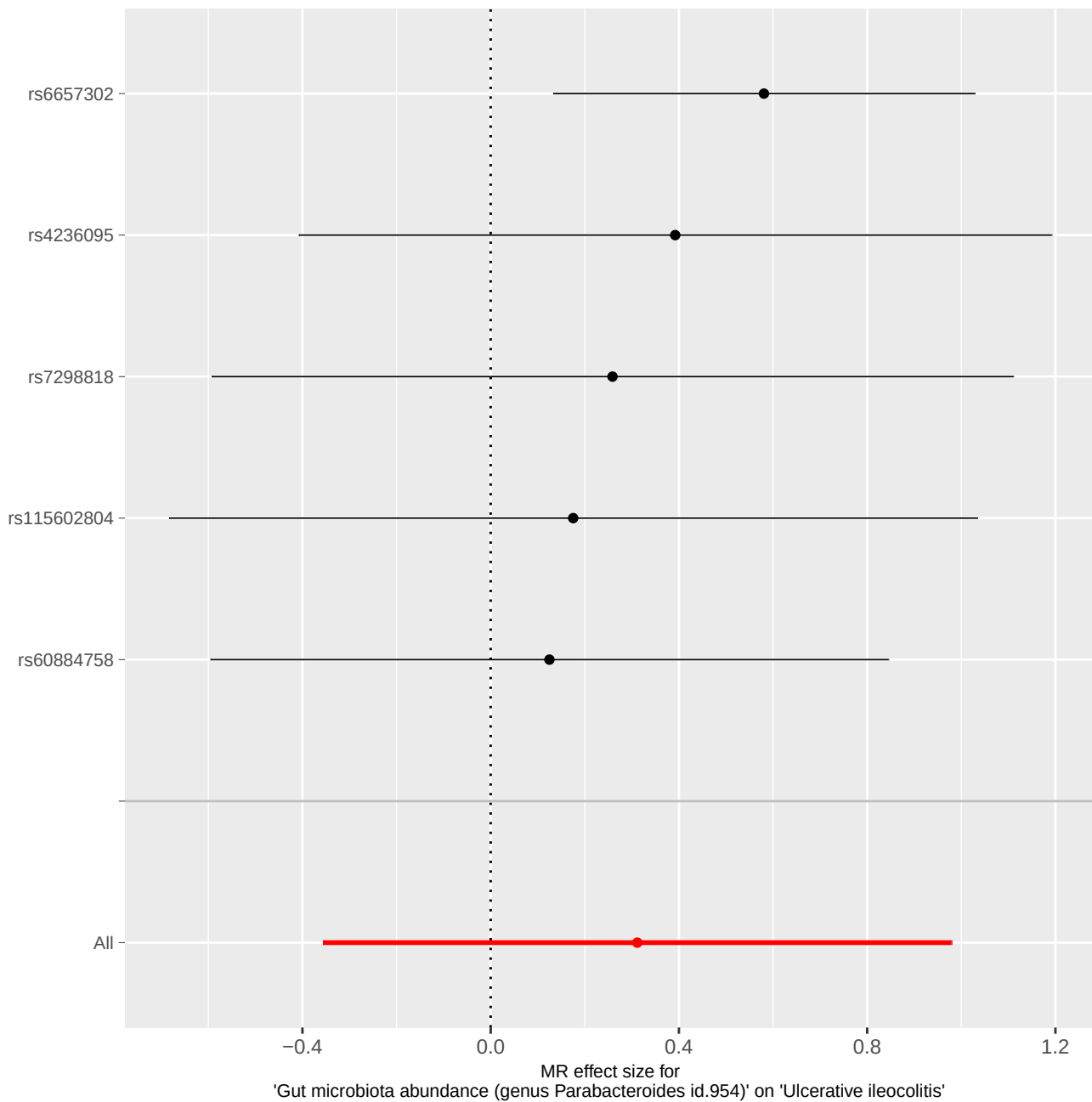


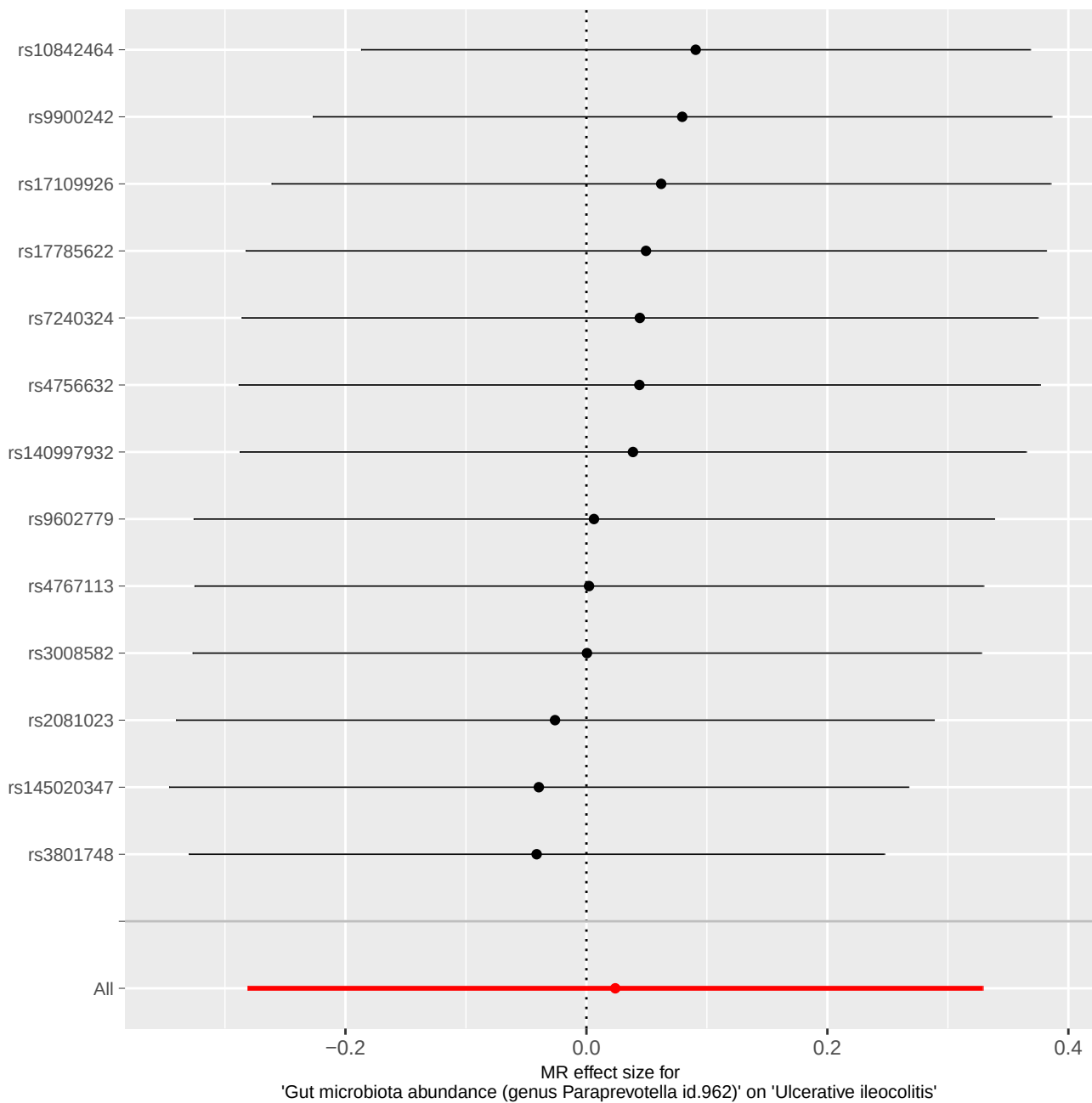




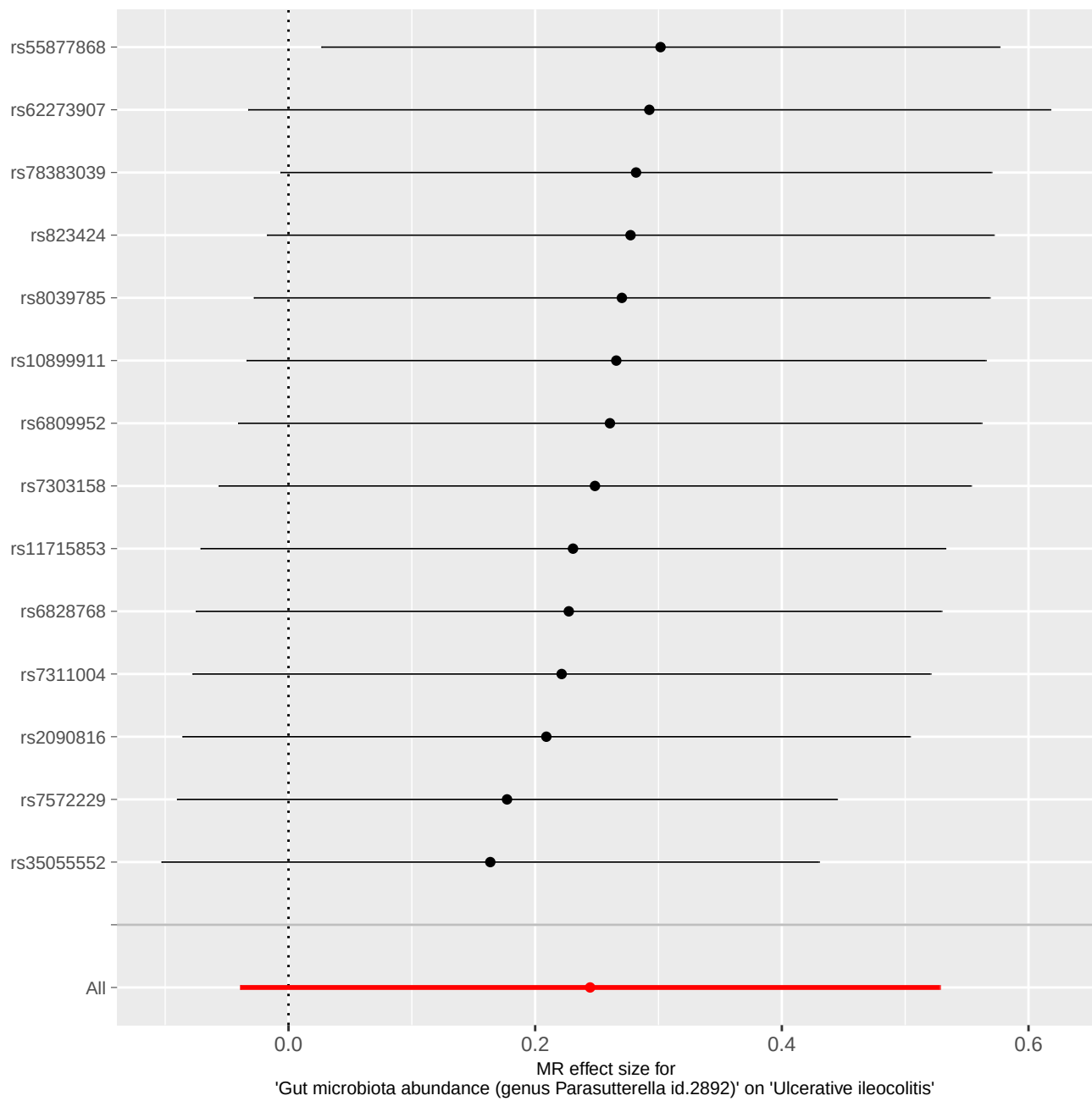


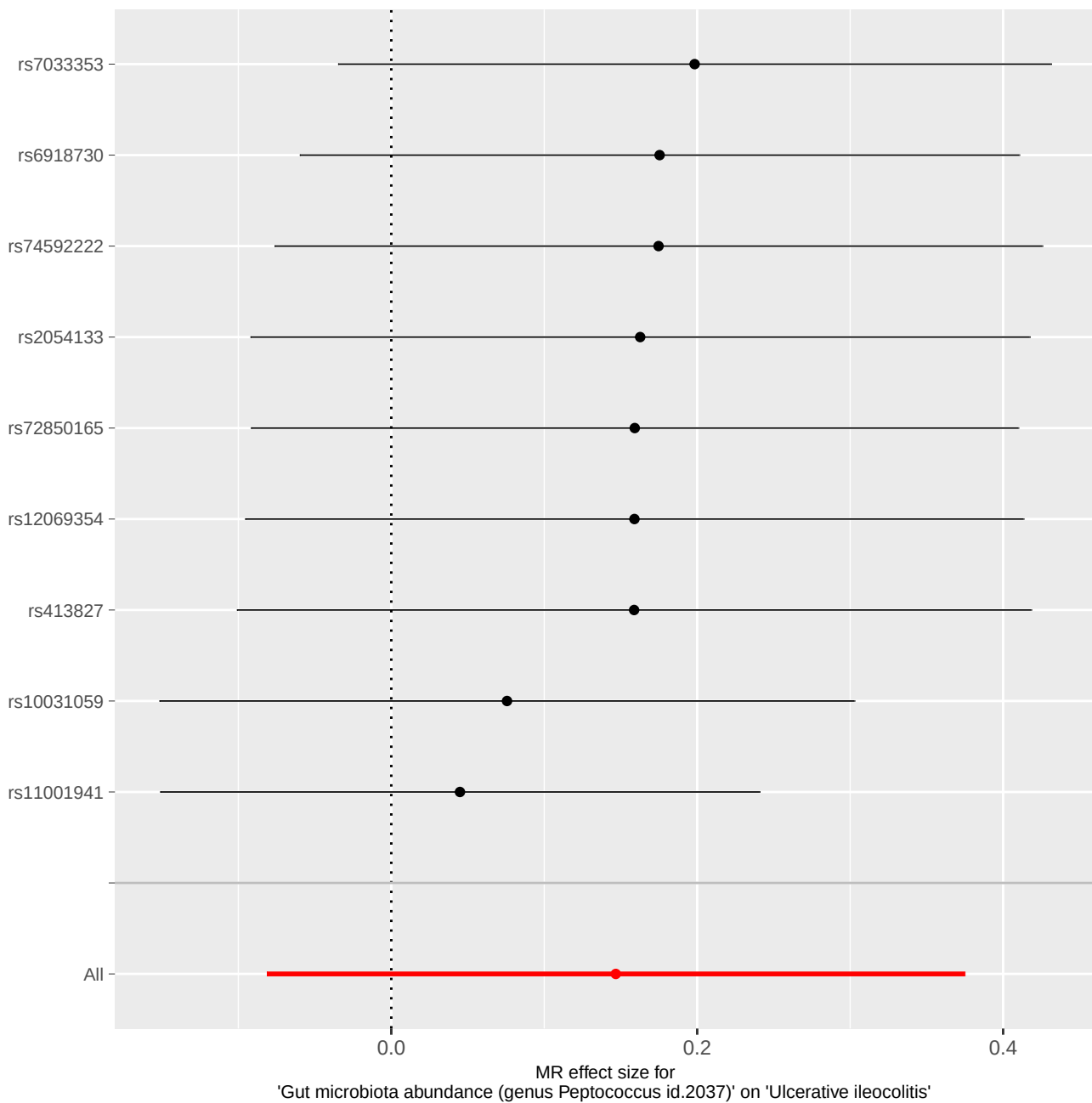


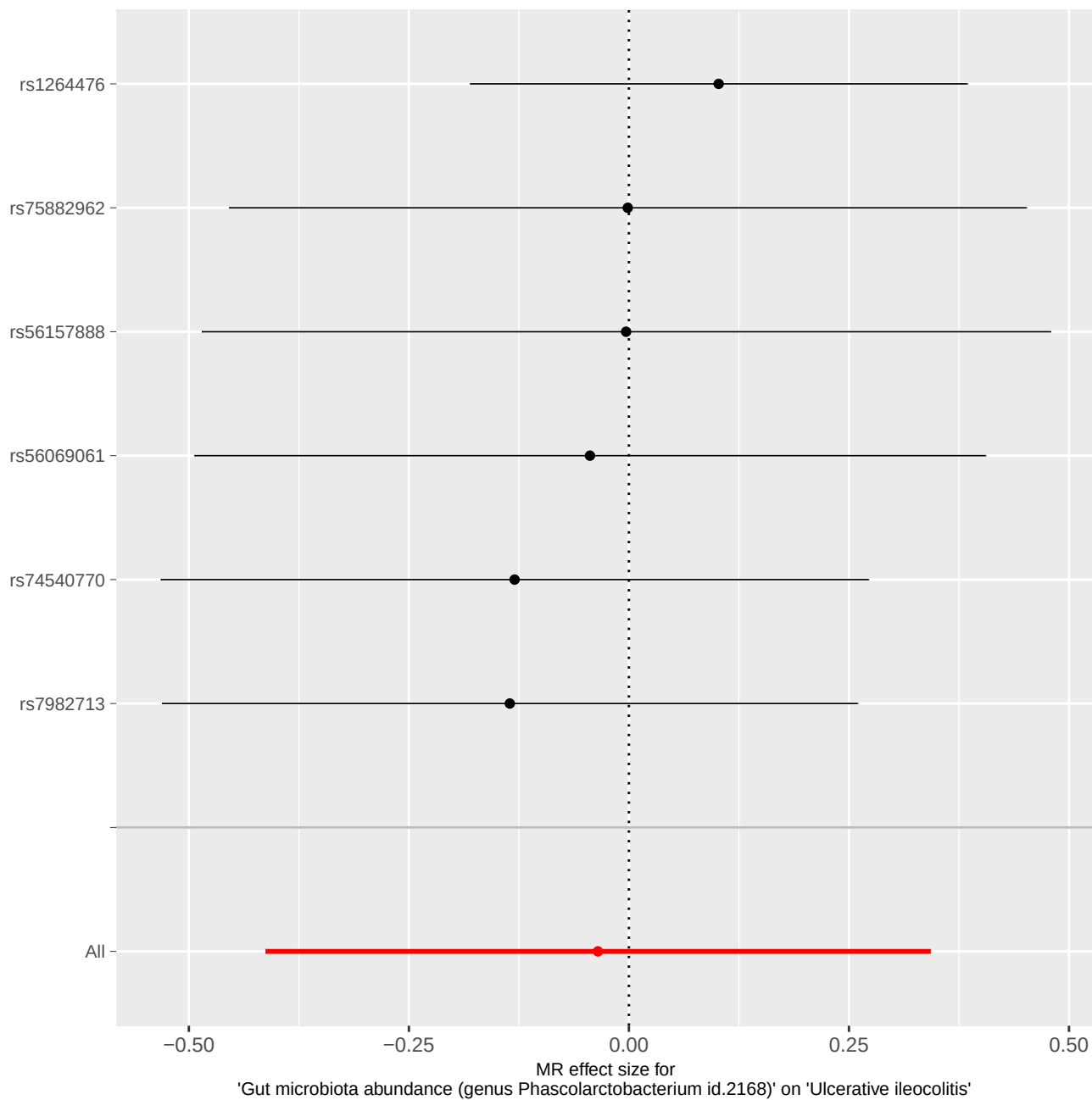




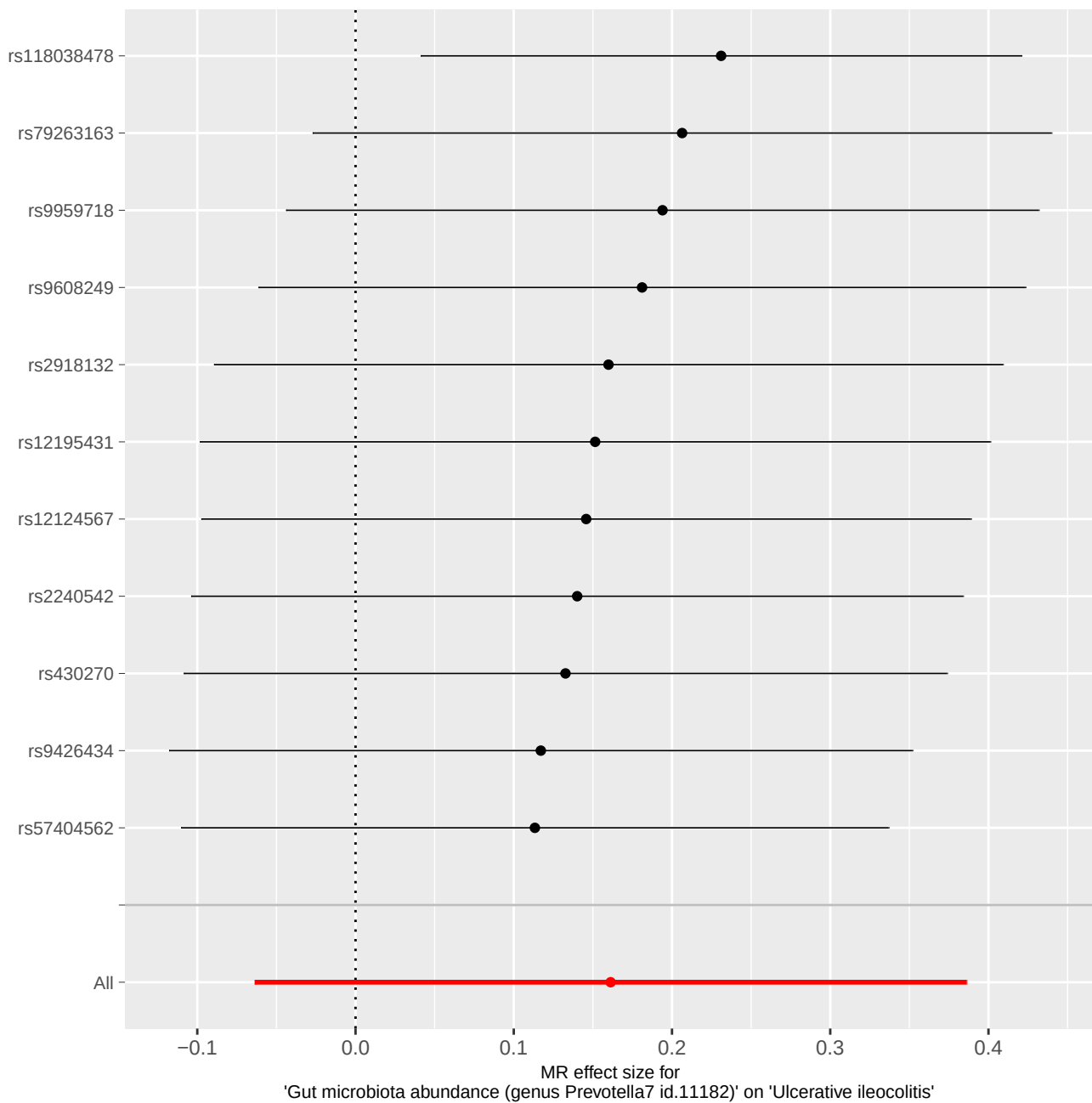
Batch 1165 : Gut microbiota abundance (genus Parasutterella id.2892) on Ulcerative ileocolitis

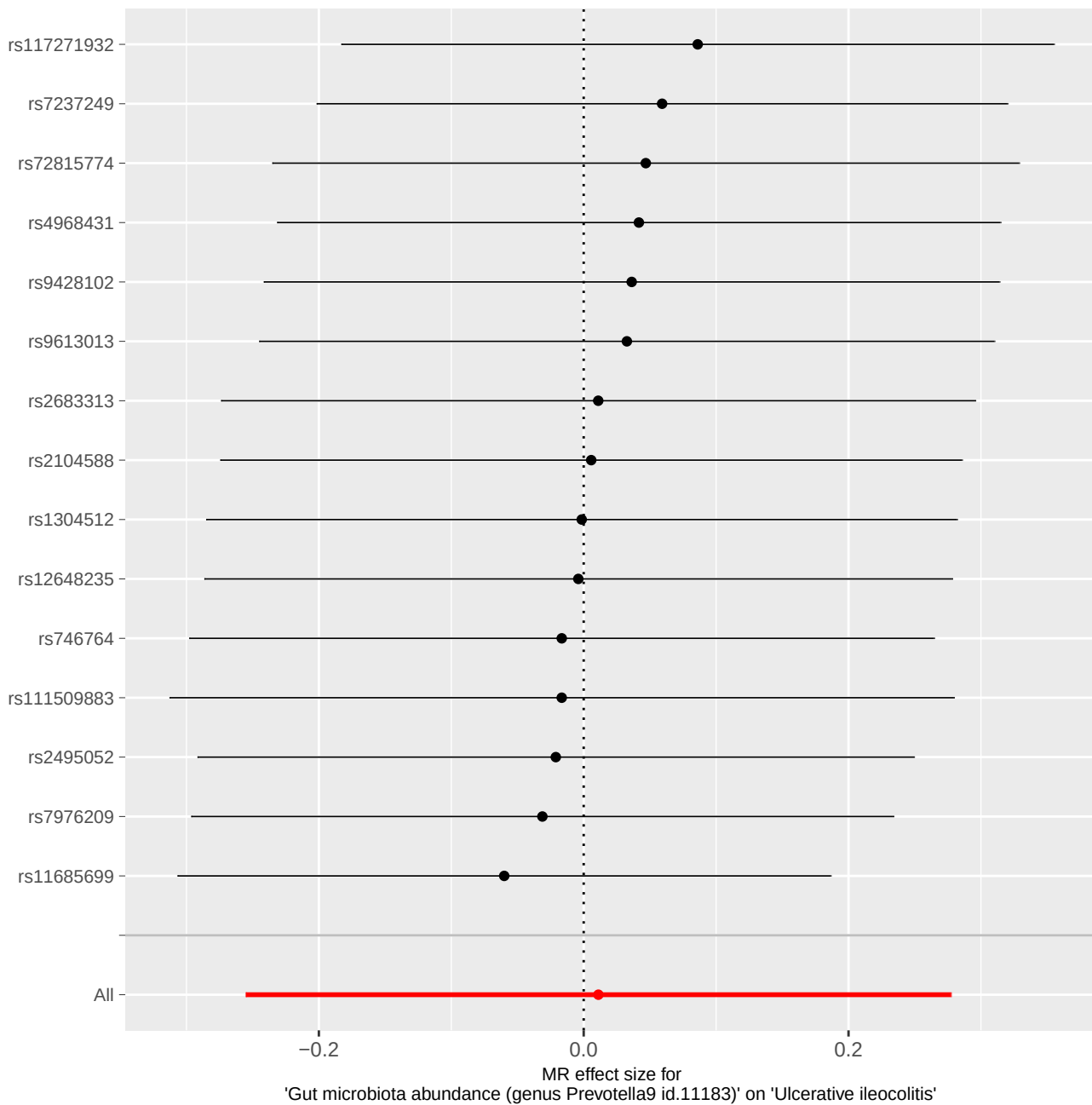


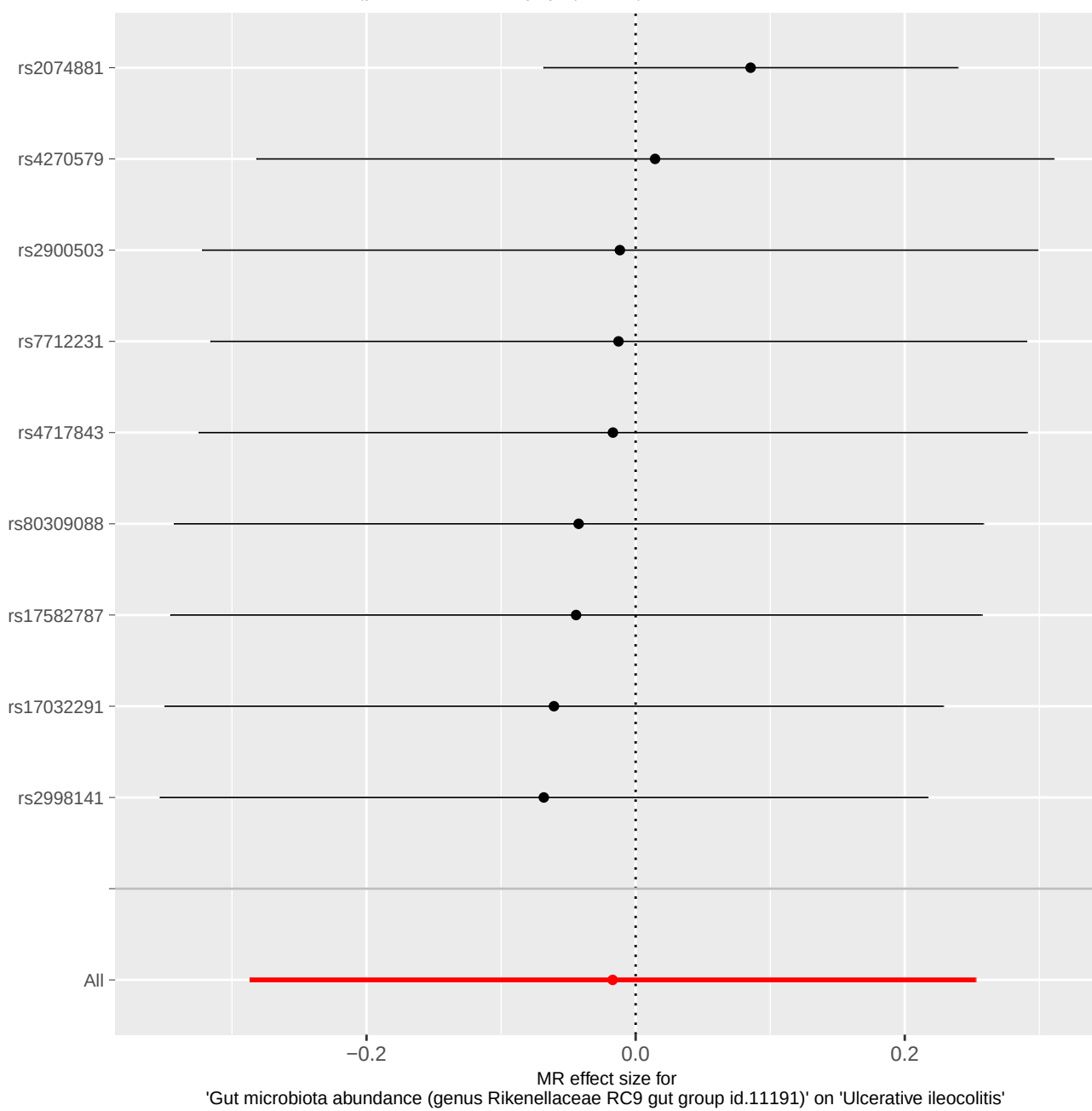


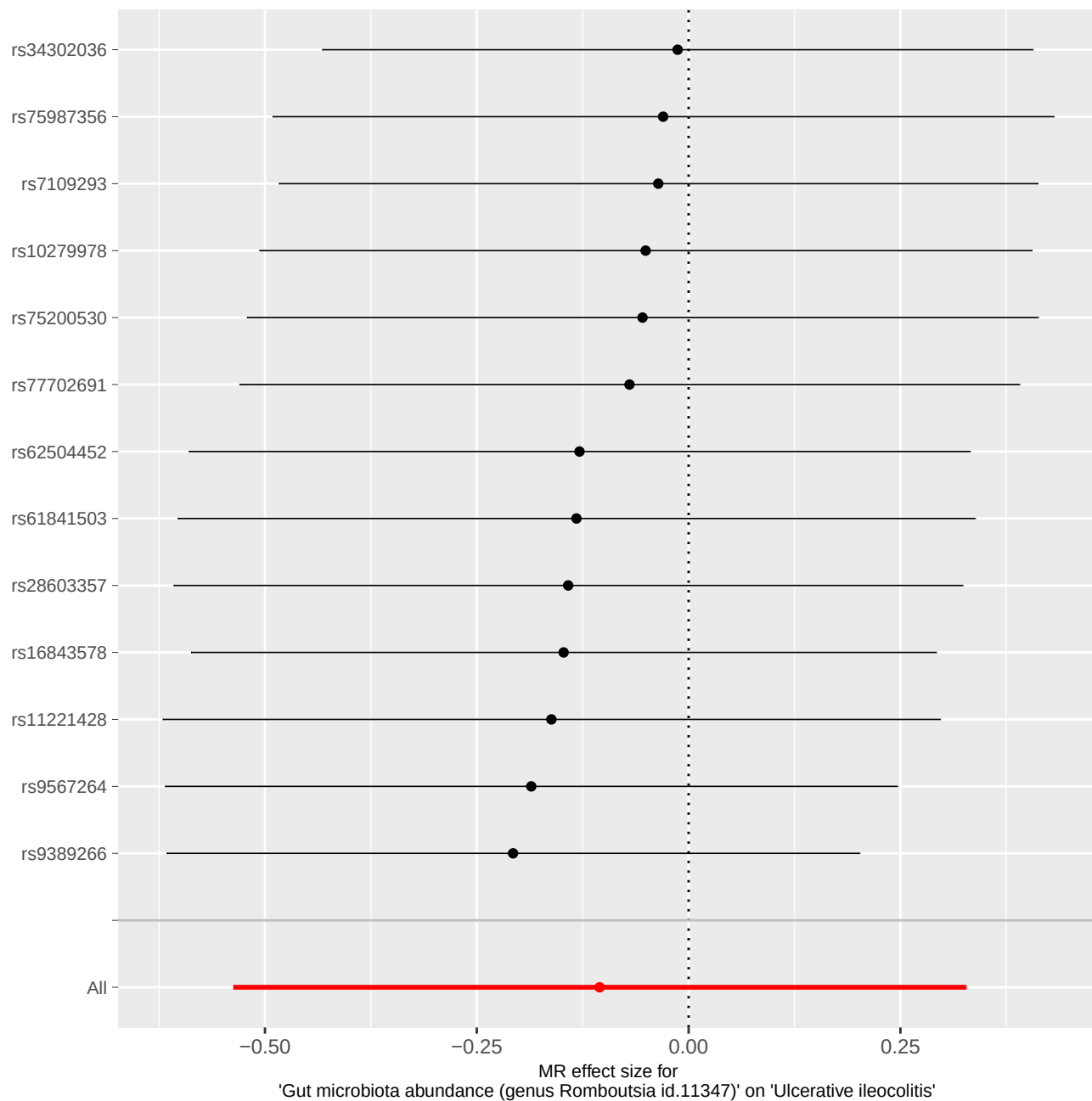


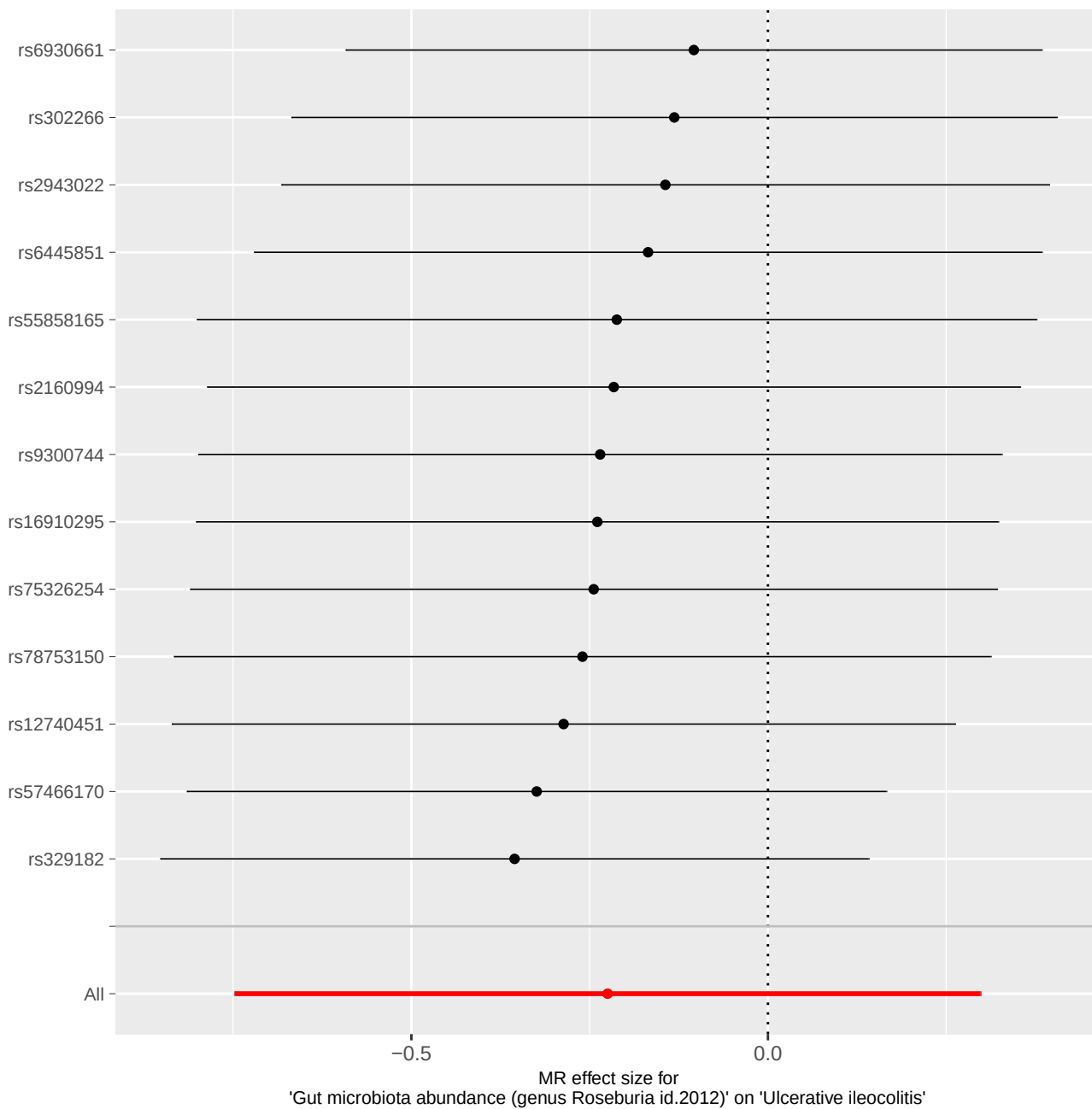
Batch 1168 : Gut microbiota abundance (genus Prevotella7 id.11182) on Ulcerative ileocolitis



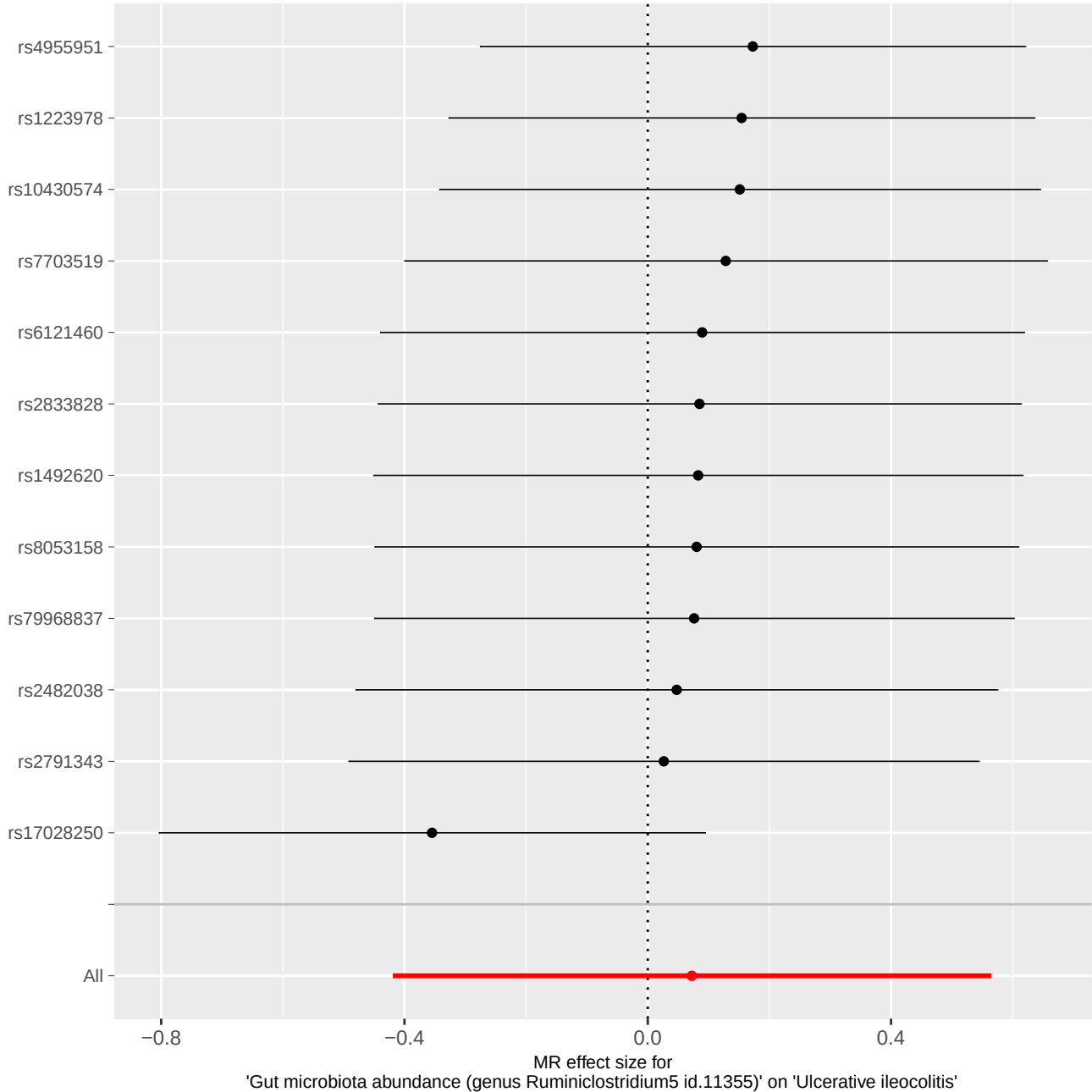


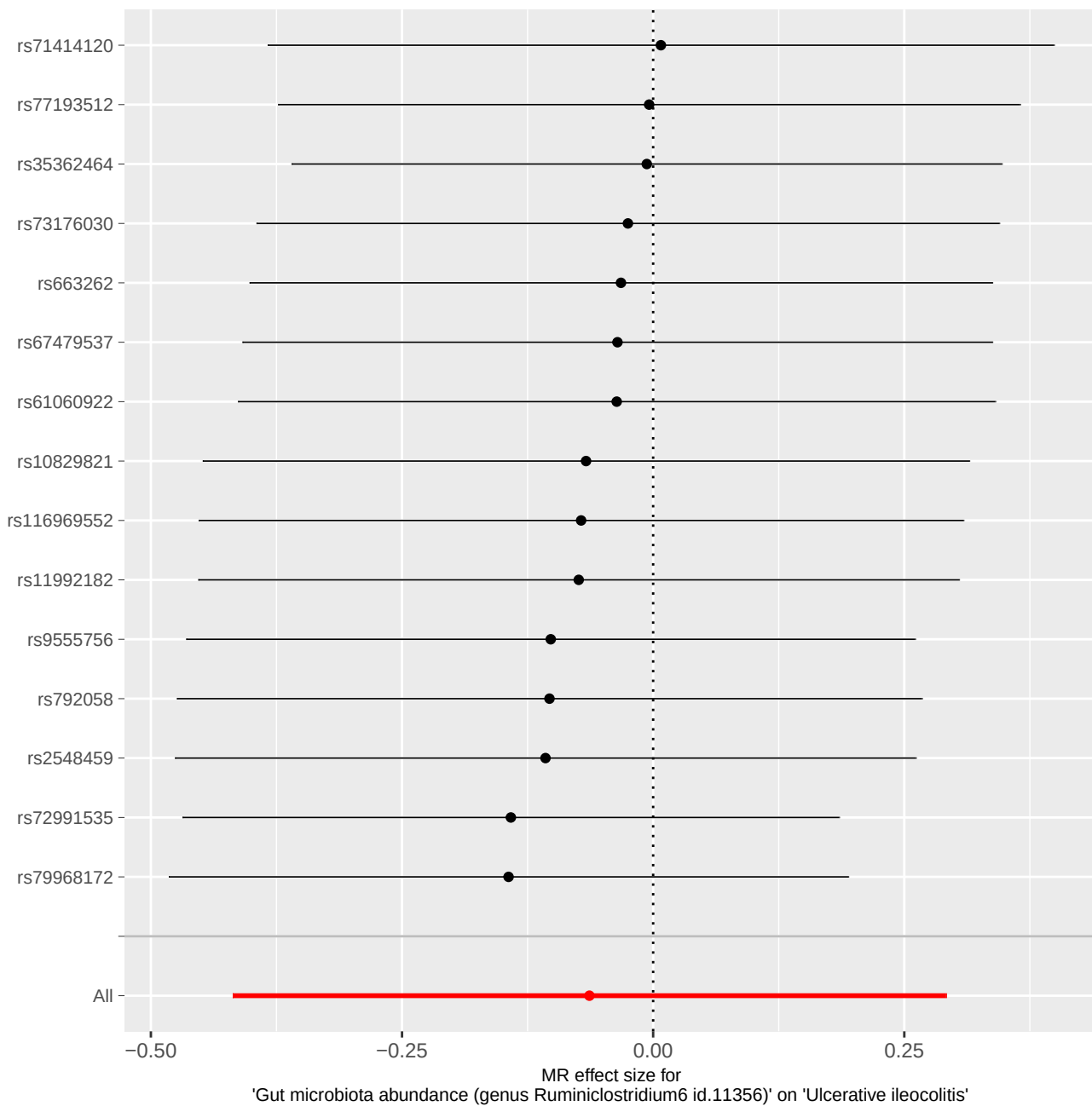




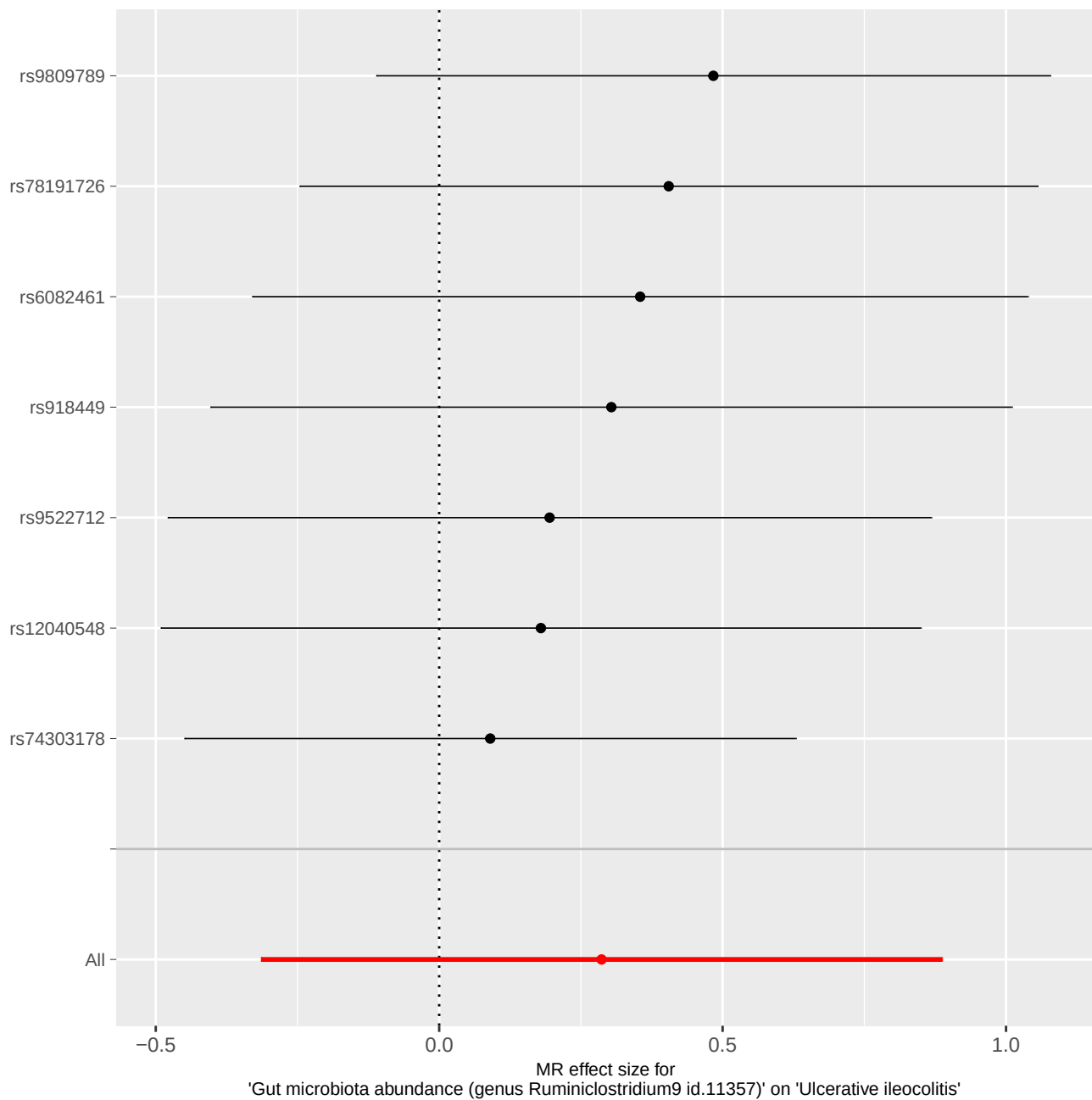


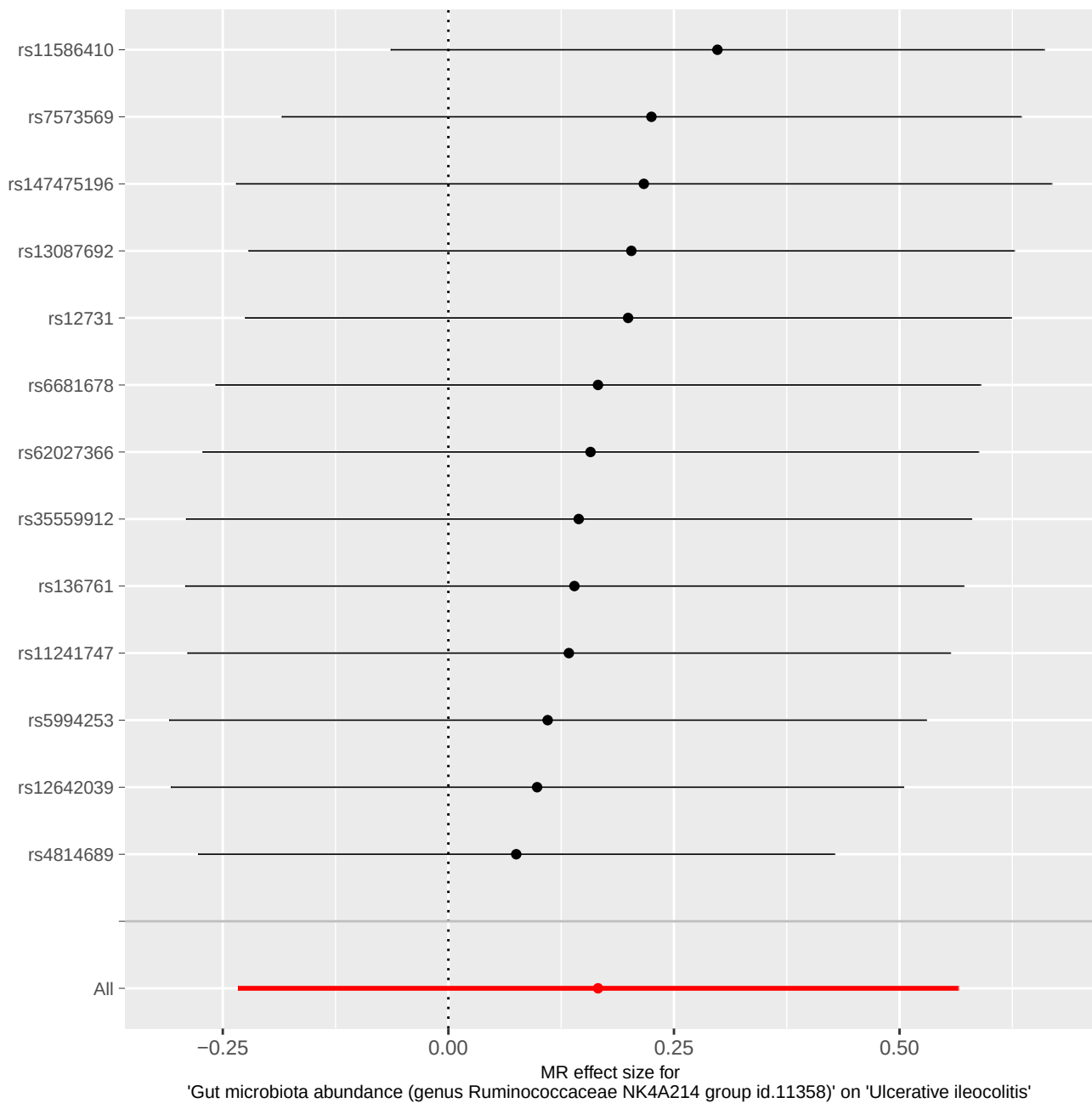
Batch 1173 : Gut microbiota abundance (genus Ruminiclostridium5 id.11355) on Ulcerative ileocolitis

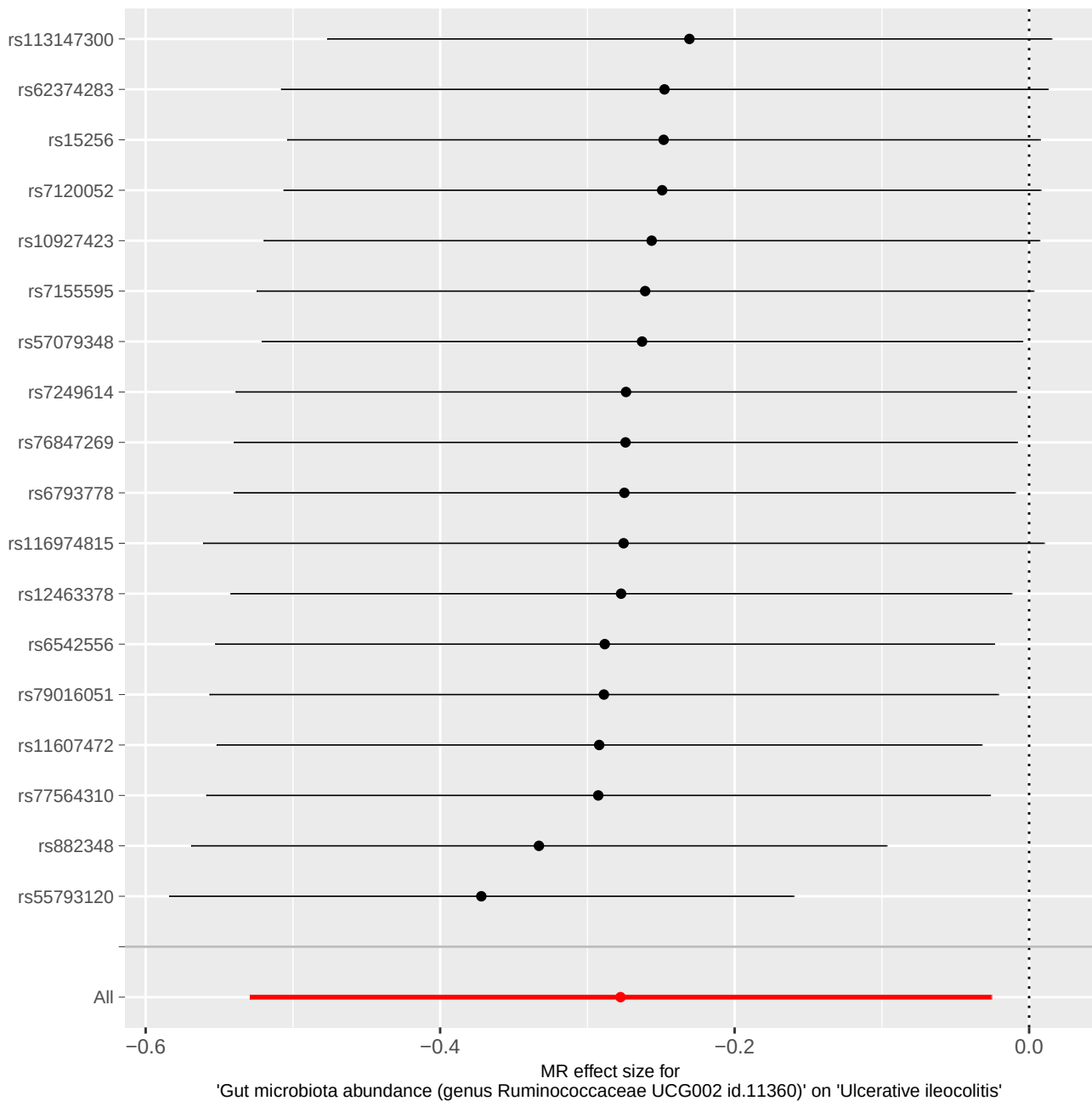


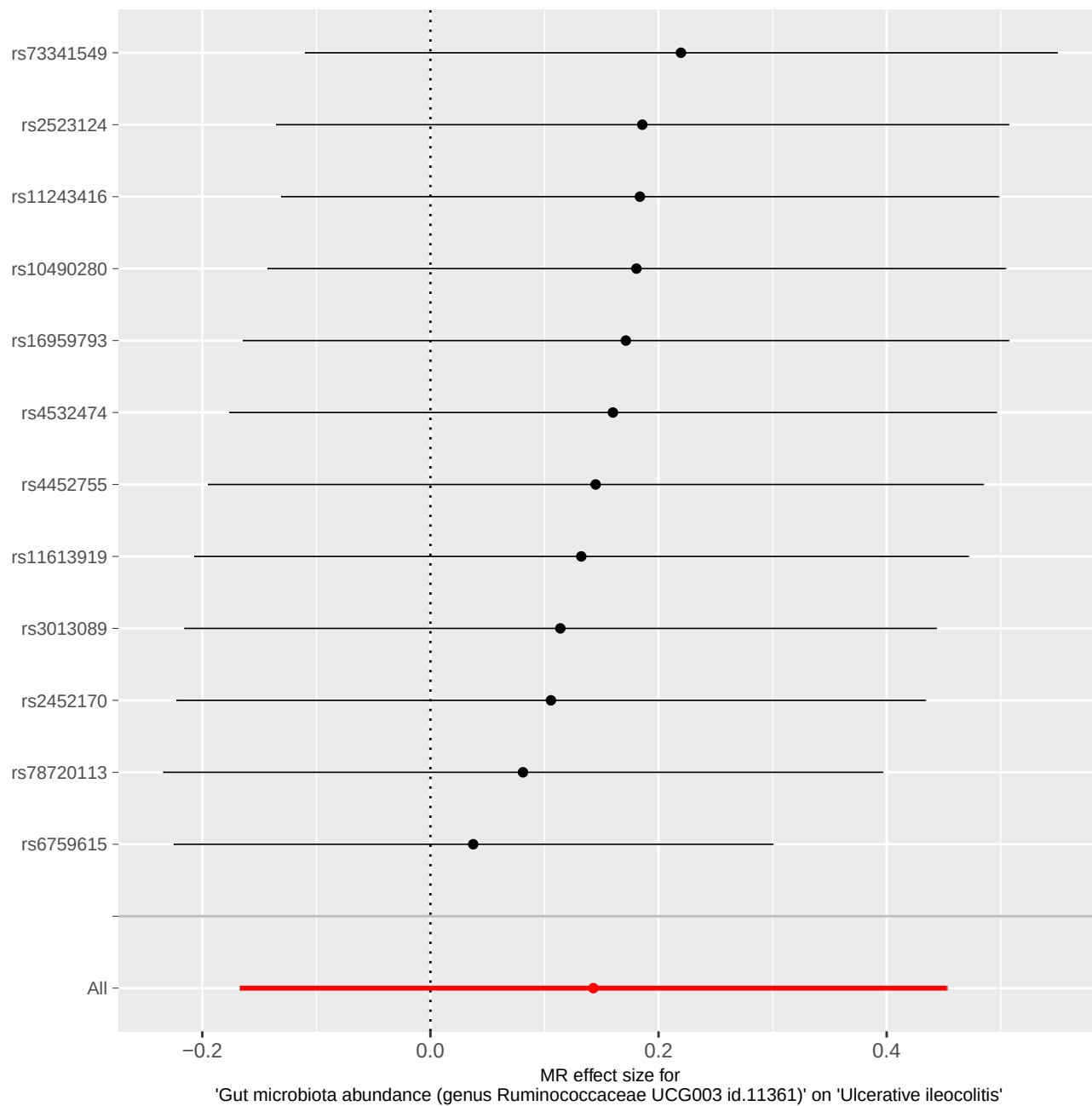


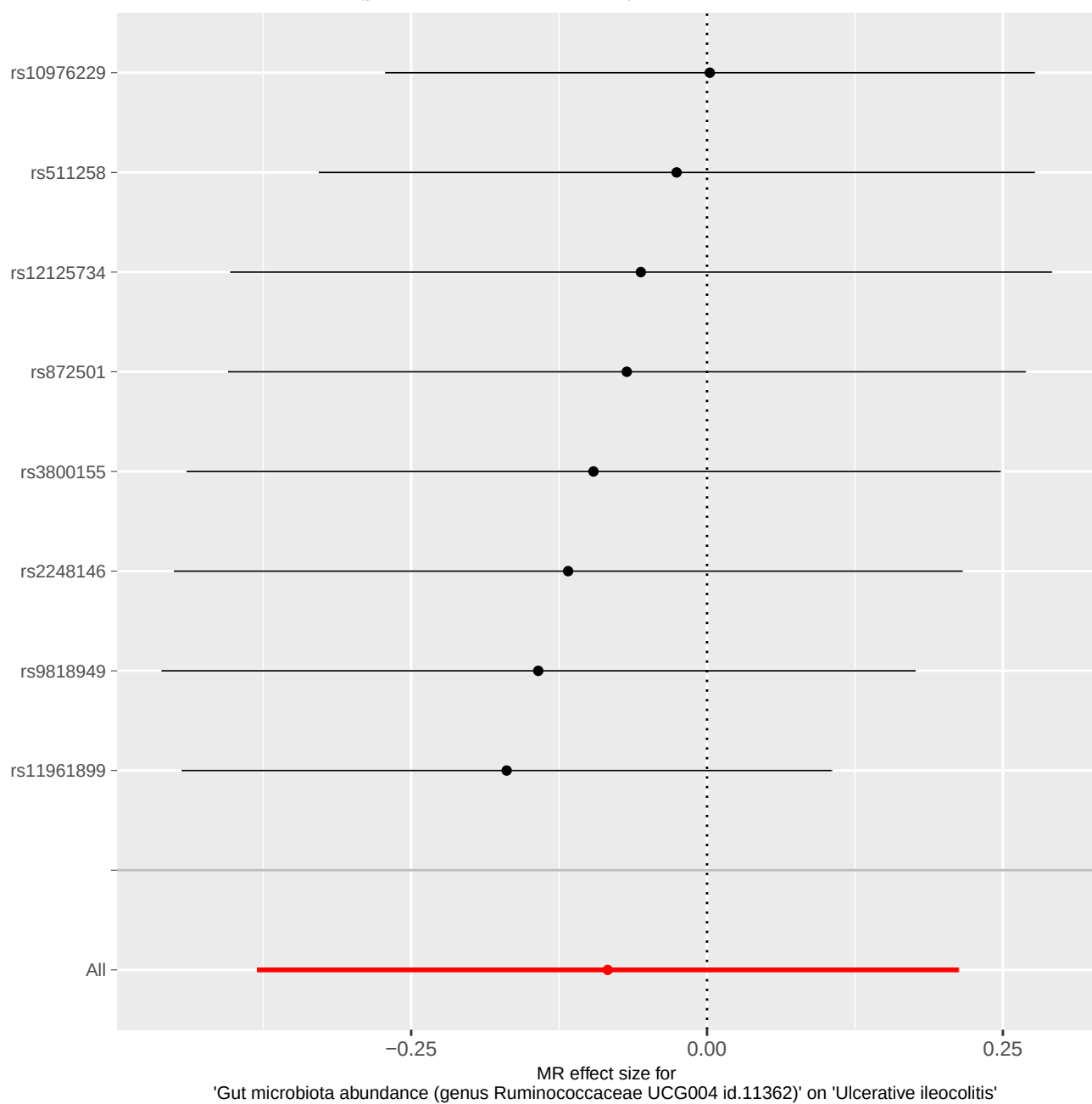
Batch 1175 : Gut microbiota abundance (genus Ruminiclostridium9 id.11357) on Ulcerative ileocolitis

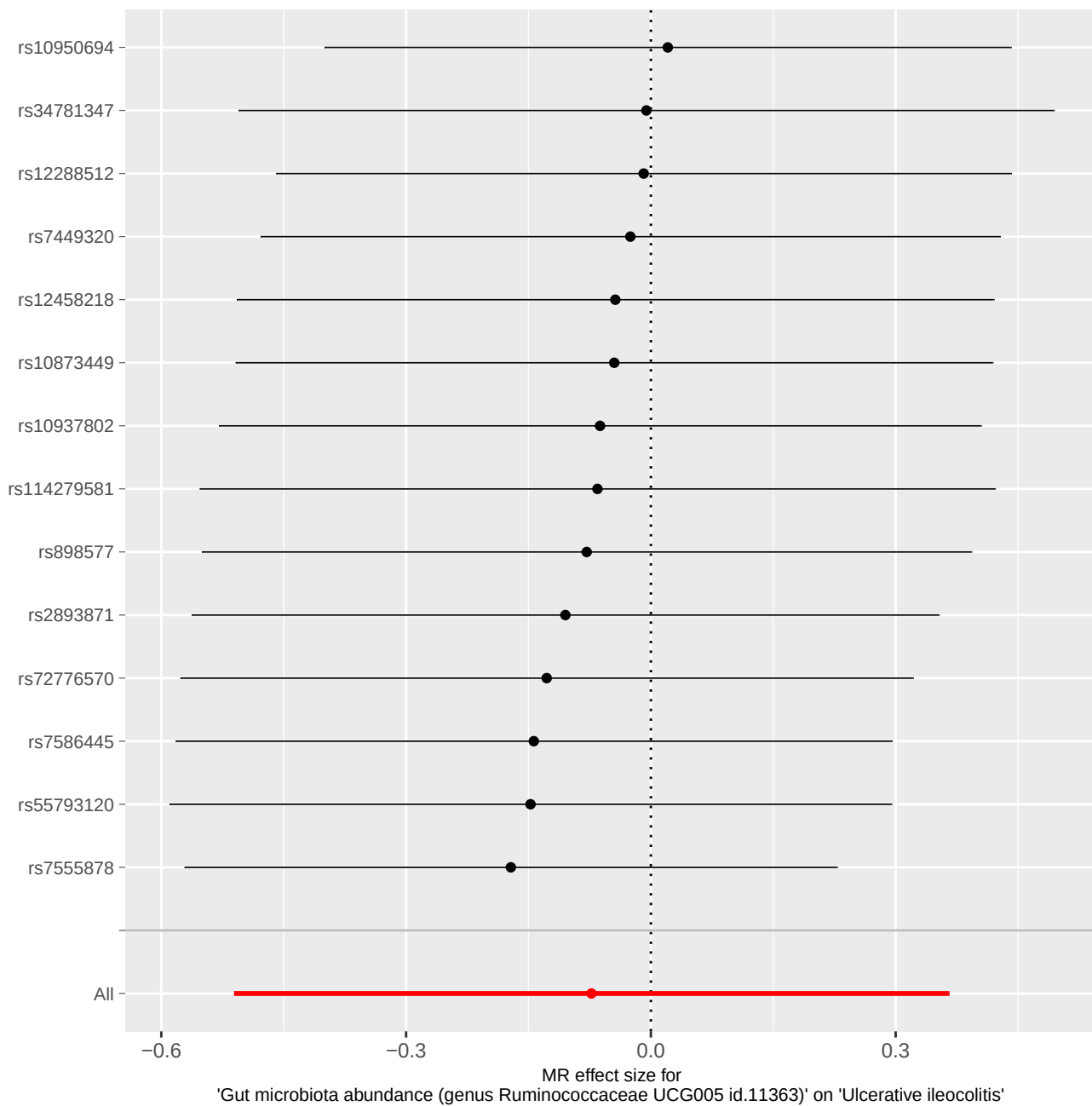


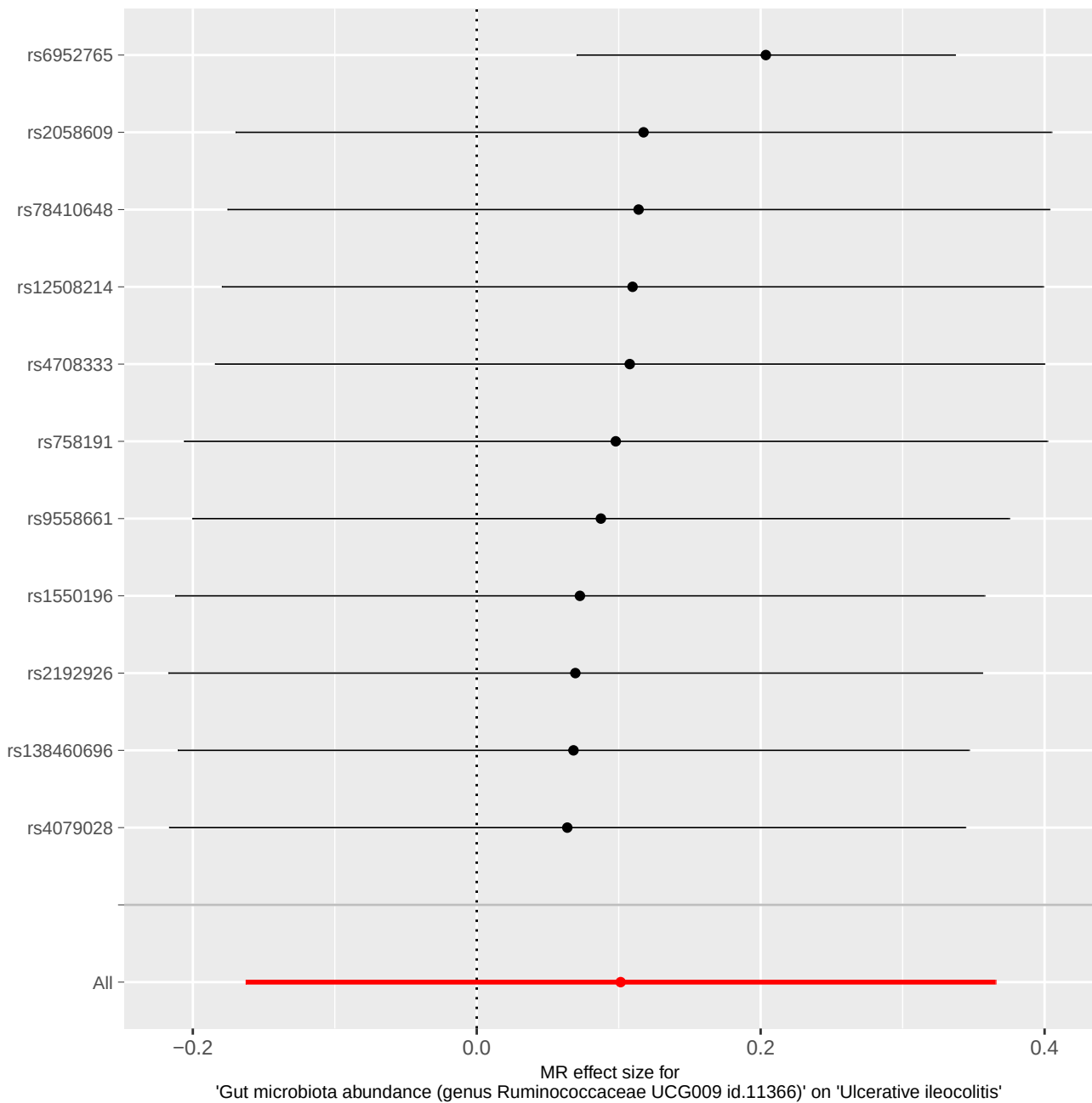


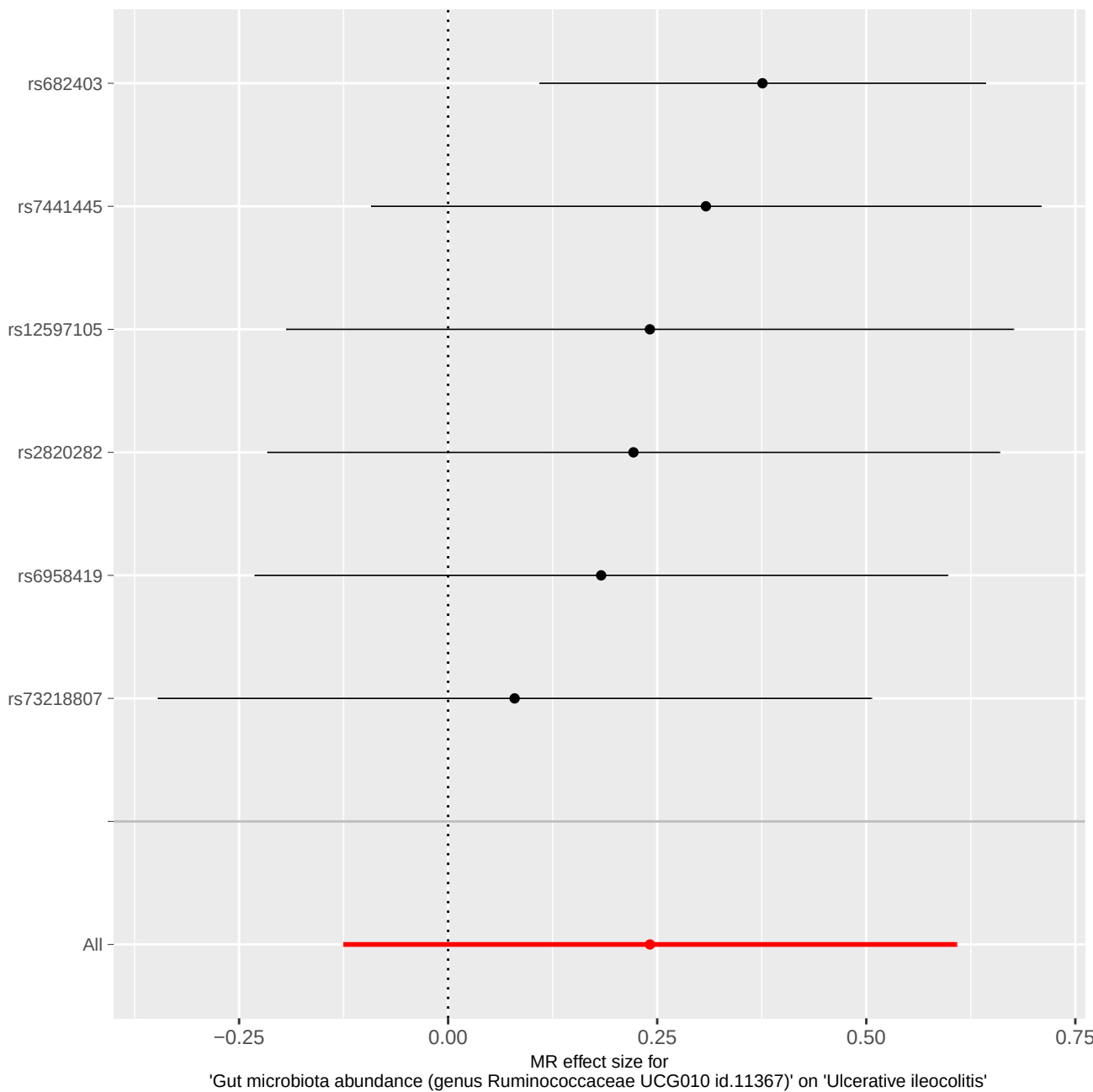


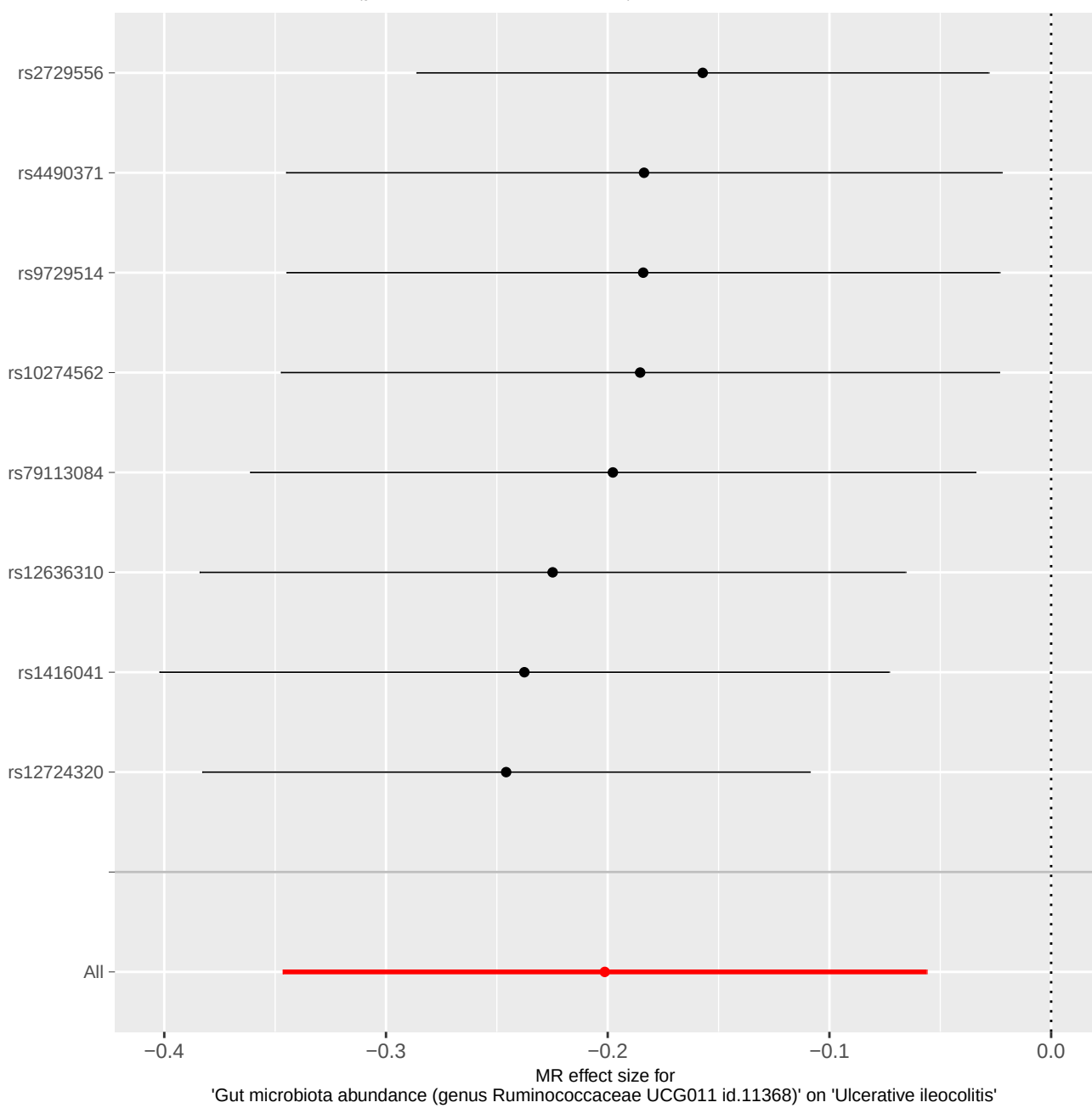


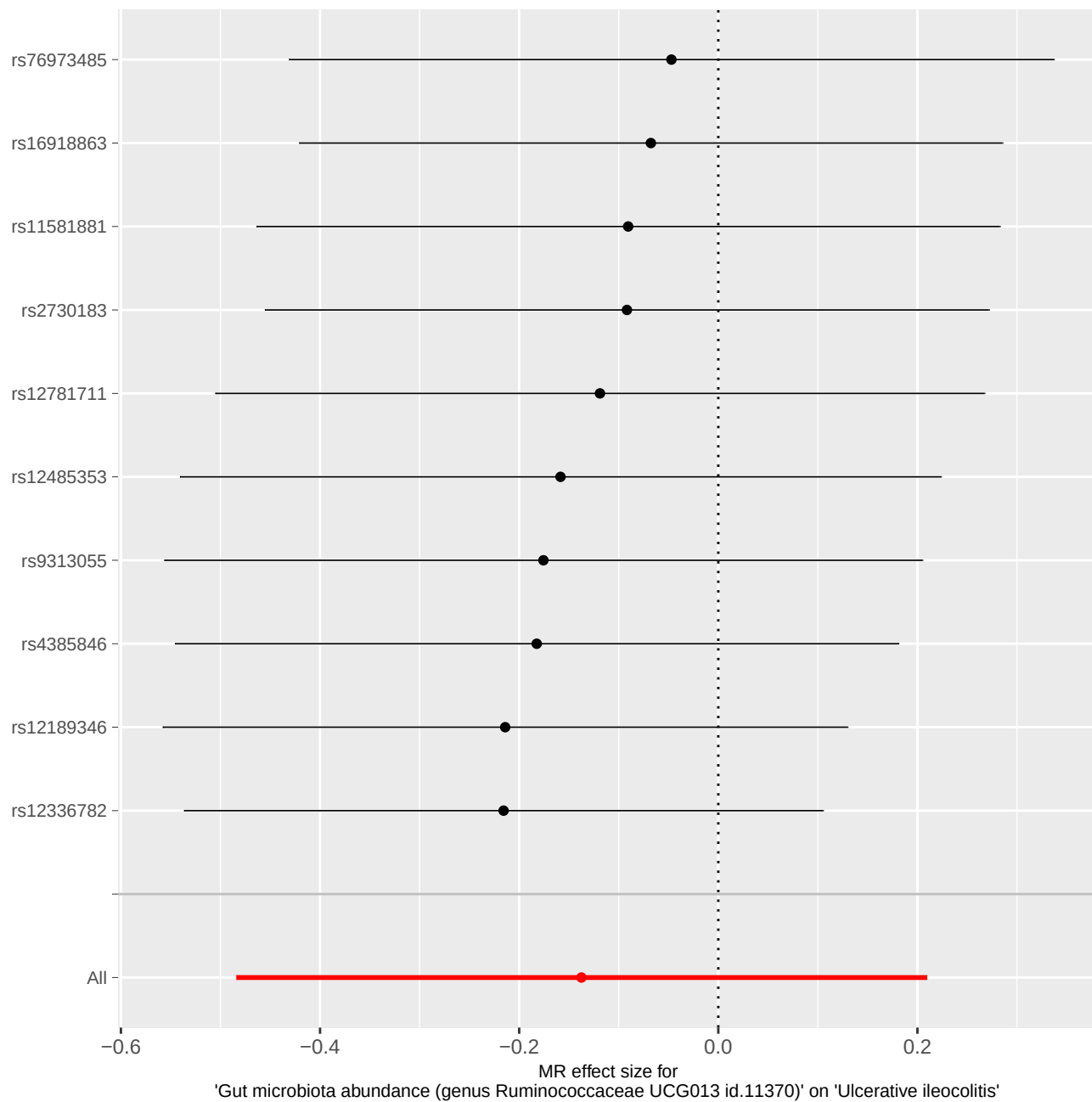


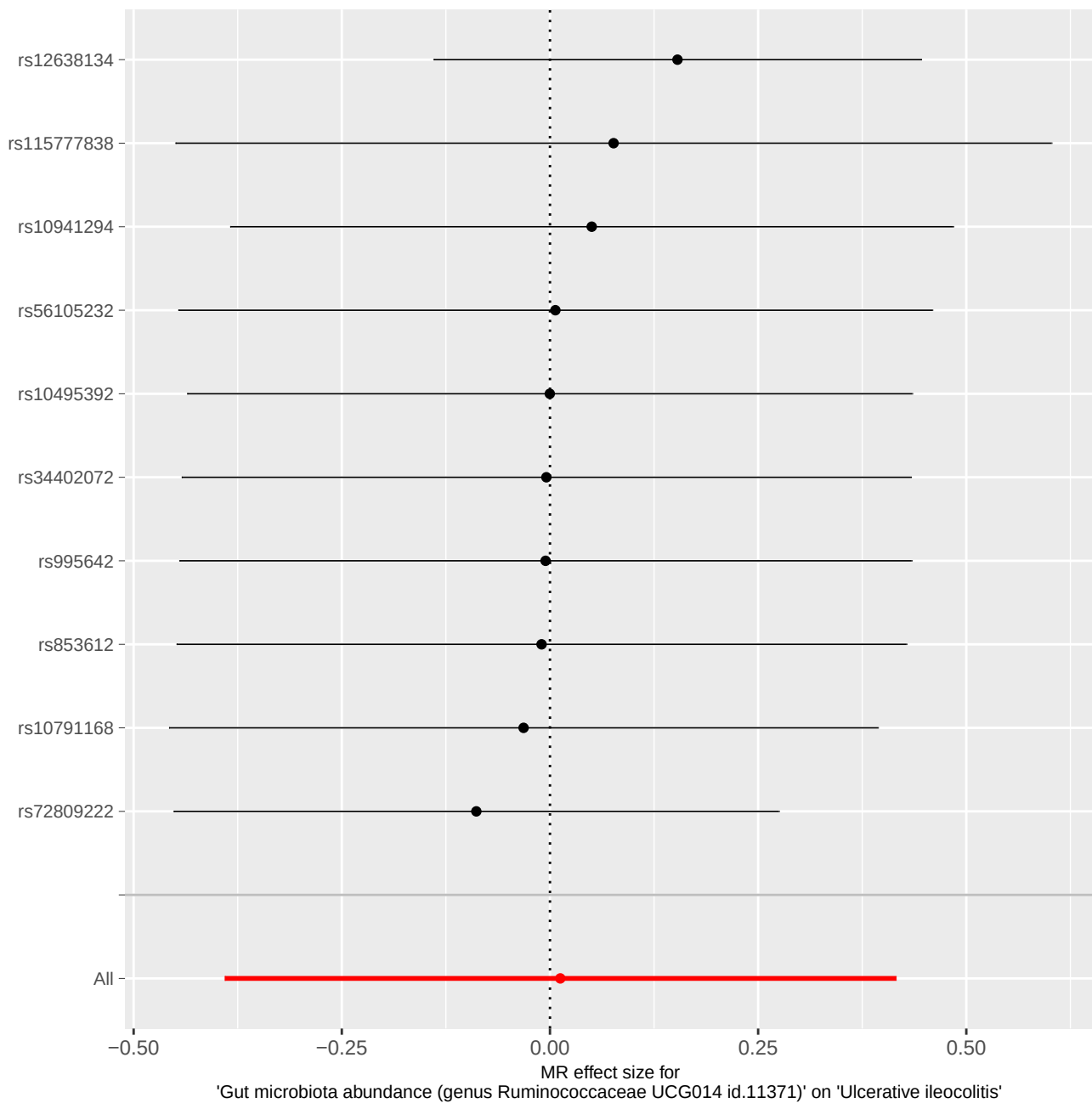


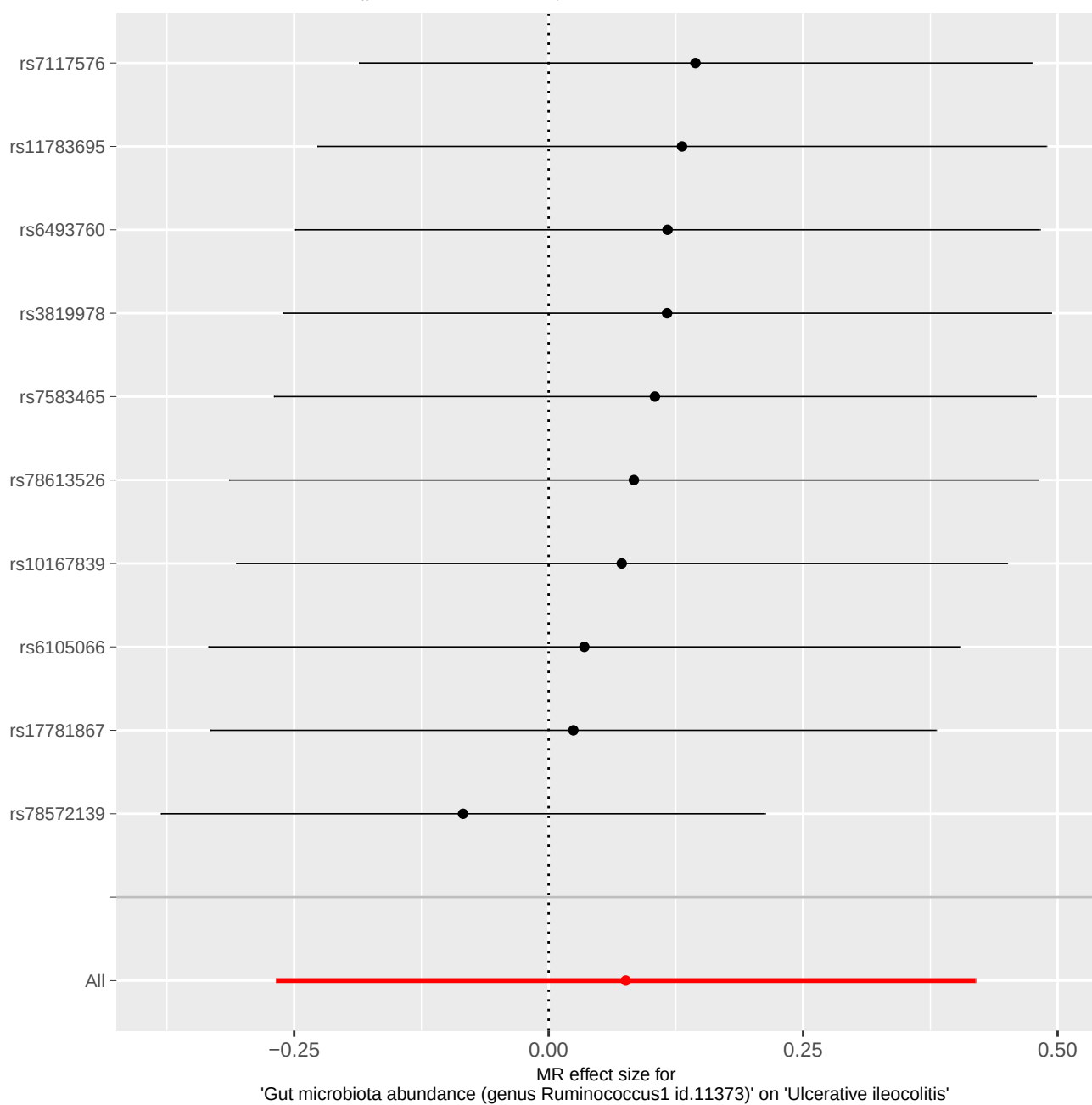




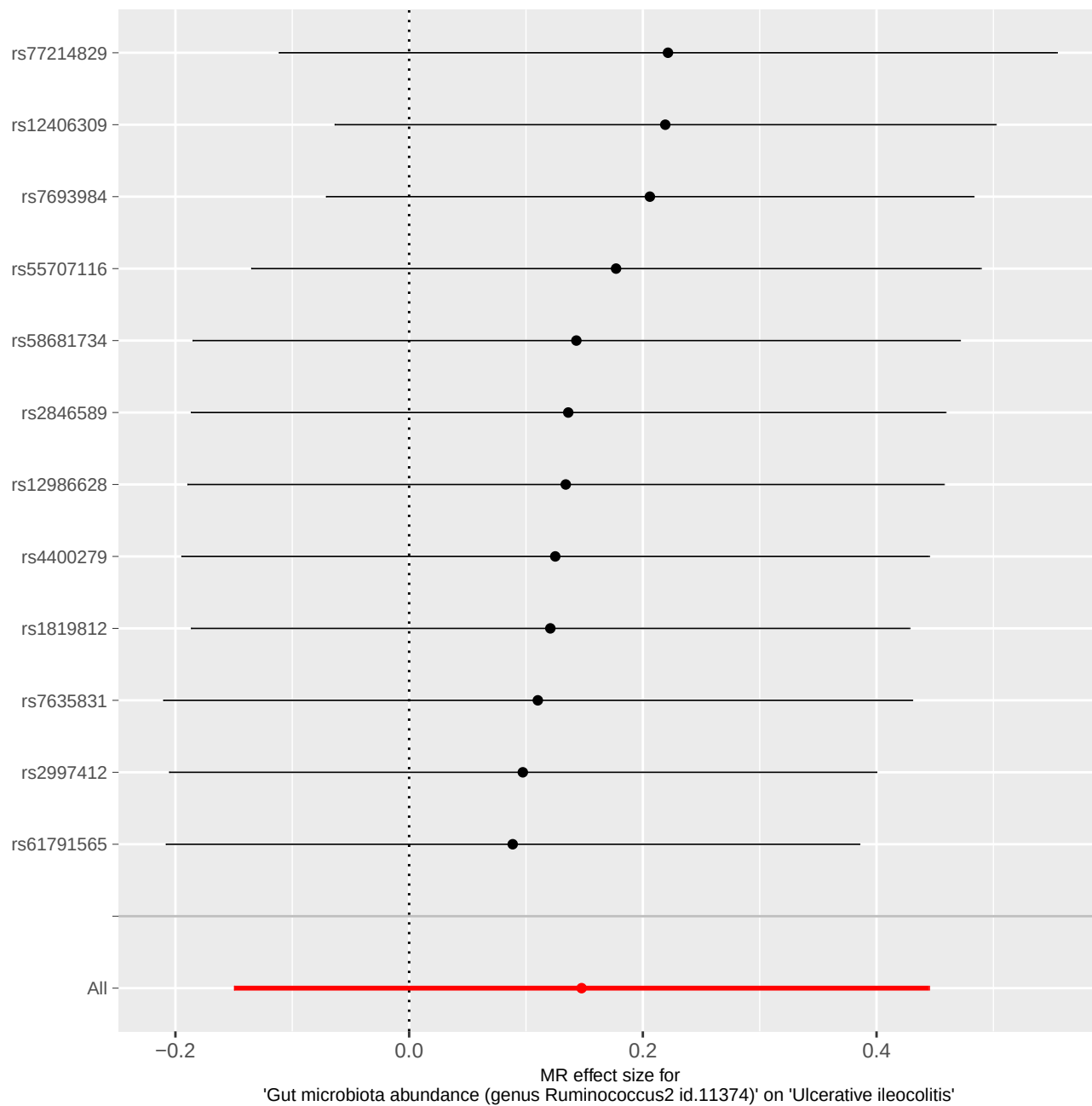


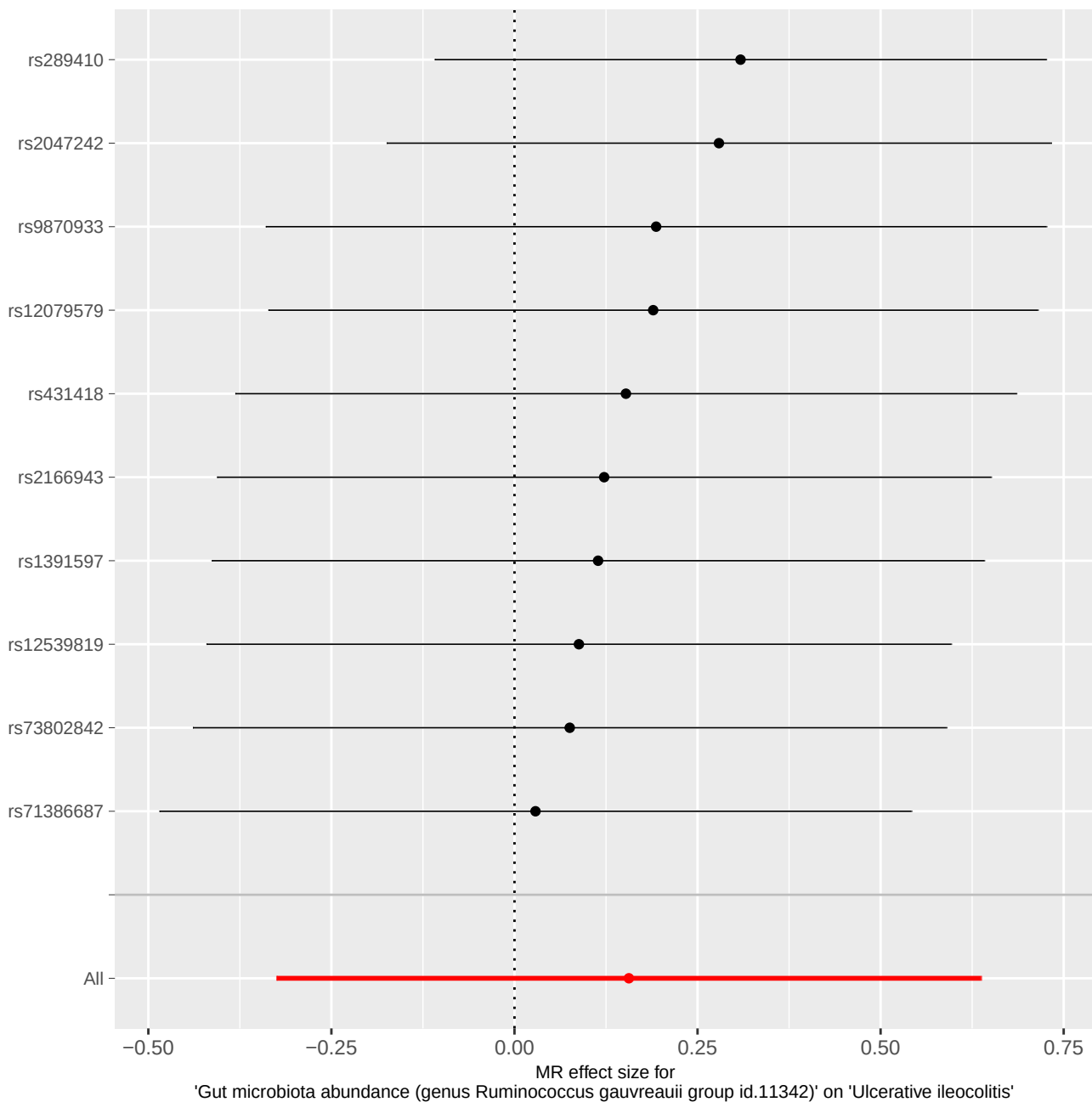


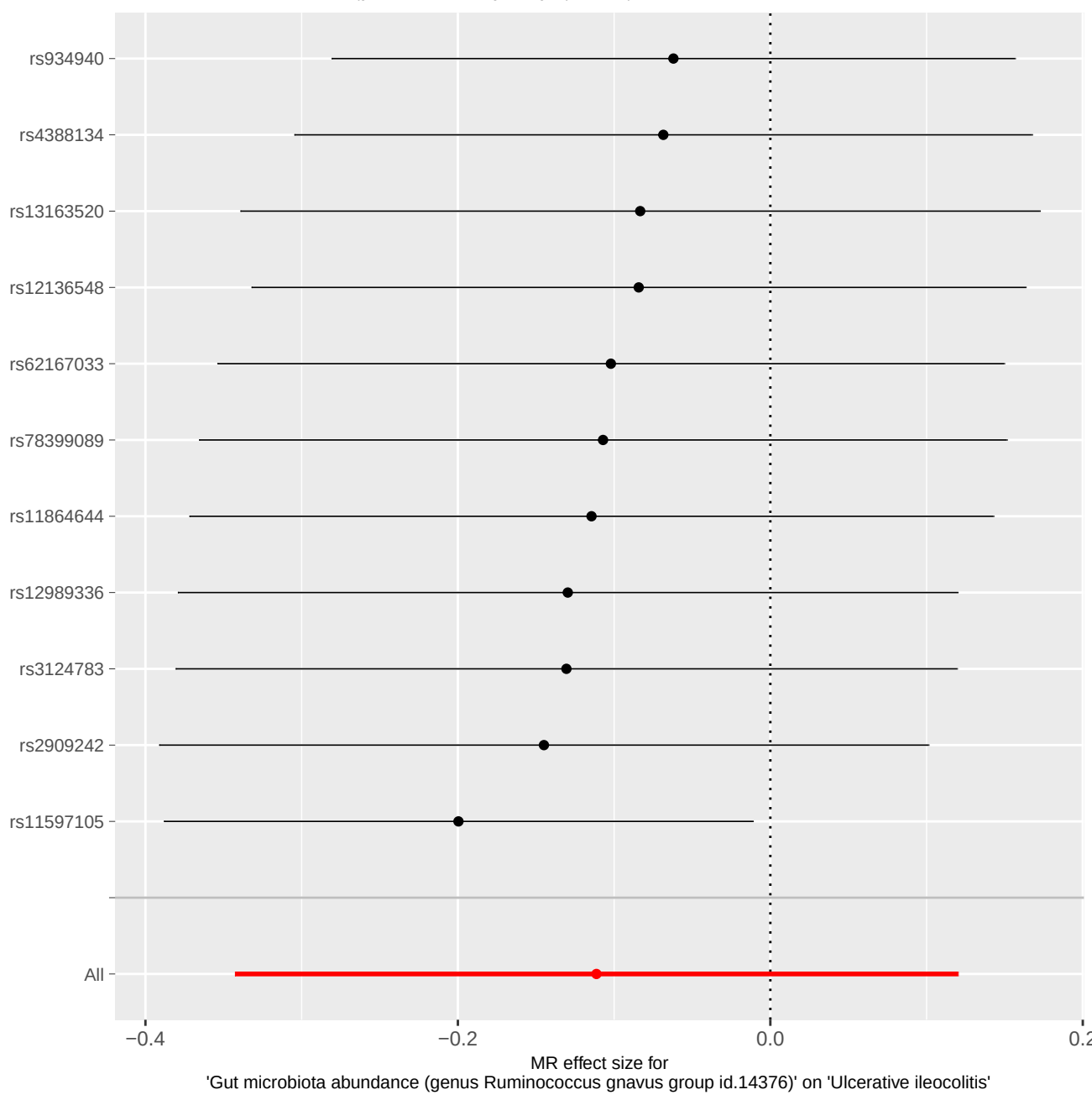


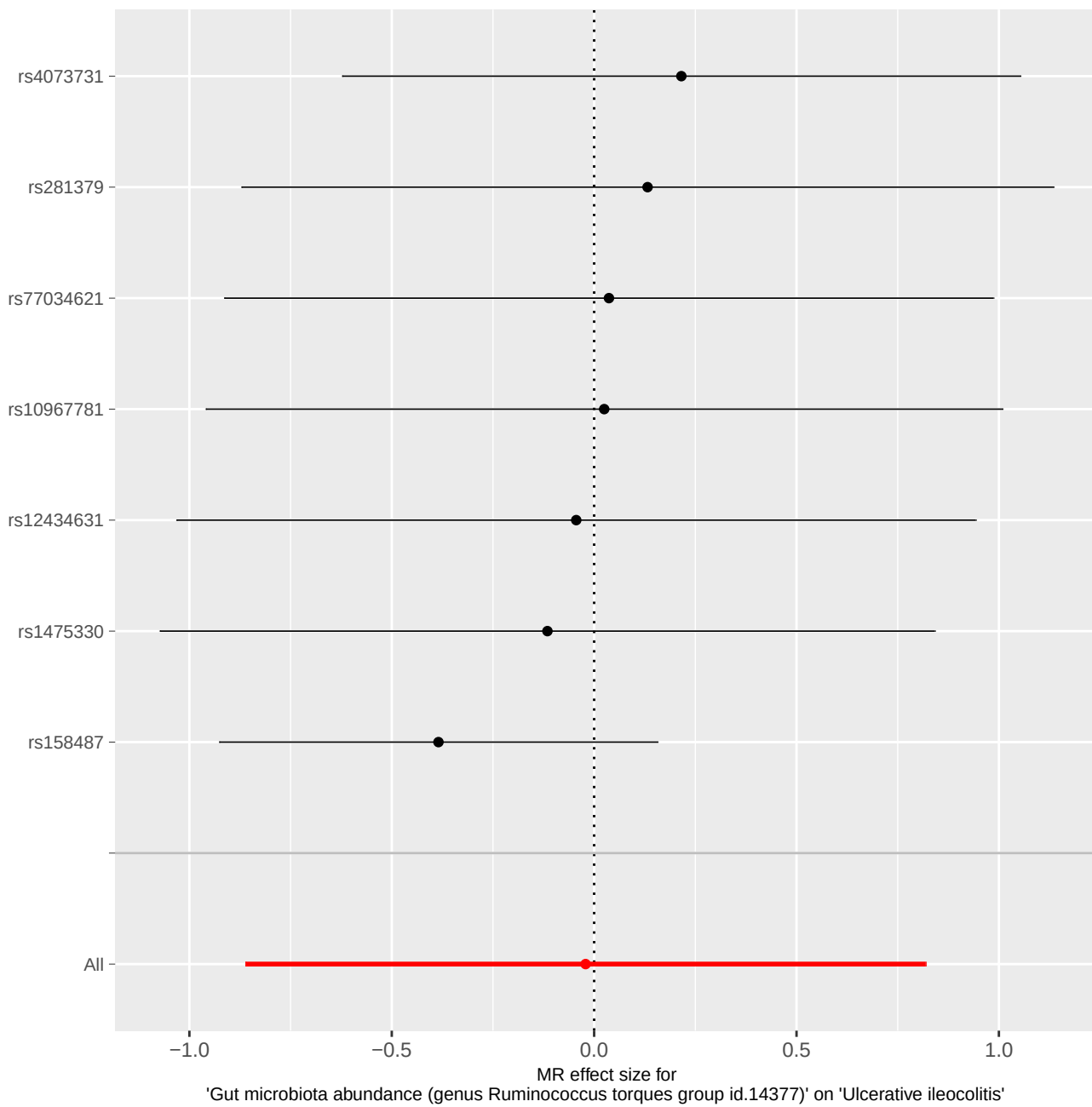


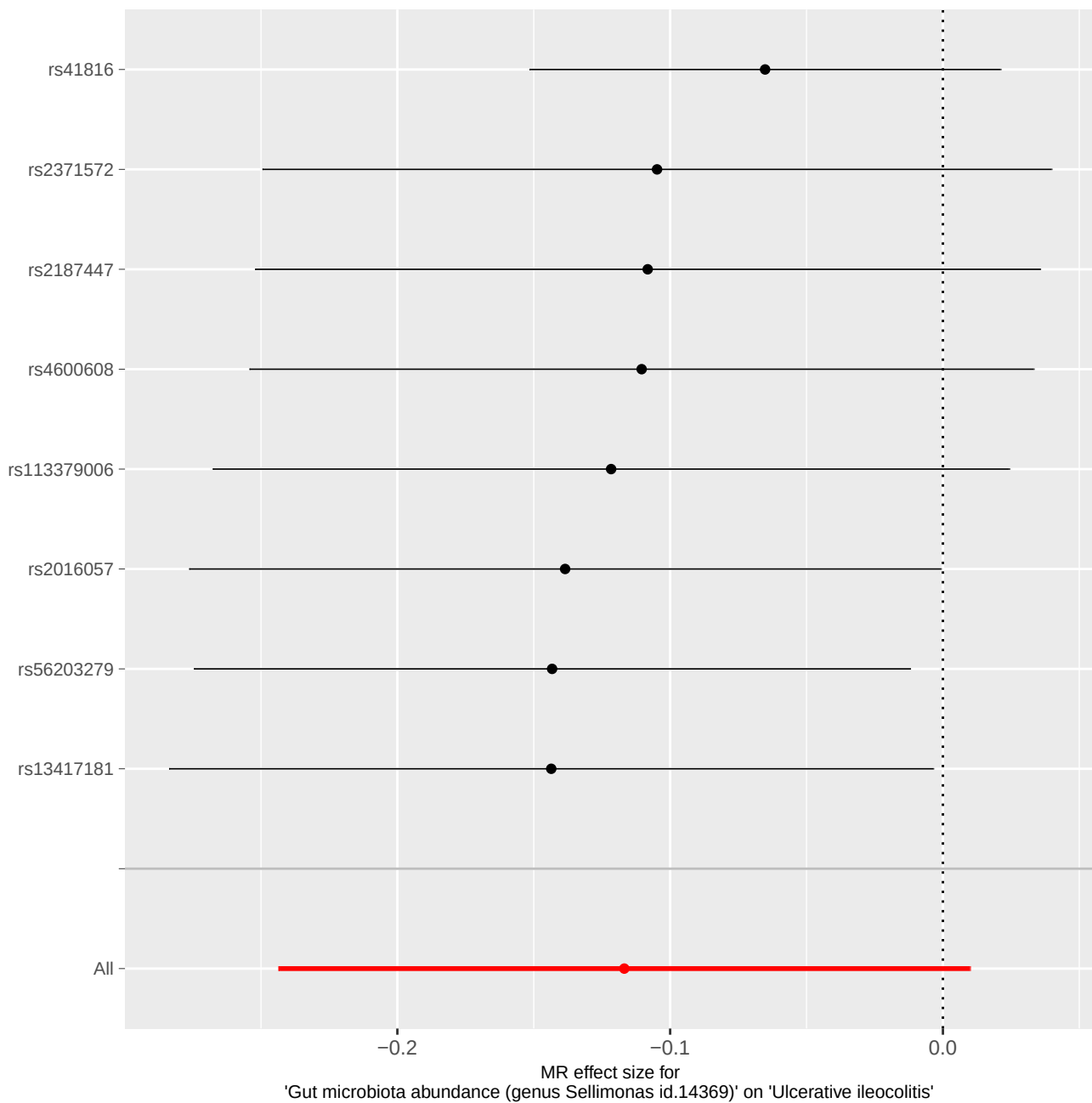
Batch 1187 : Gut microbiota abundance (genus Ruminococcus2 id.11374) on Ulcerative ileocolitis

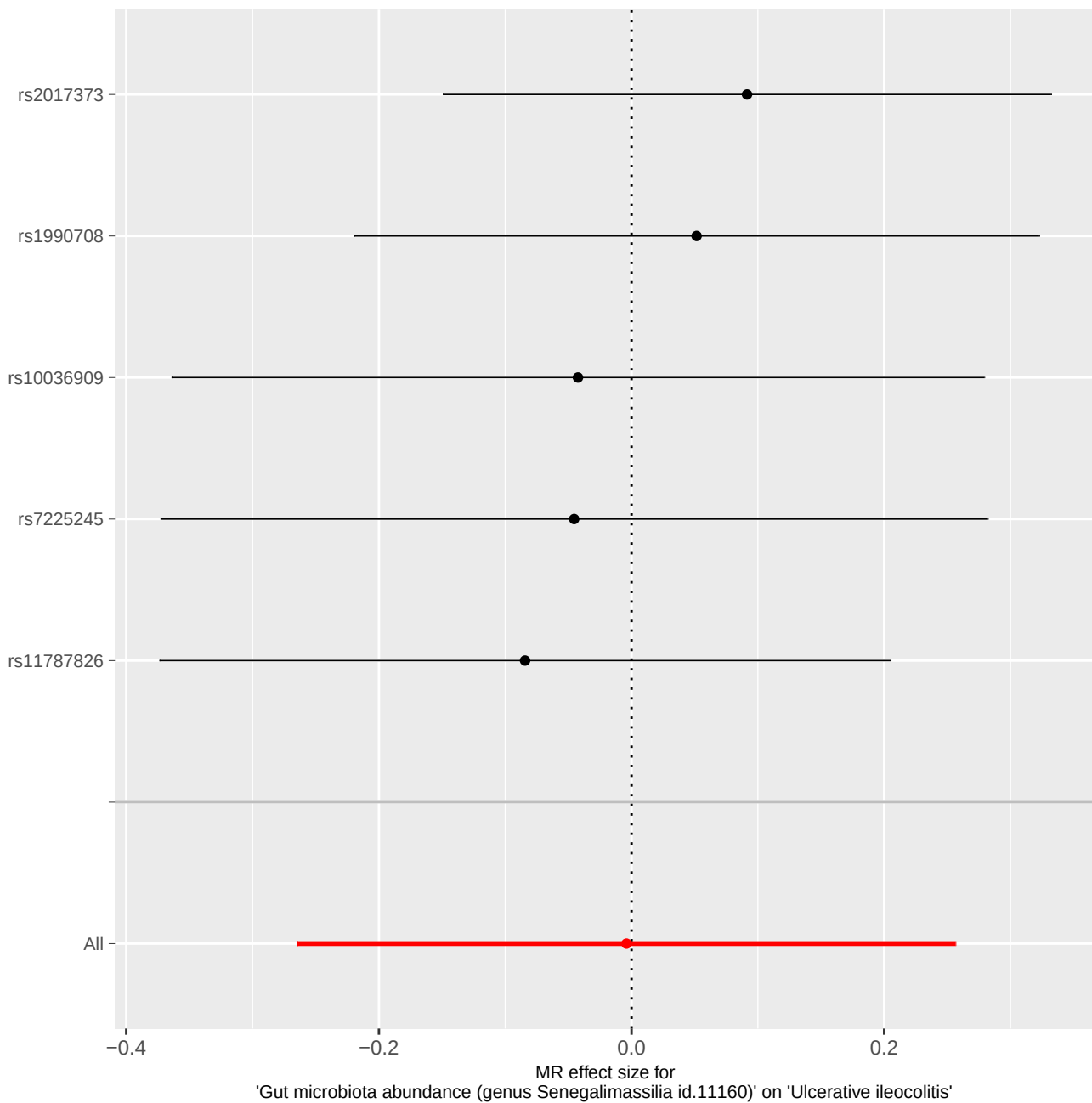


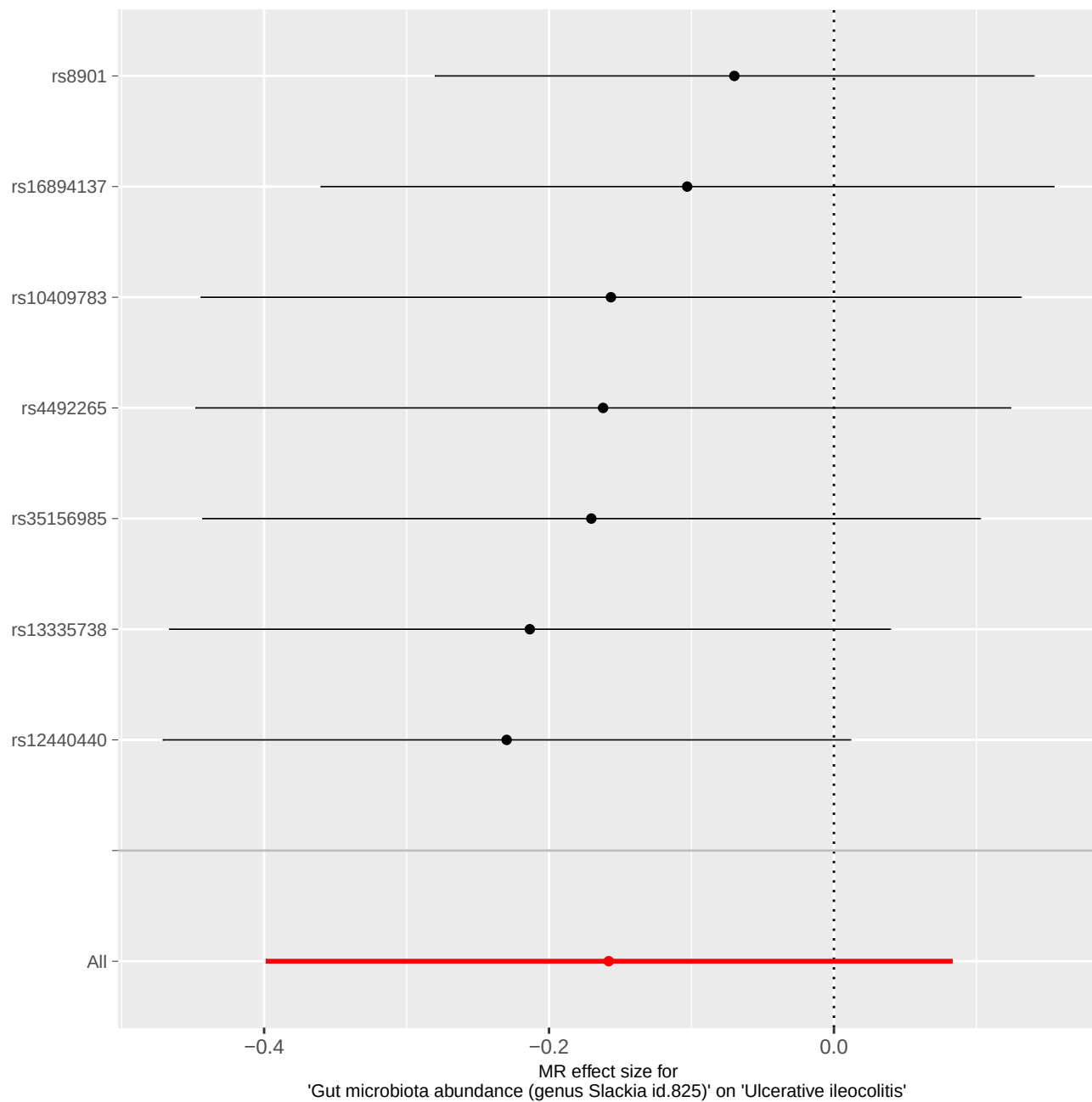


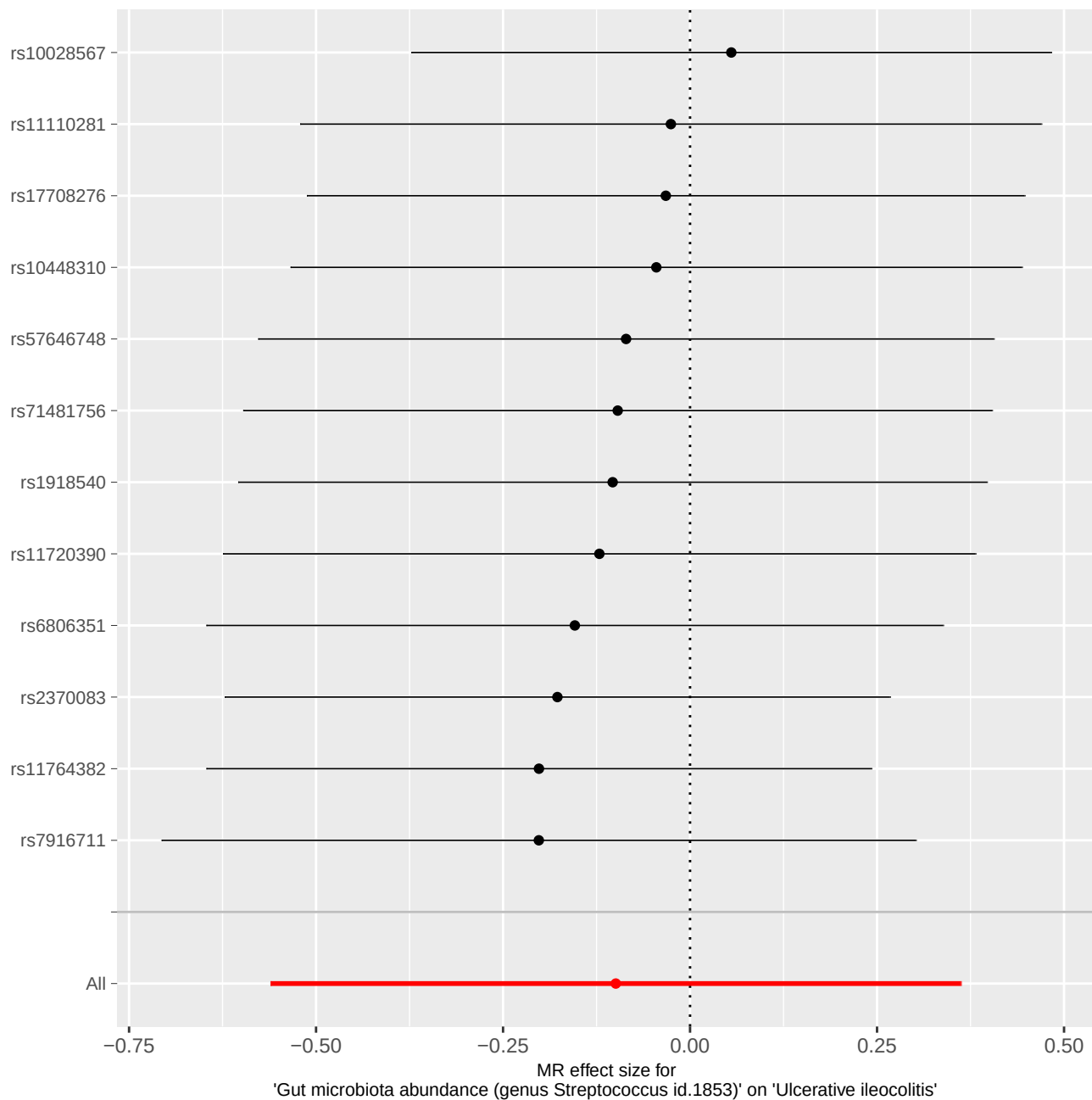


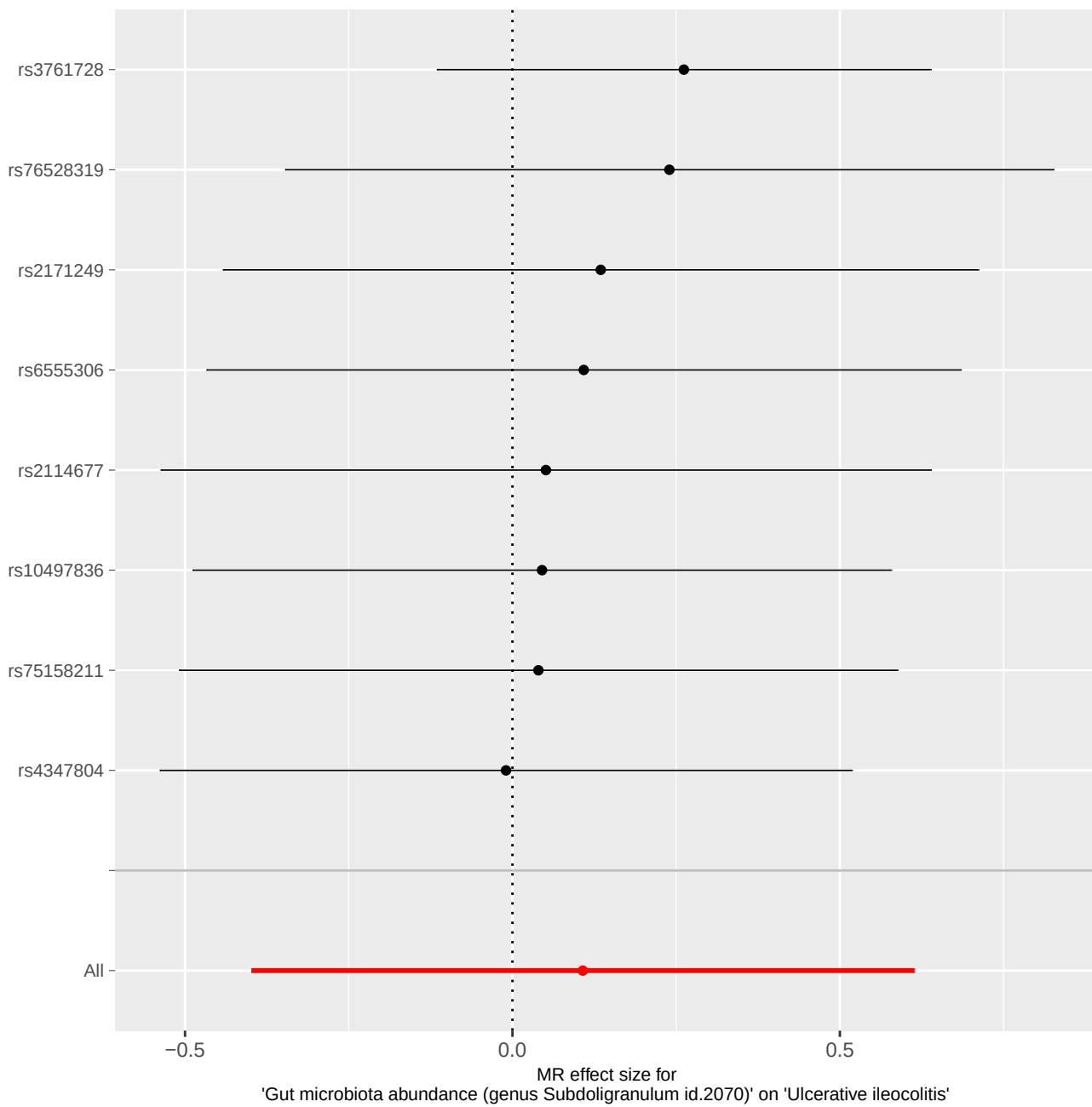


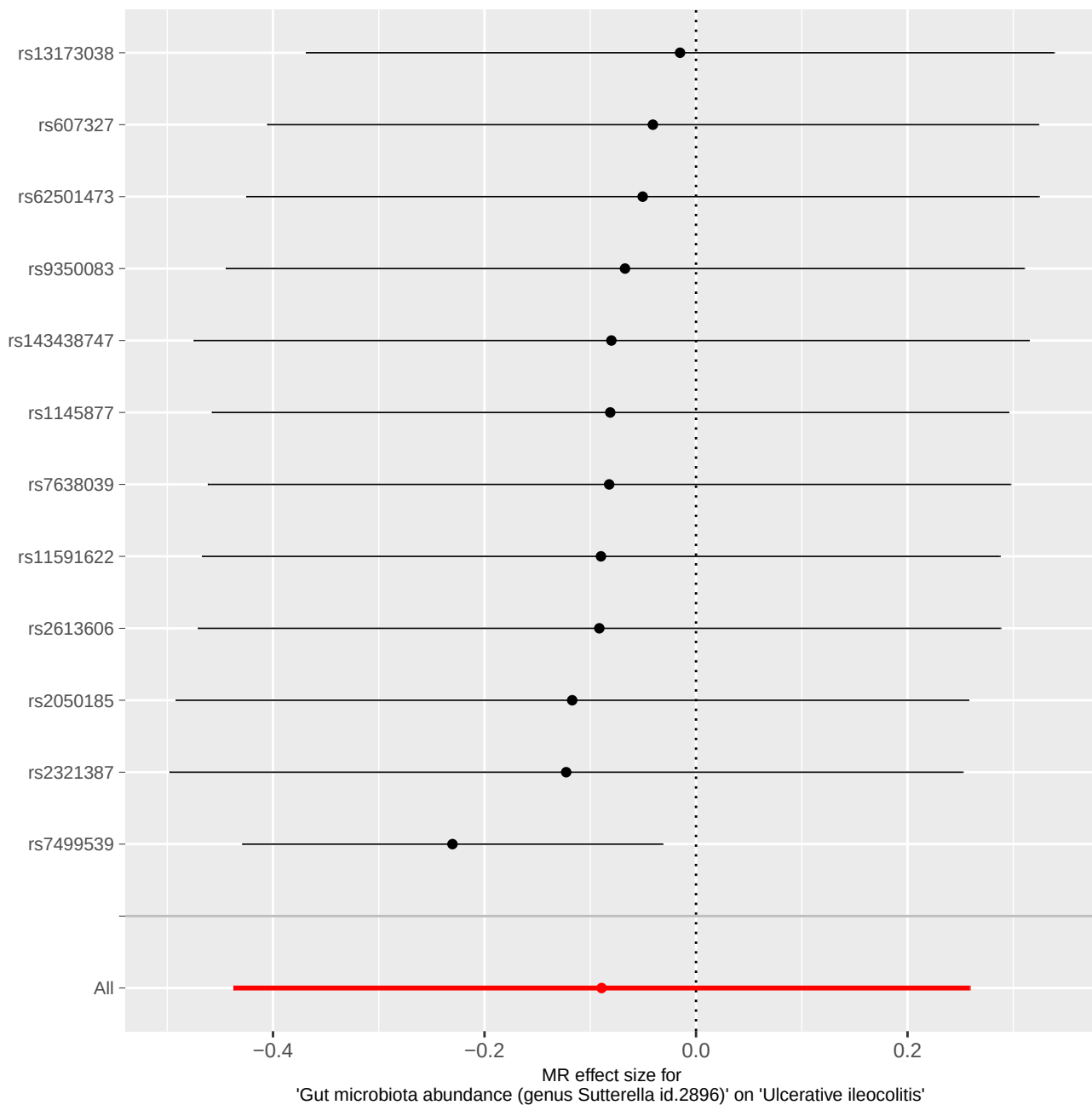


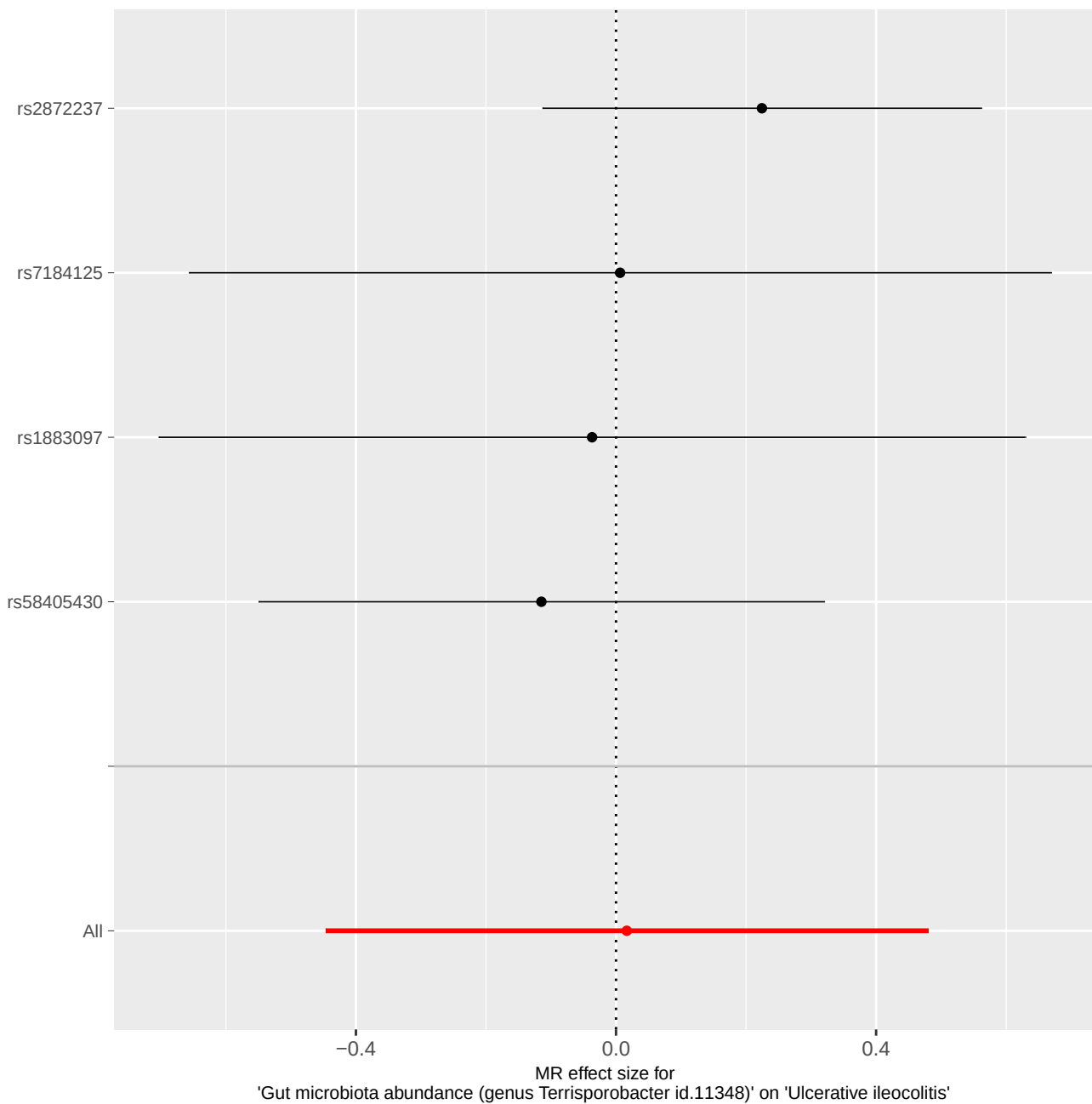


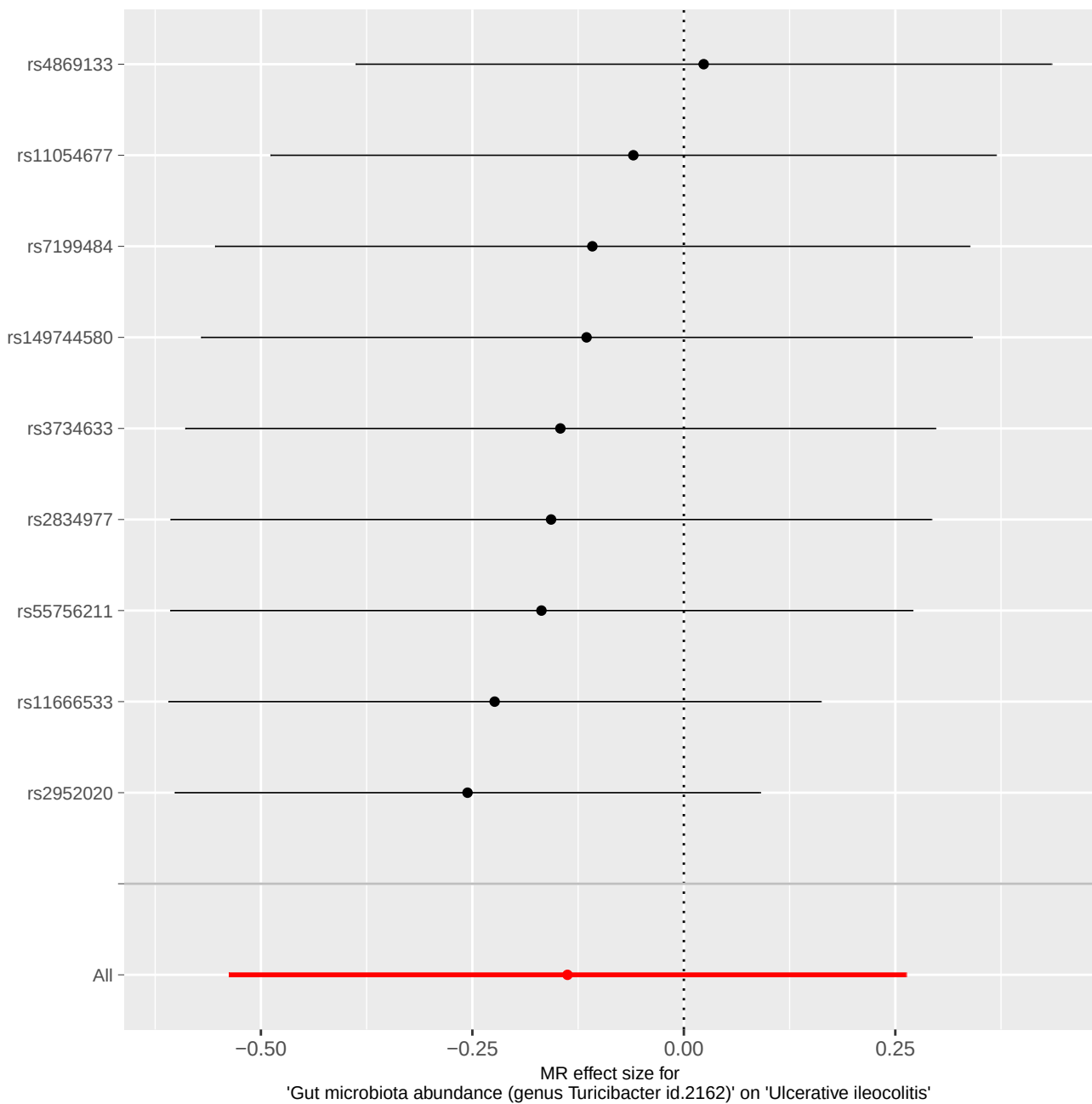


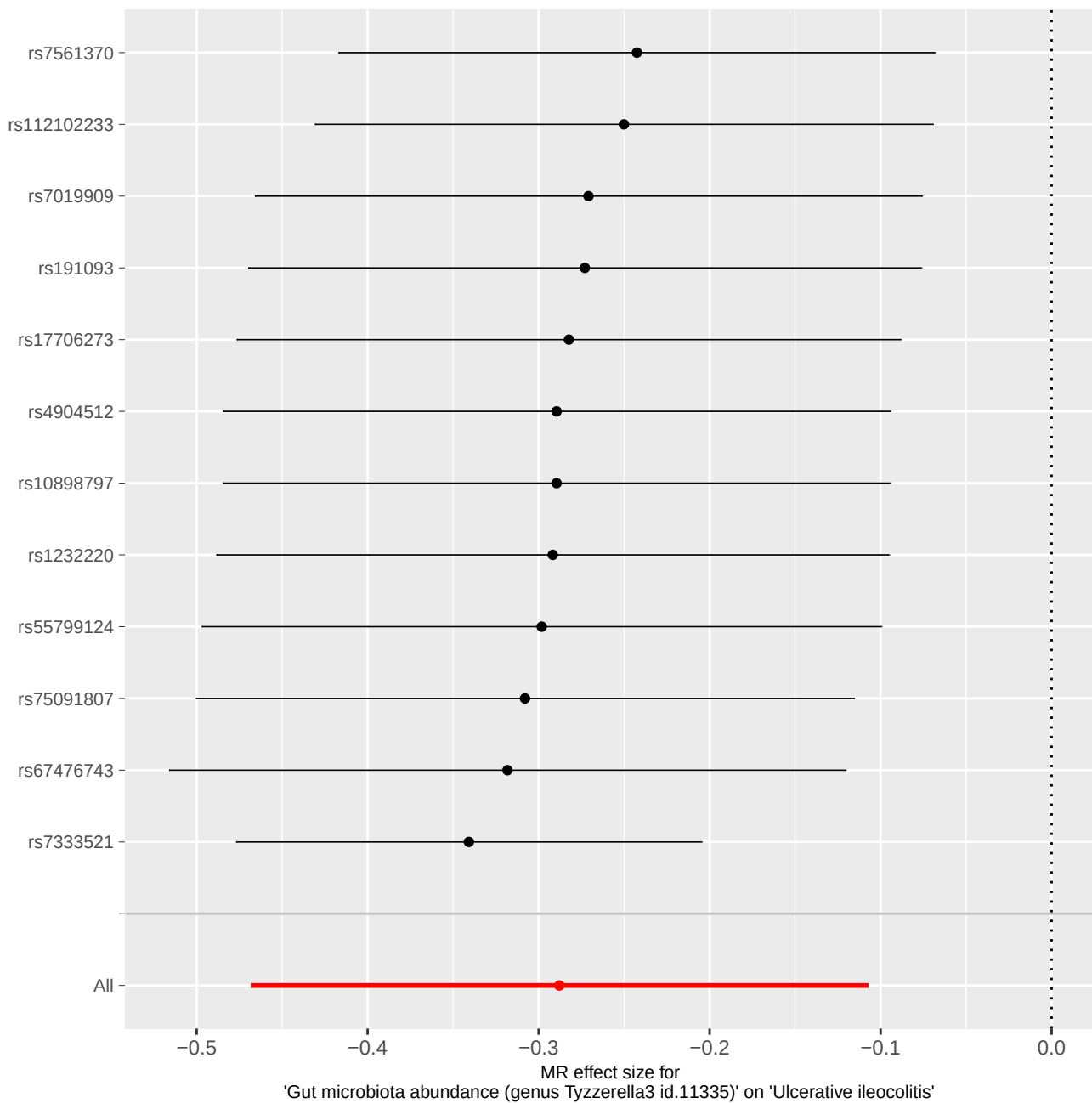


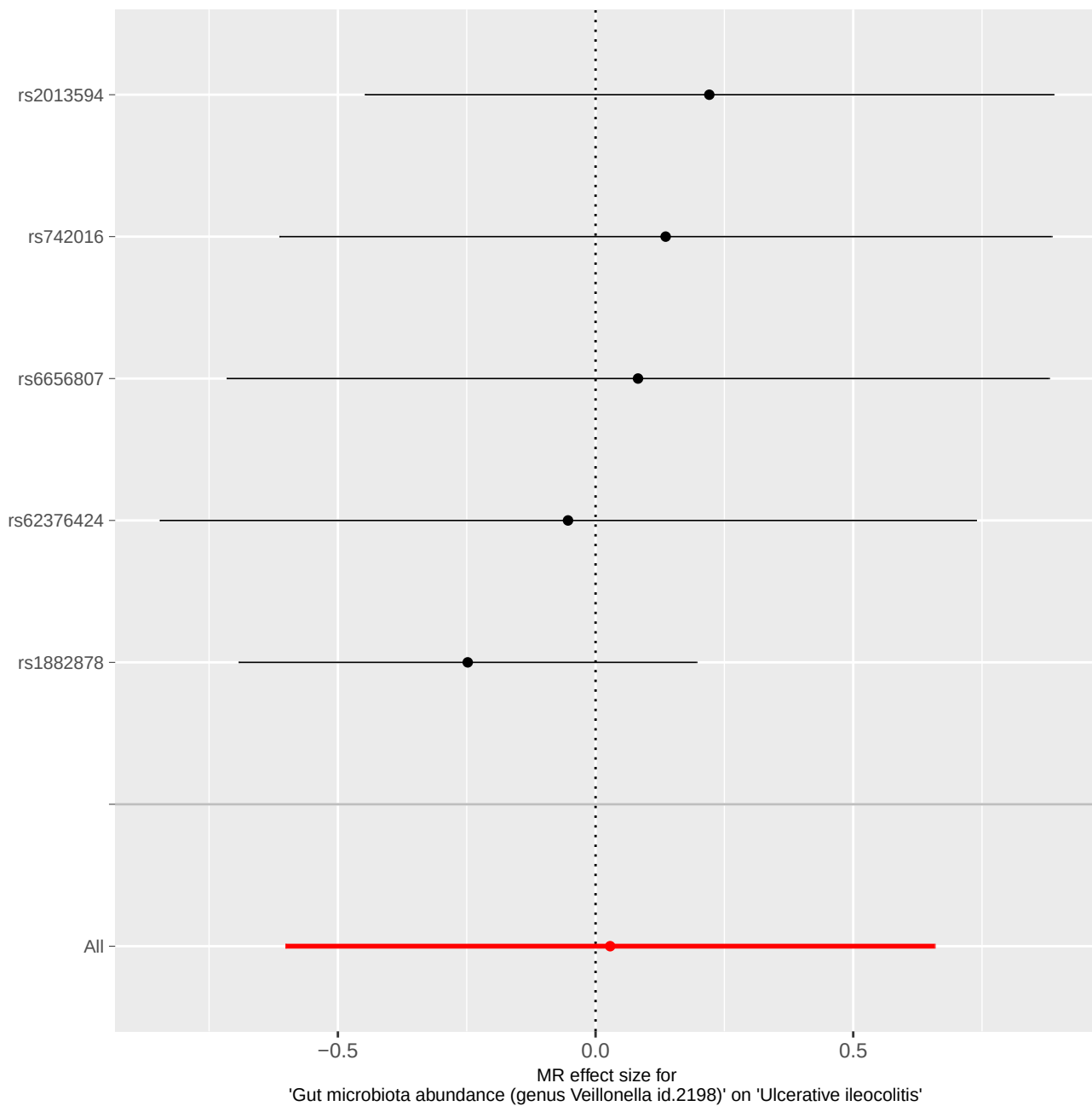


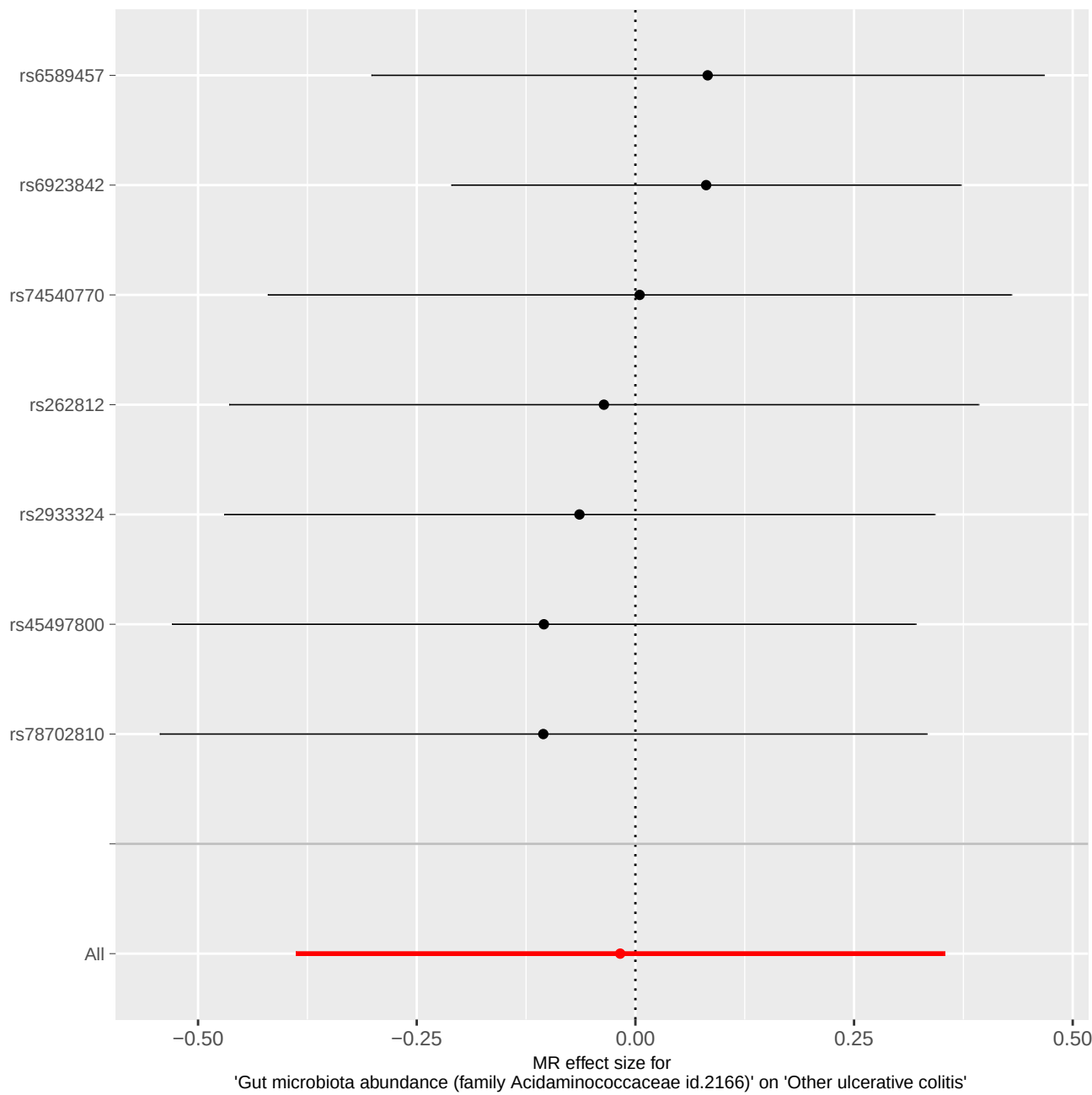


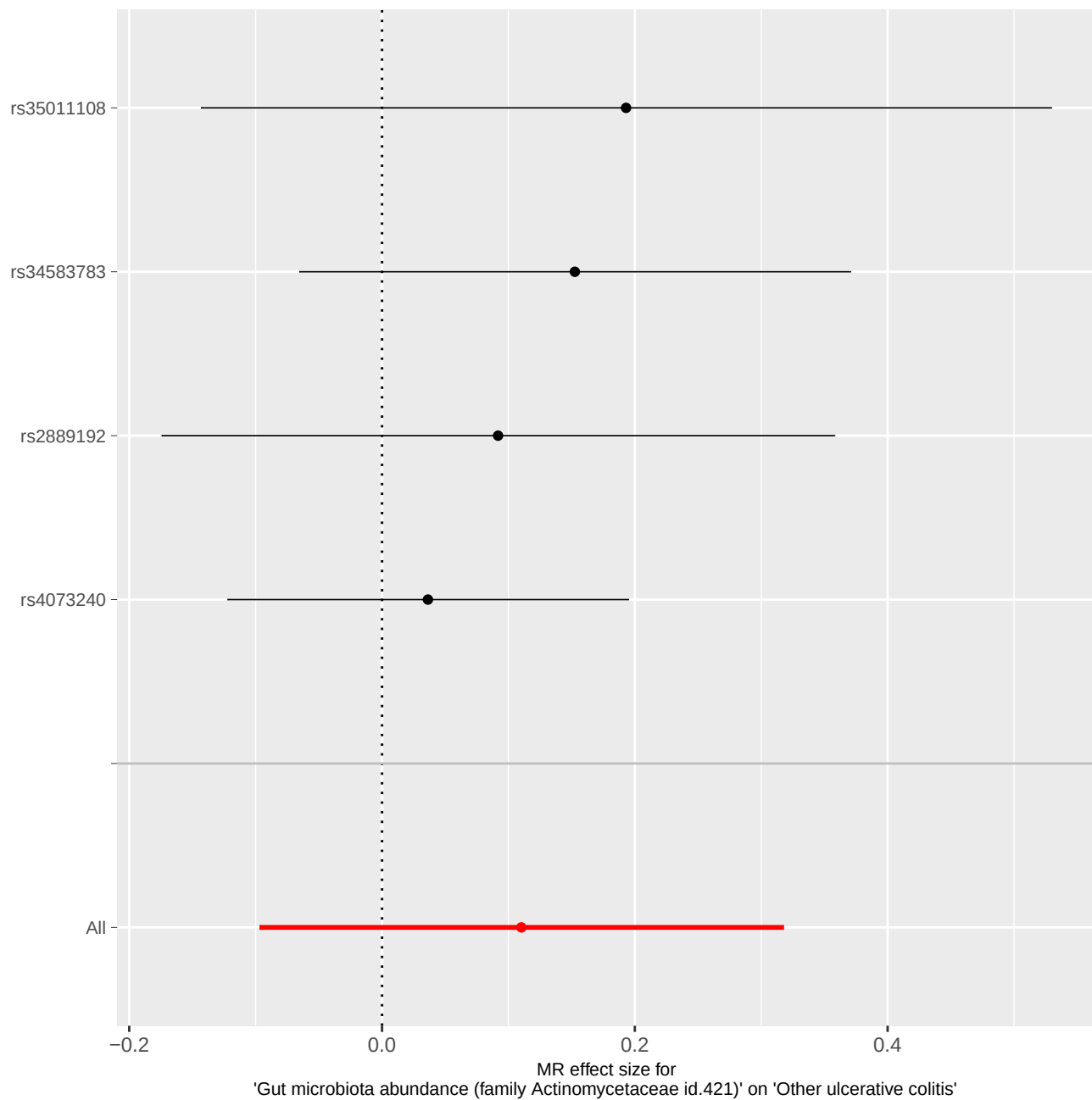


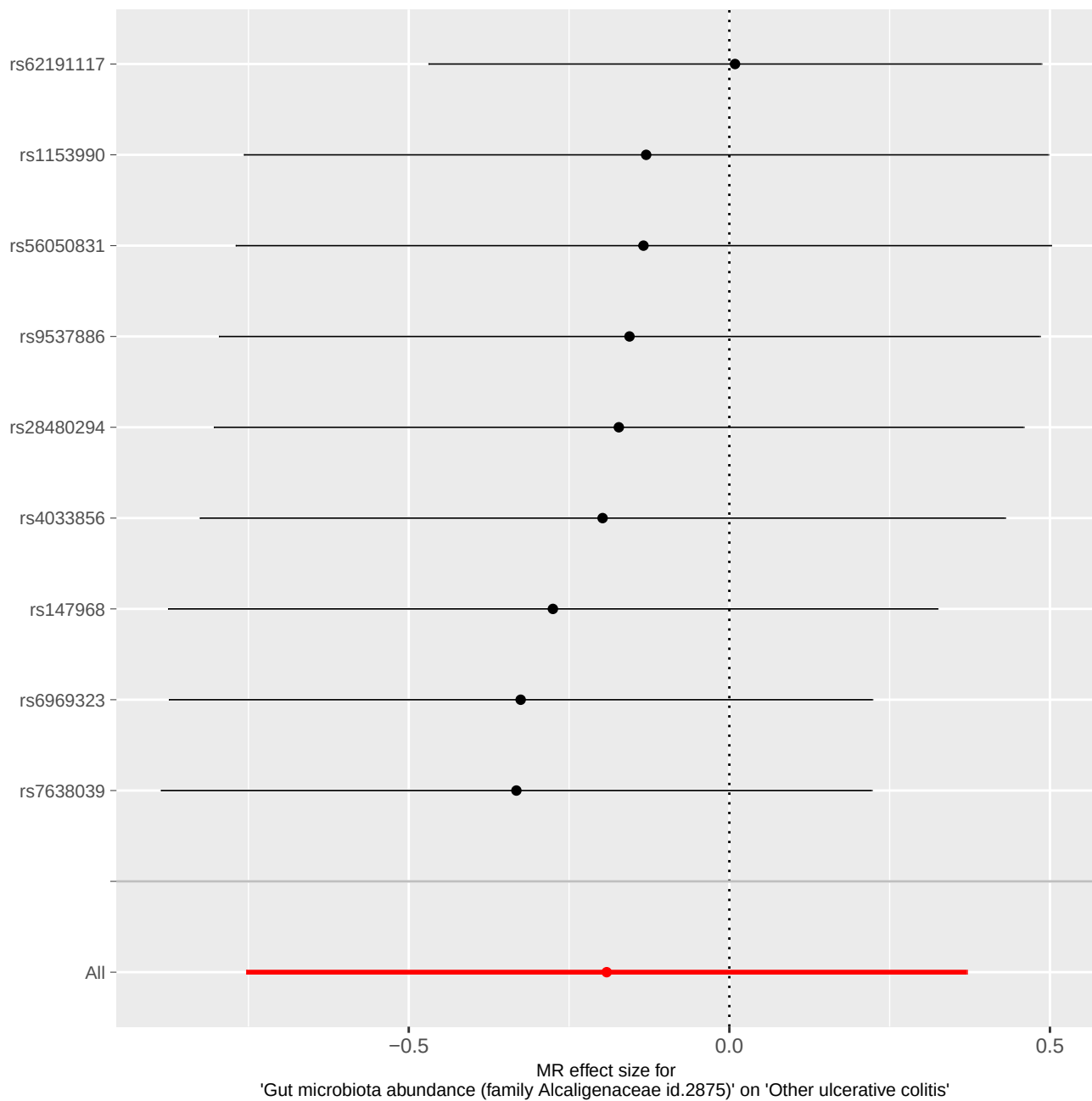


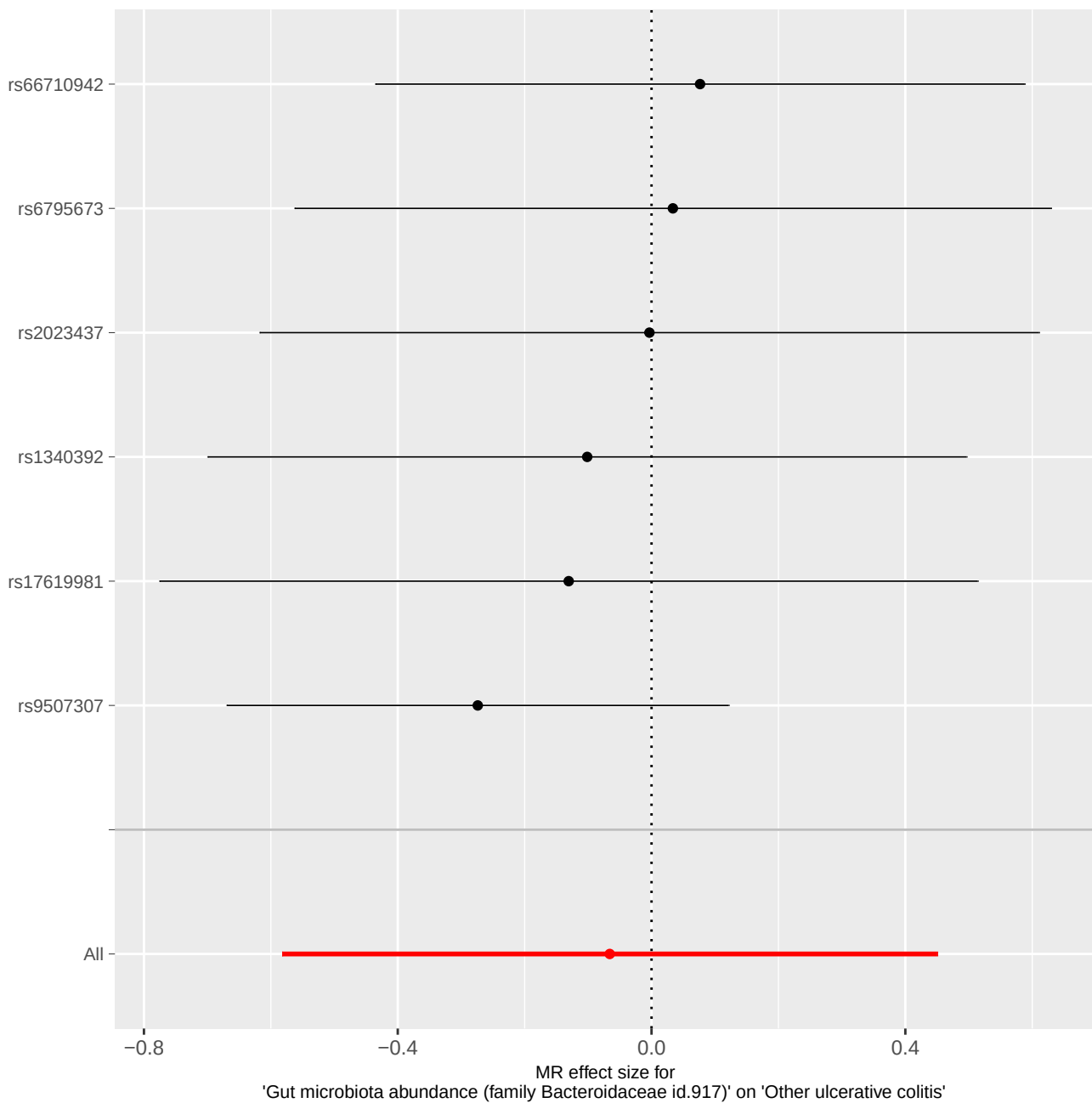


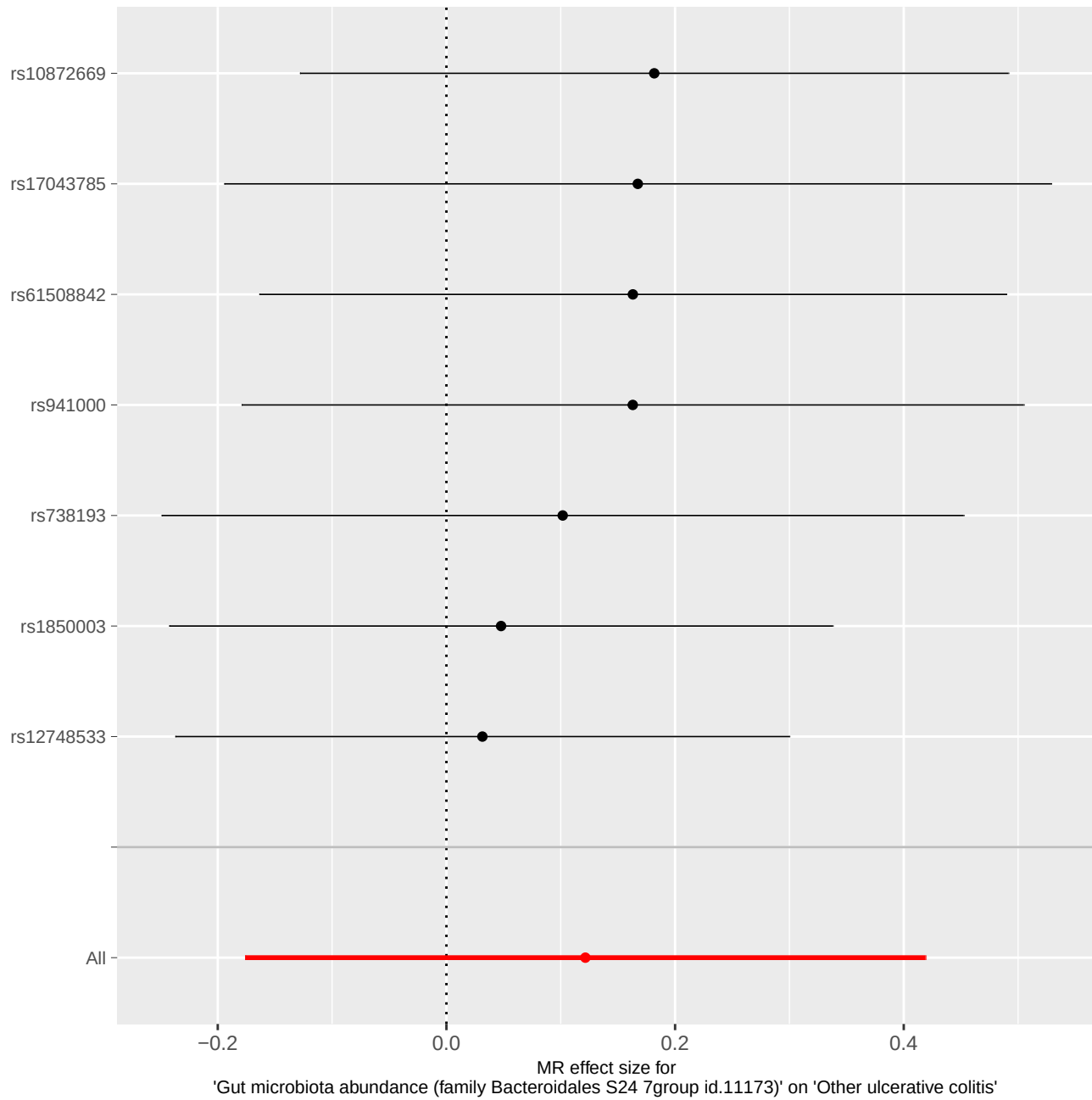


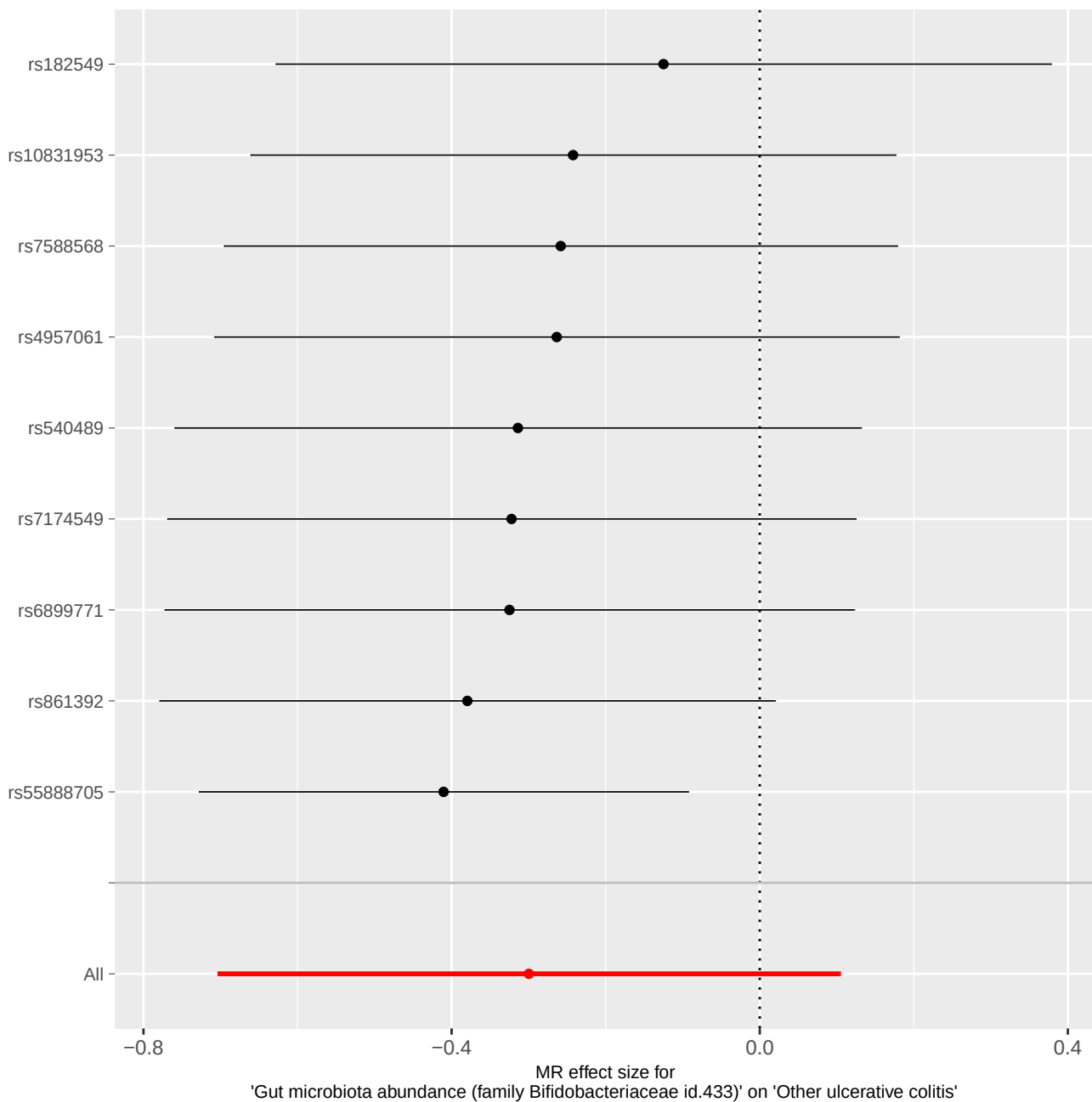


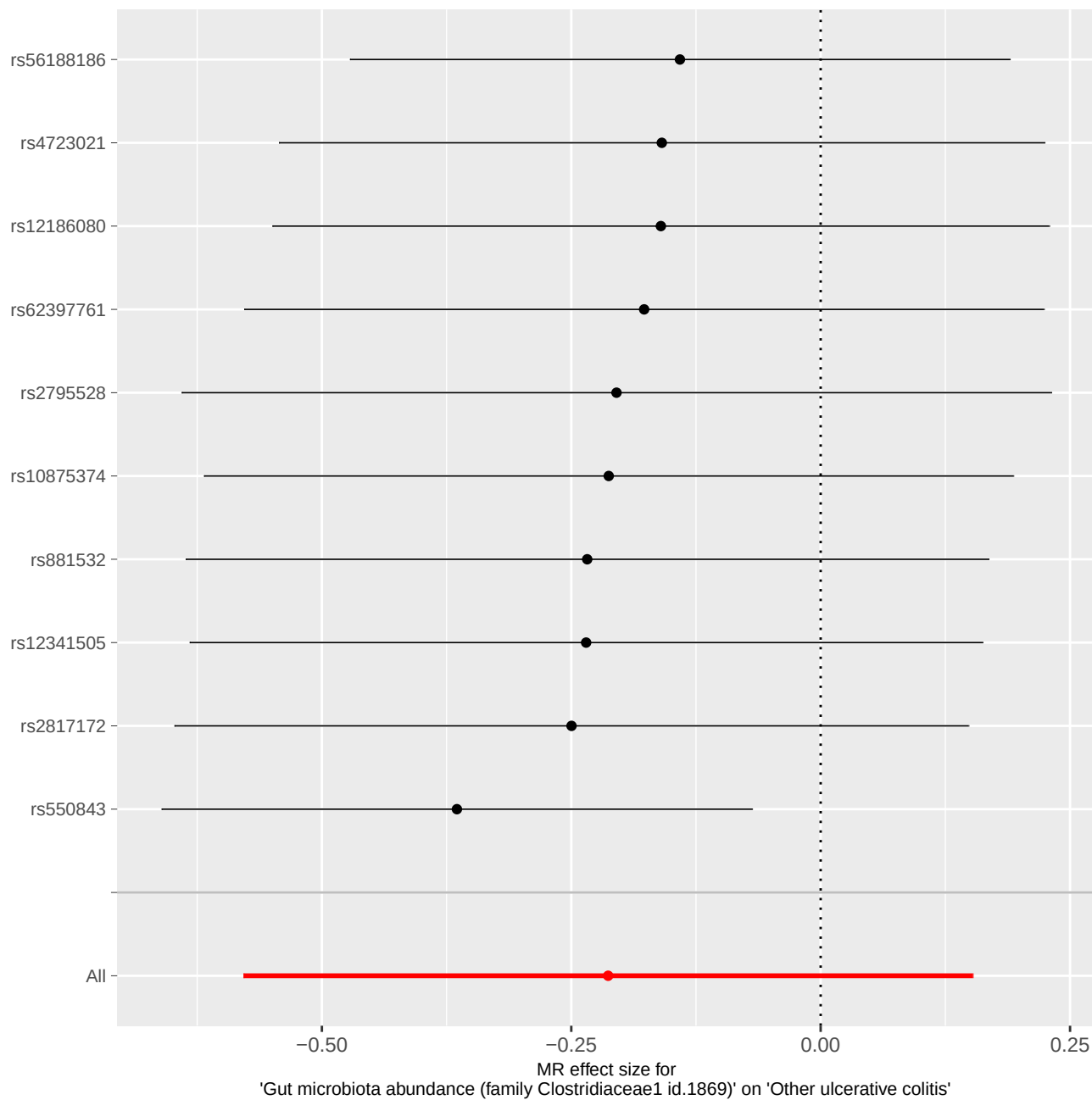


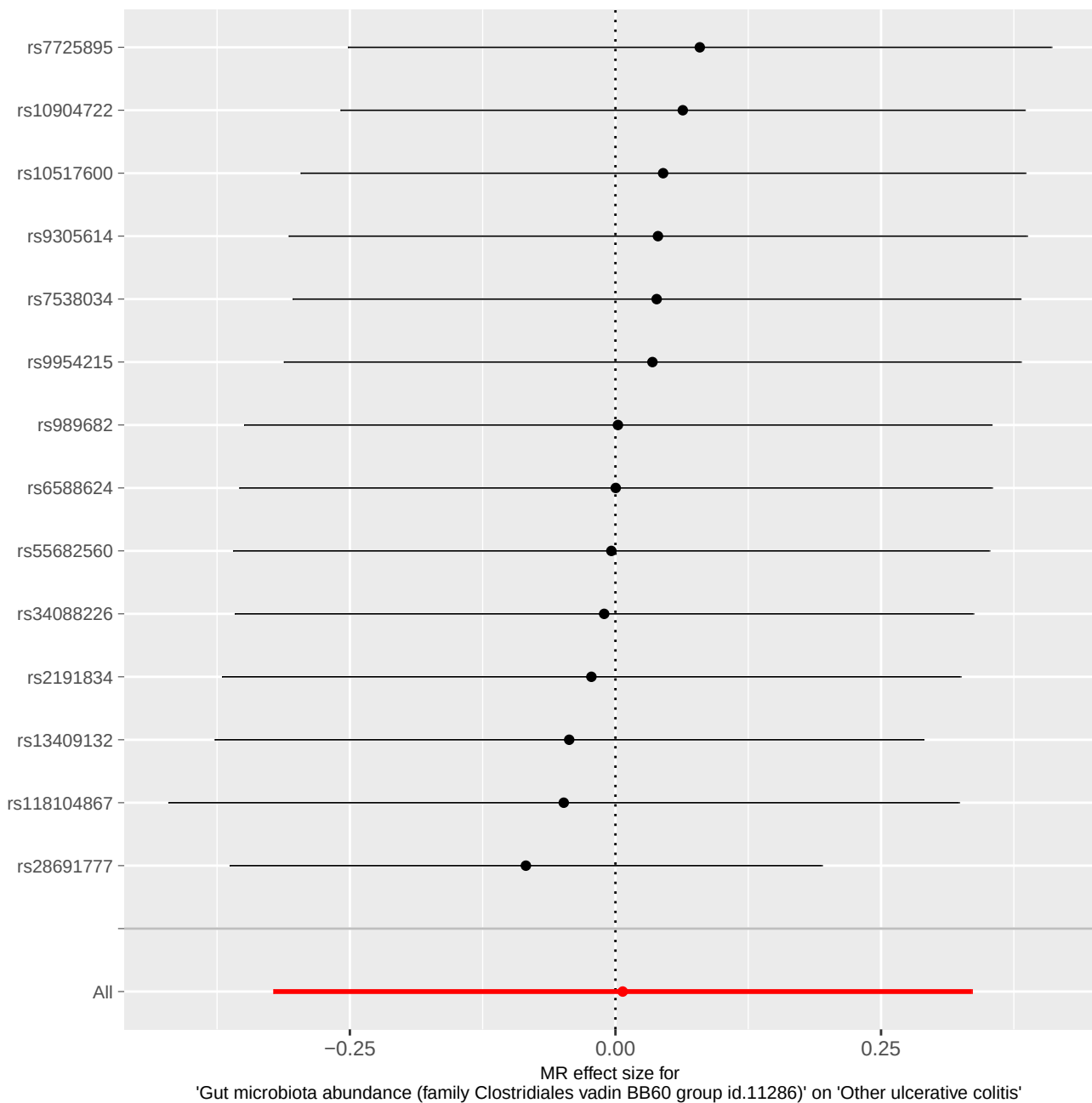


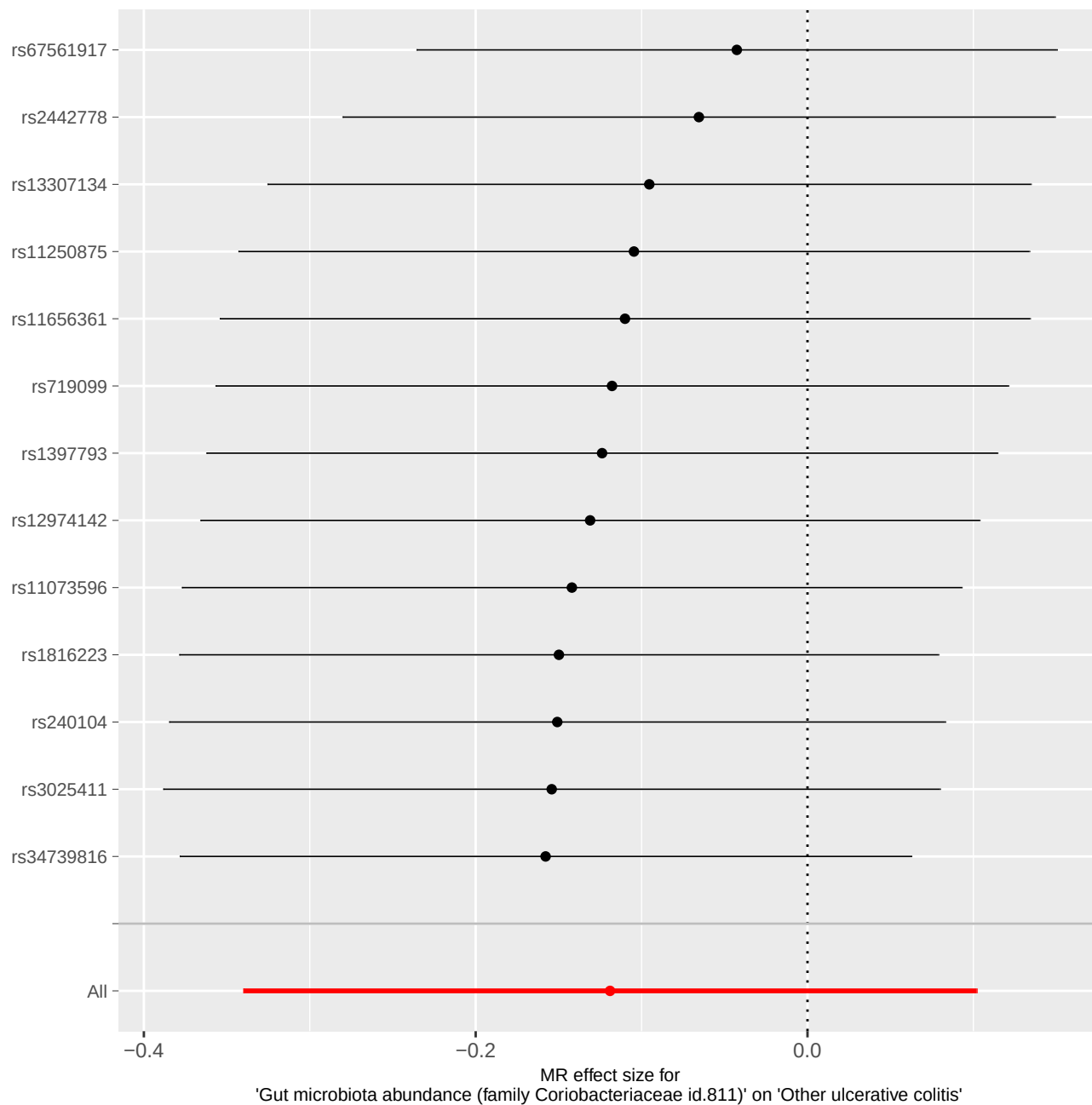


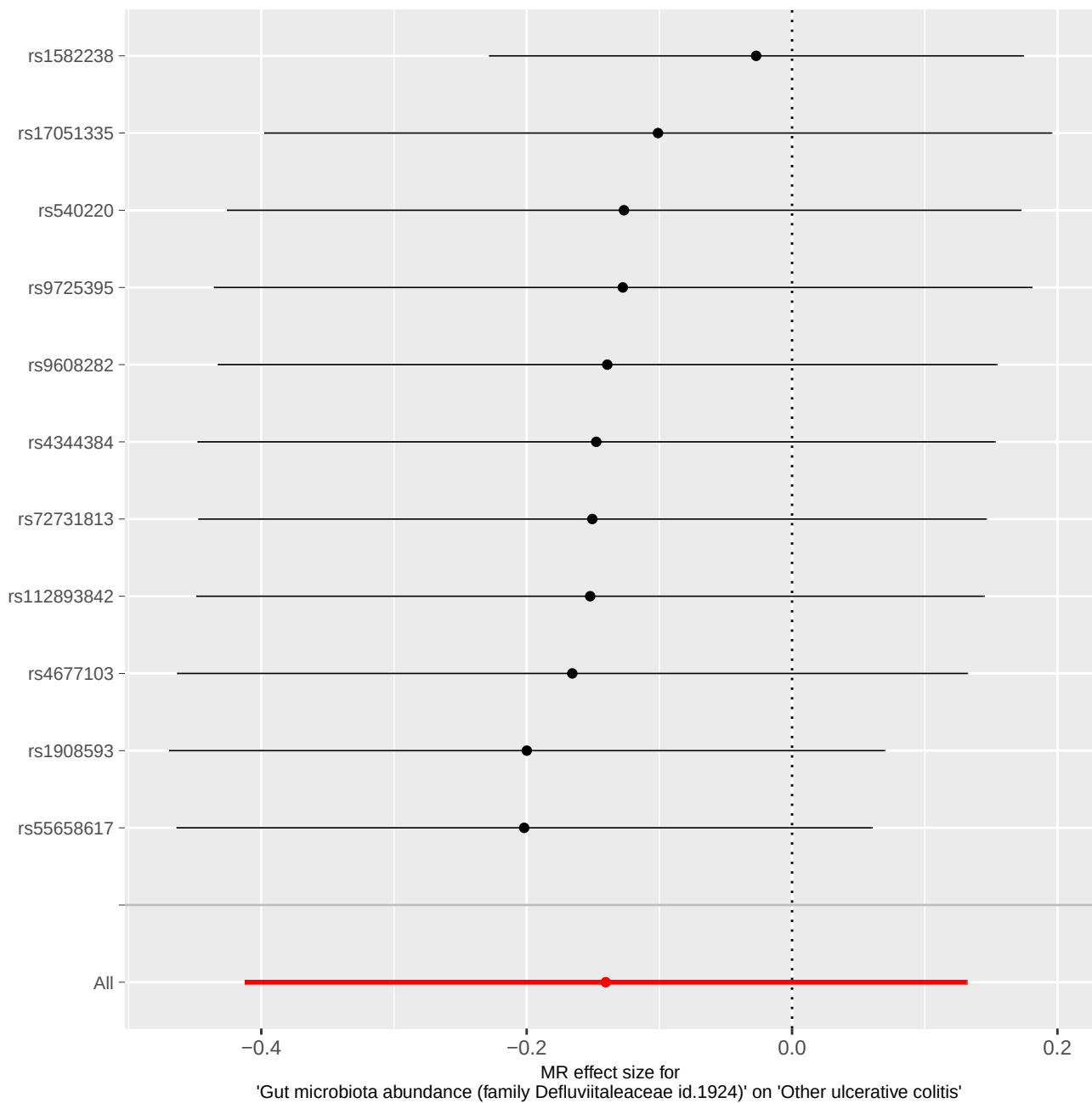


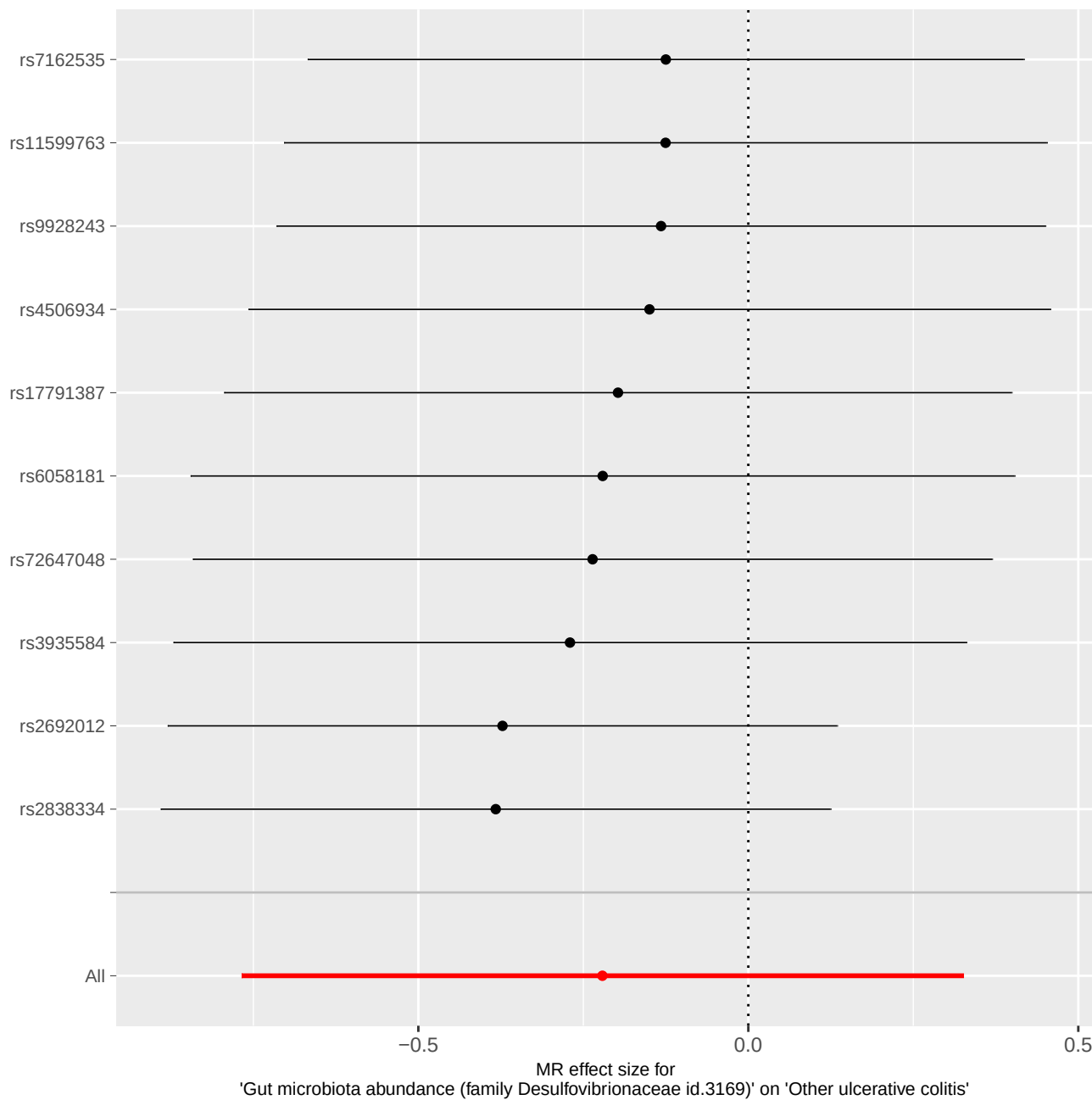


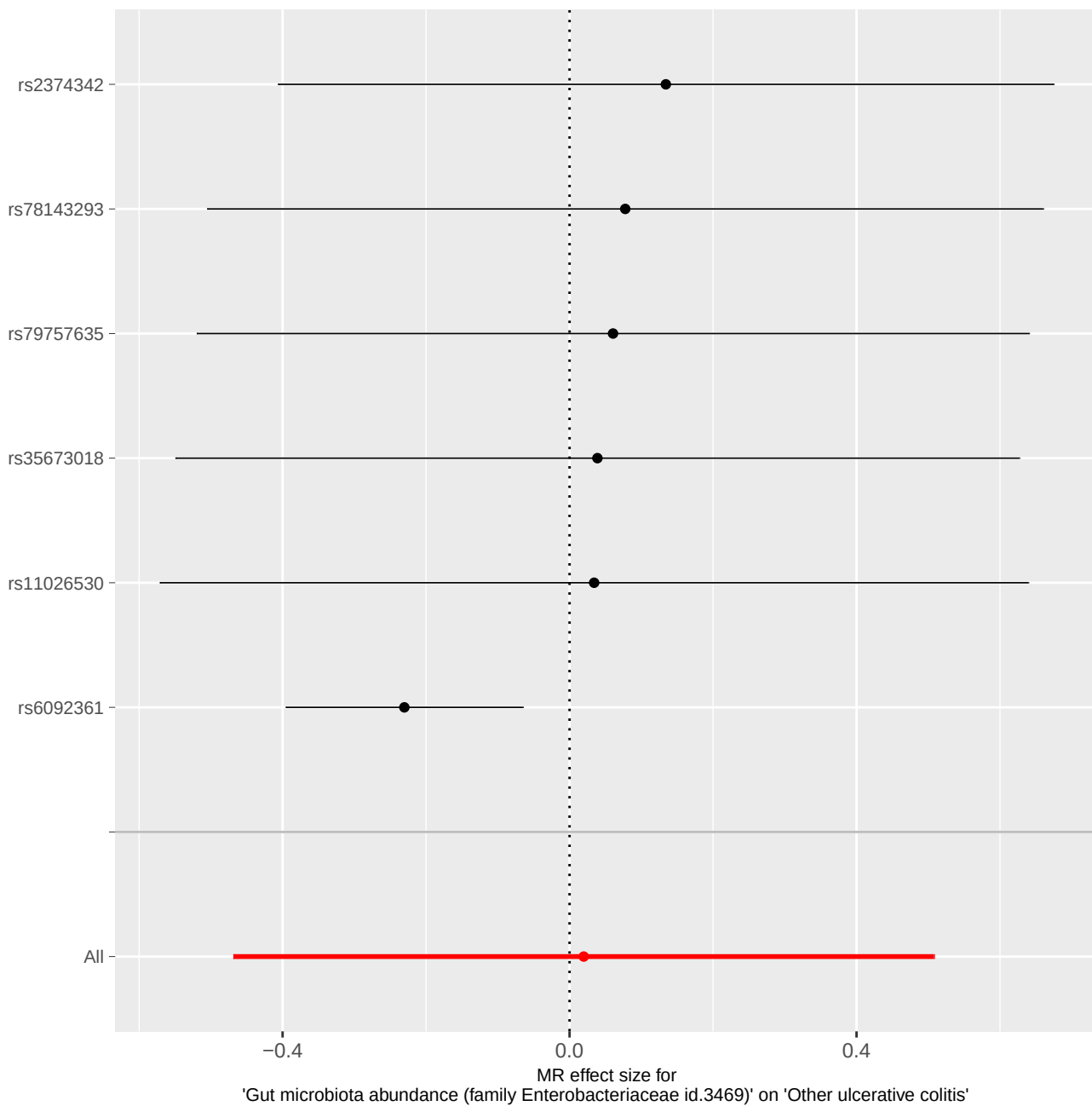


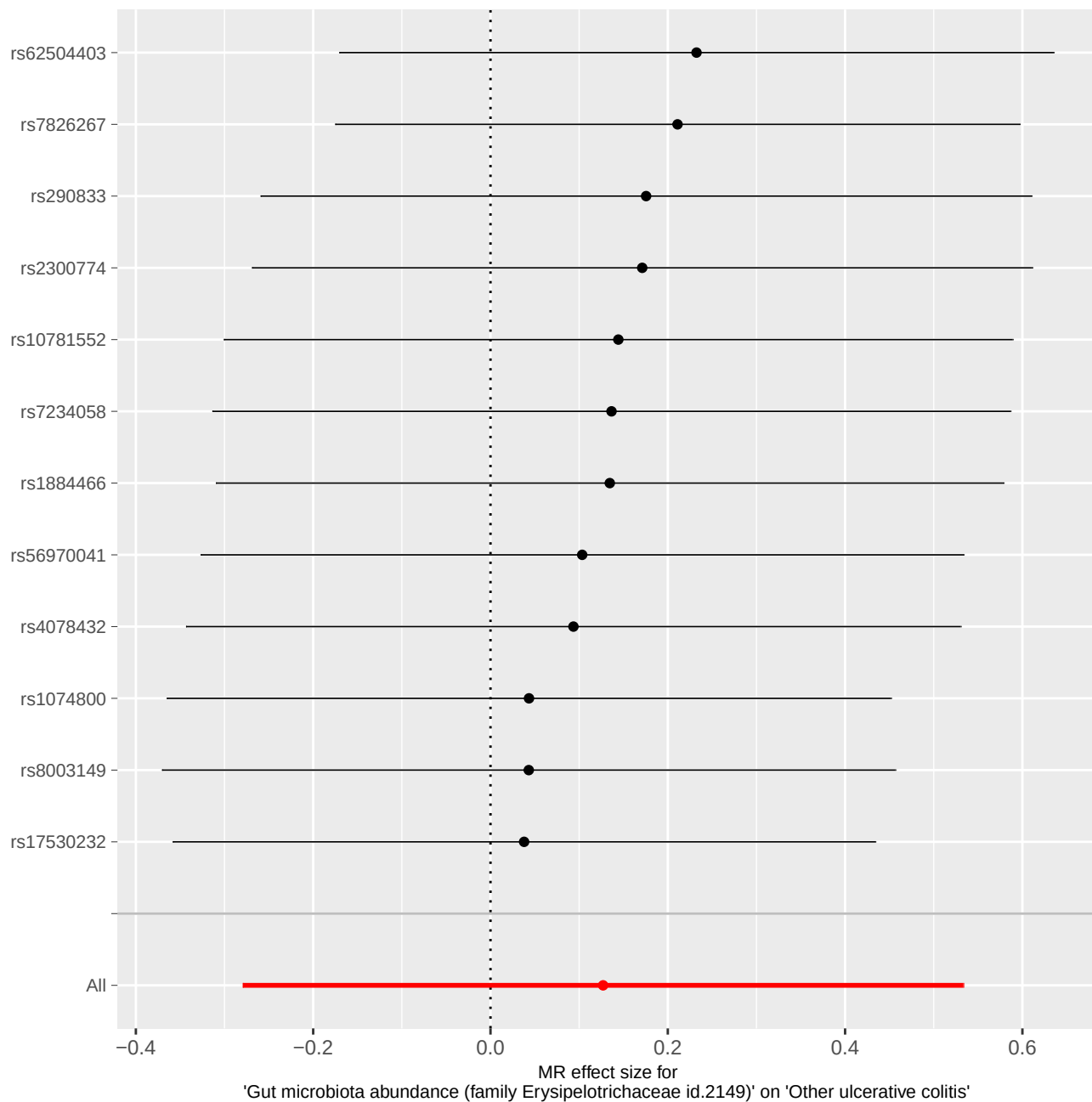




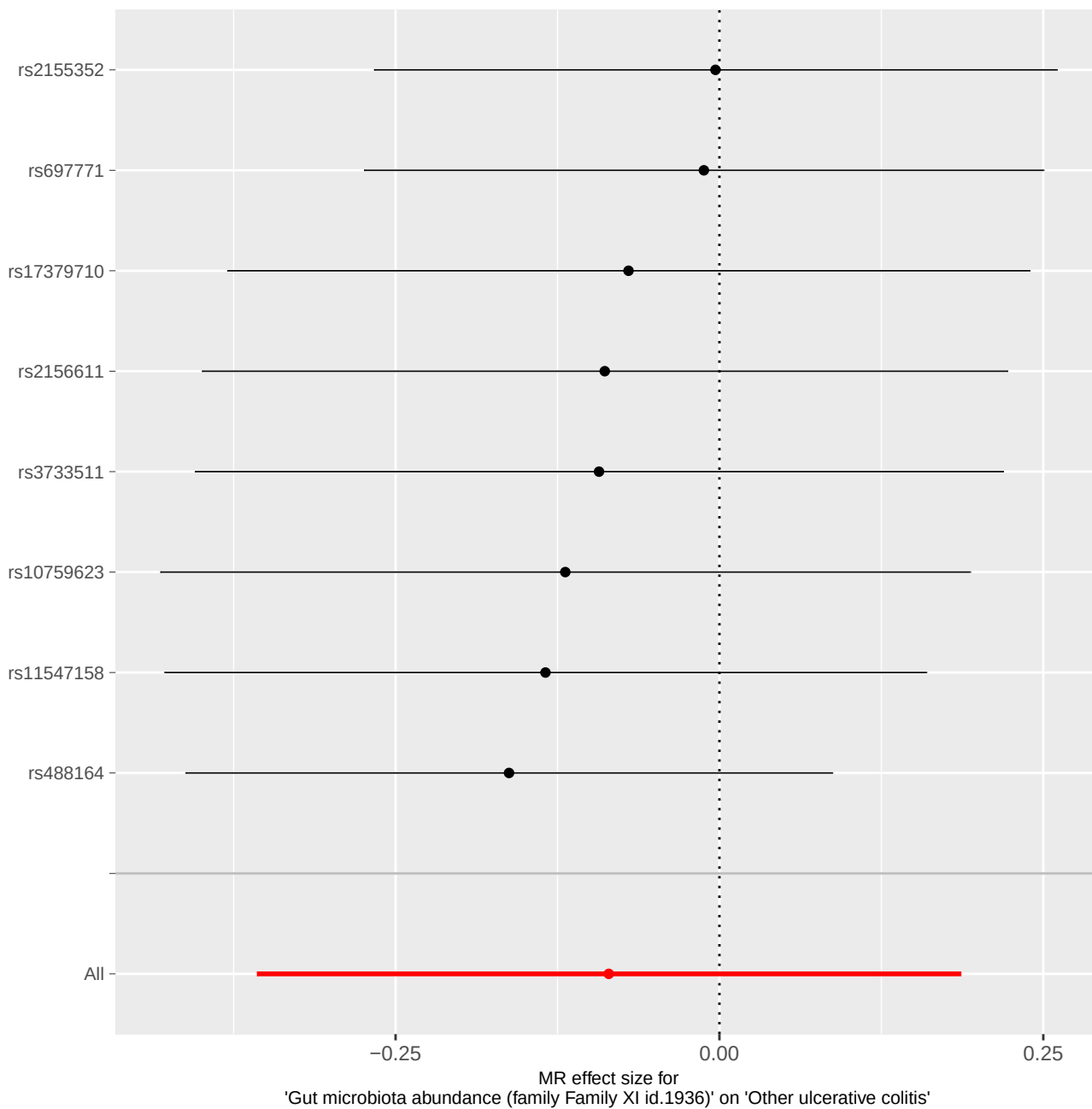


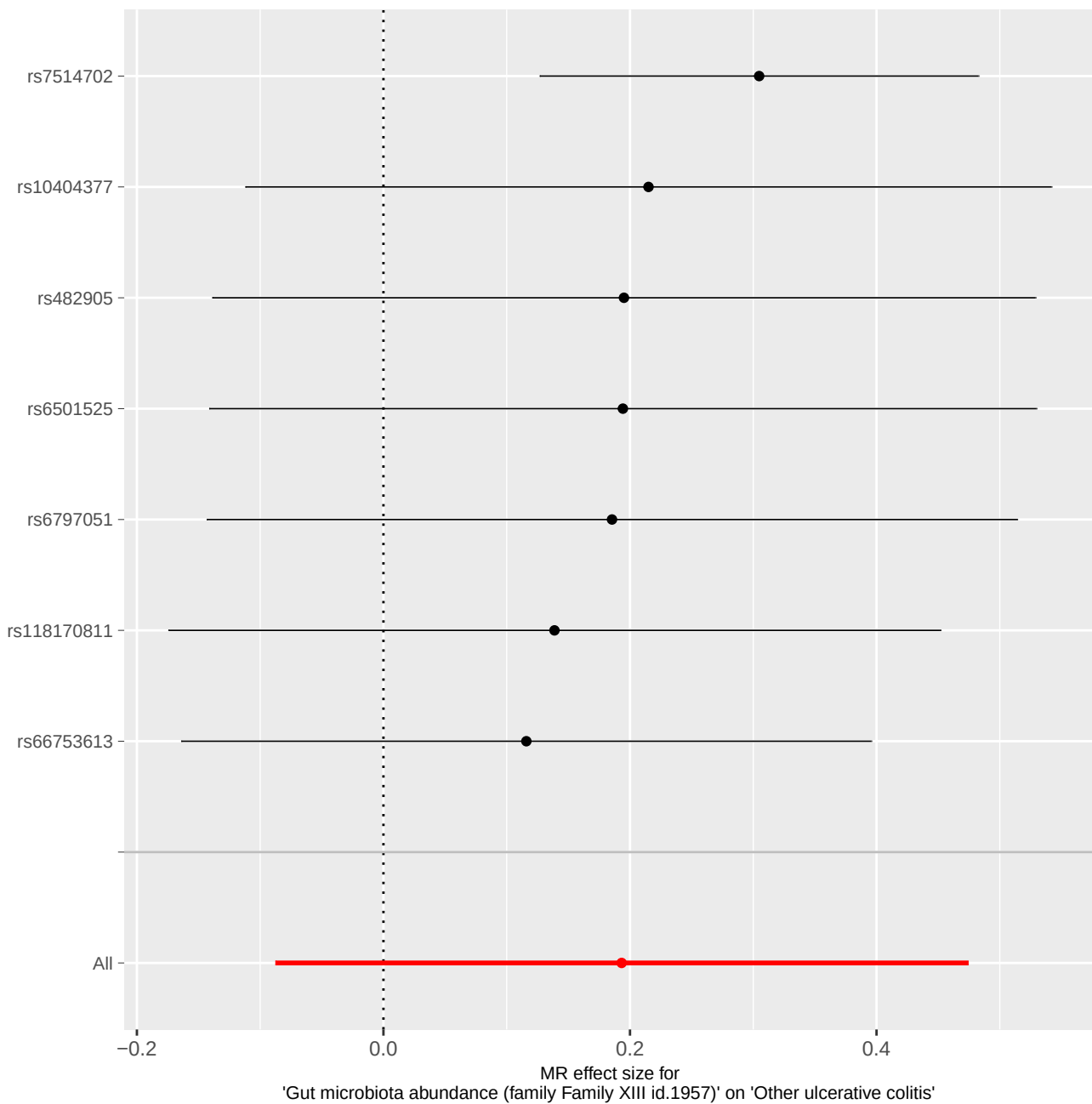




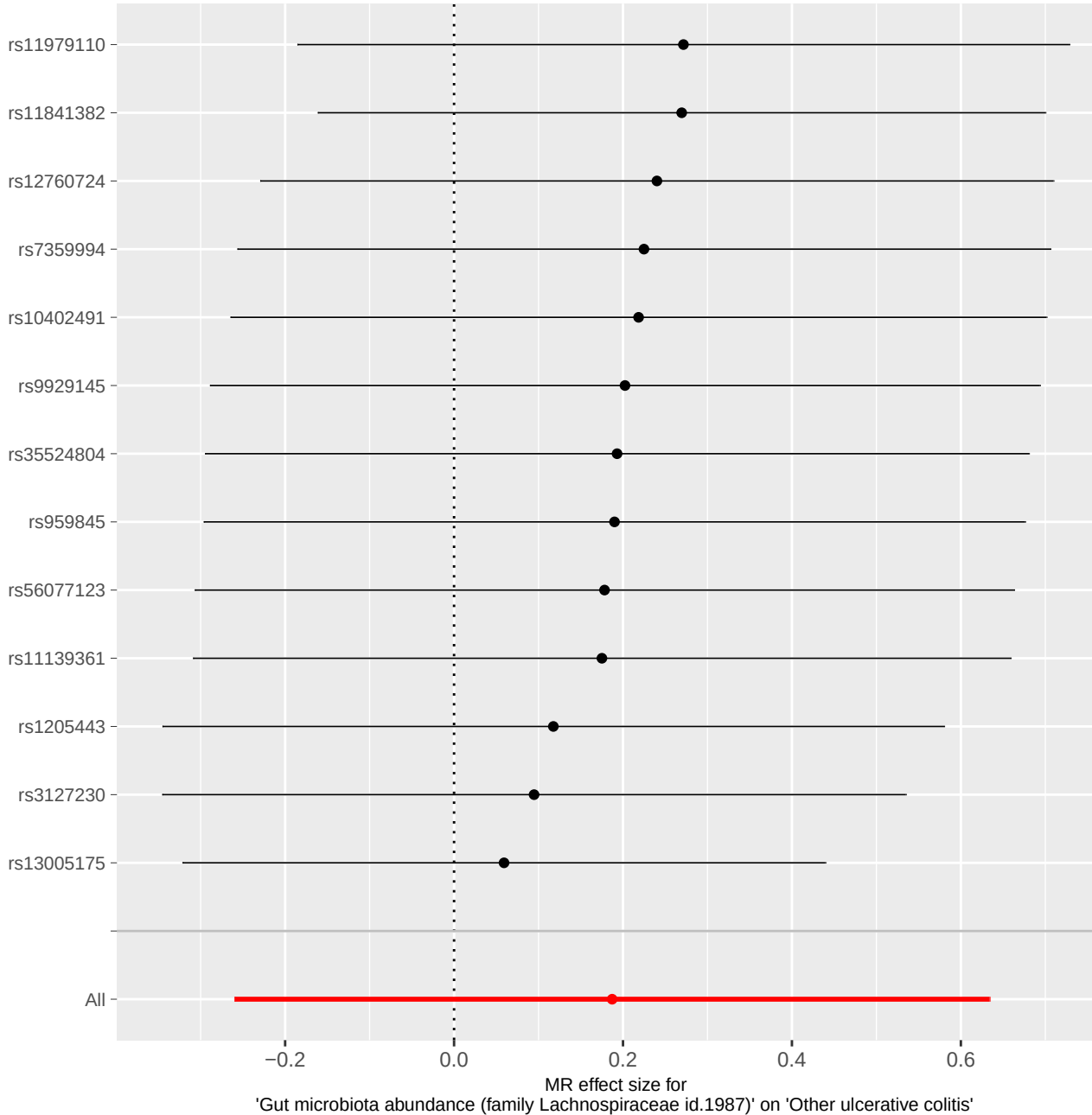


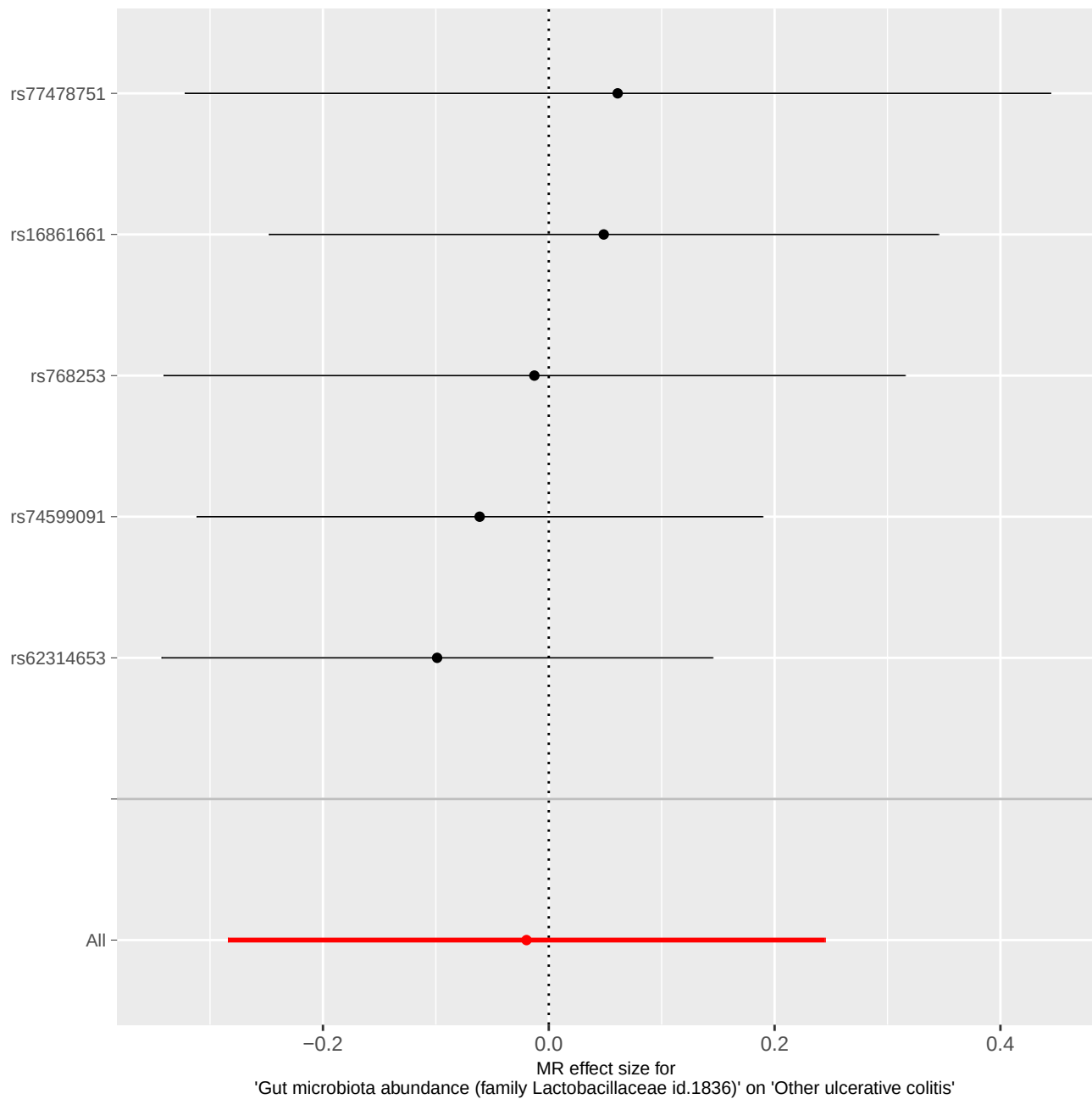
Batch 1215 : Gut microbiota abundance (family Family XI id.1936) on Other ulcerative colitis



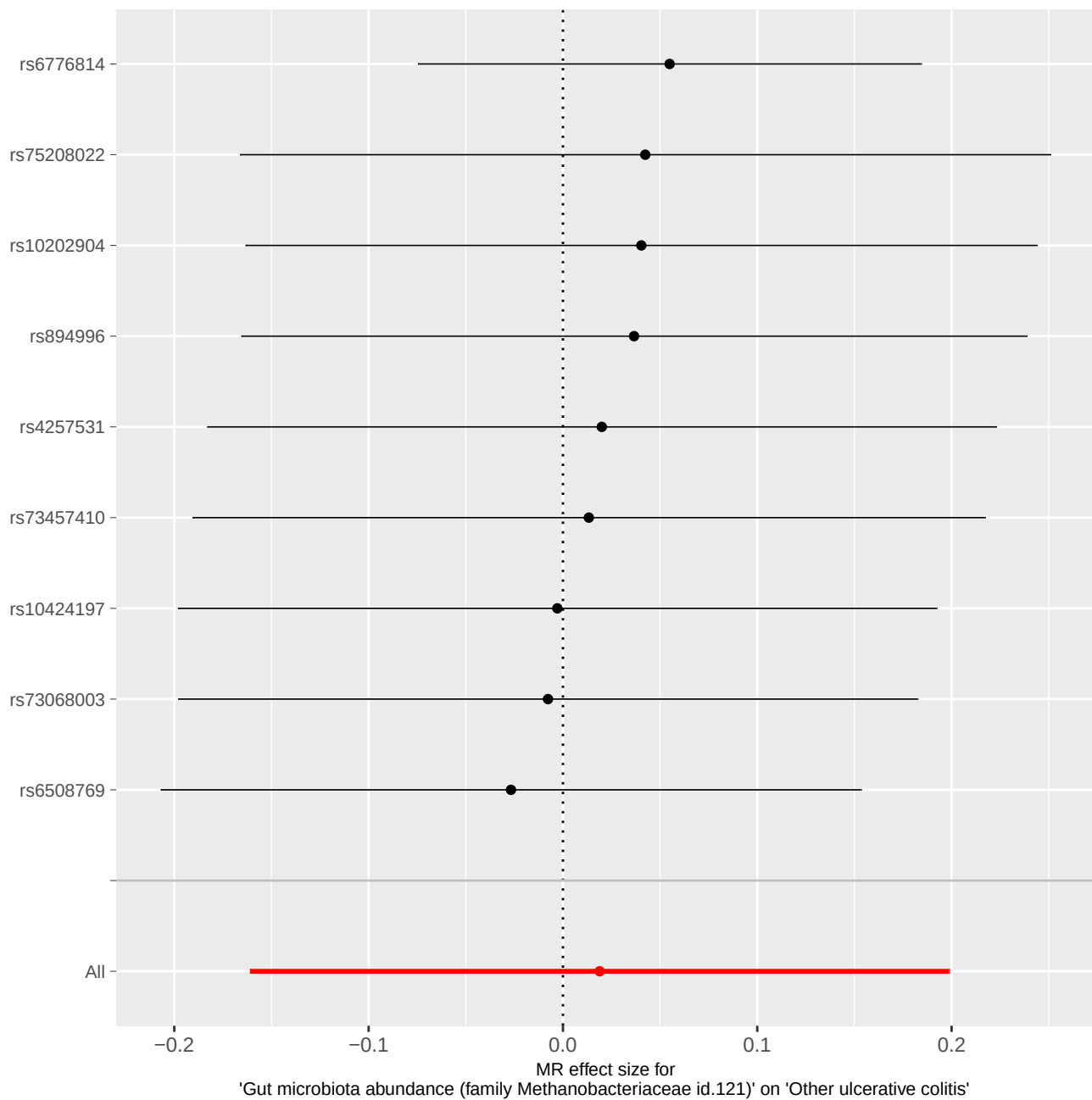


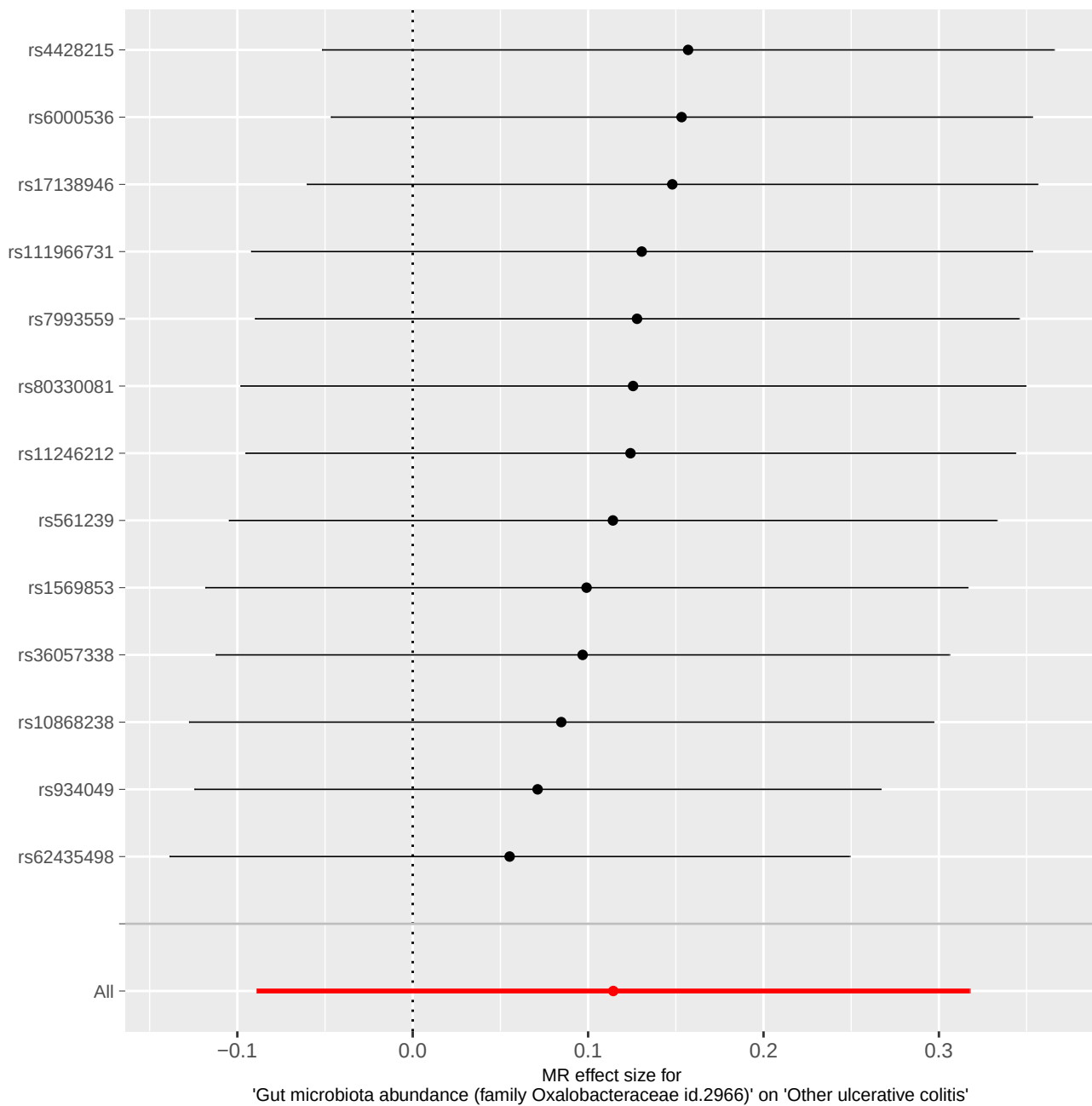
Batch 1217 : Gut microbiota abundance (family Lachnospiraceae id.1987) on Other ulcerative colitis

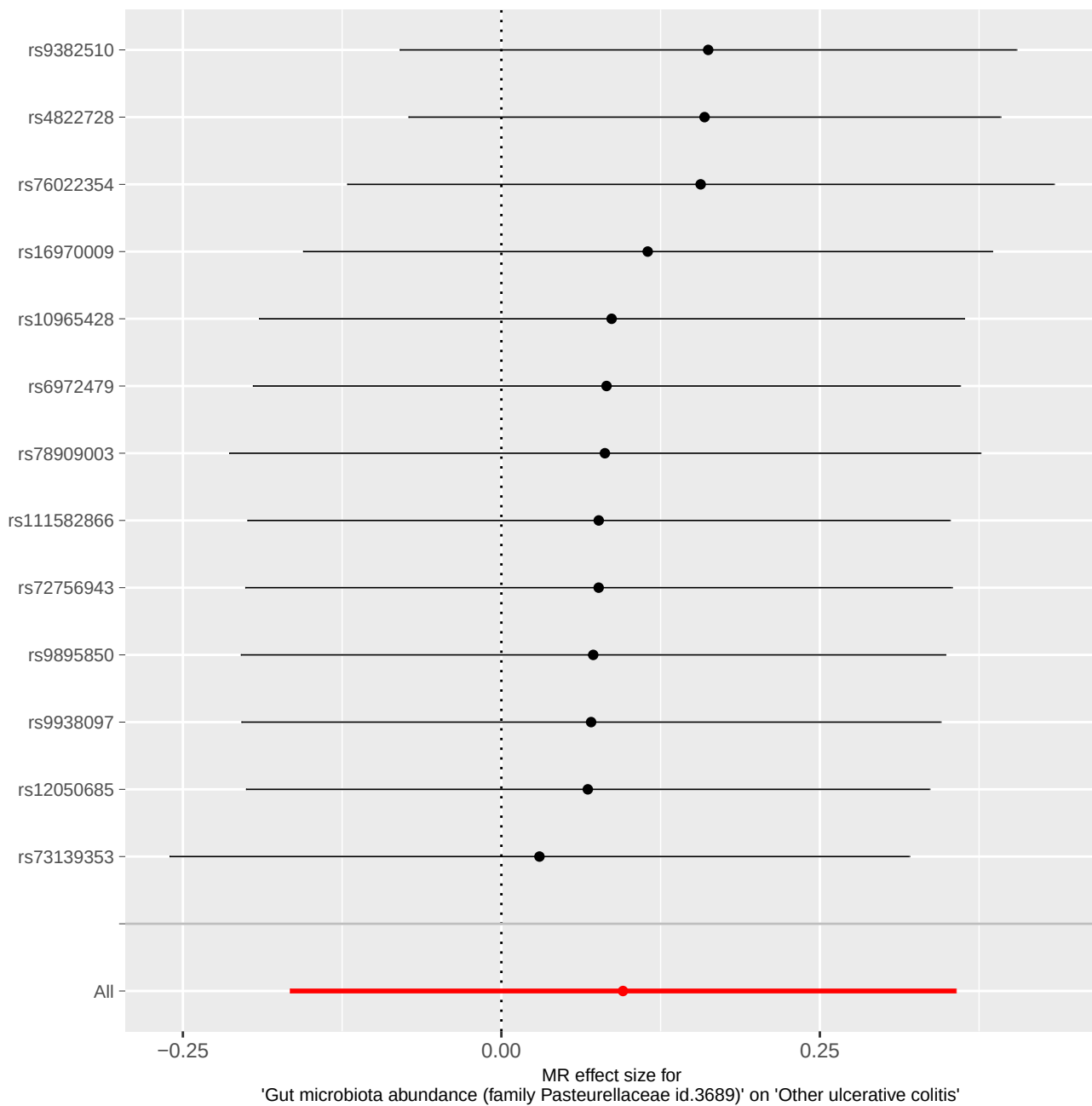


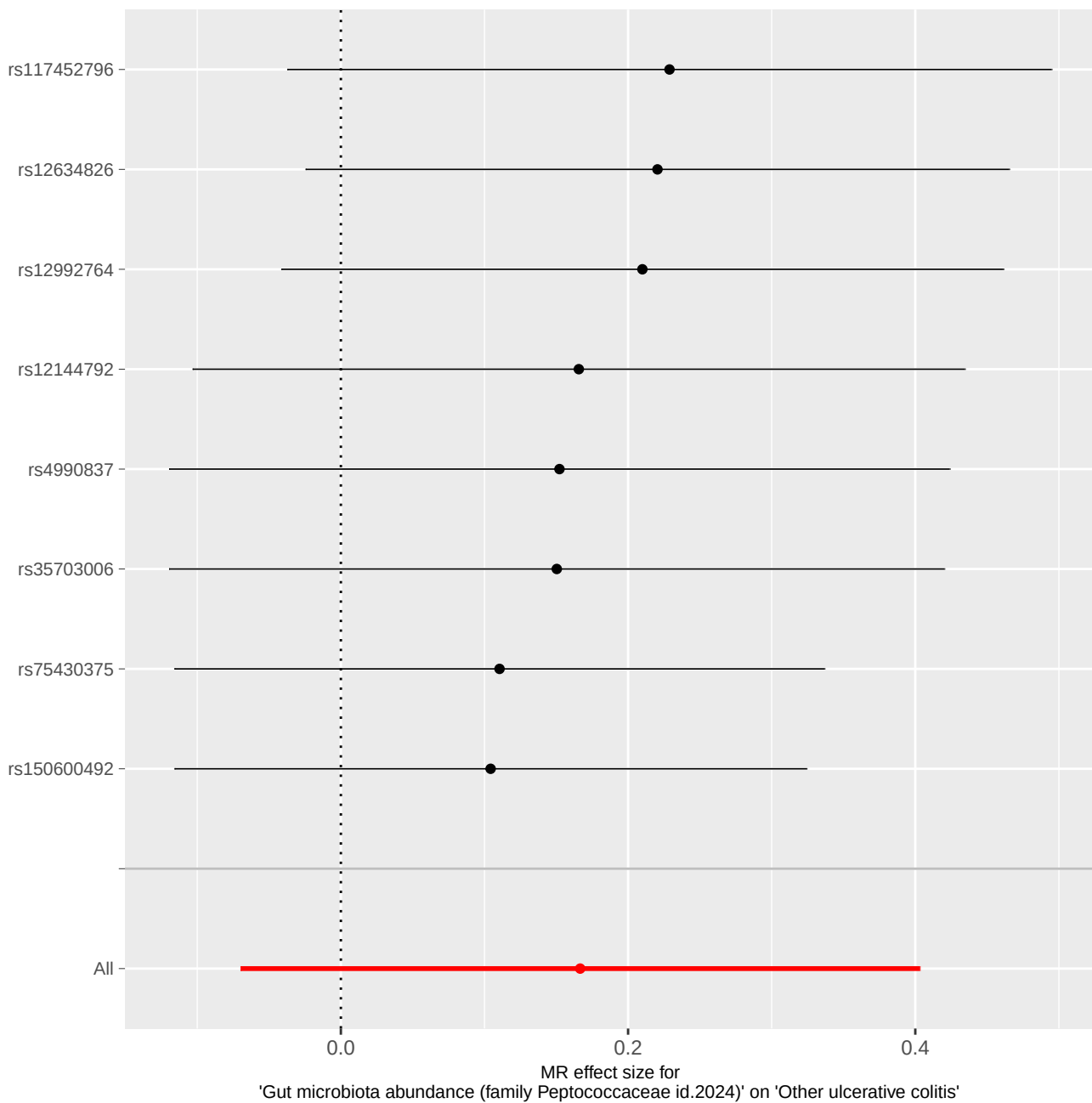


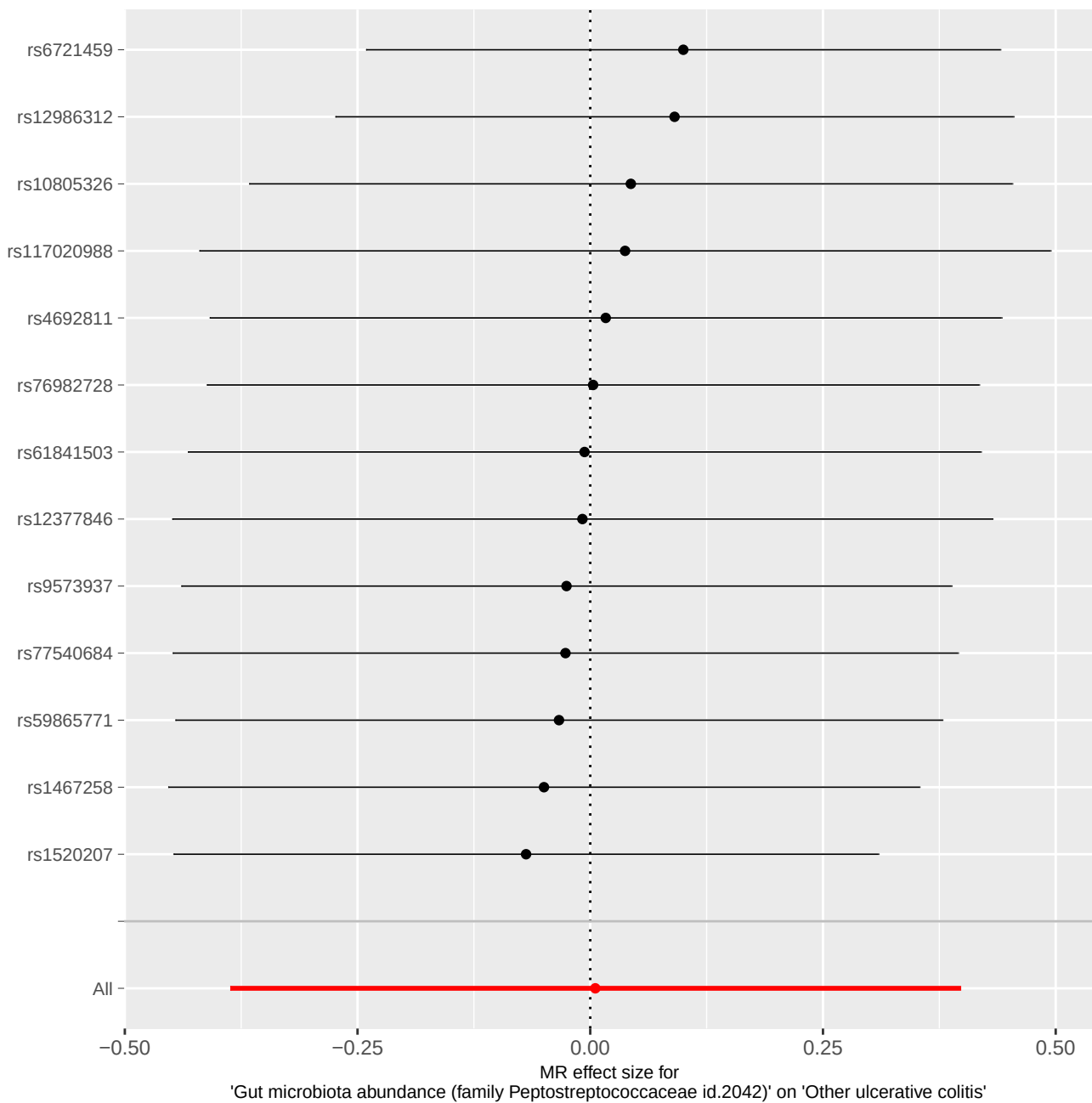
Batch 1219 : Gut microbiota abundance (family Methanobacteriaceae id.121) on Other ulcerative colitis

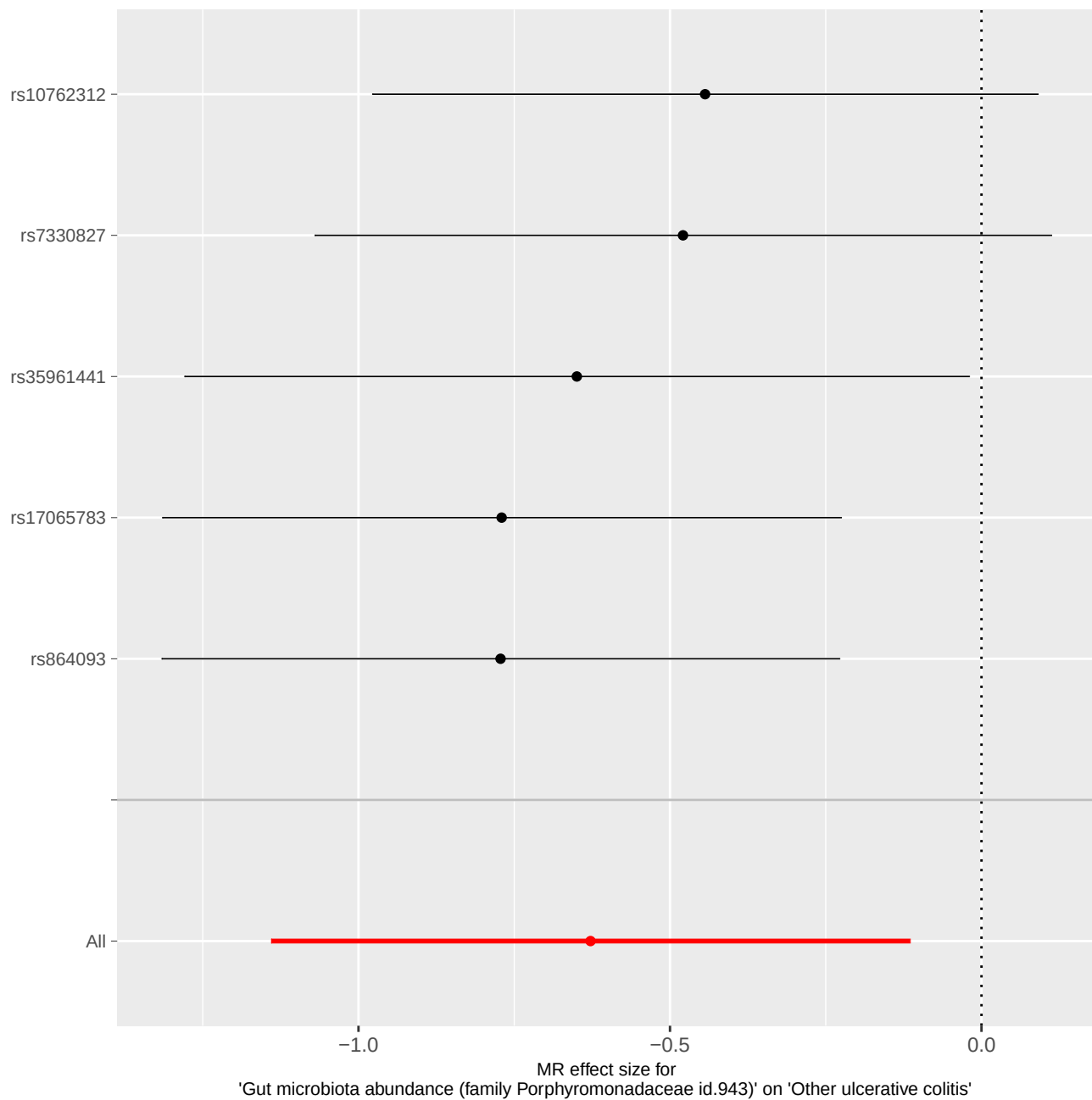


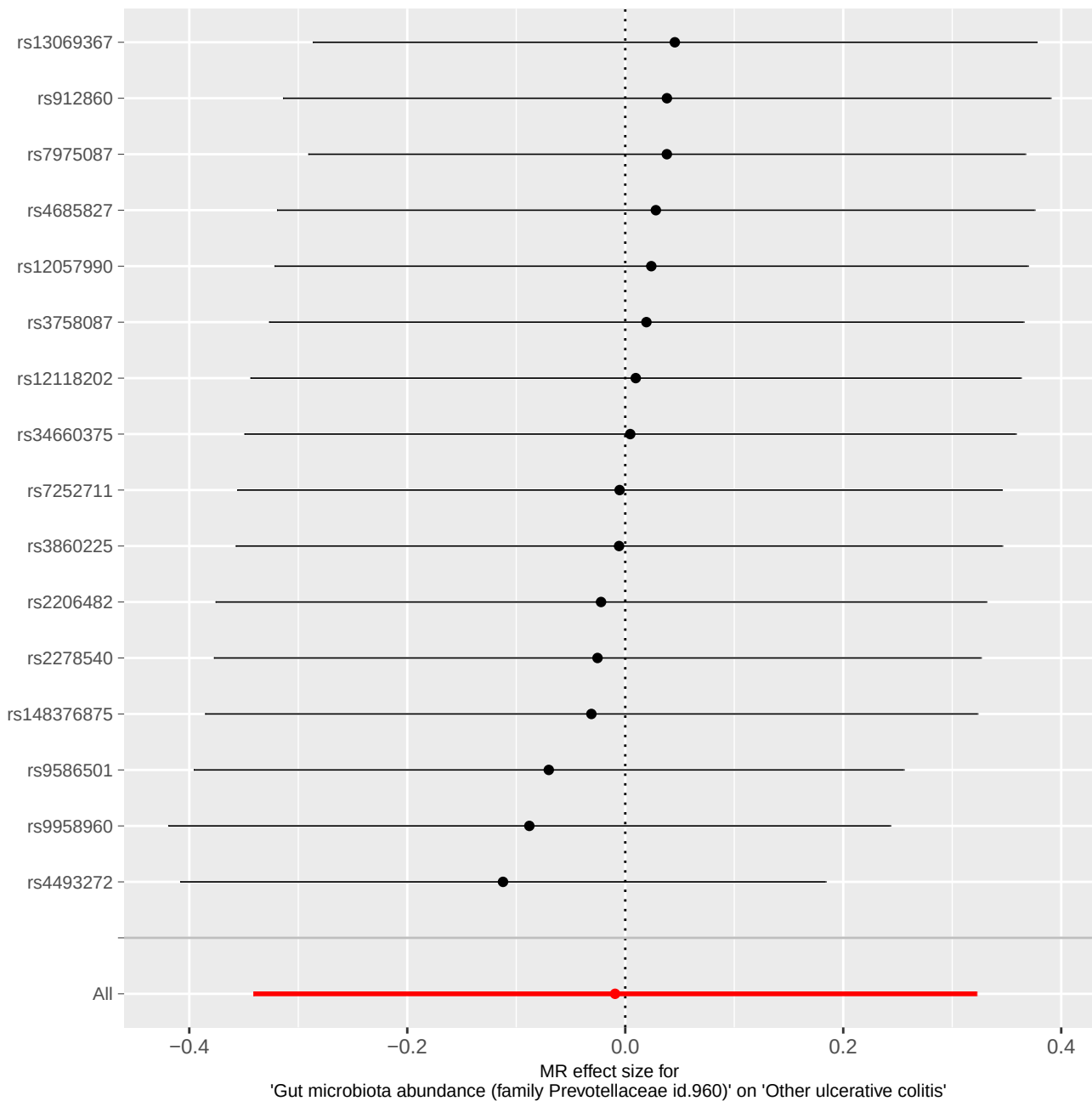


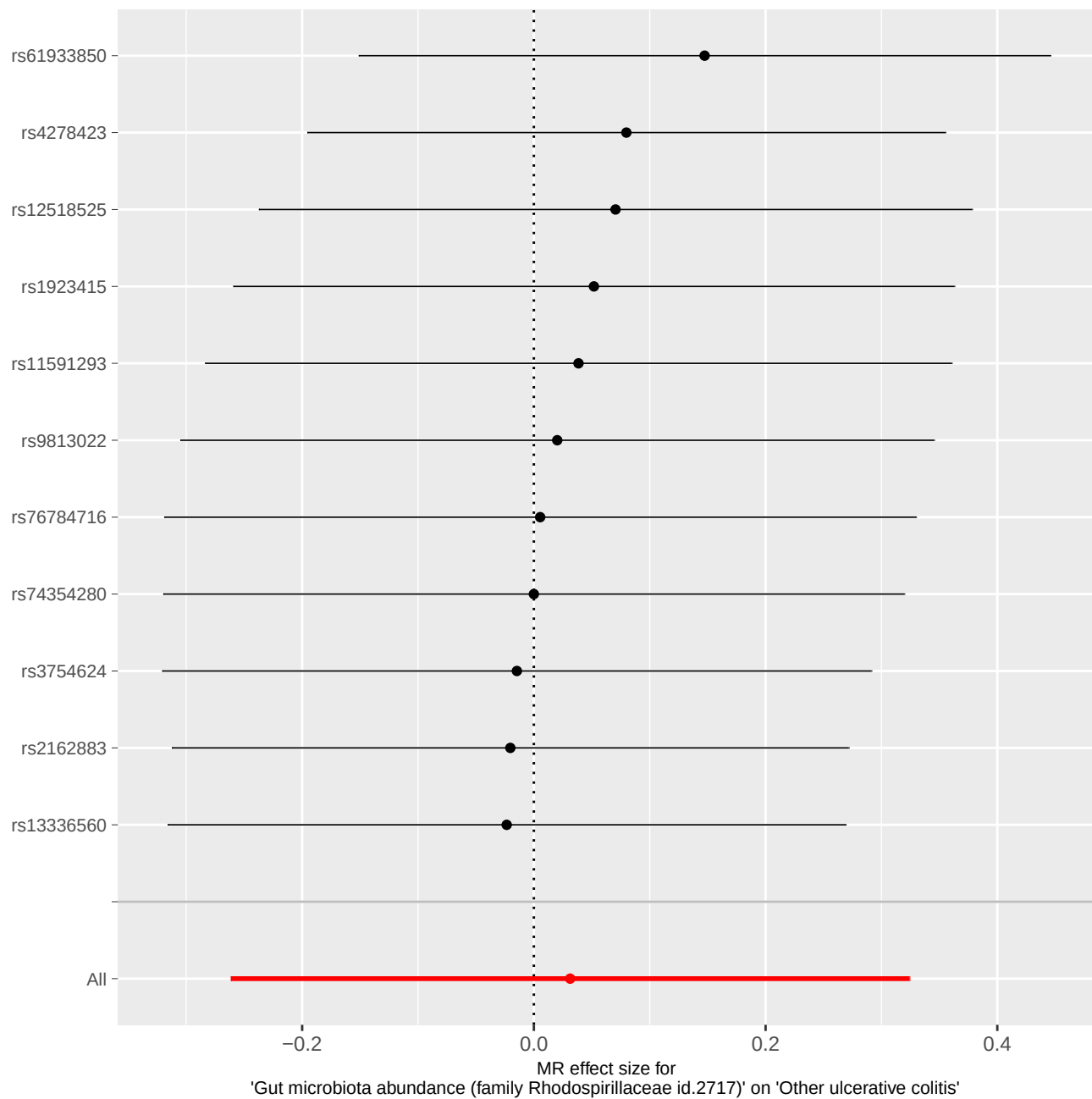


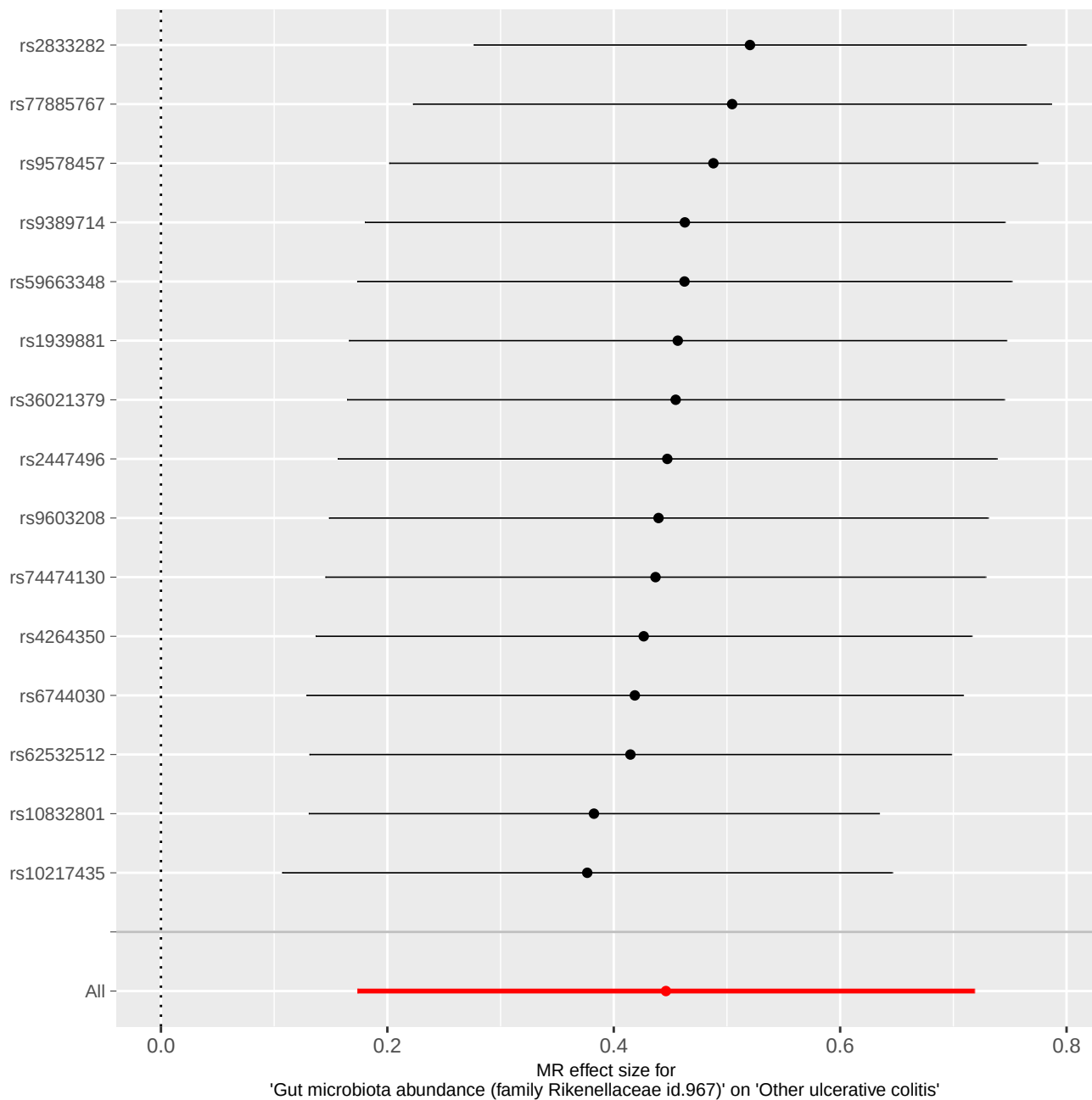


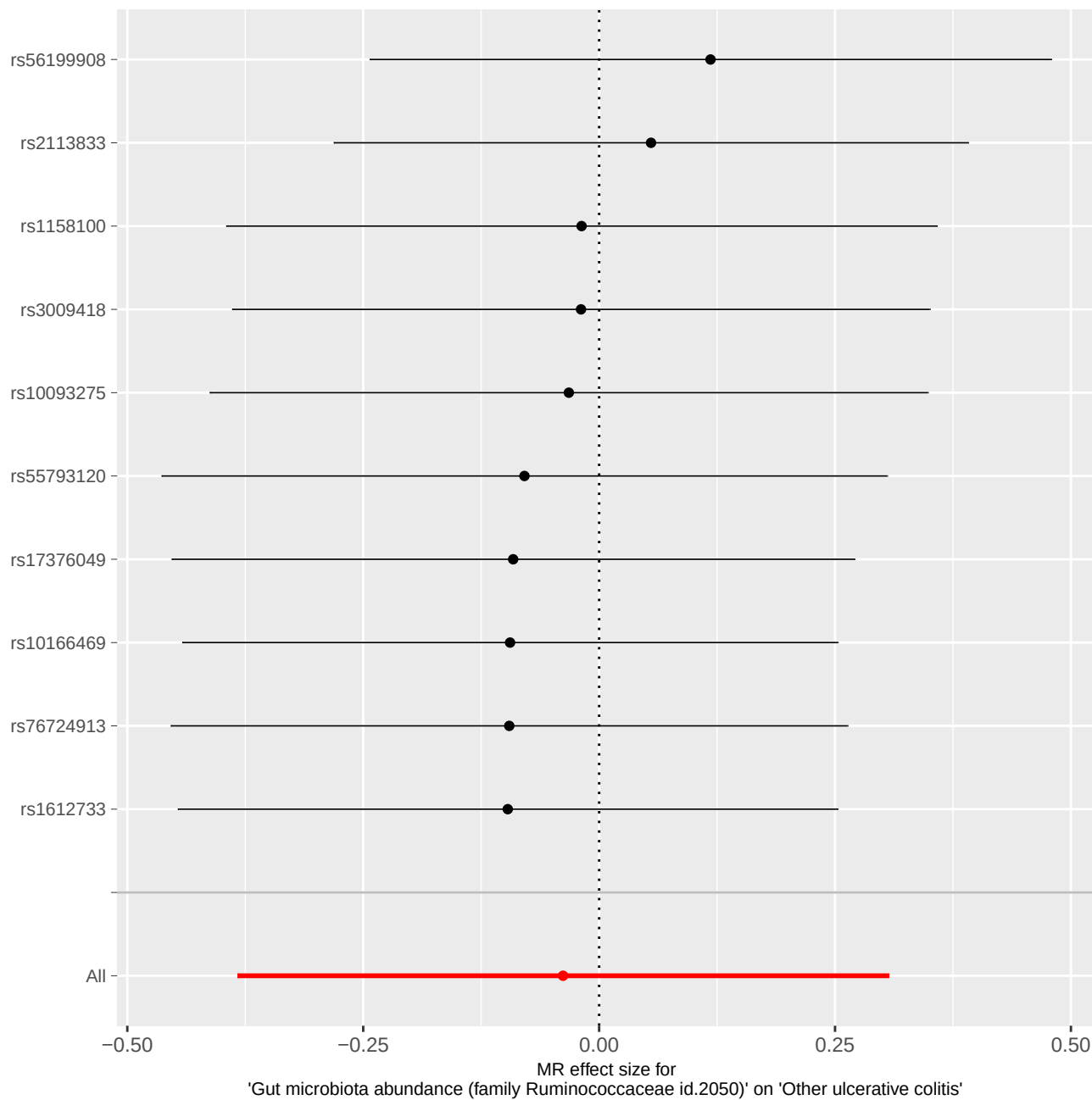


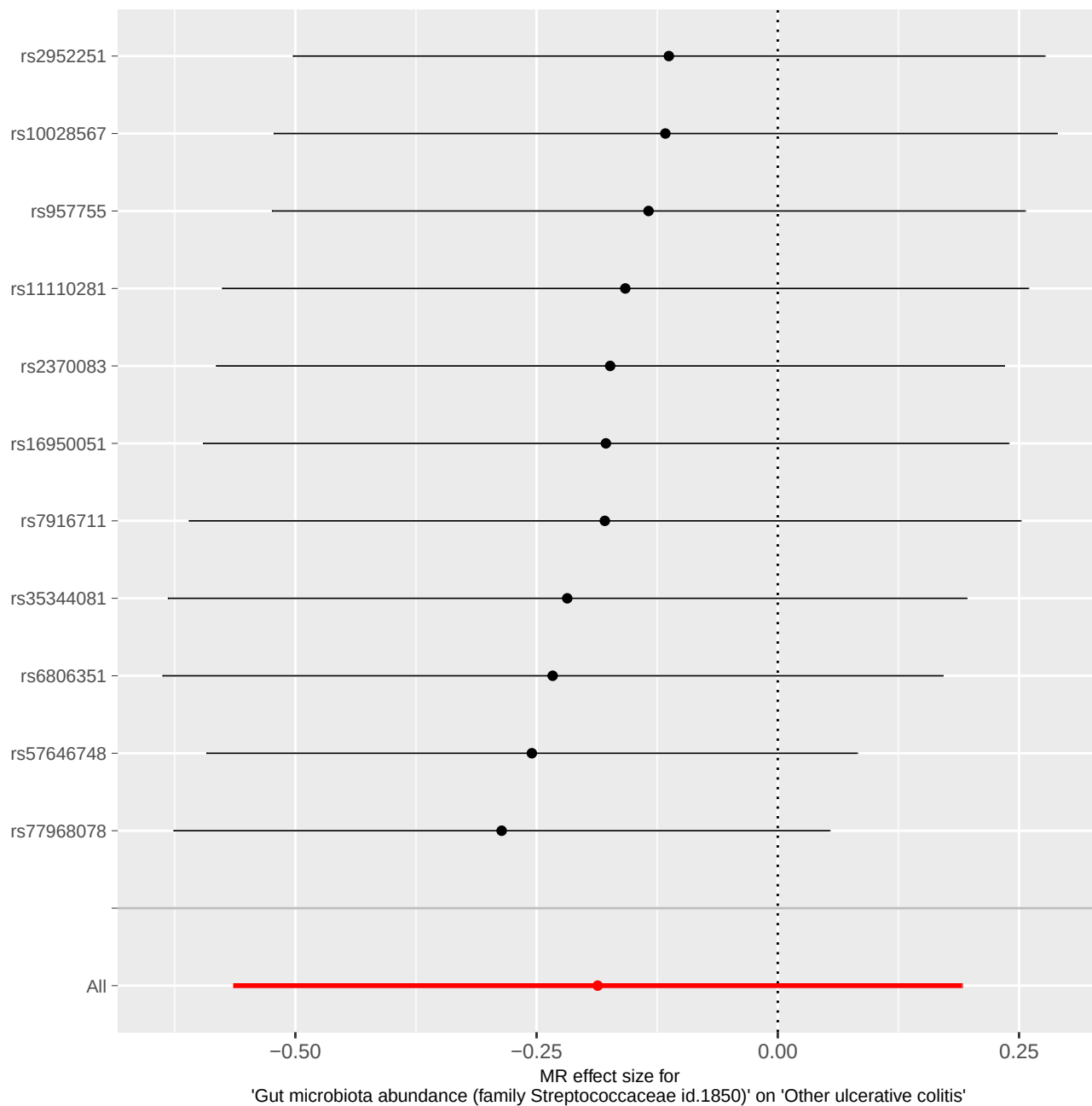


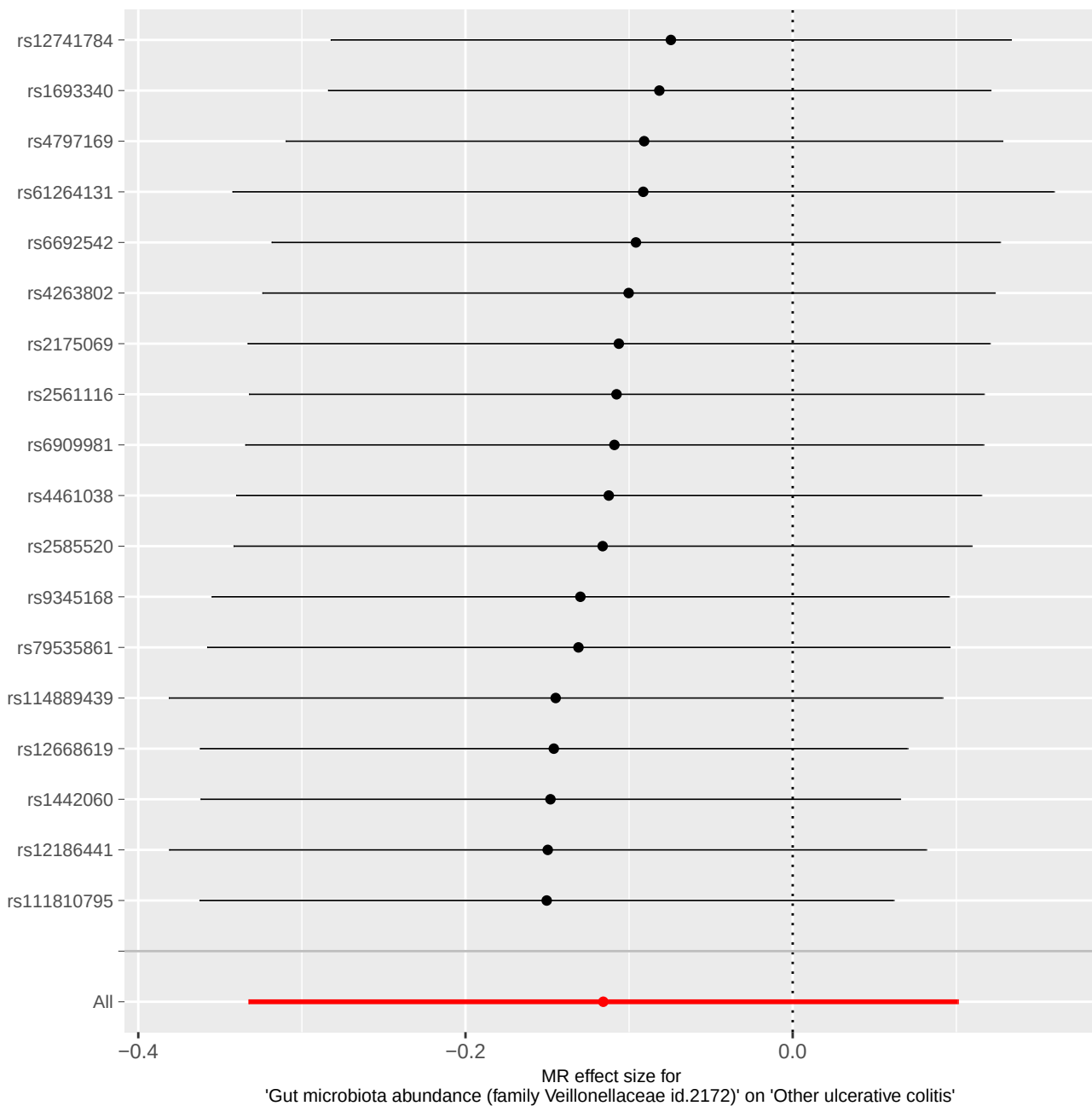


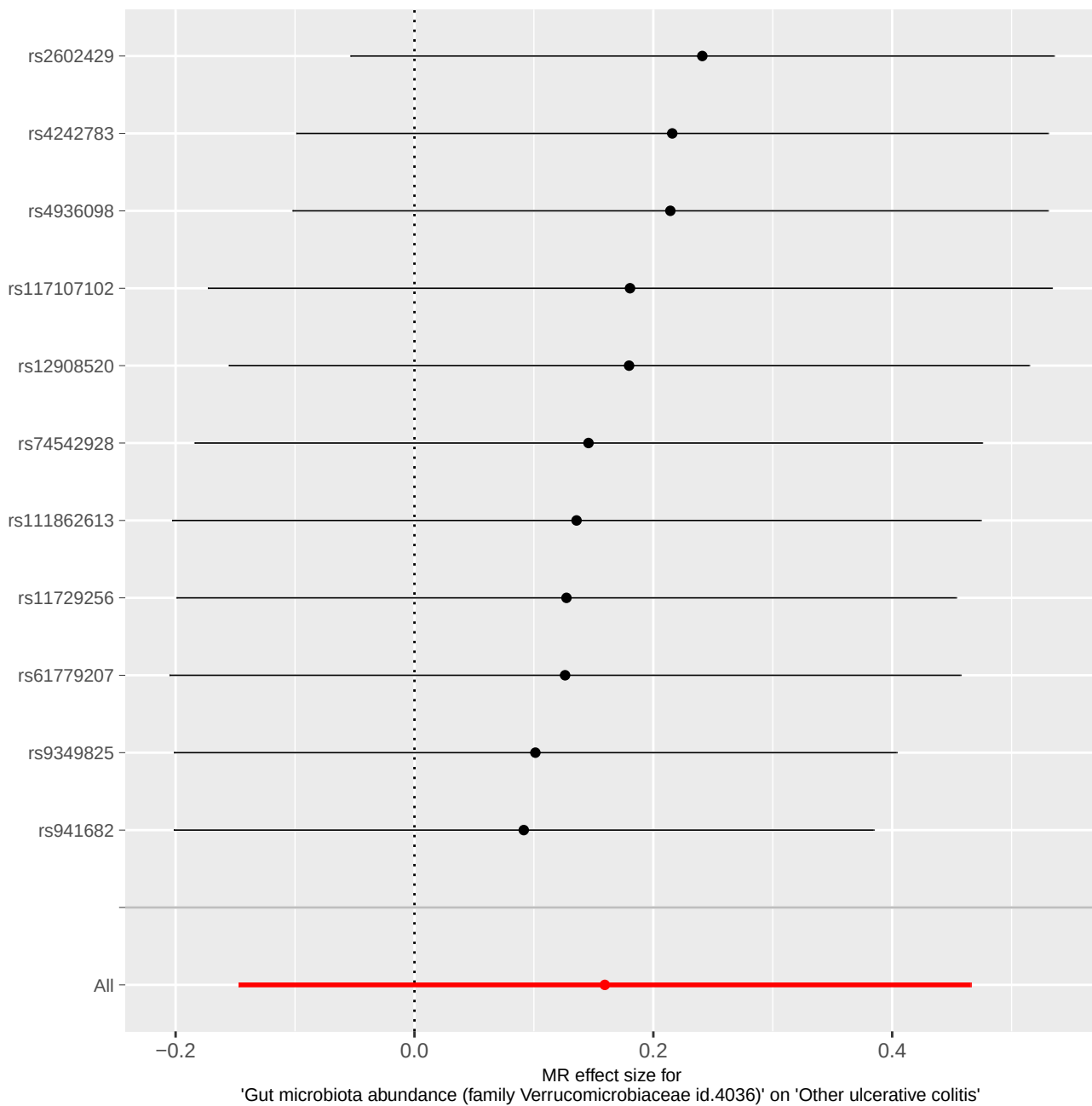


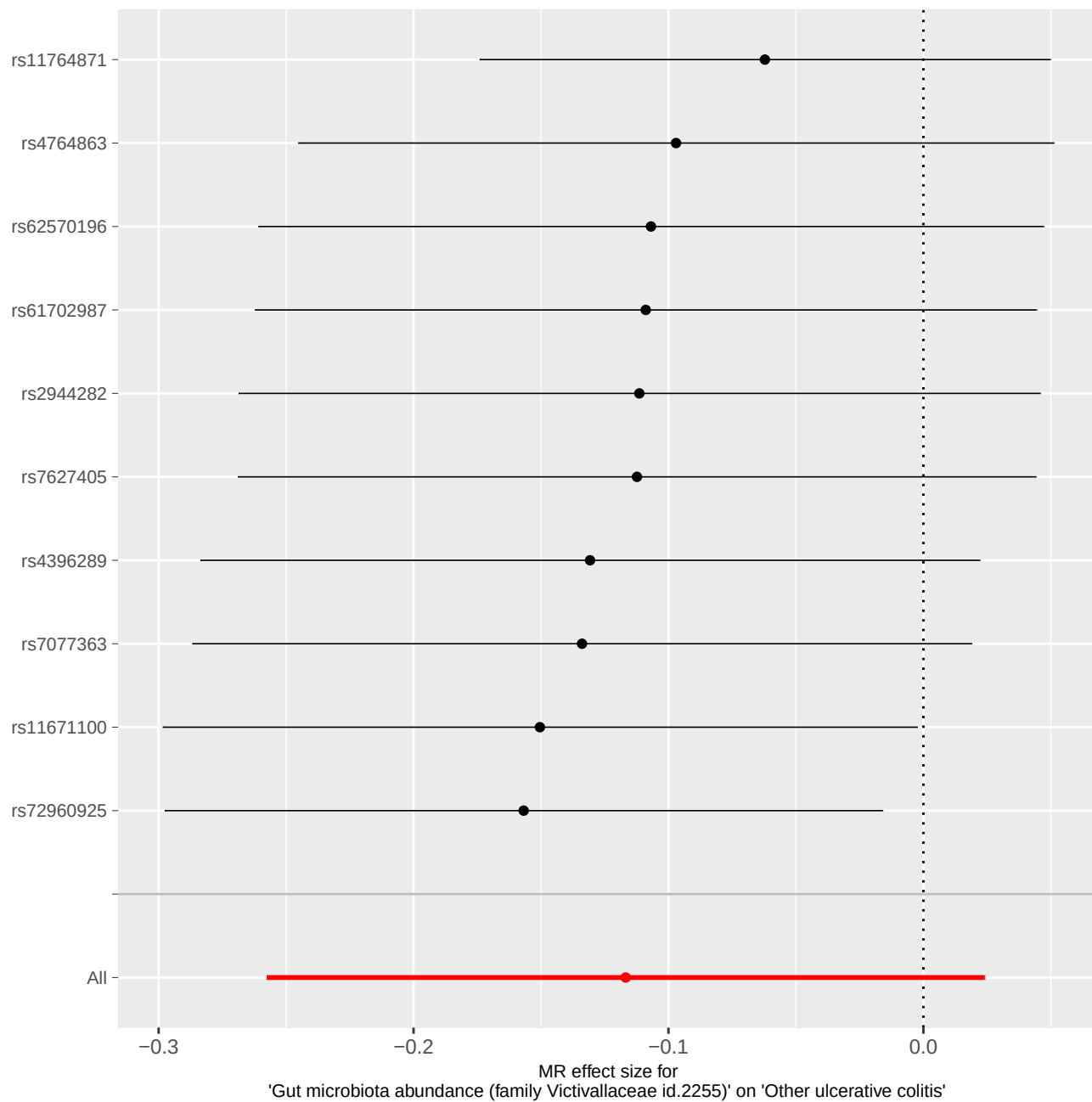


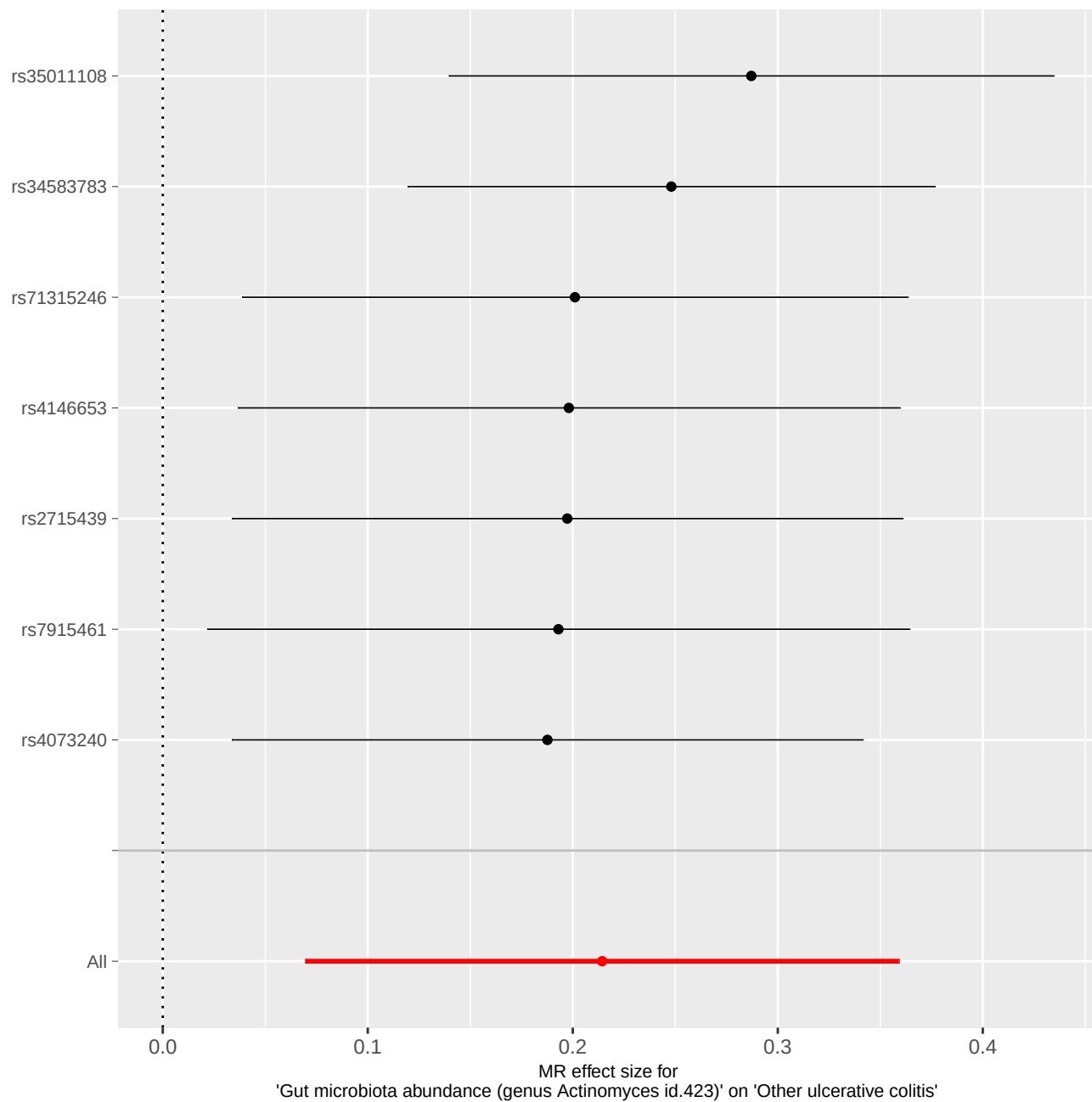


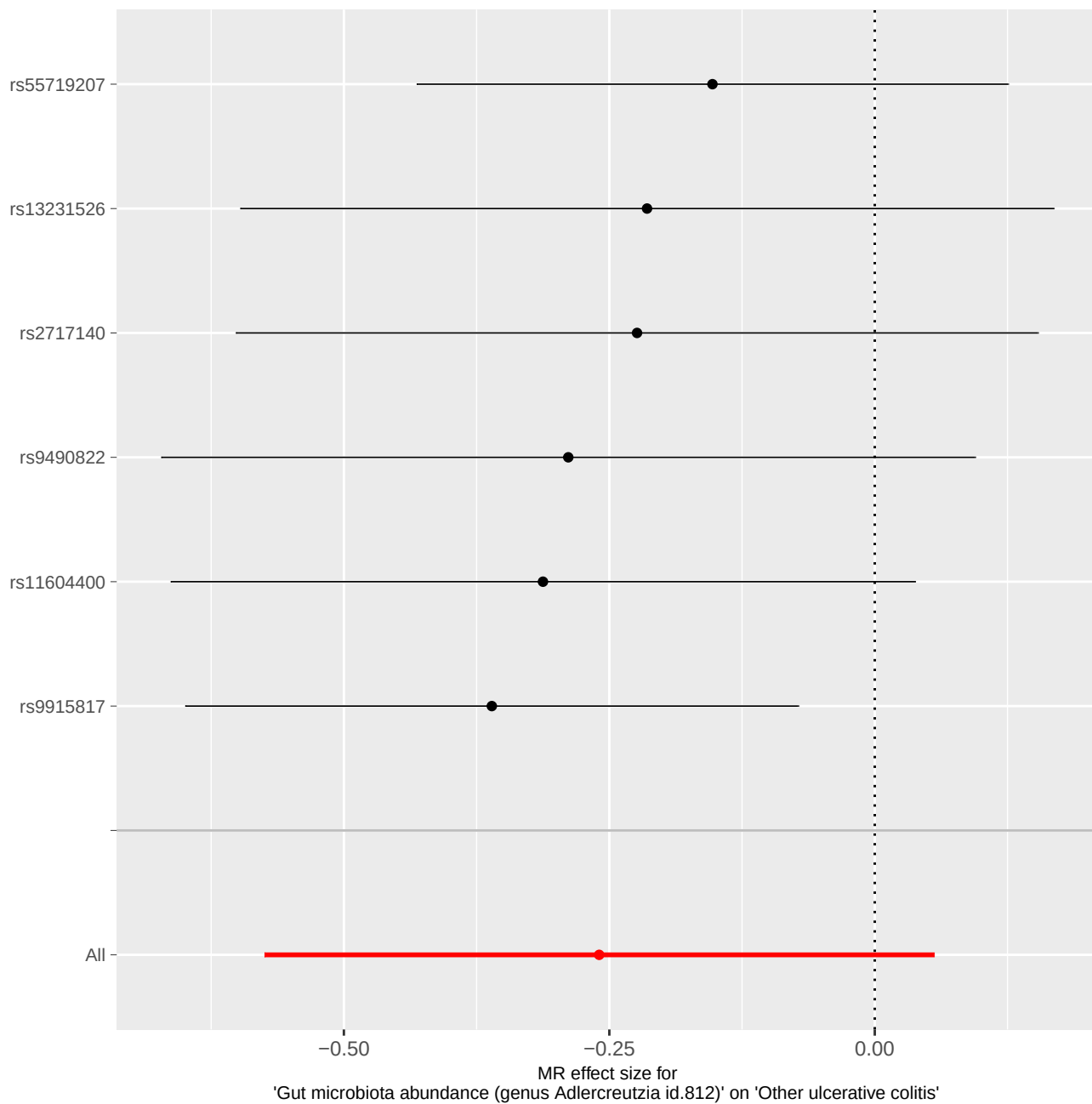


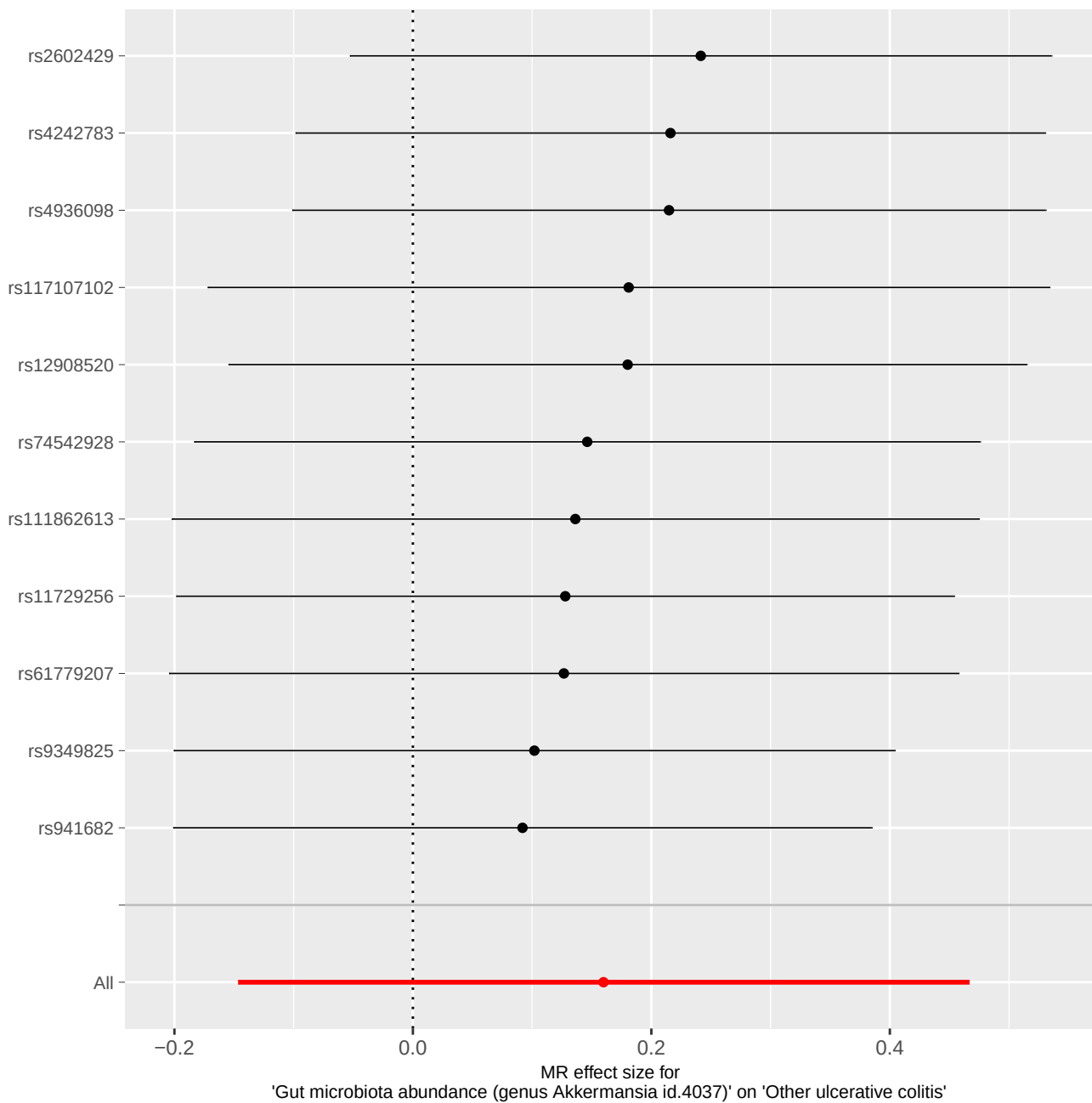




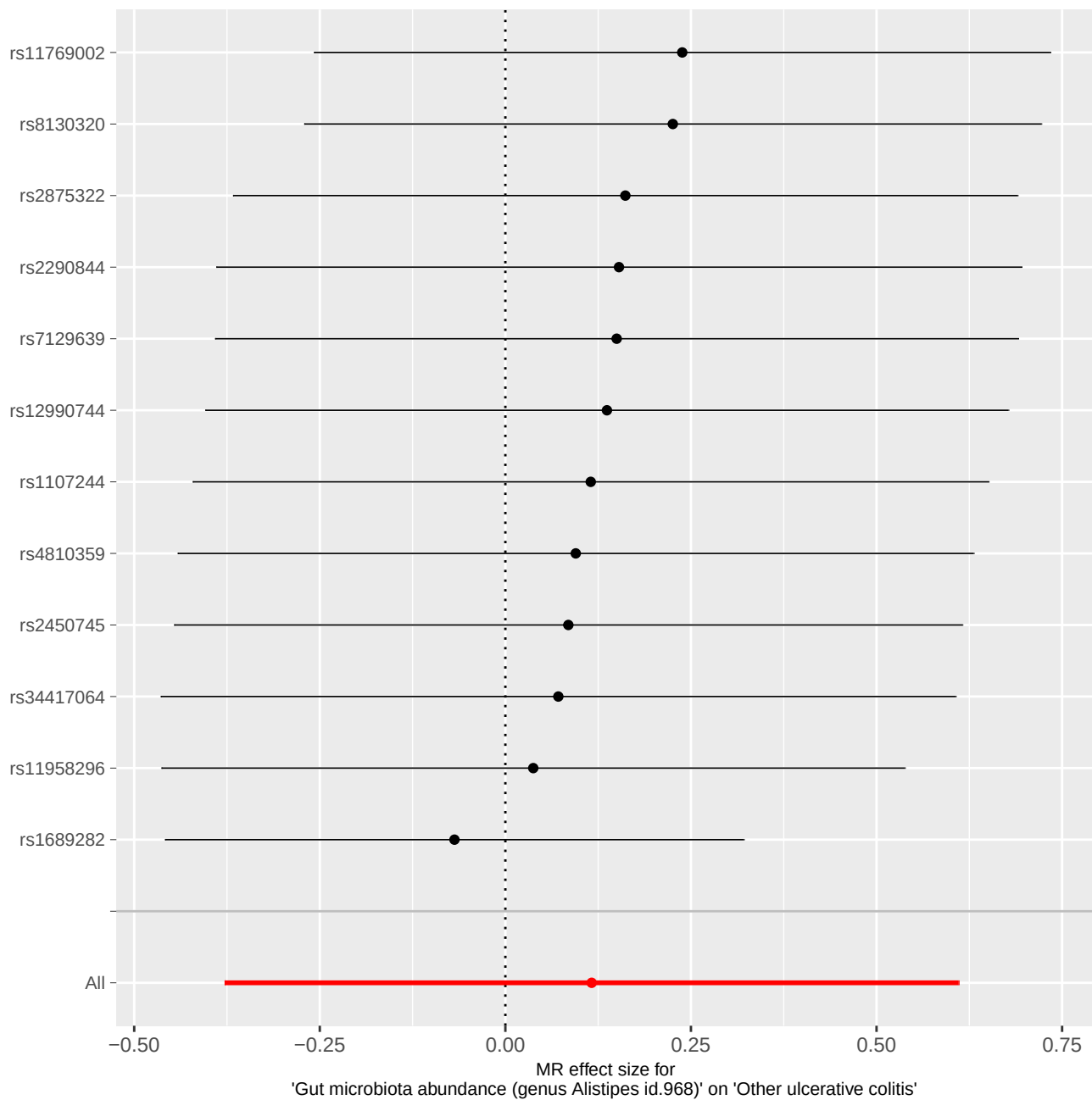


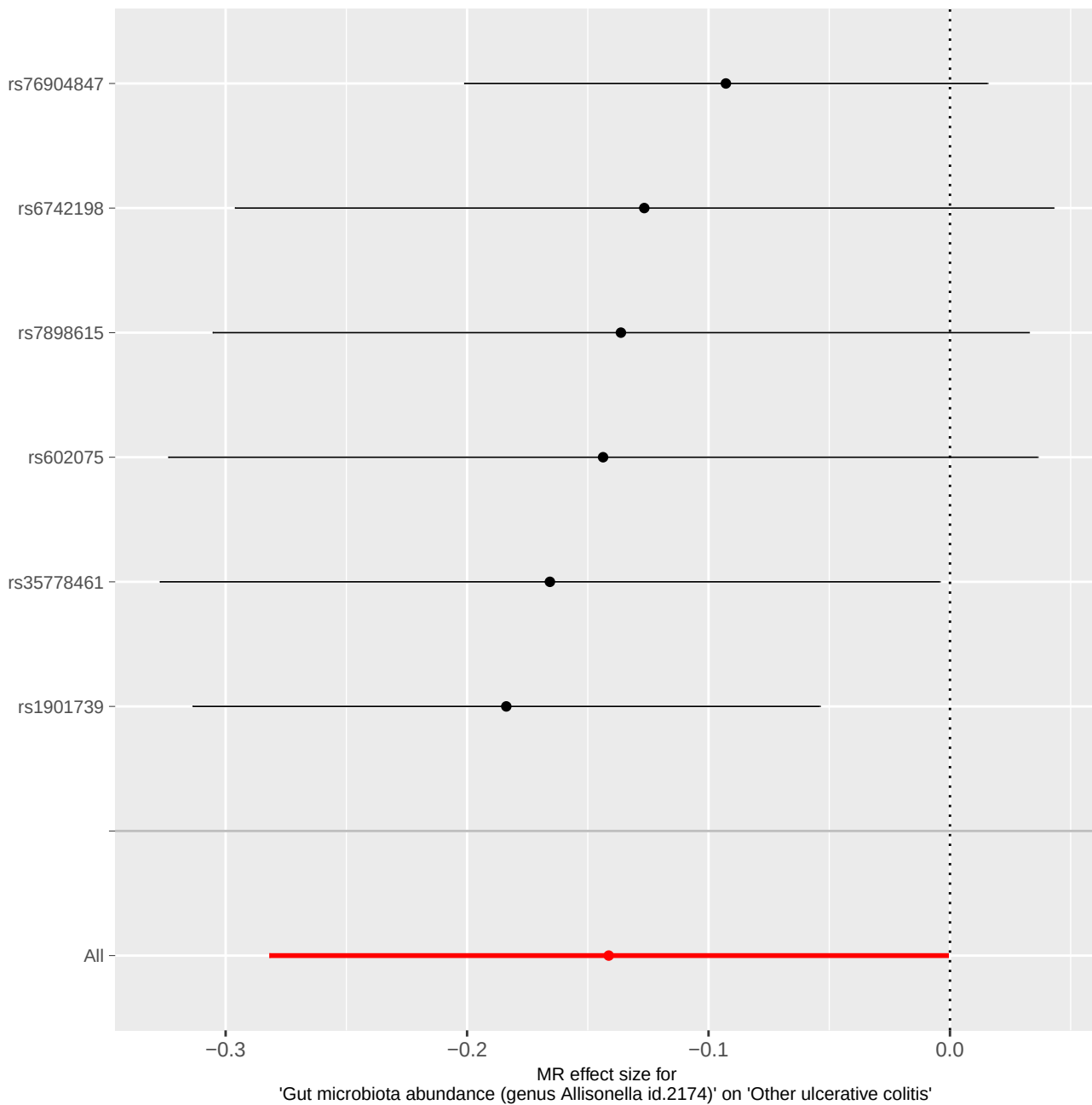


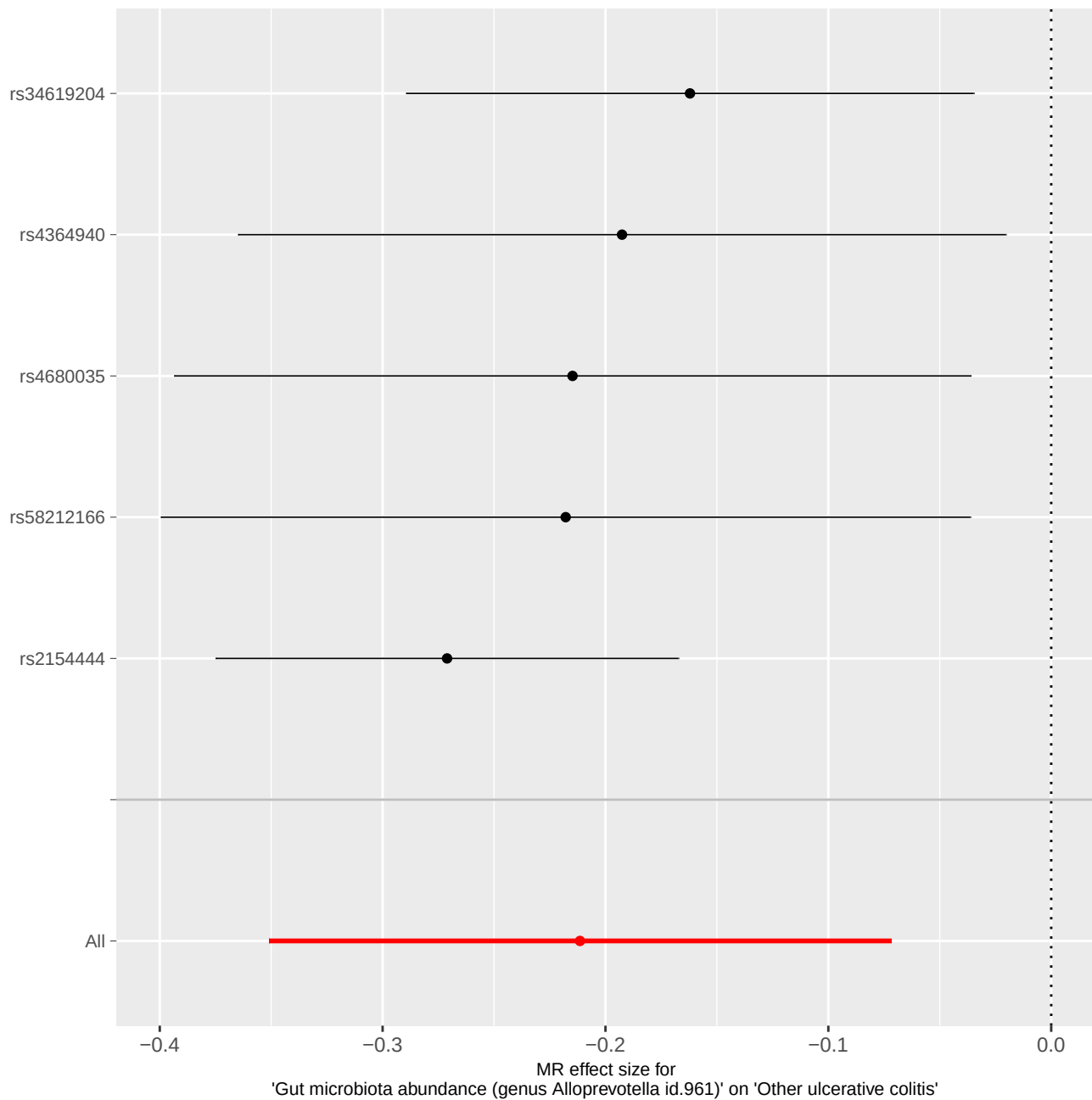


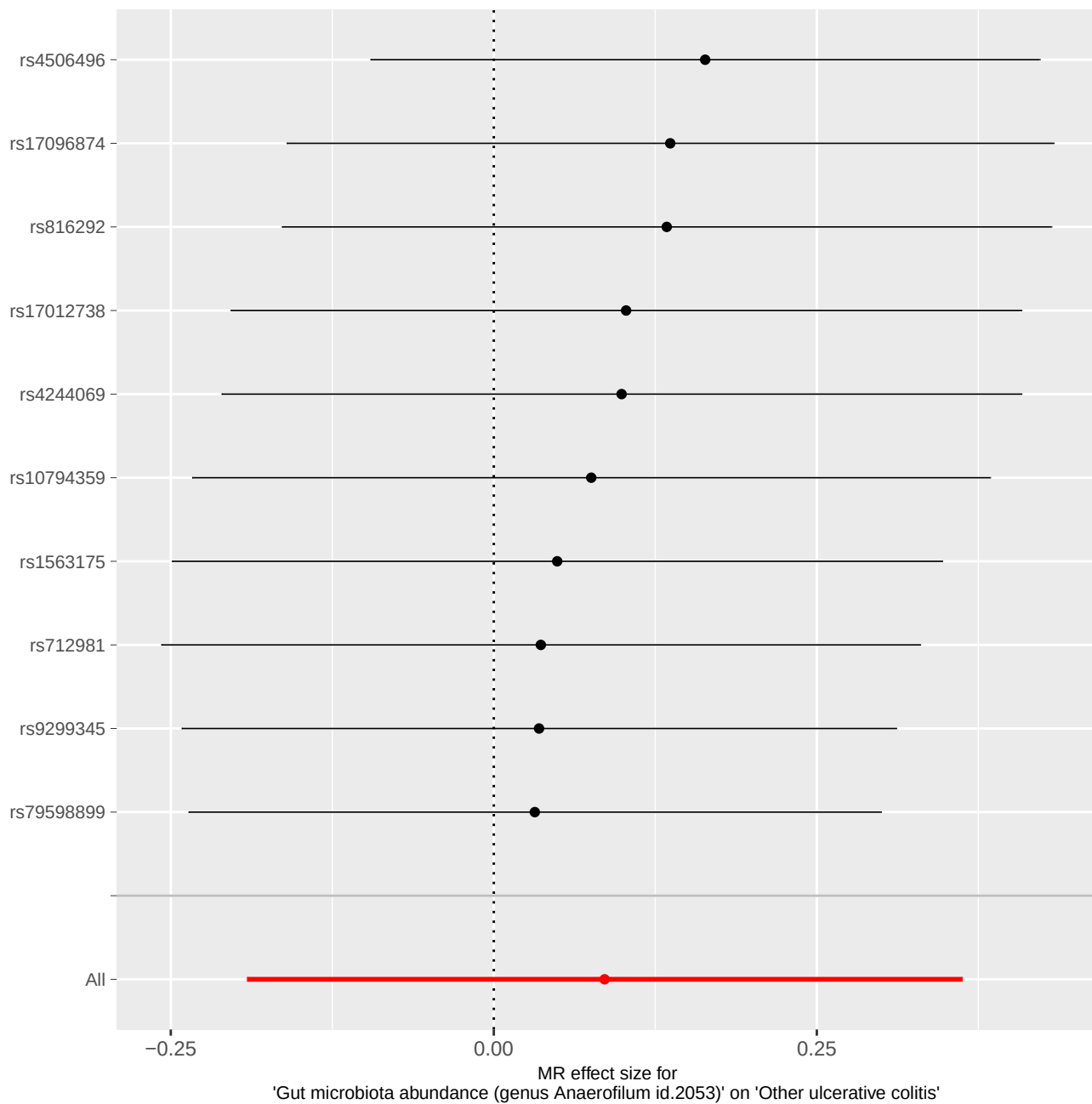


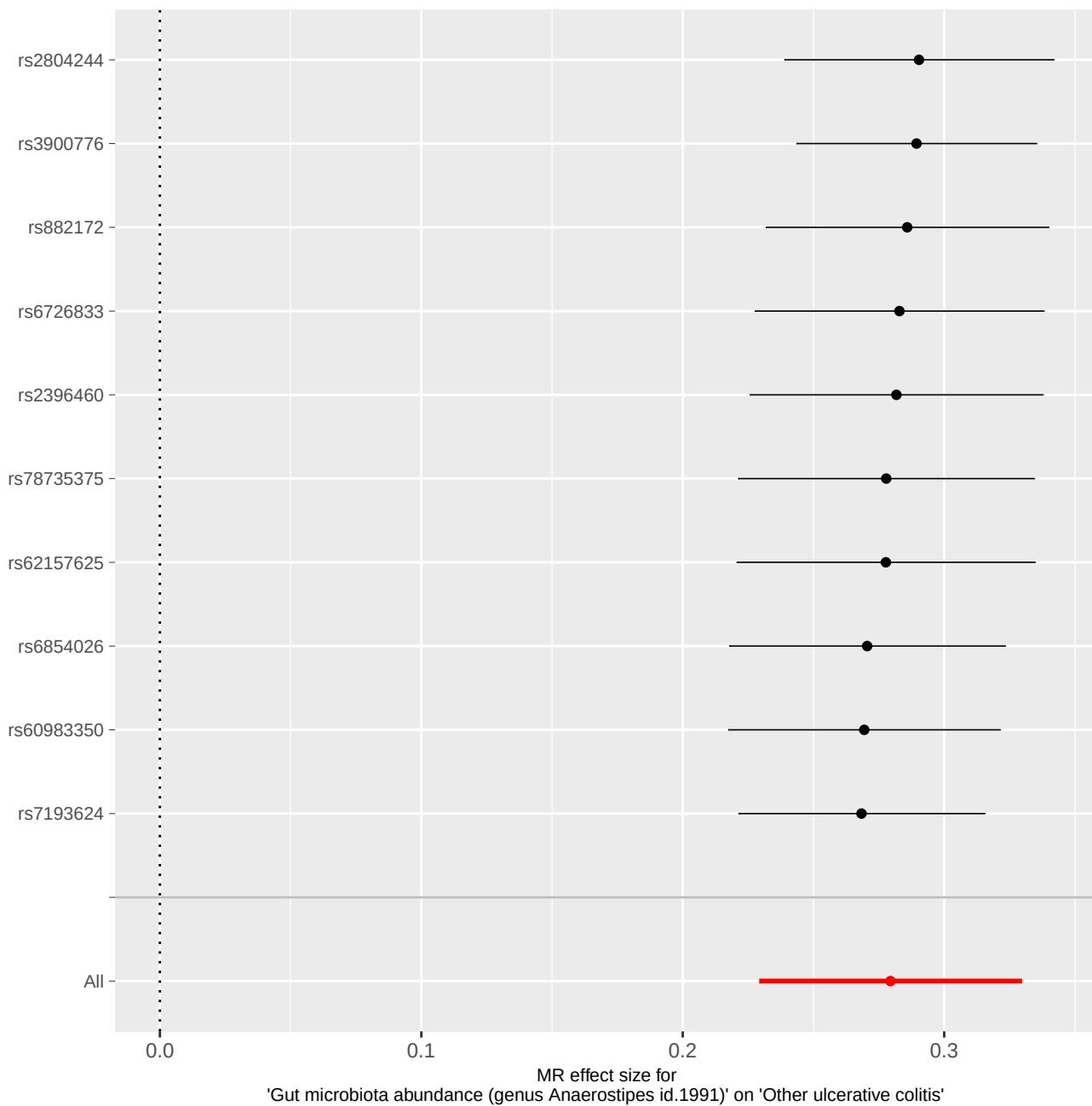
Batch 1236 : Gut microbiota abundance (genus Alistipes id.968) on Other ulcerative colitis

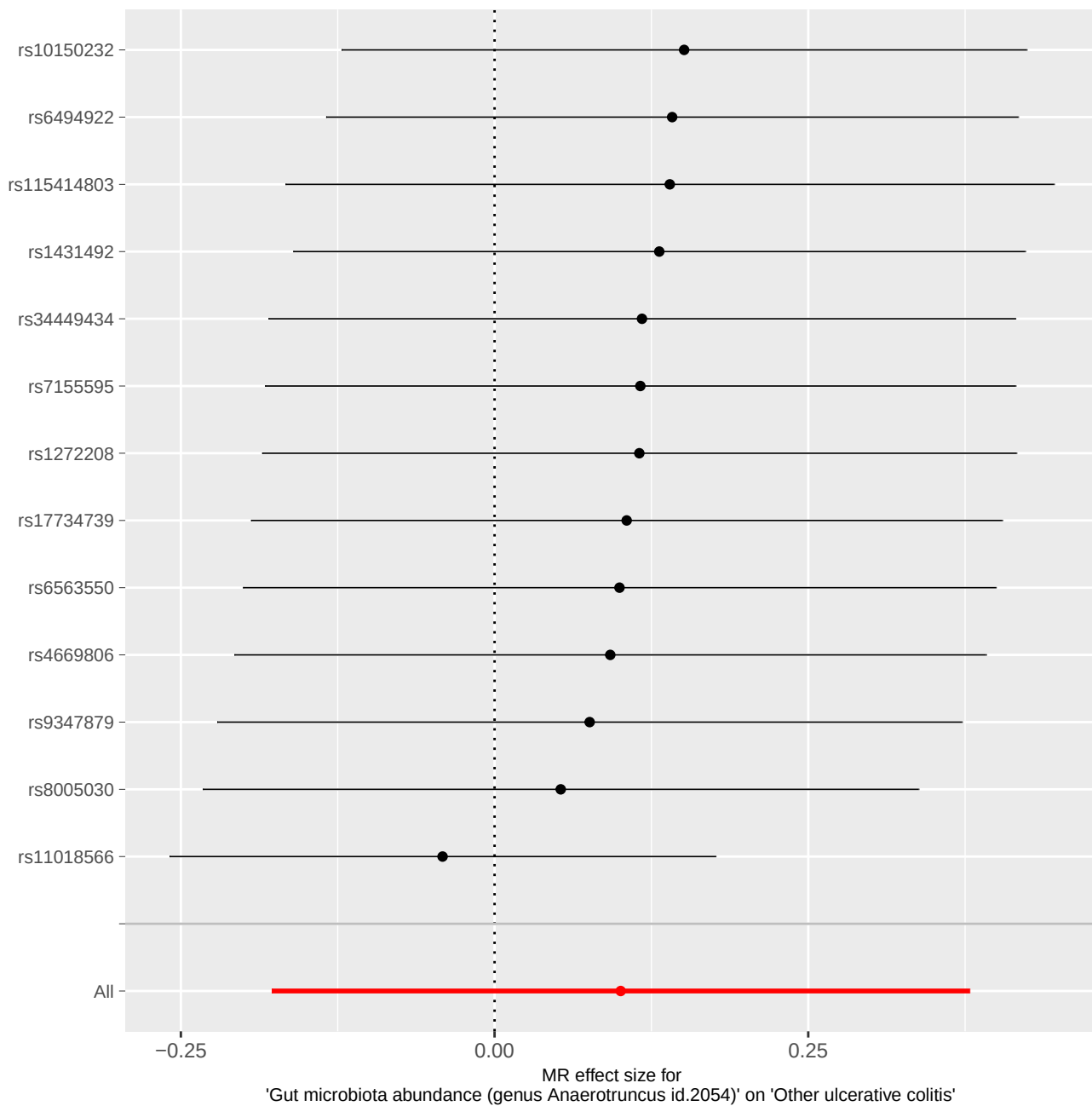


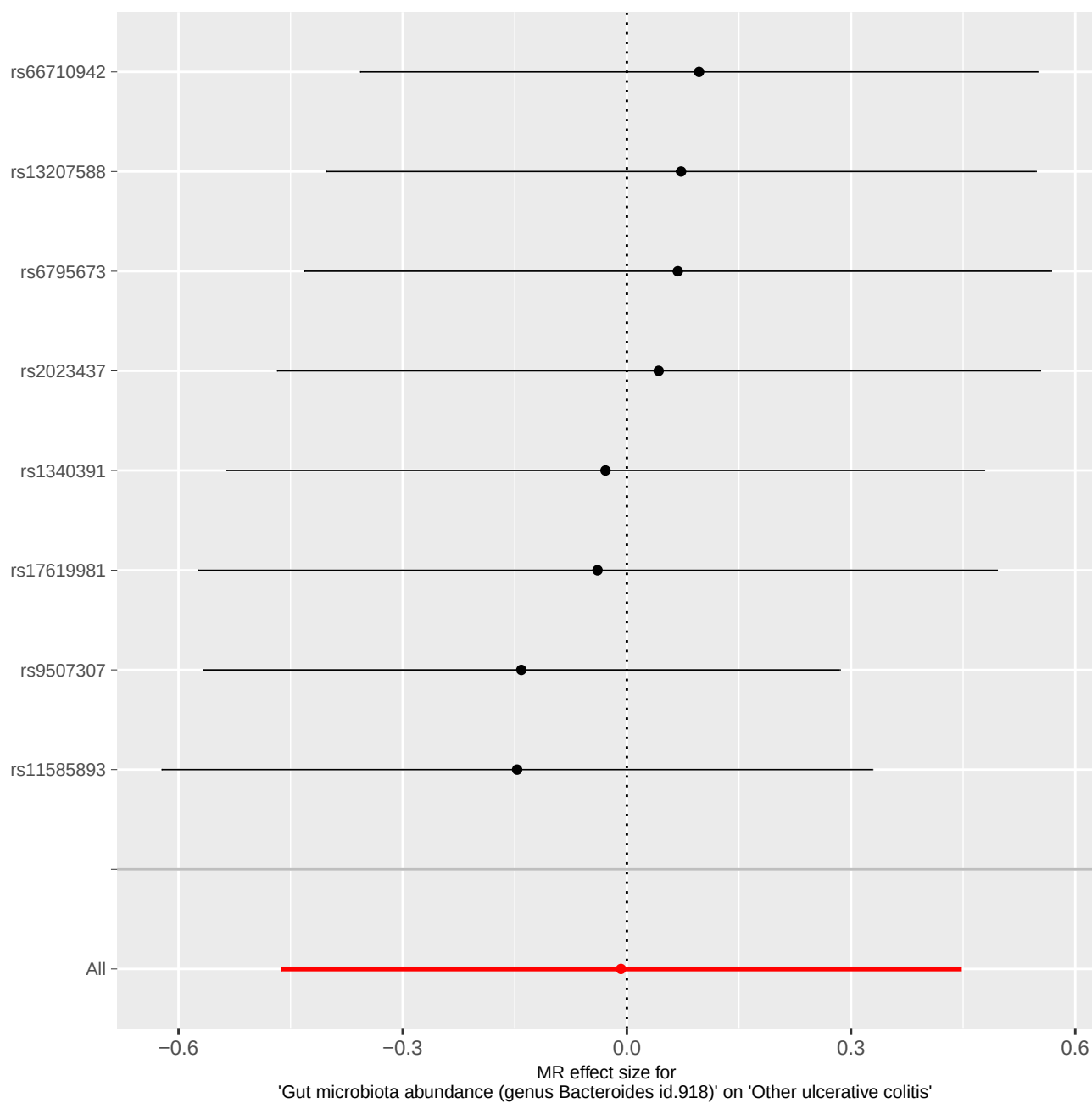


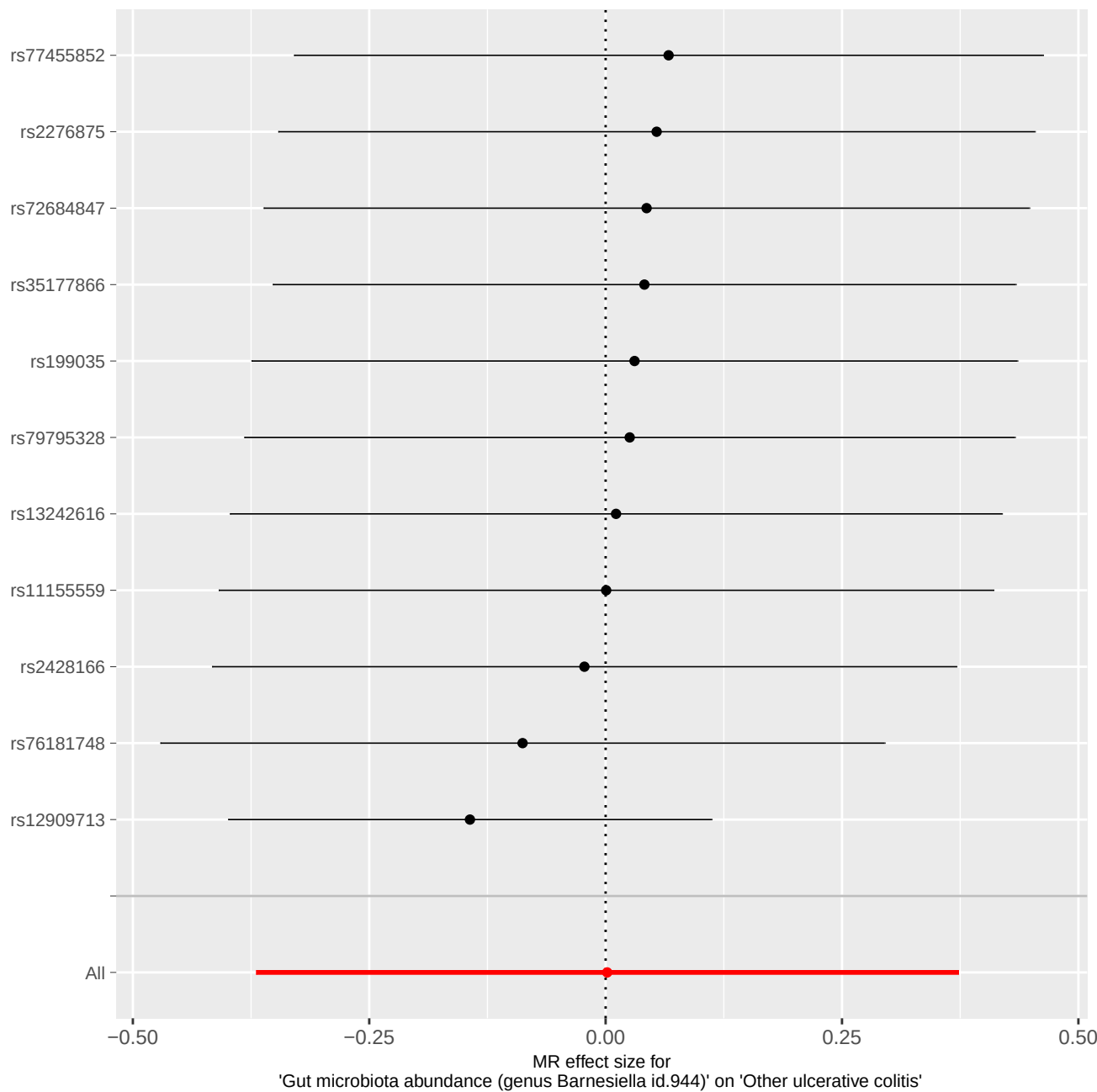


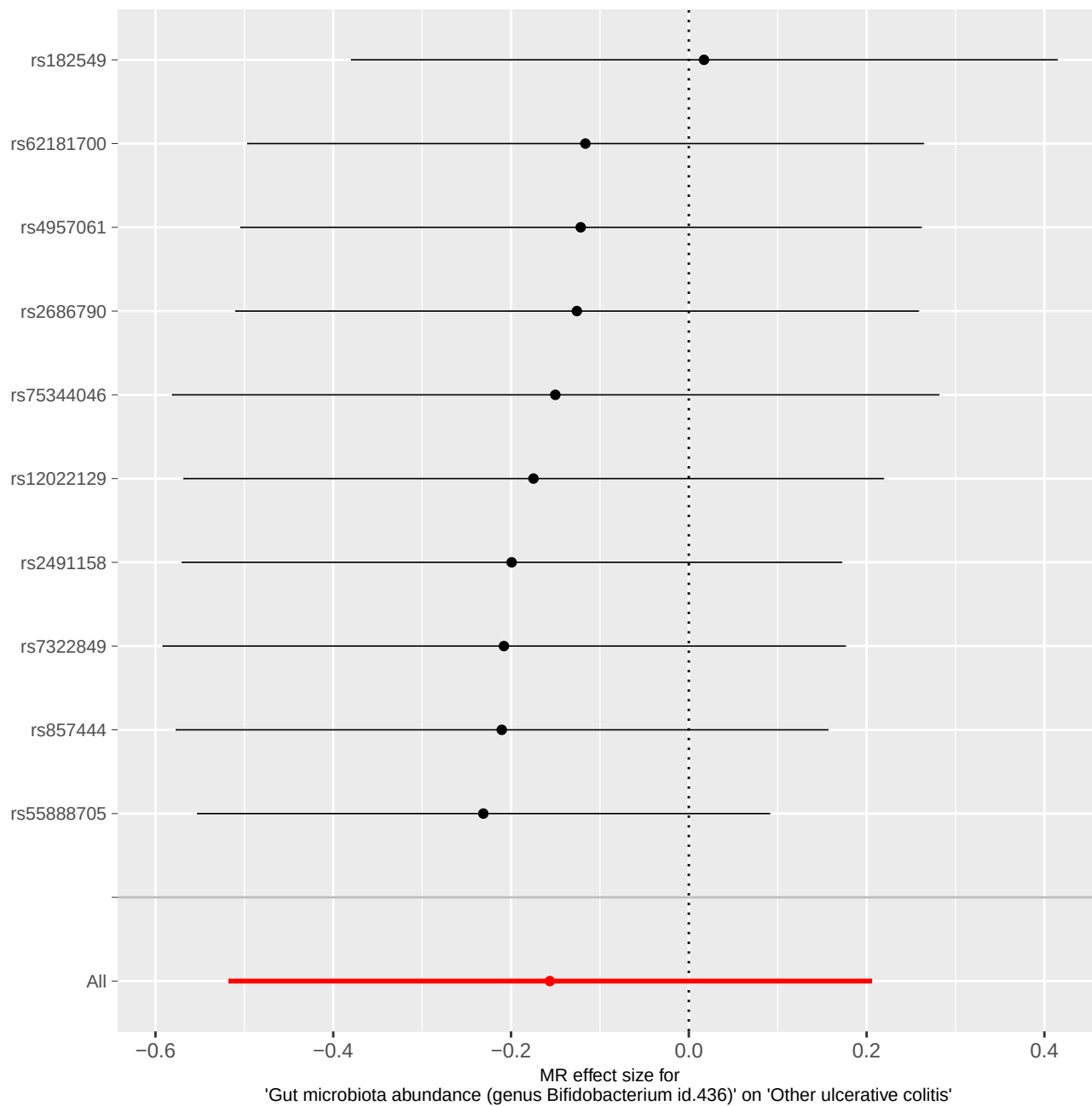


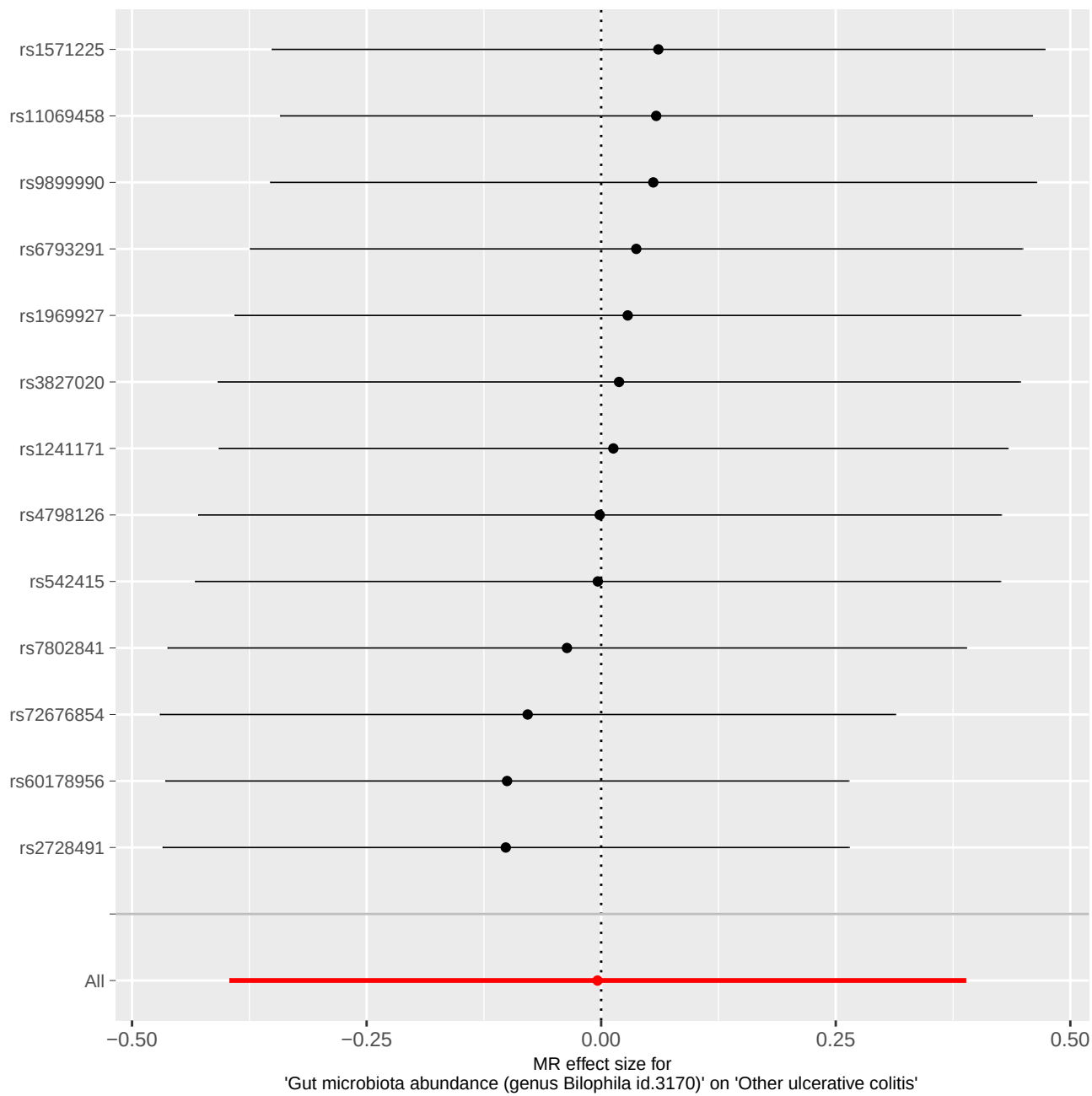


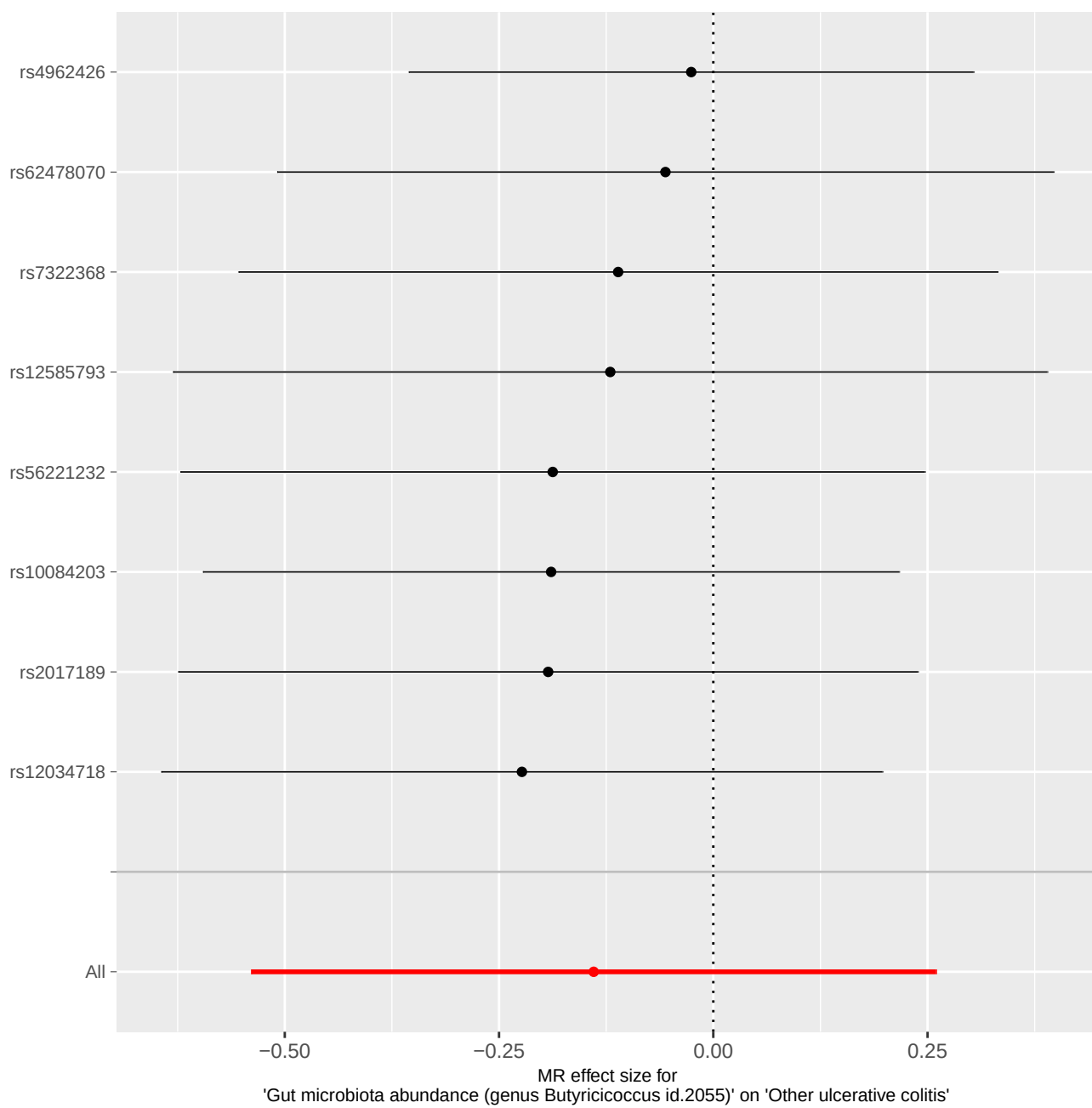


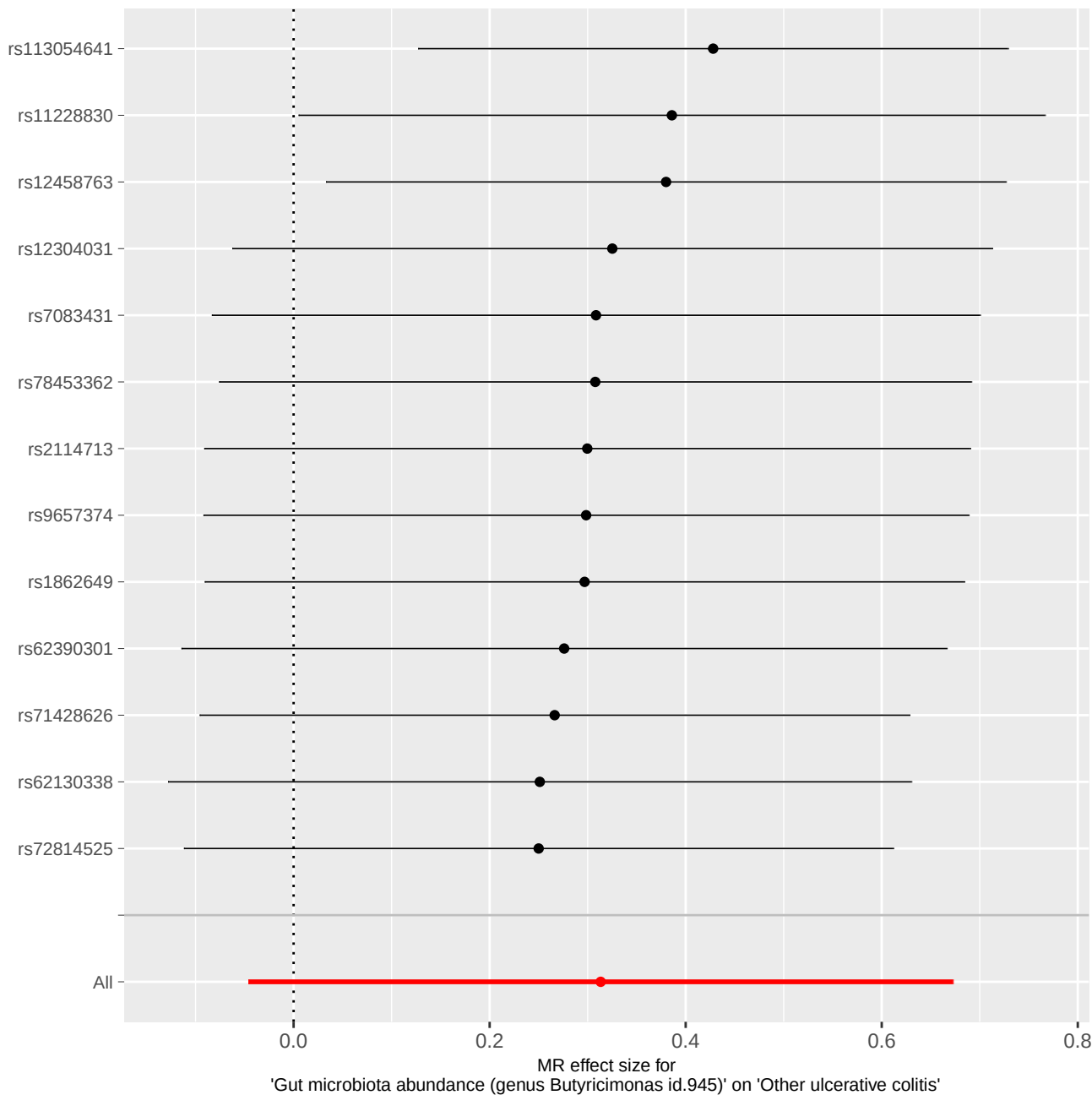


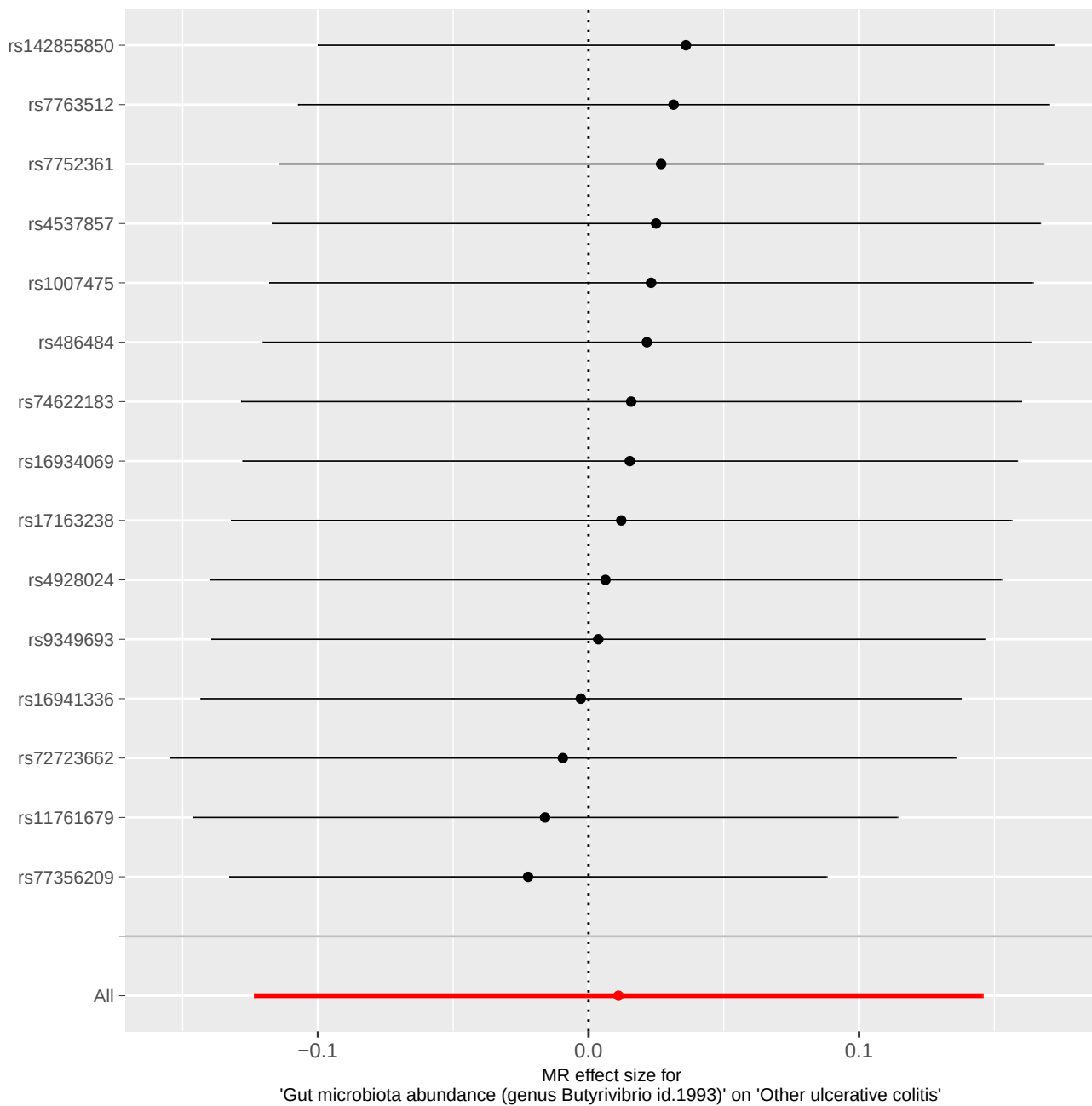


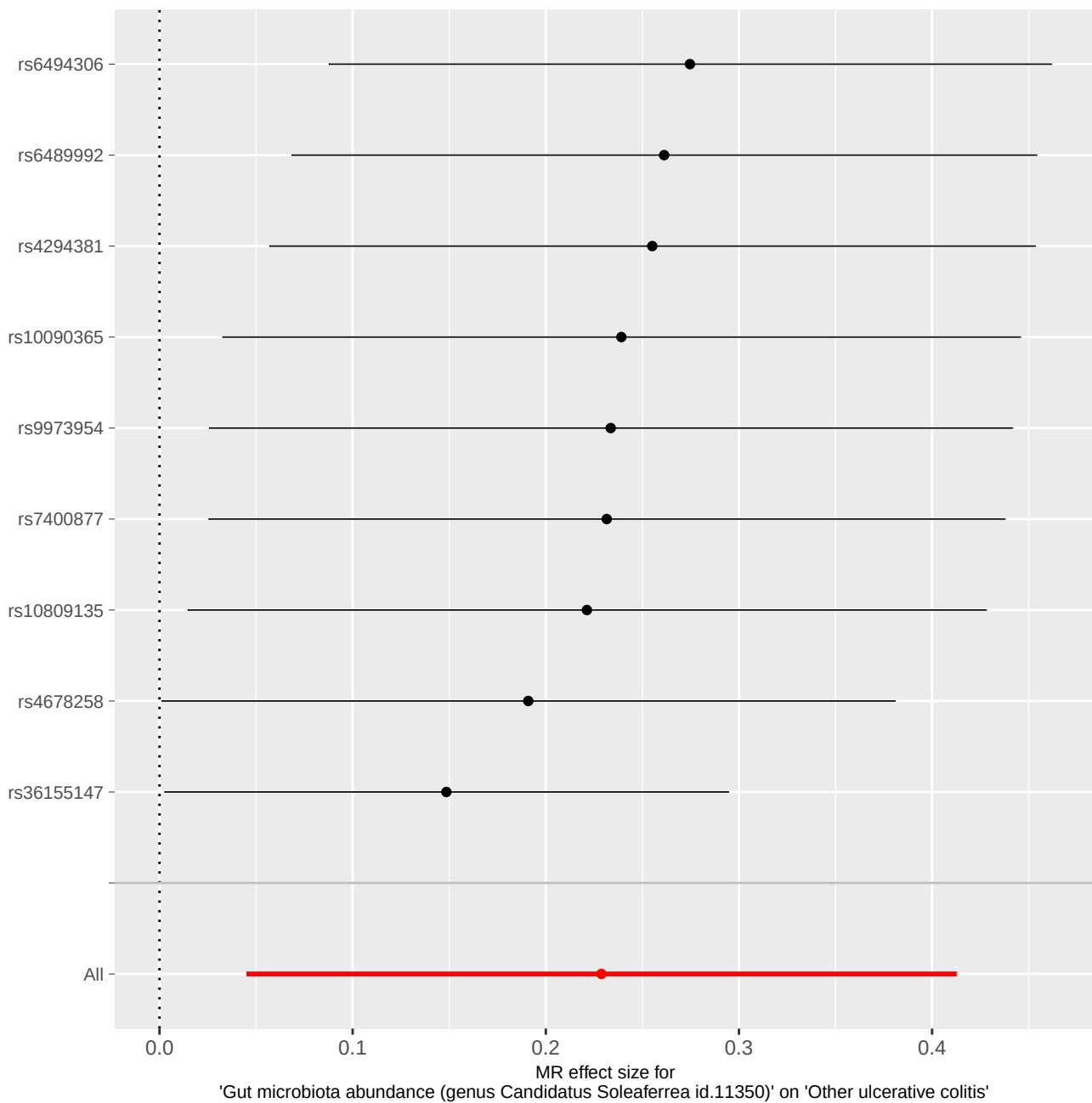


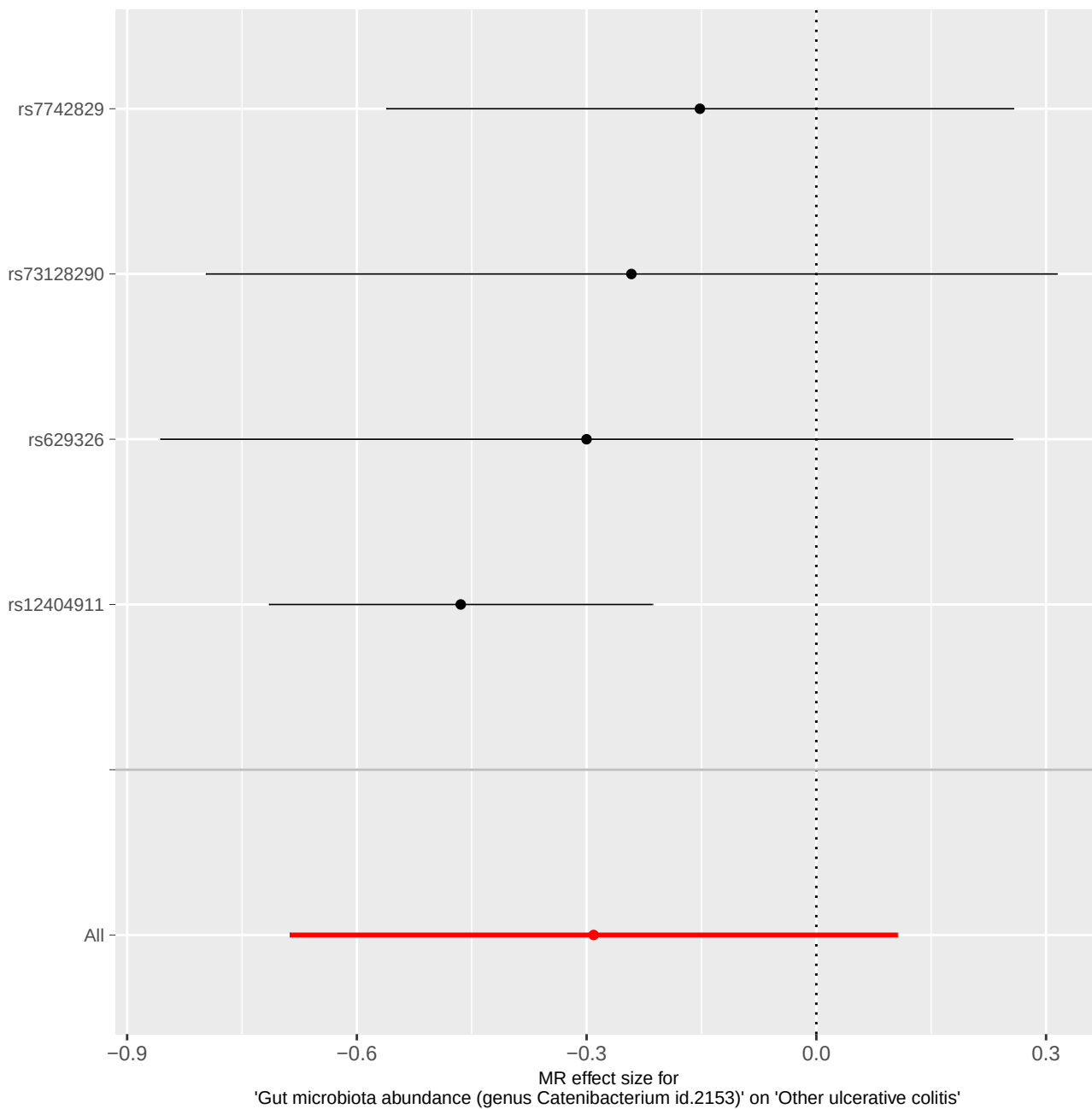


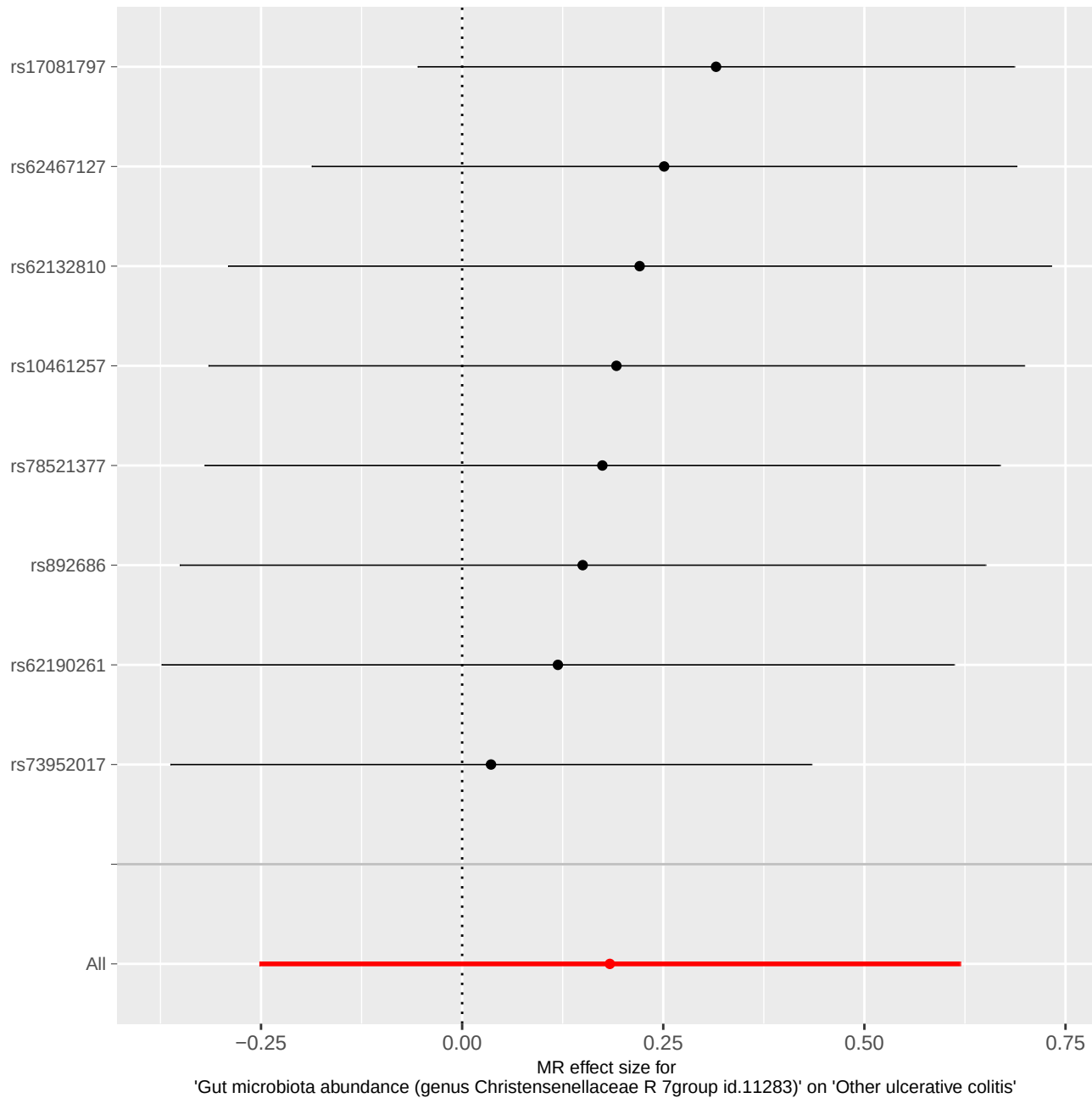


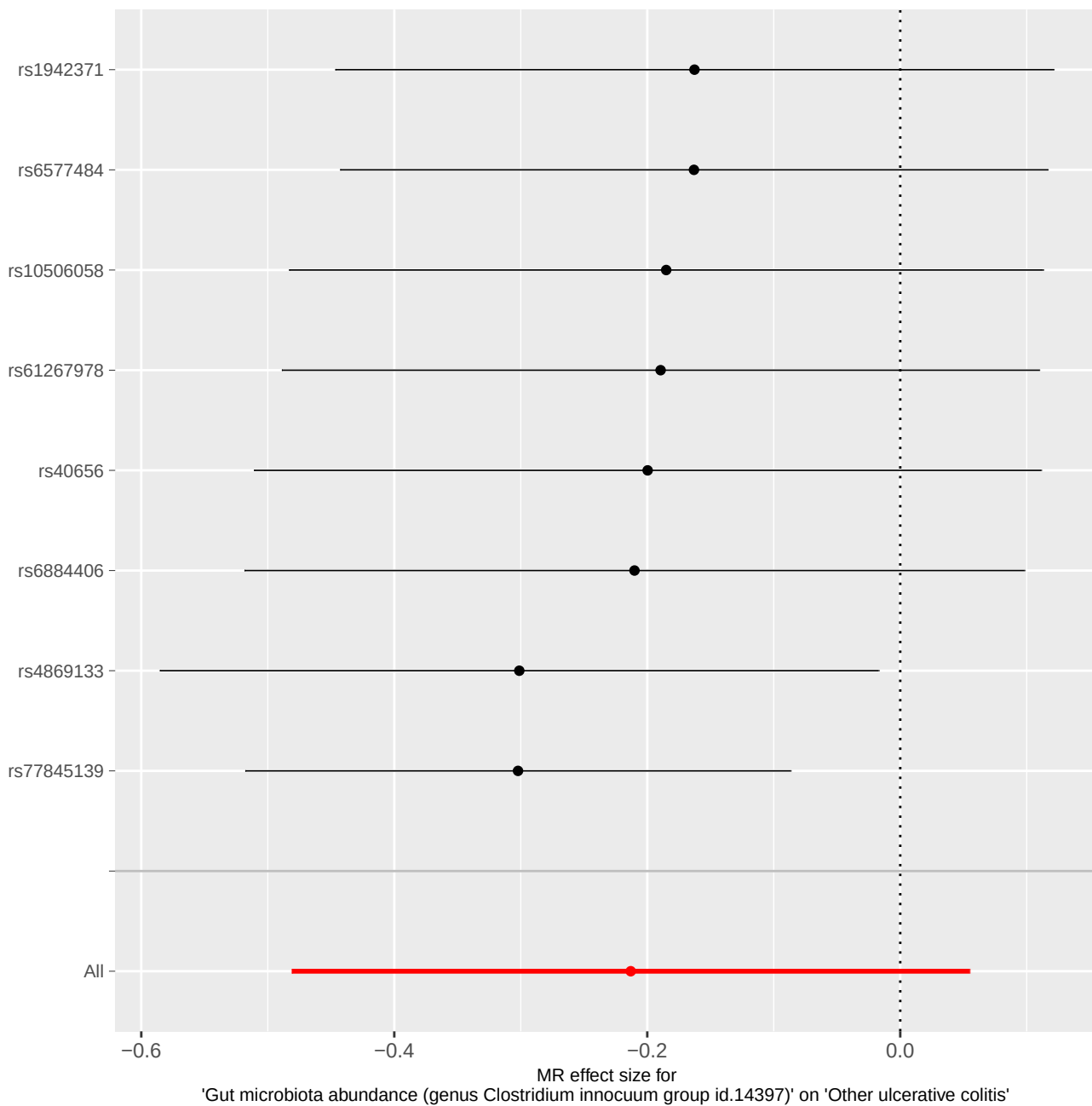


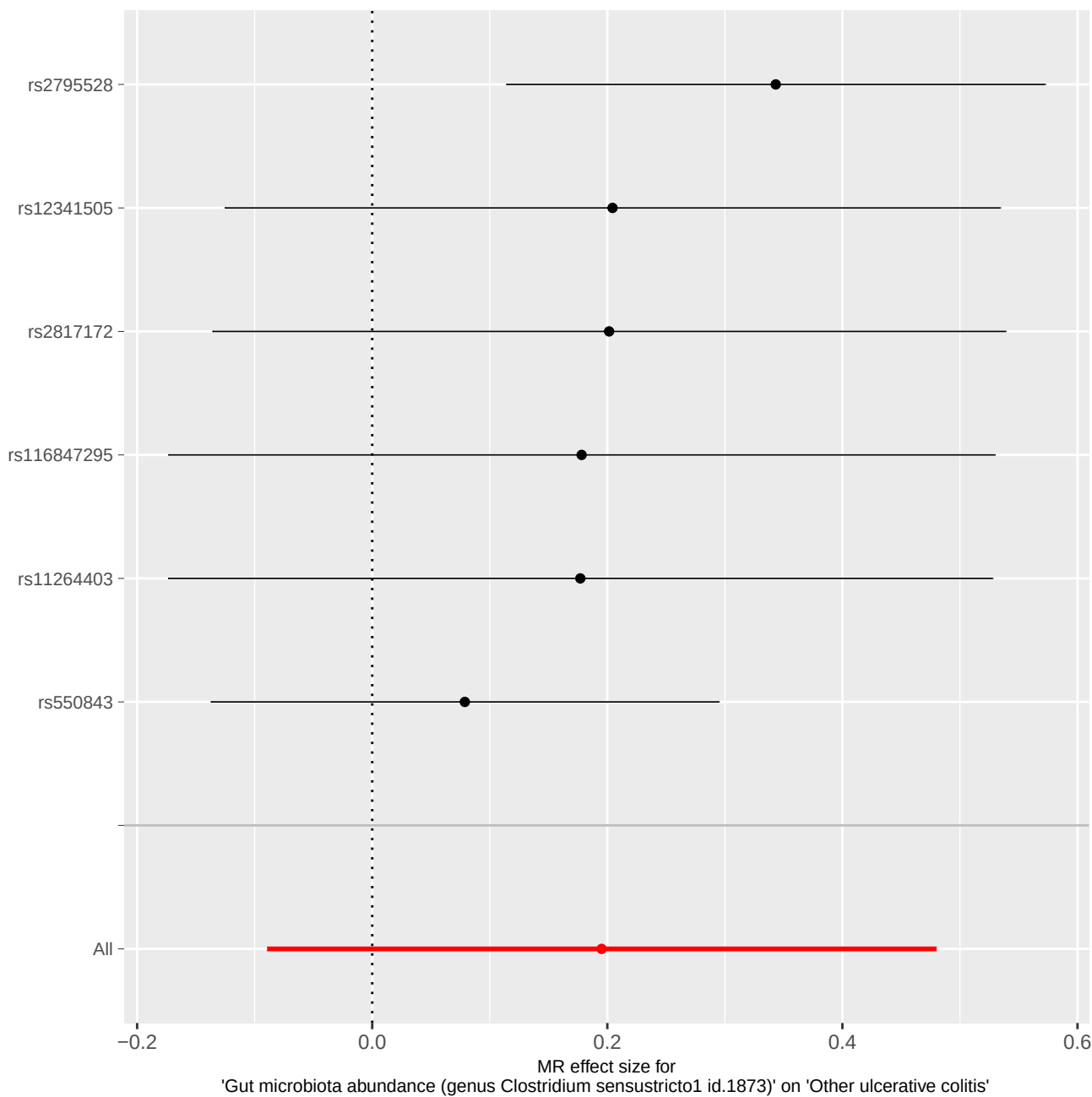


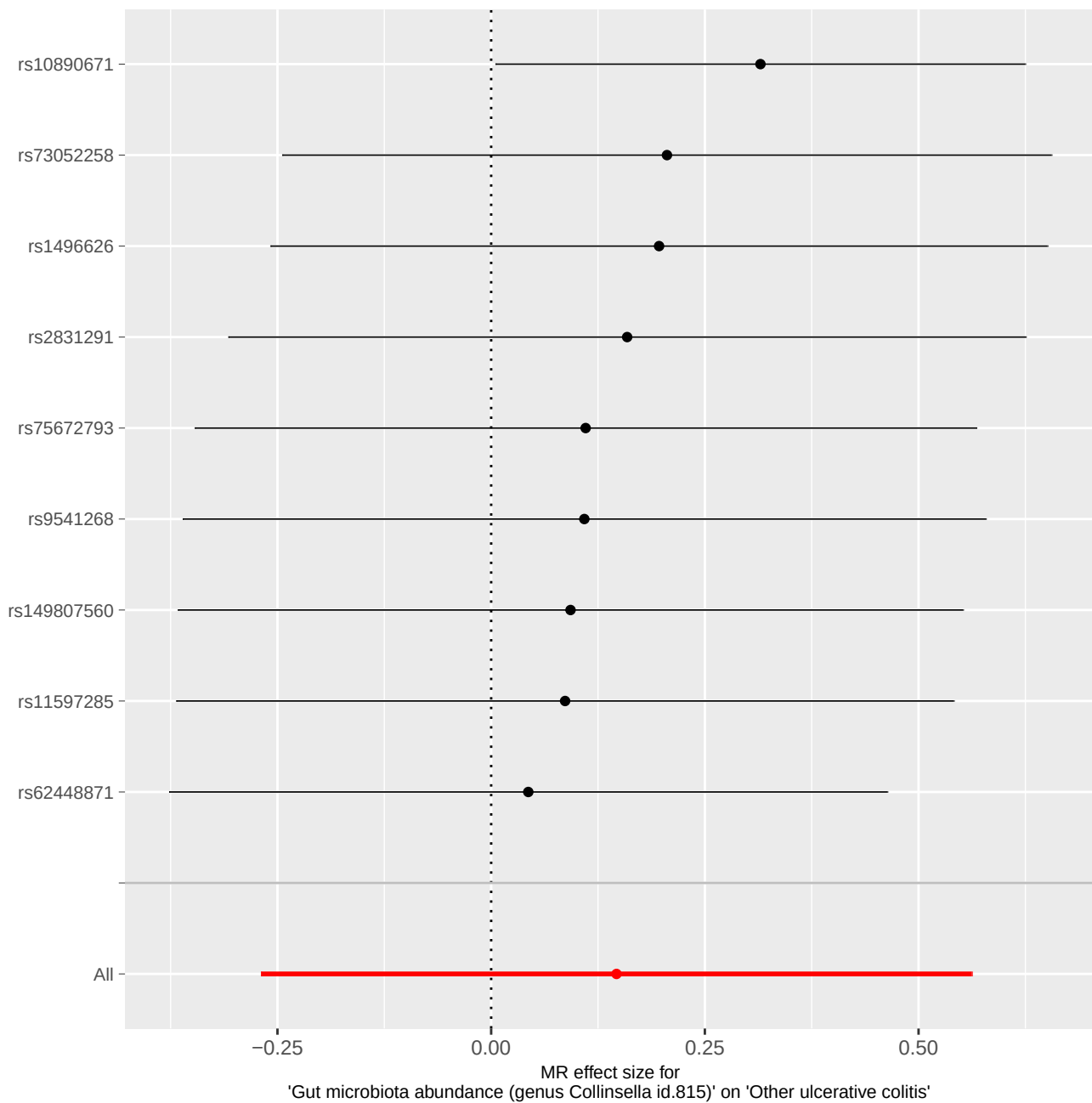


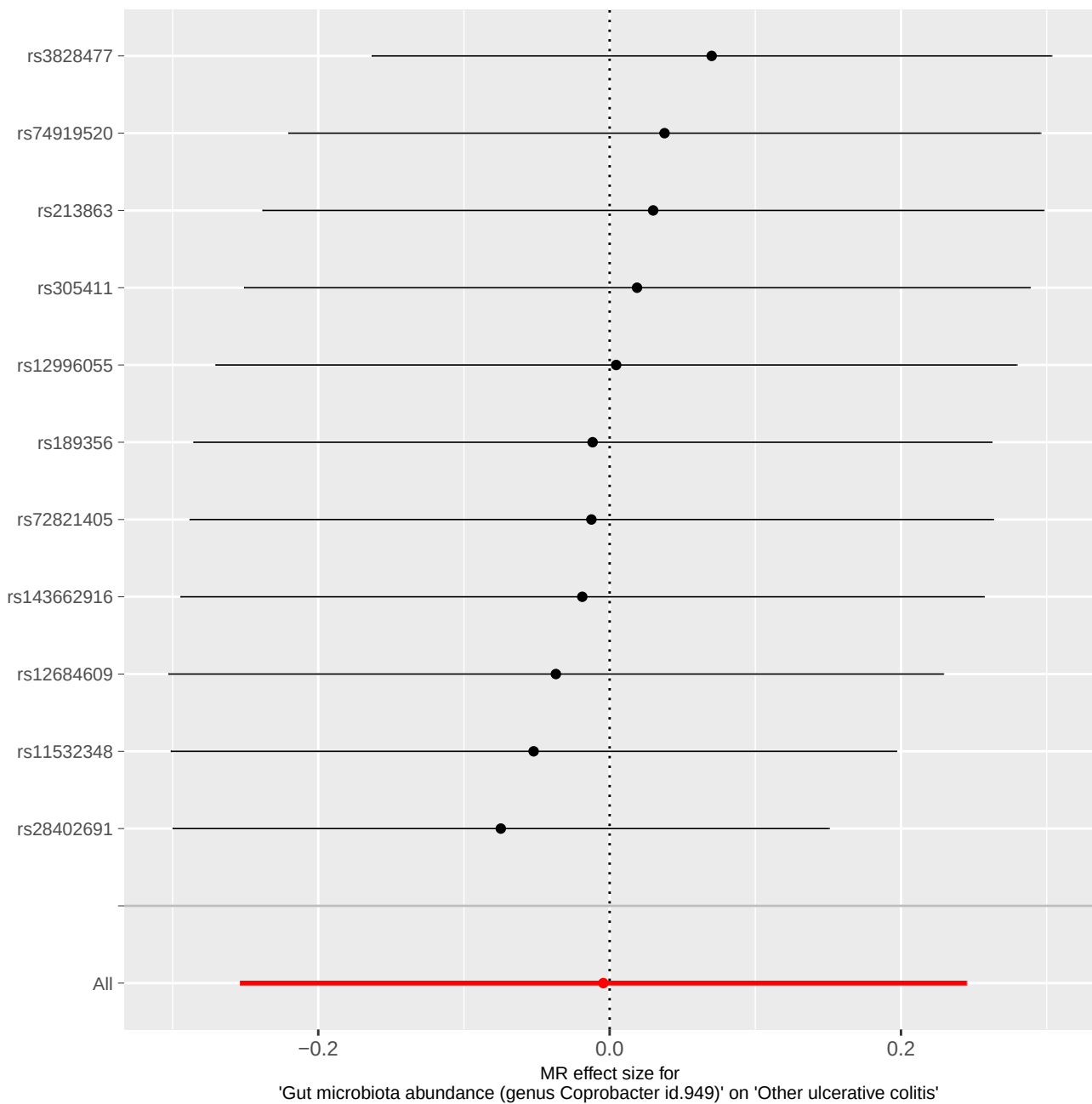


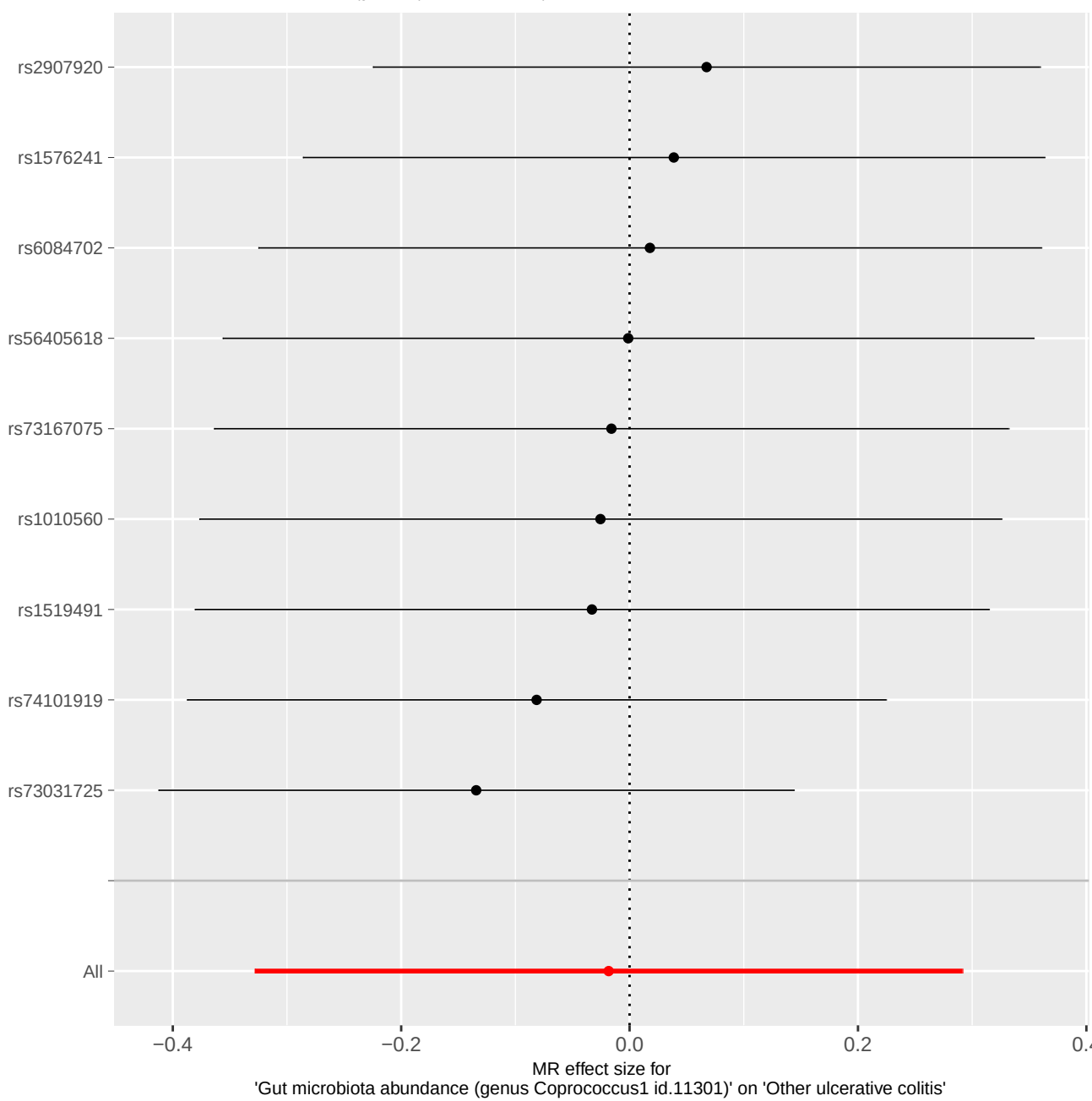


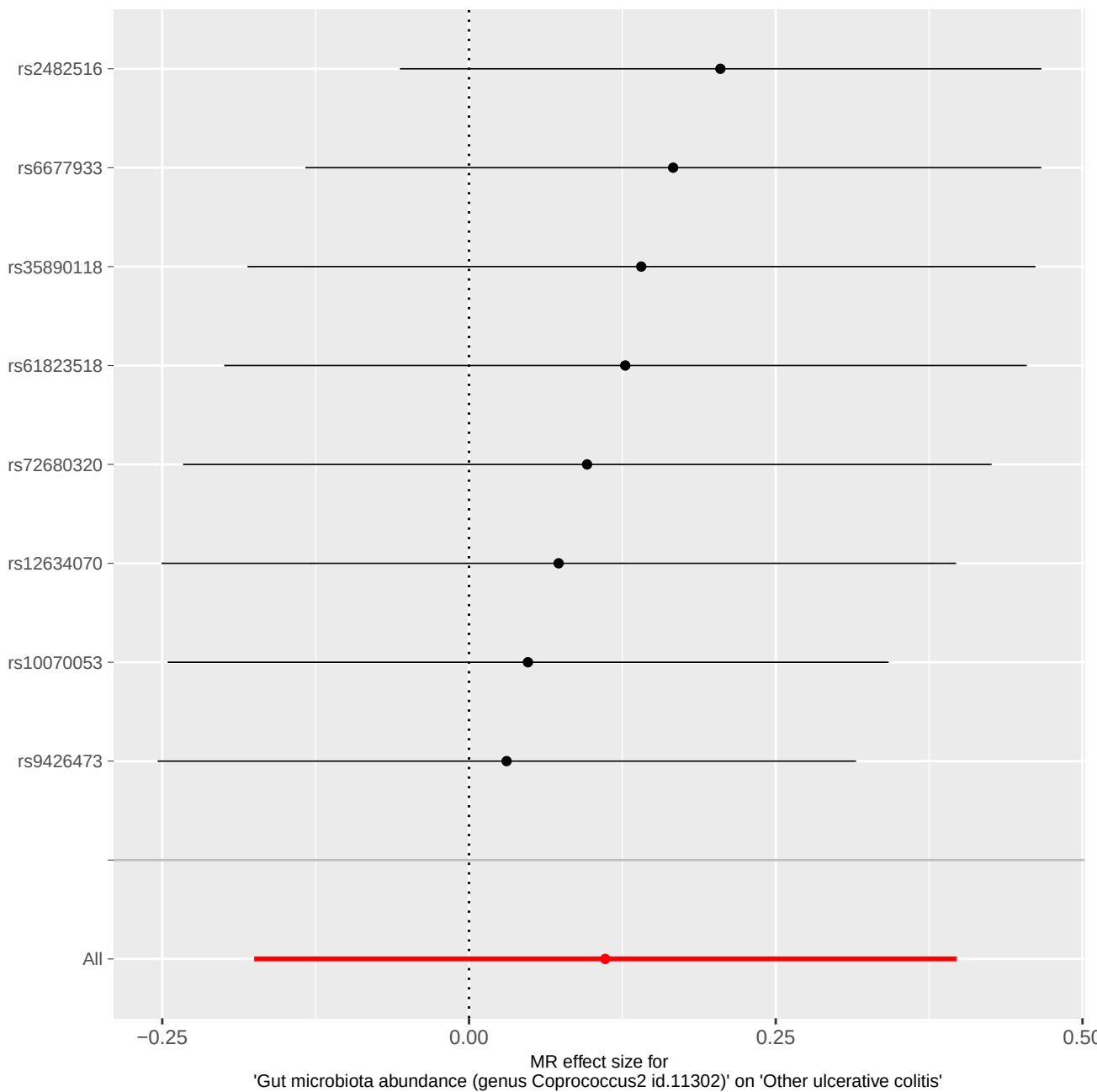




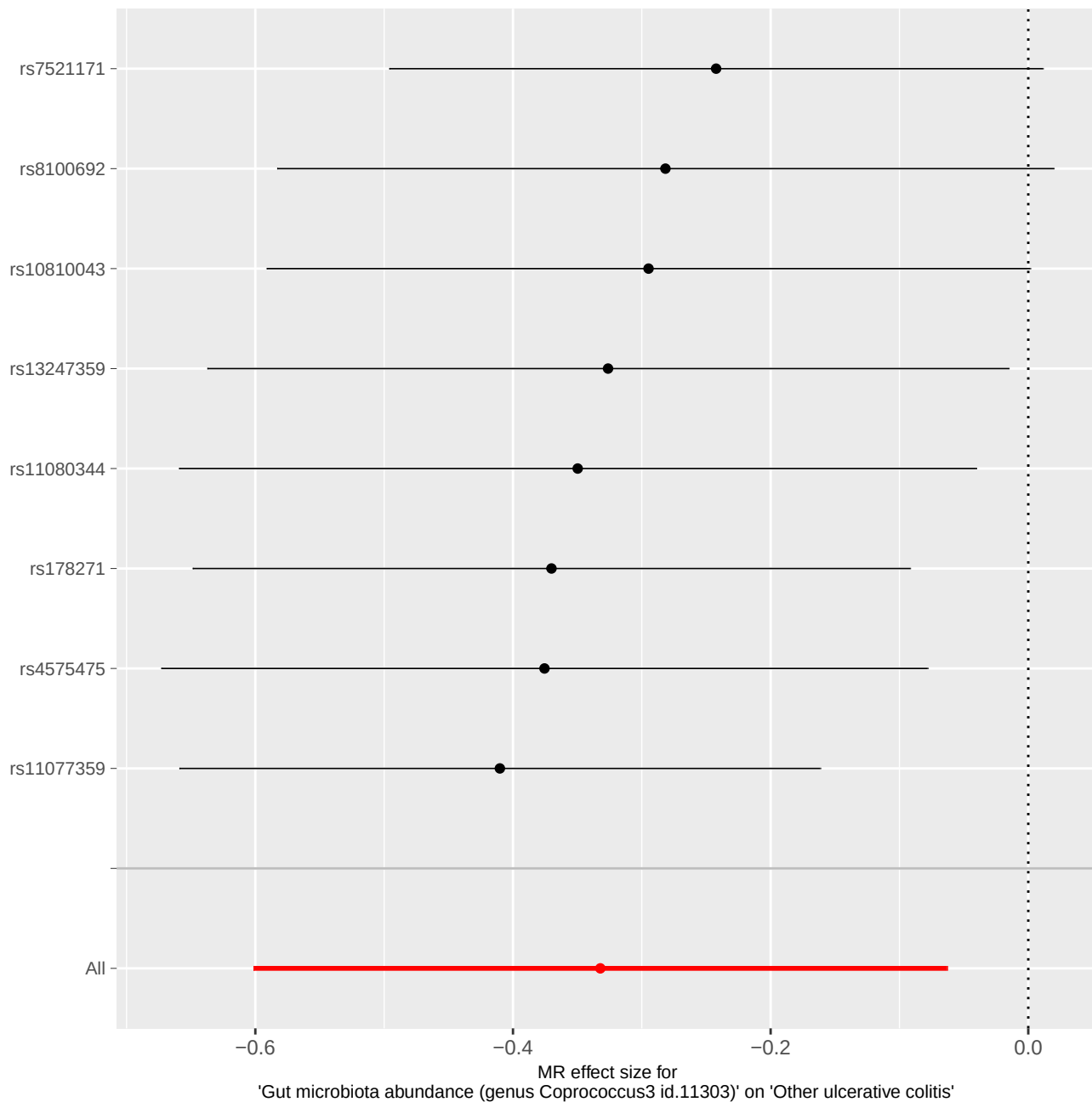


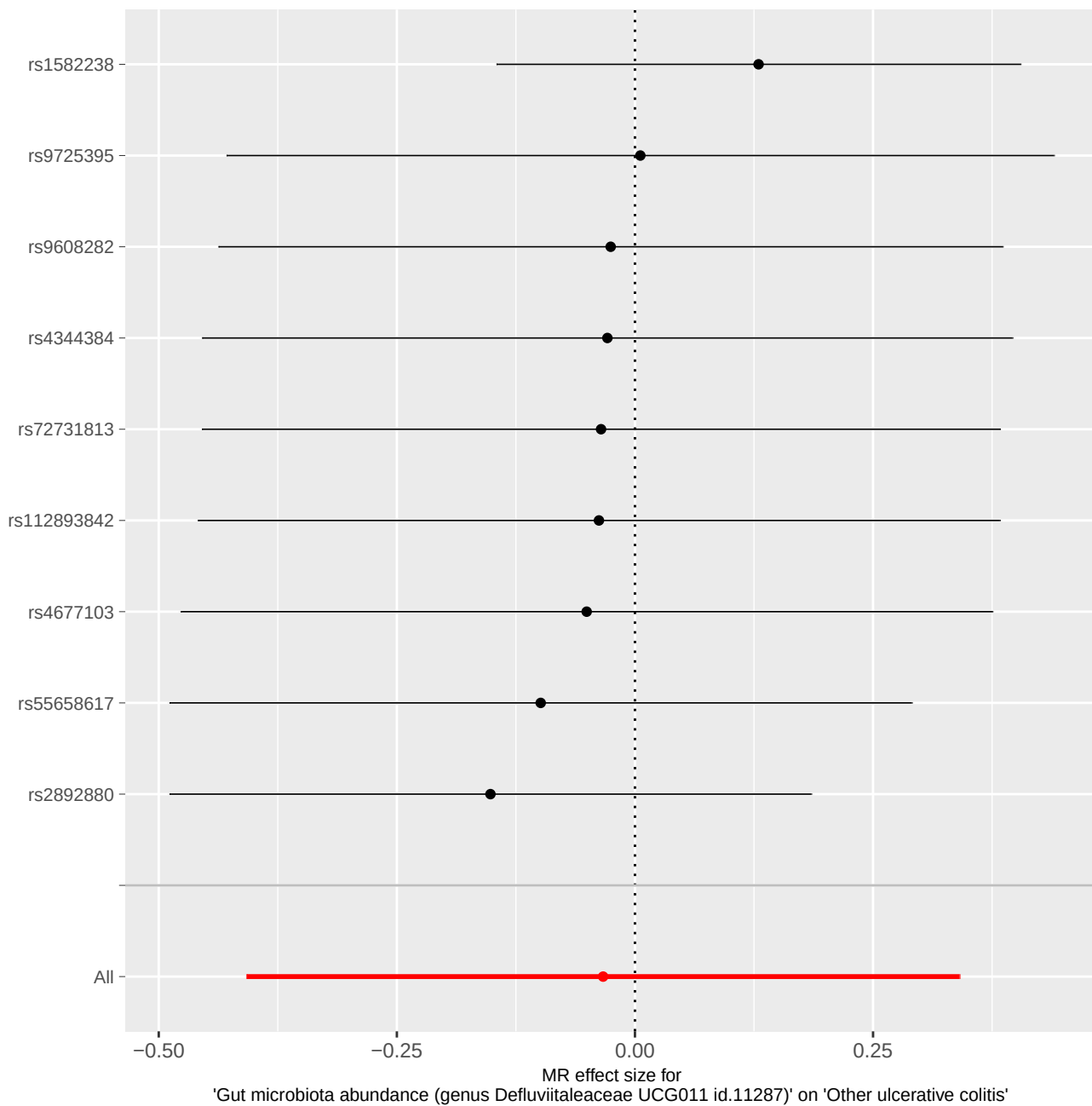


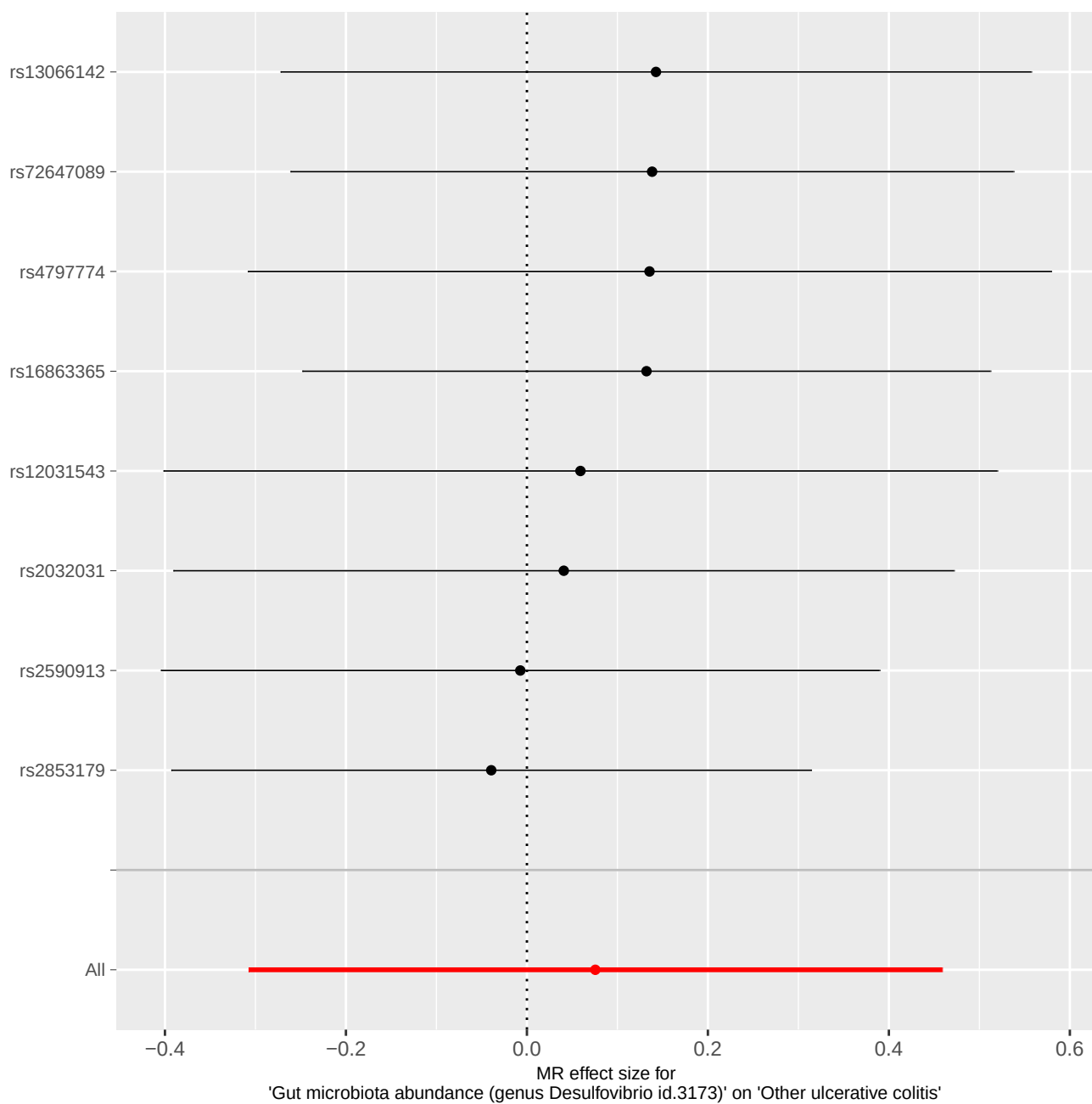


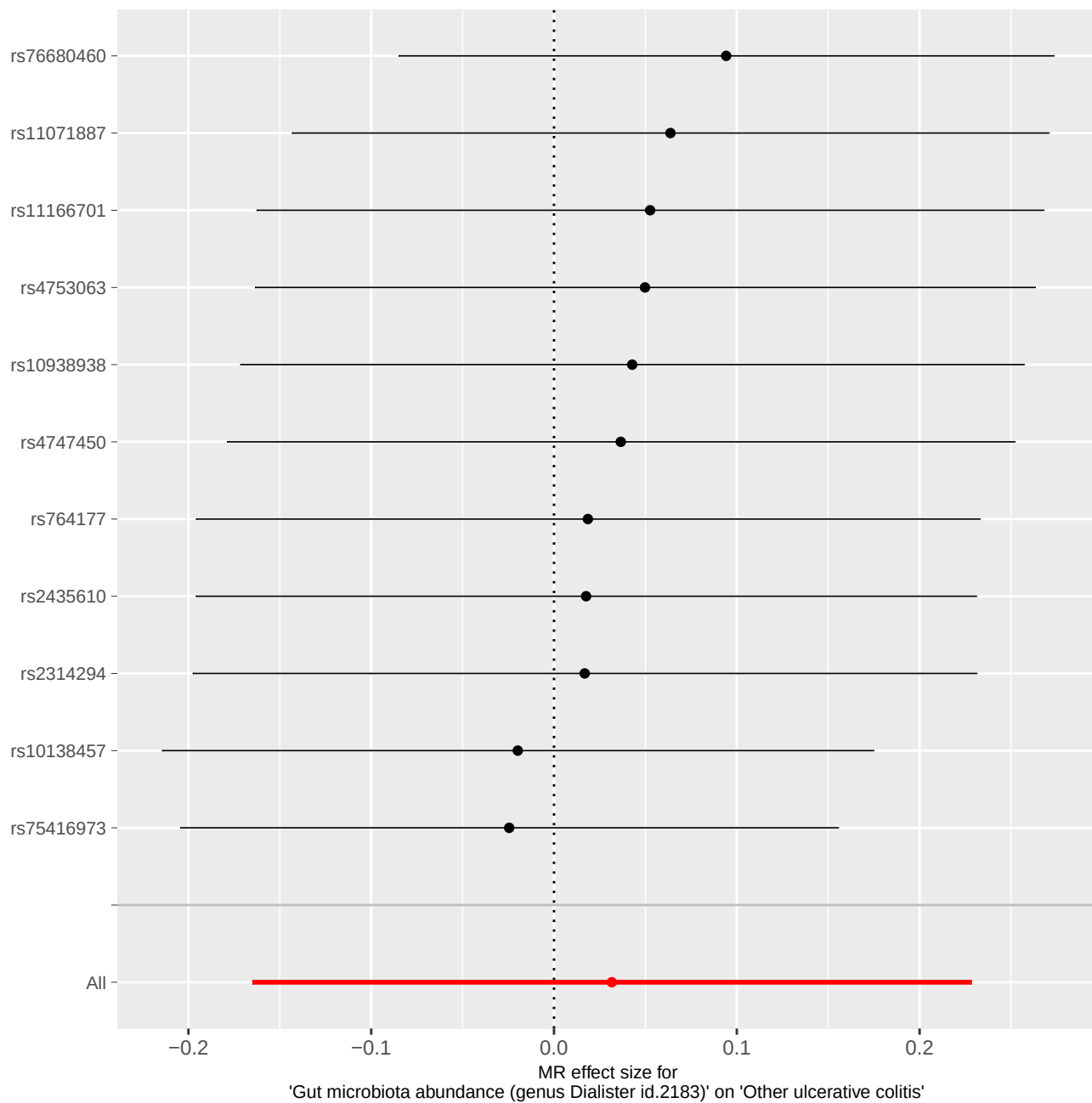


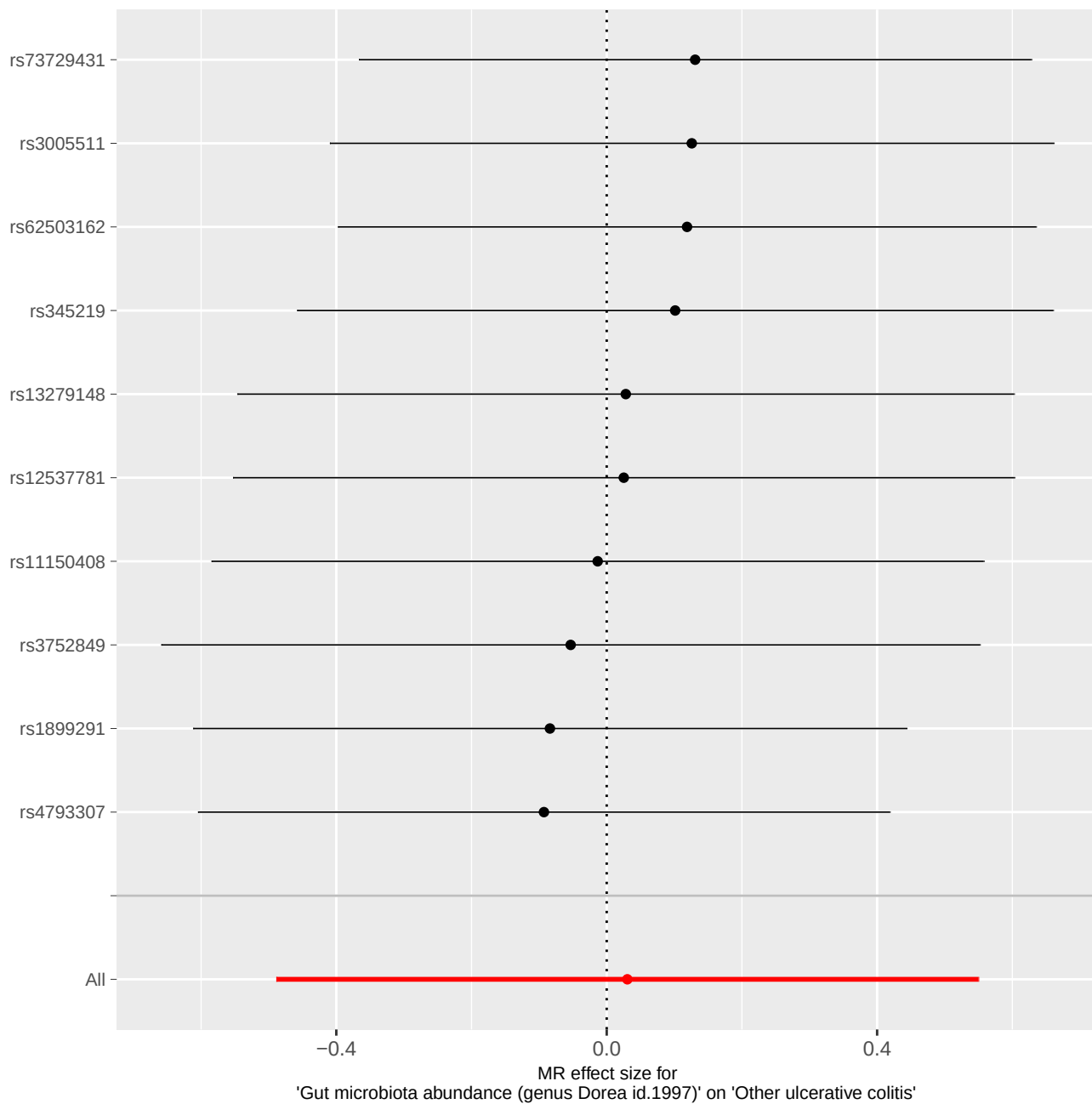
MR effect size for
'Gut microbiota abundance (genus Coprococcus2 id.11302)' on 'Other ulcerative colitis'

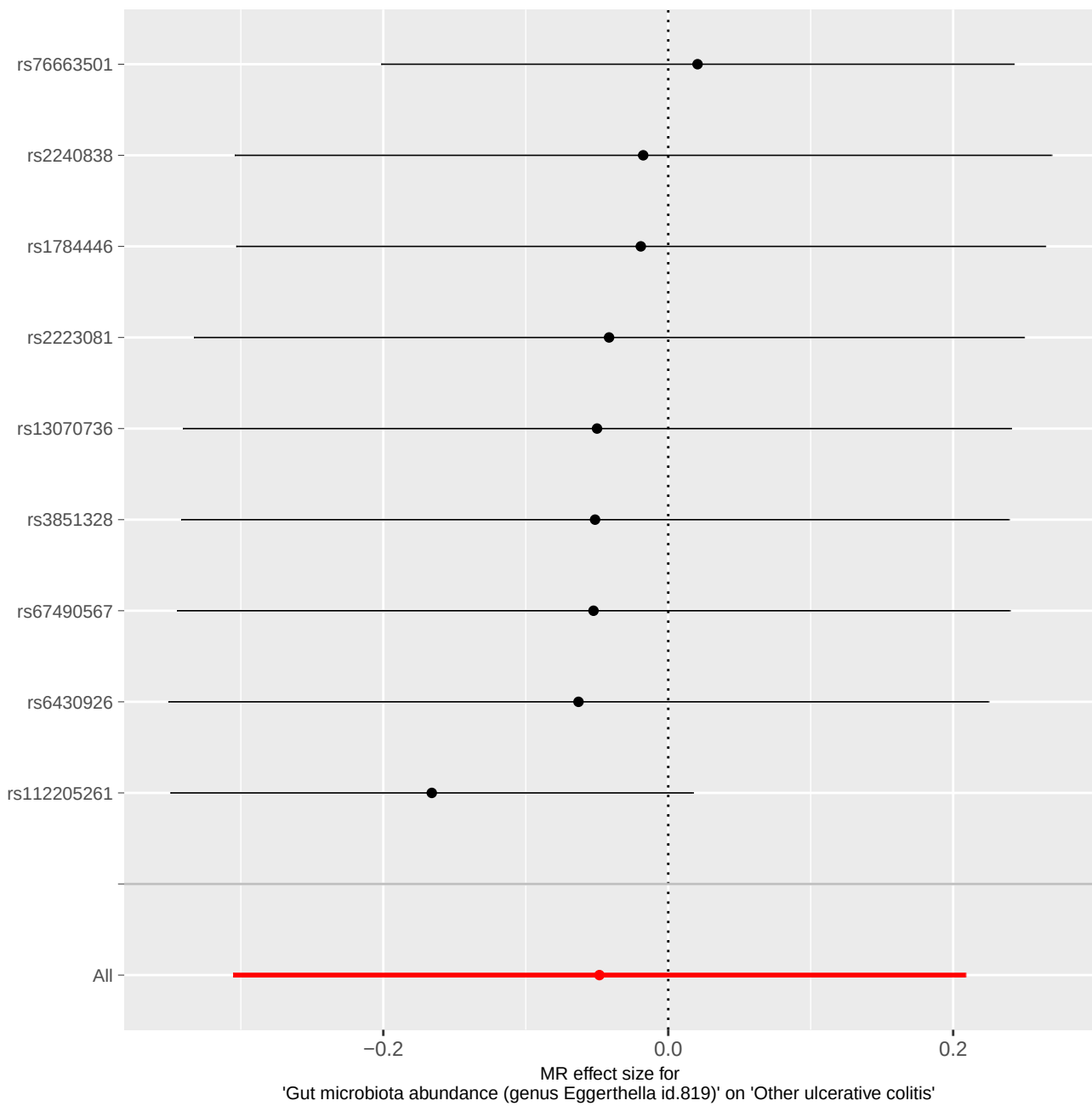


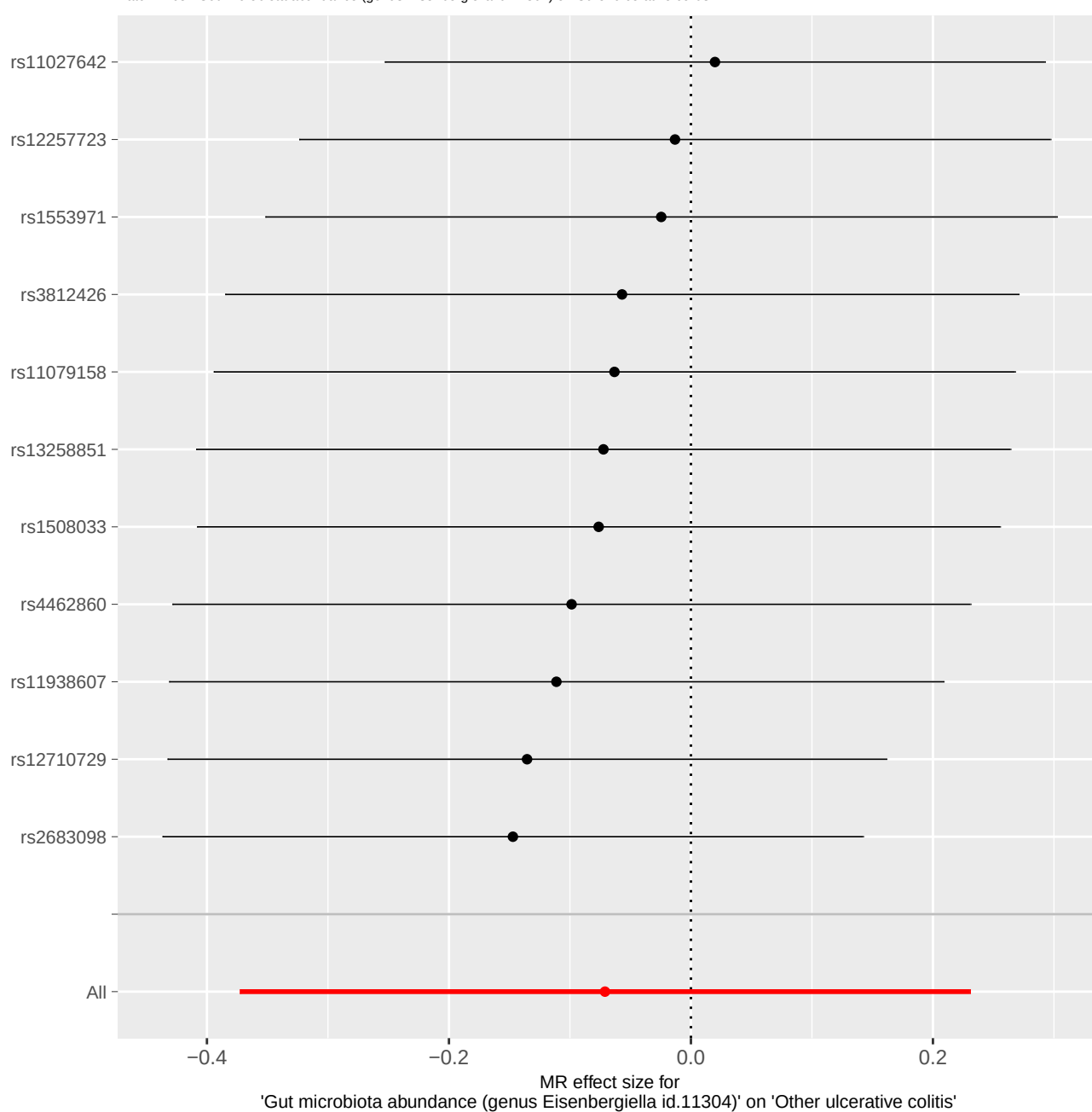


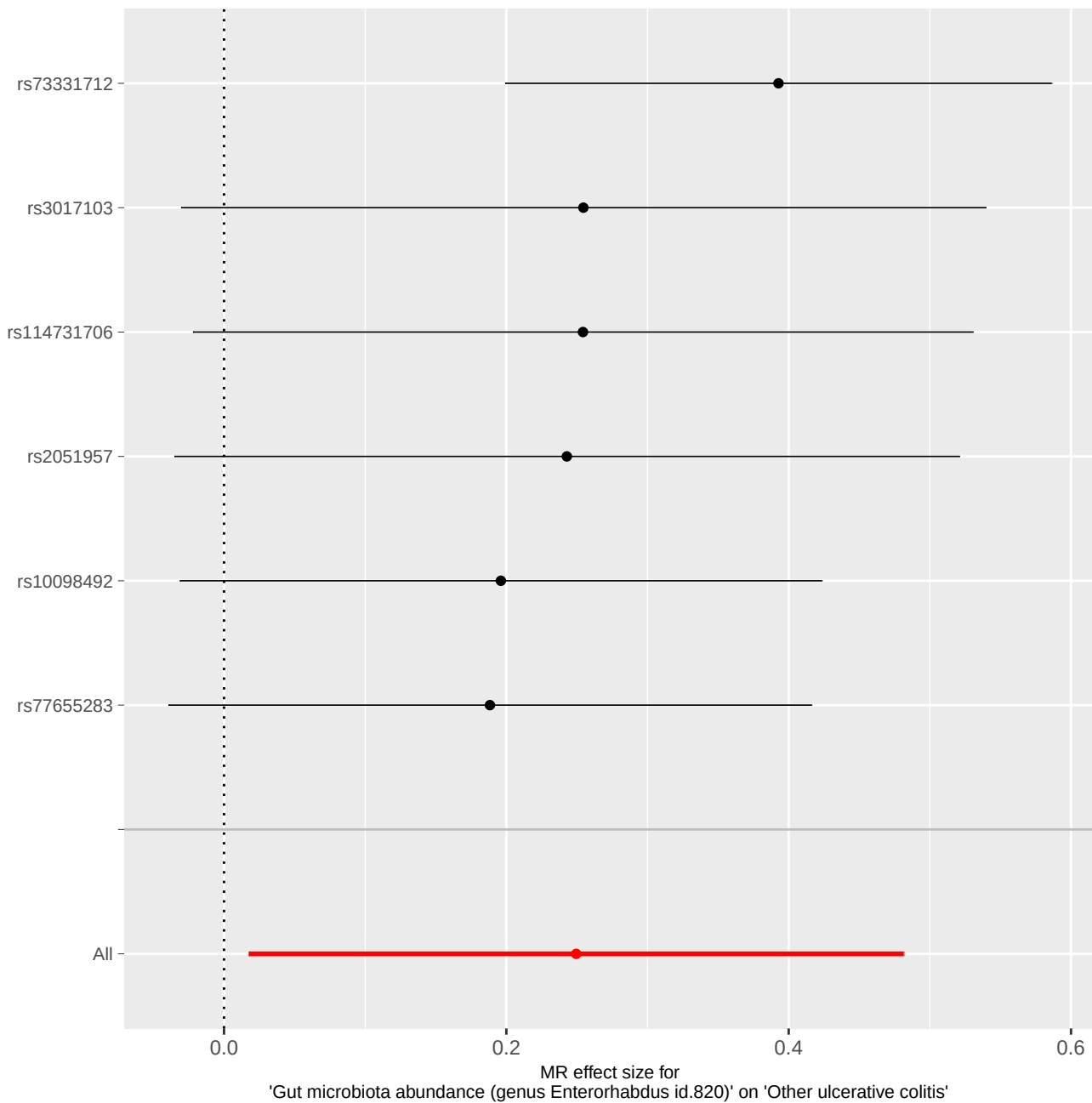




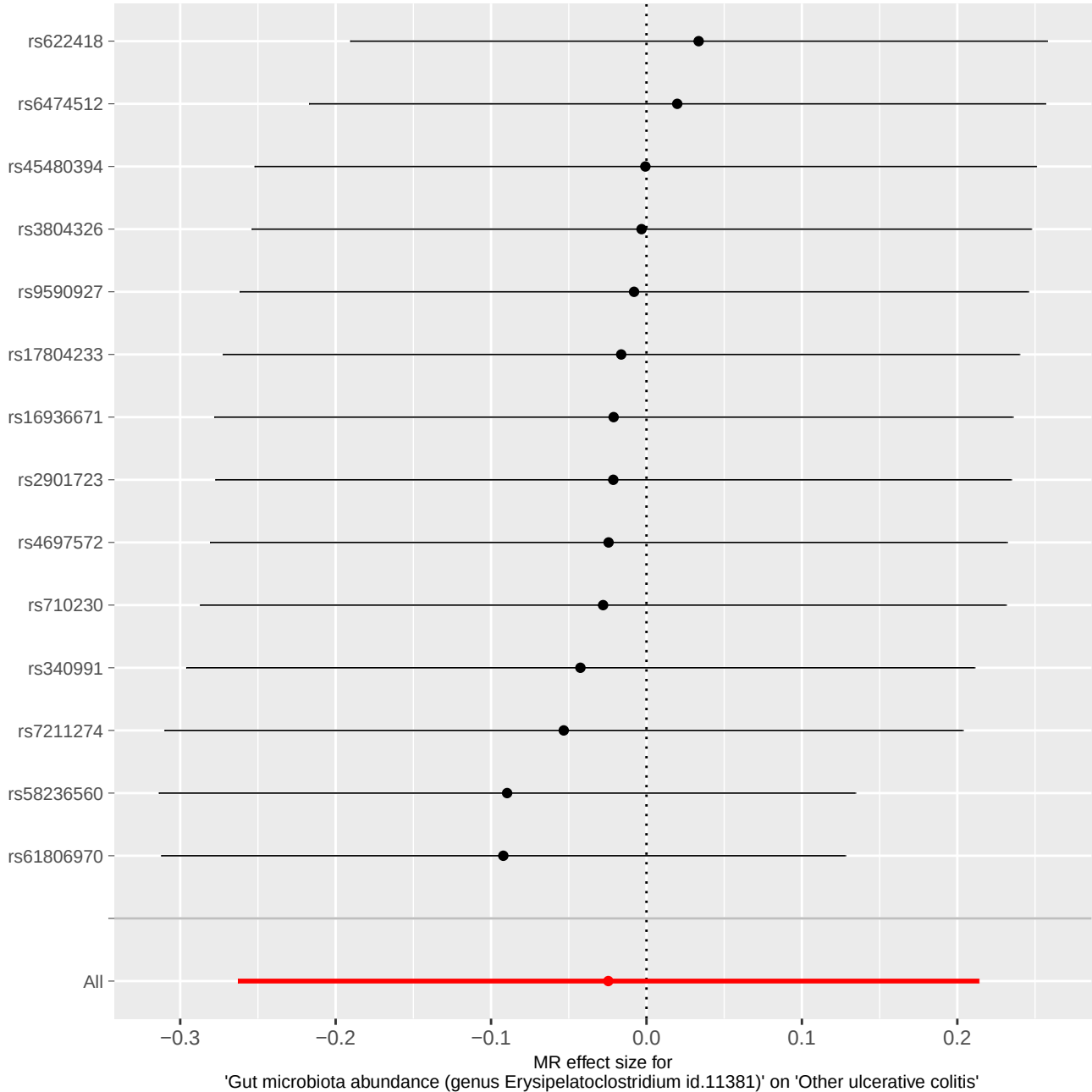


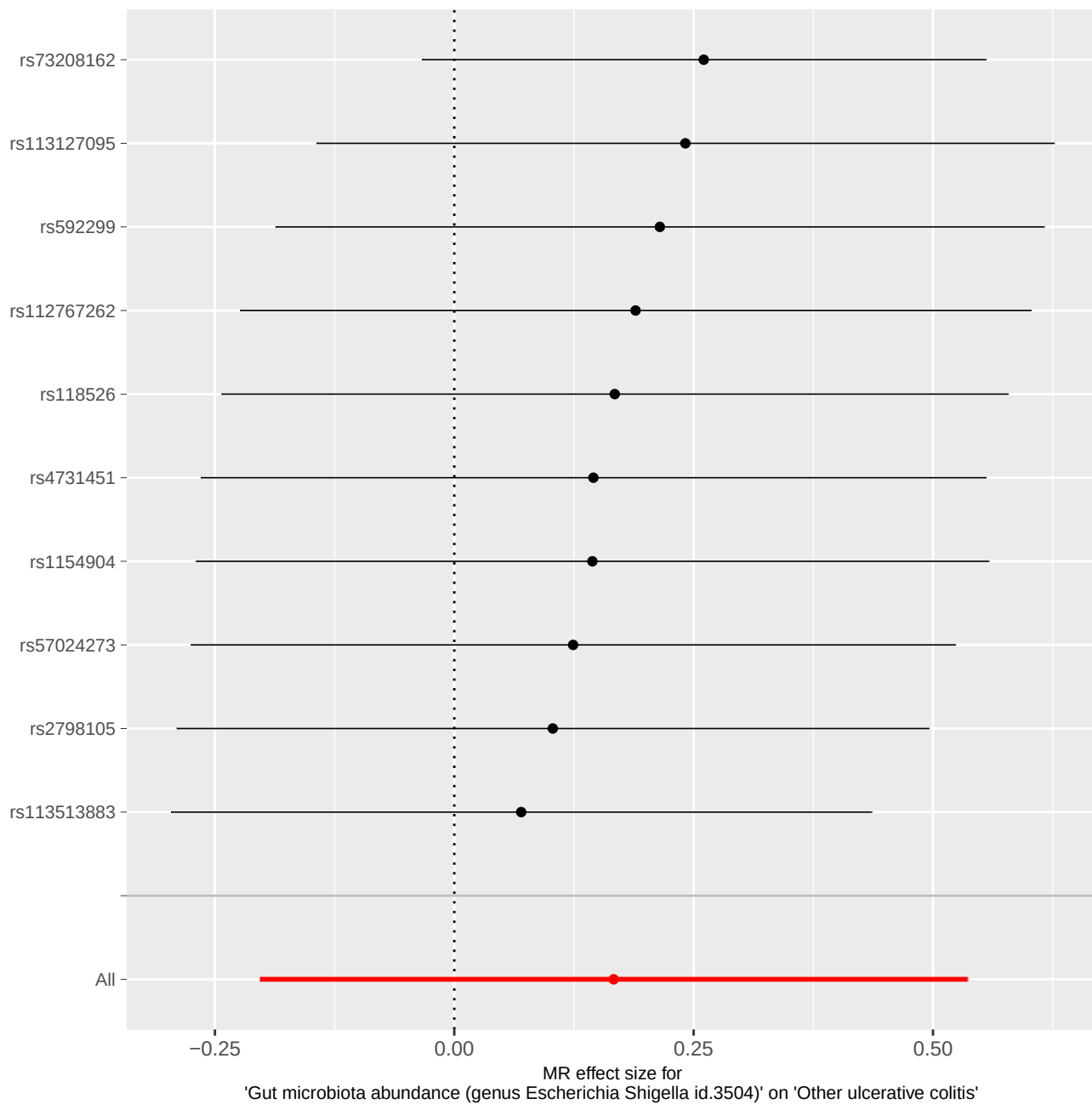


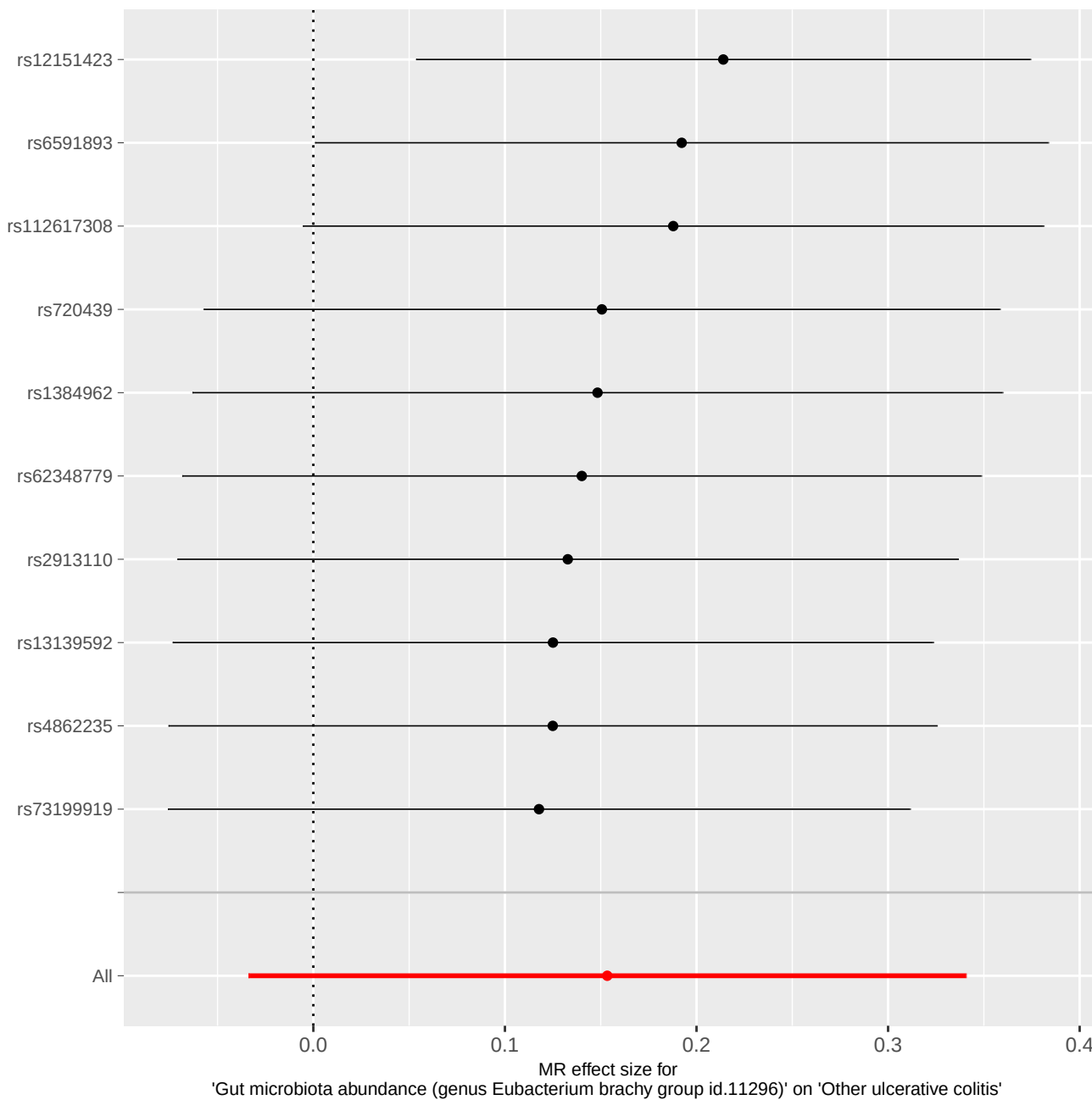


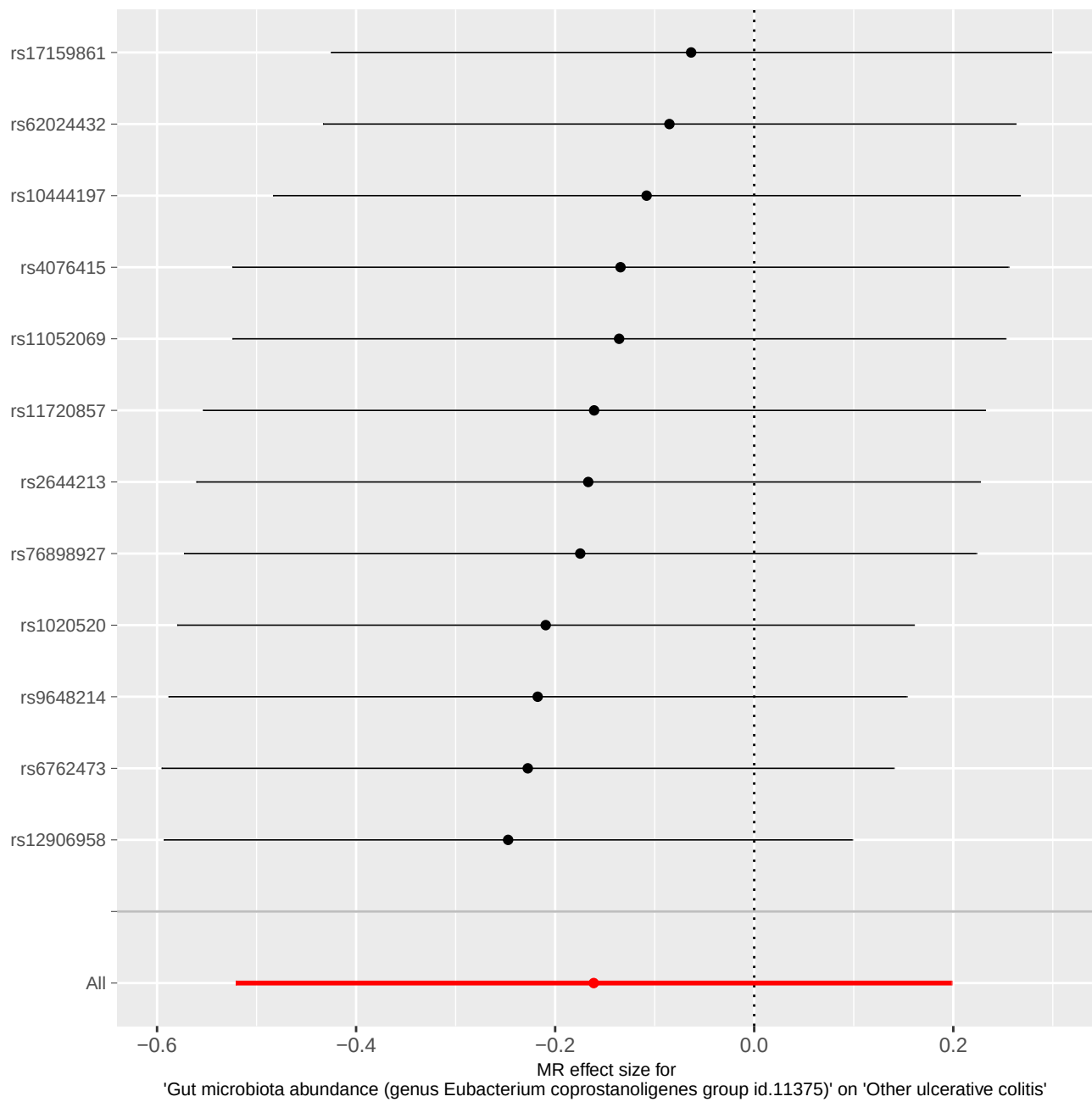


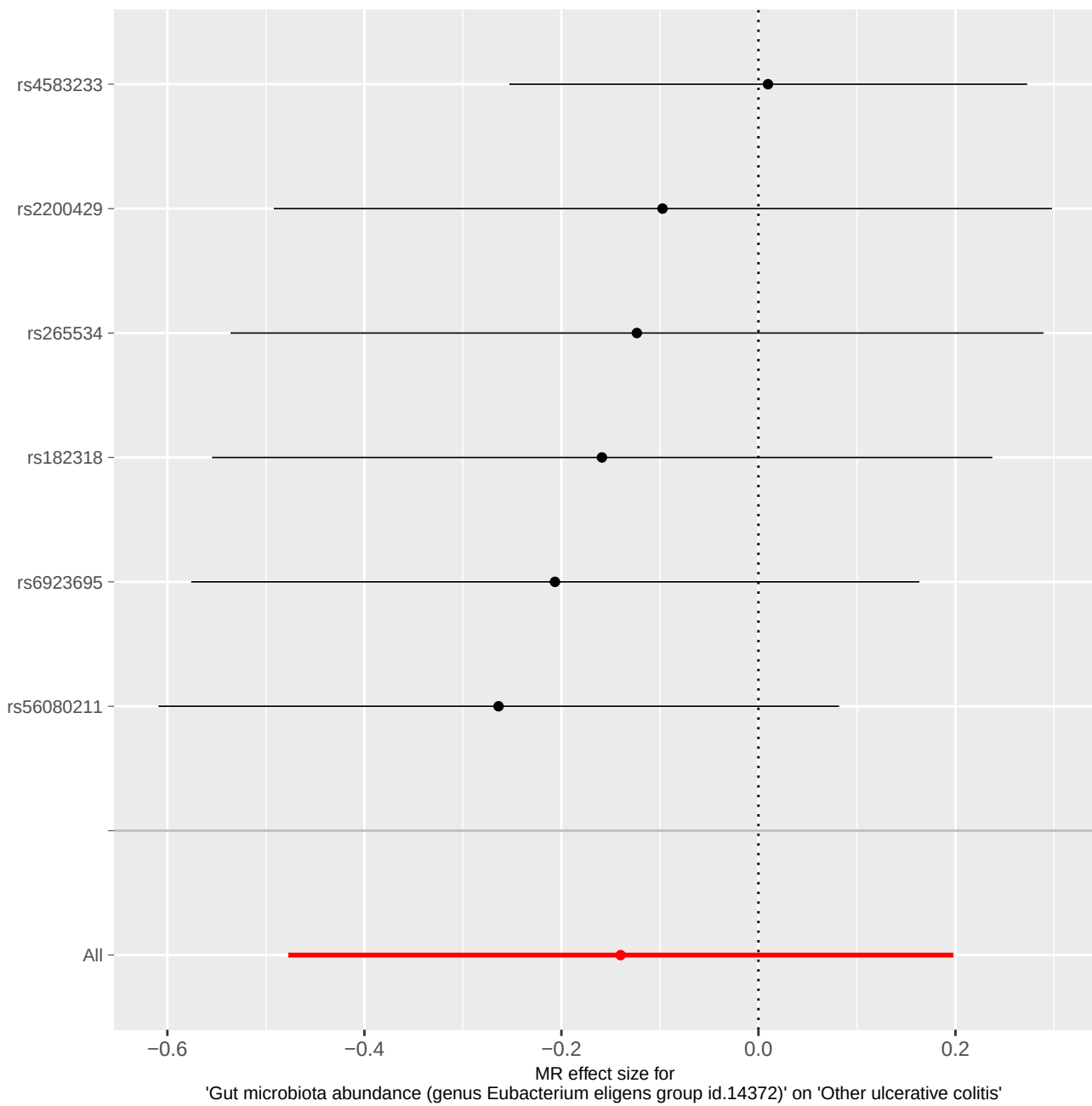
Batch 1267 : Gut microbiota abundance (genus Erysipelatoclostridium id.11381) on Other ulcerative colitis

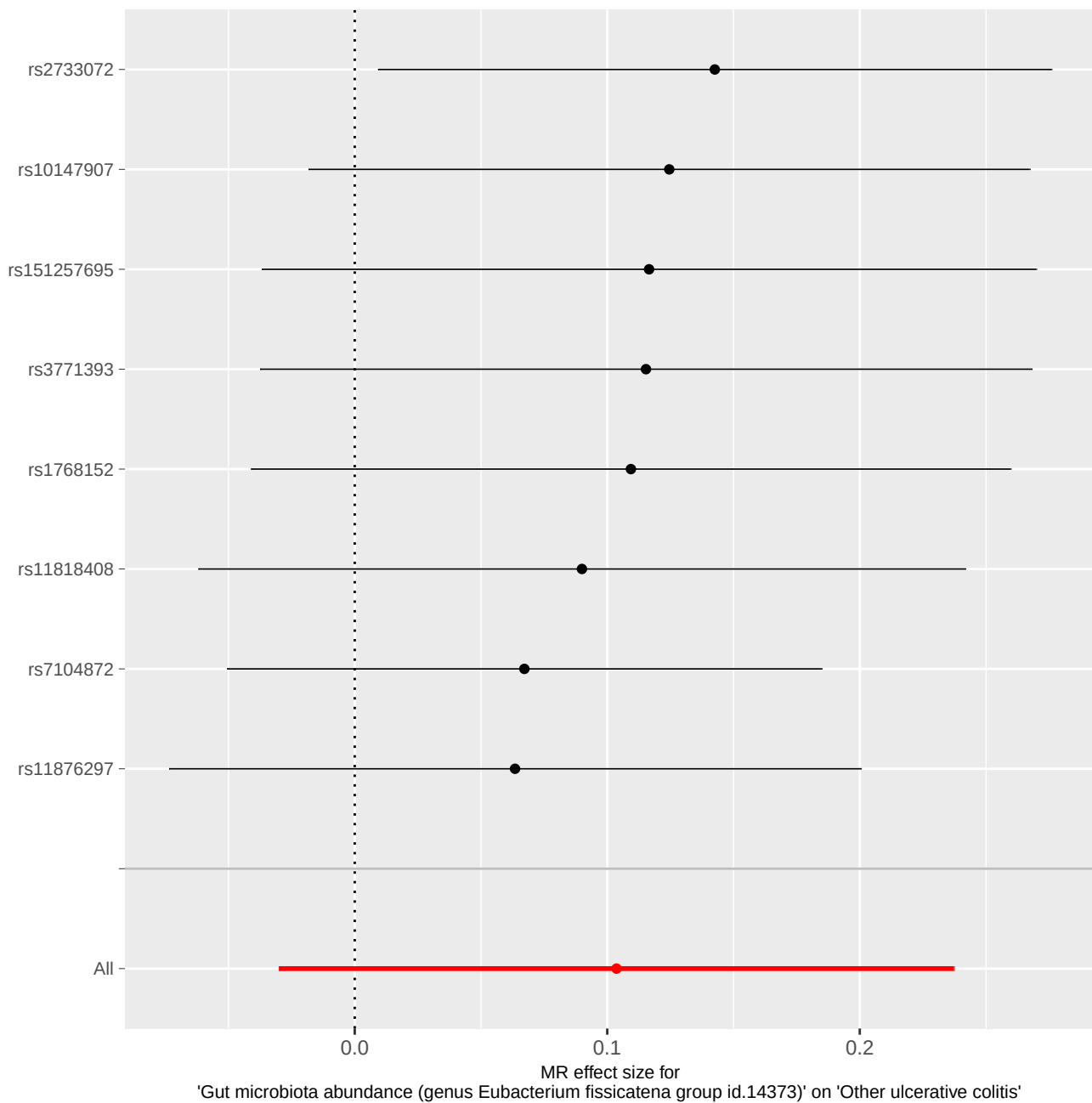


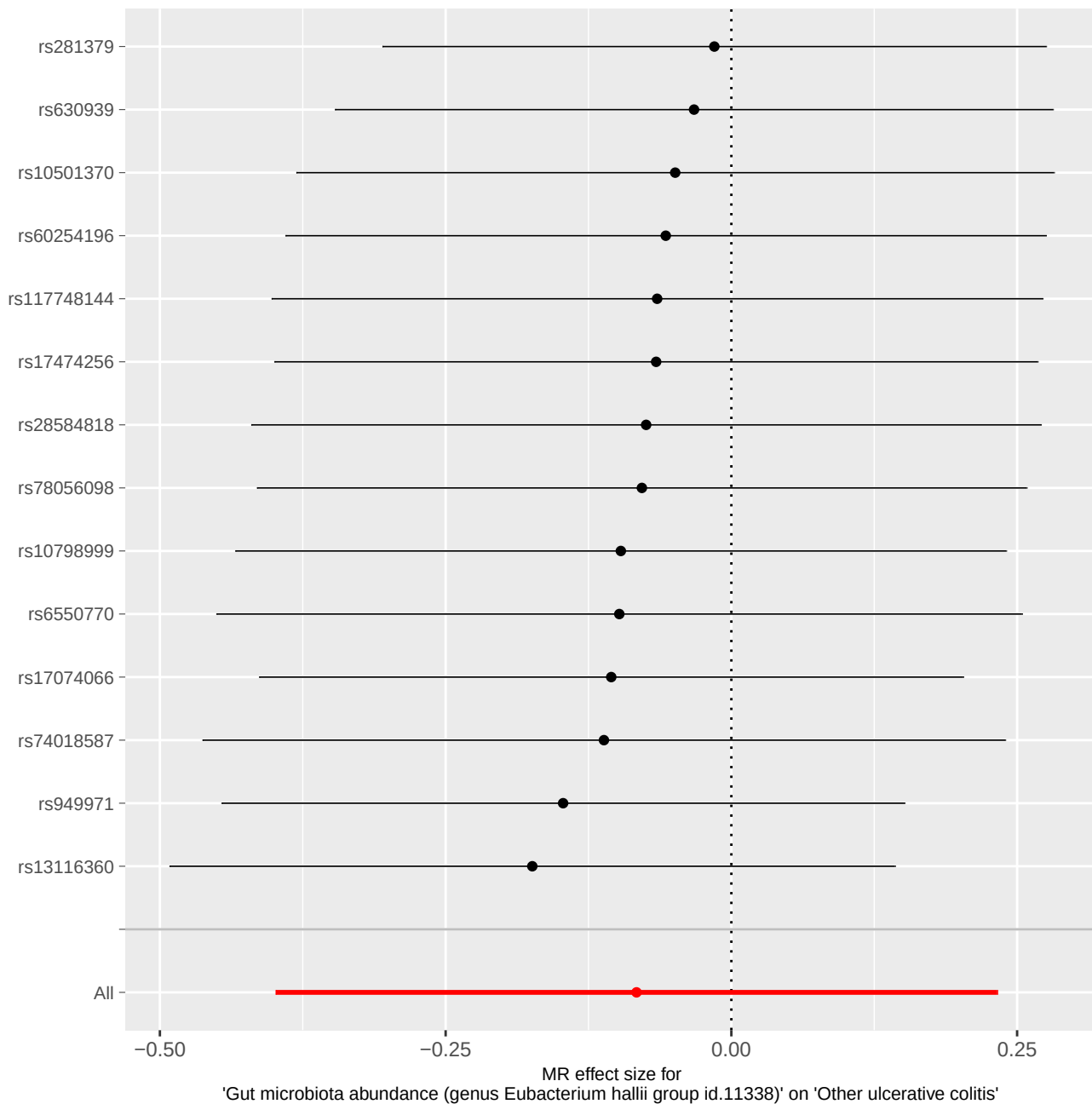


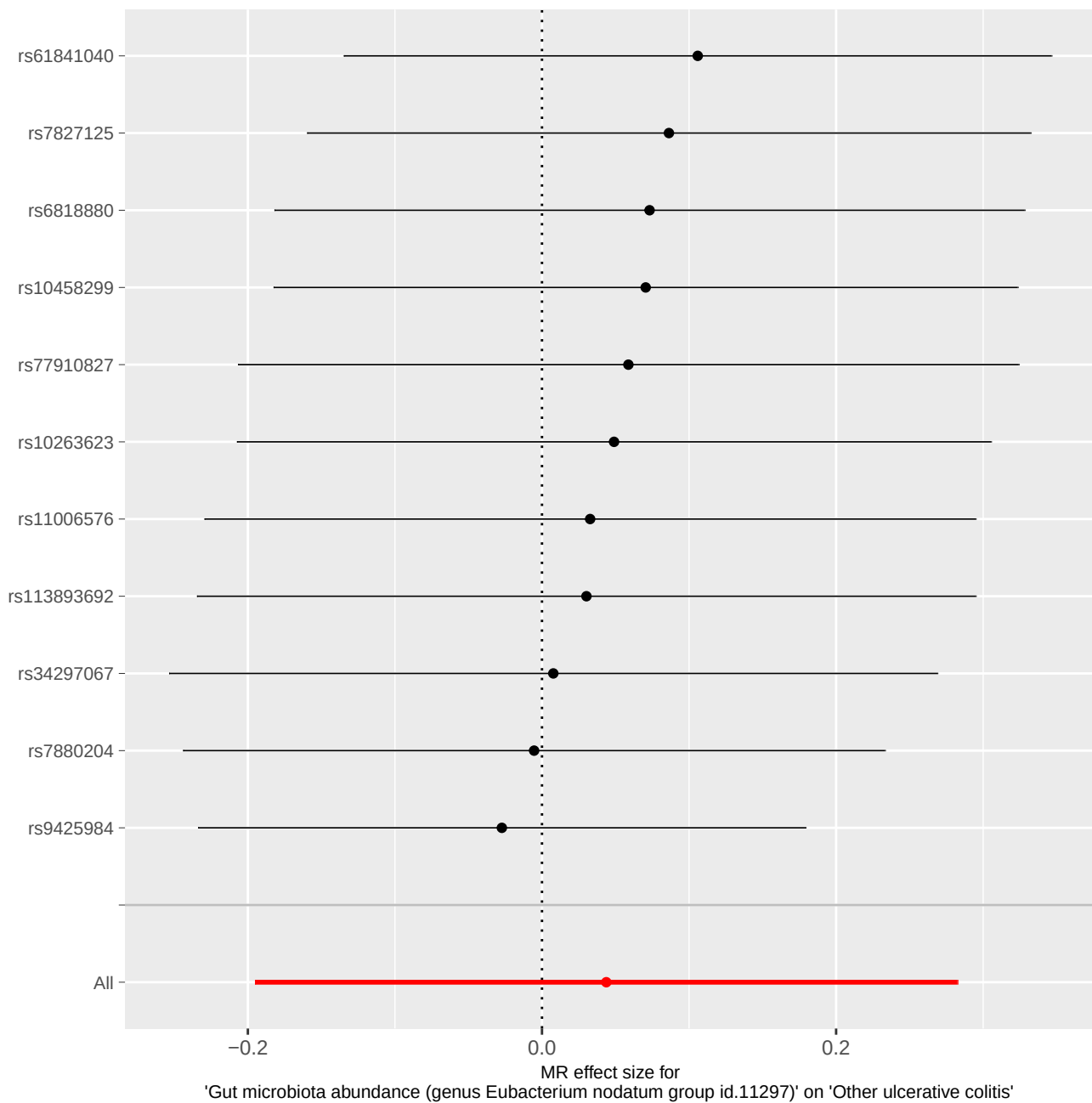


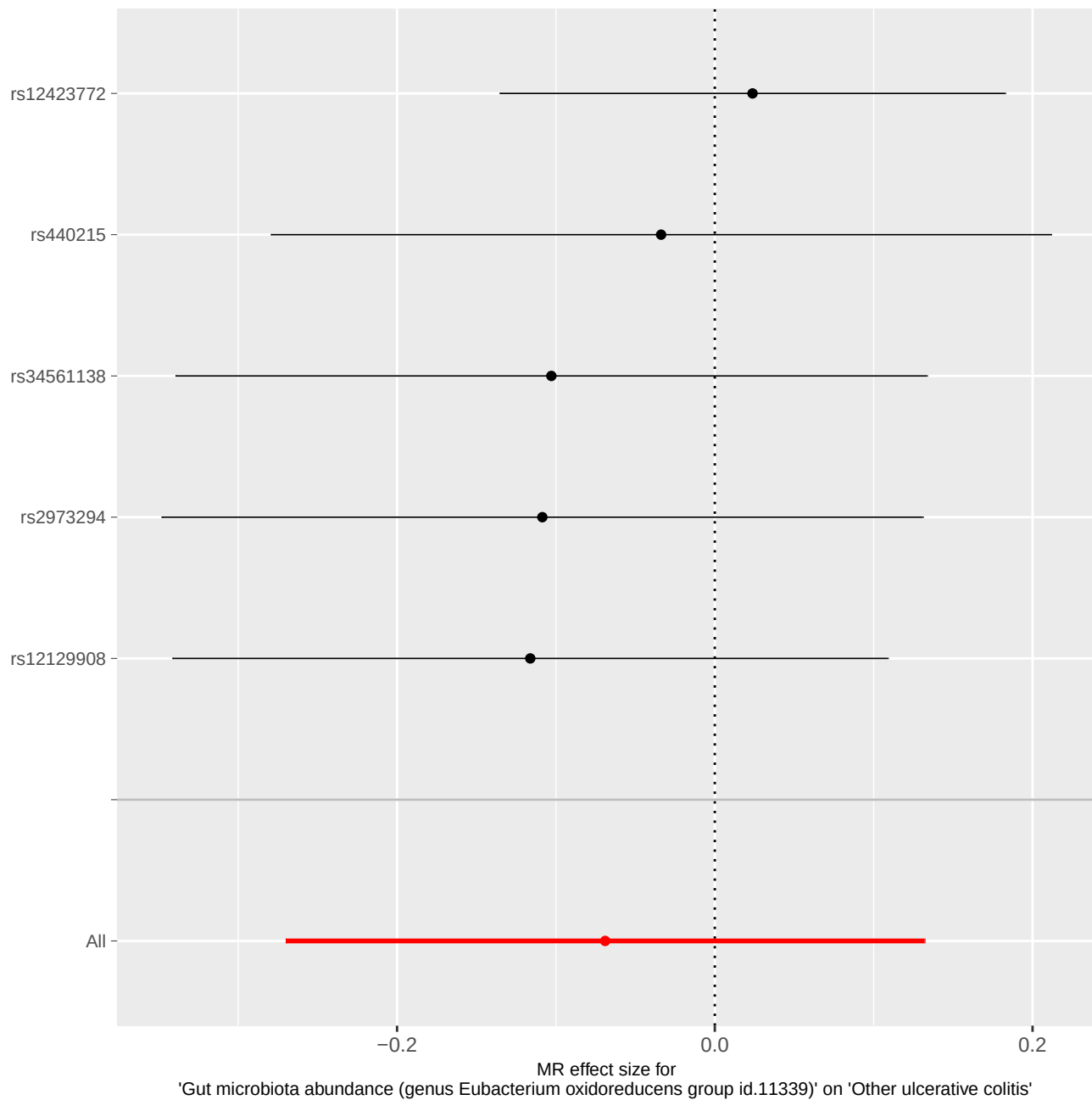


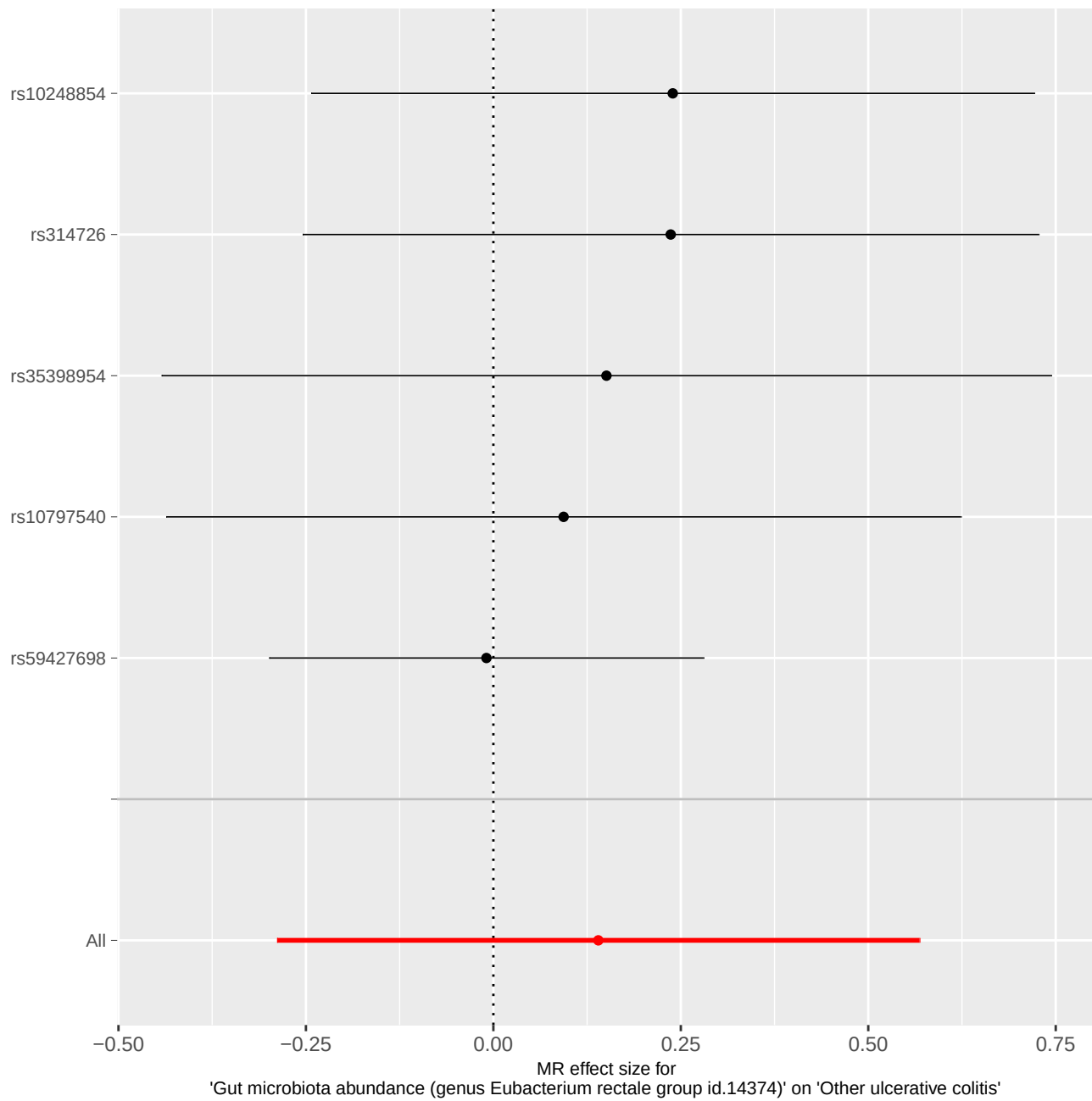


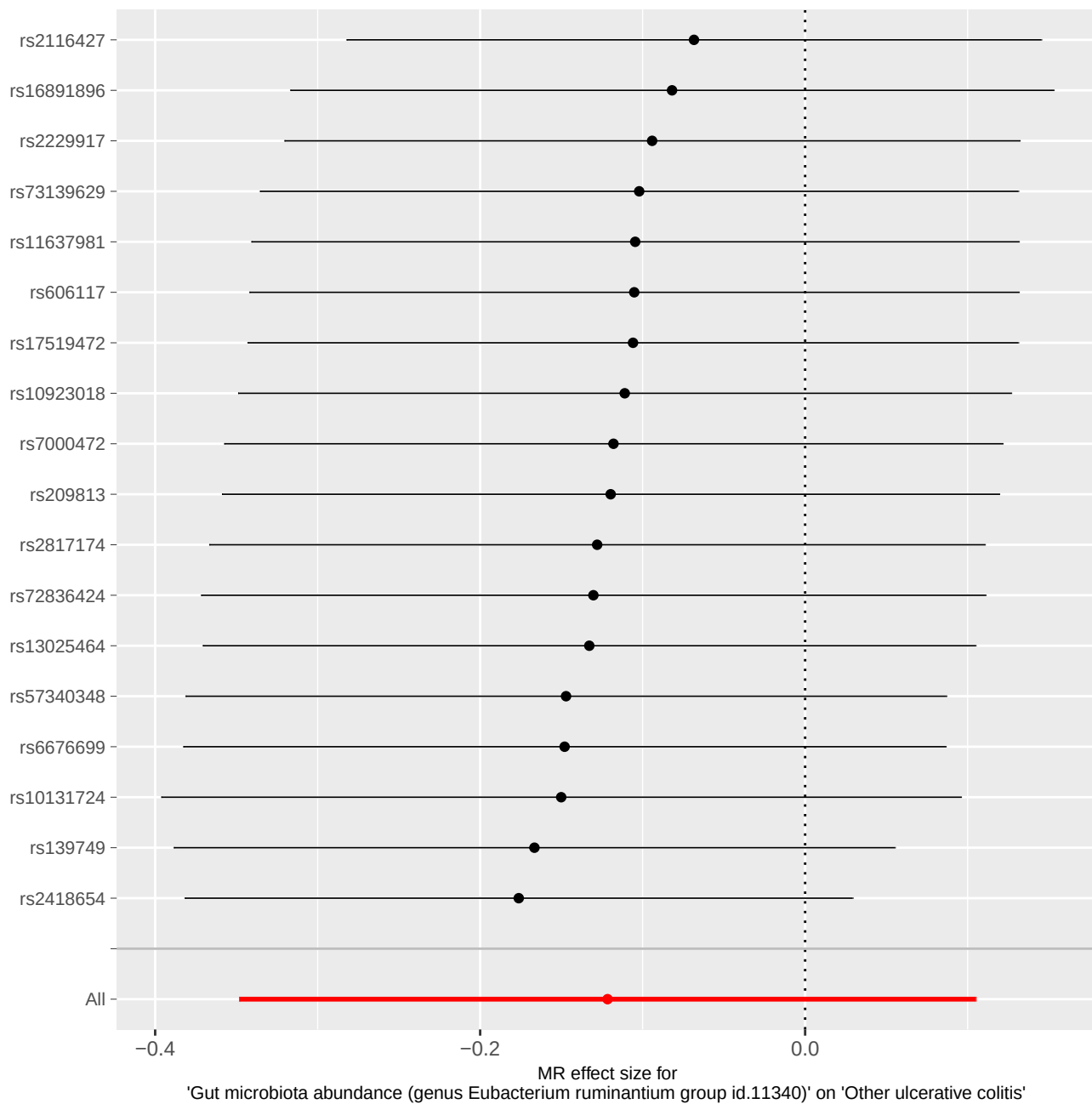












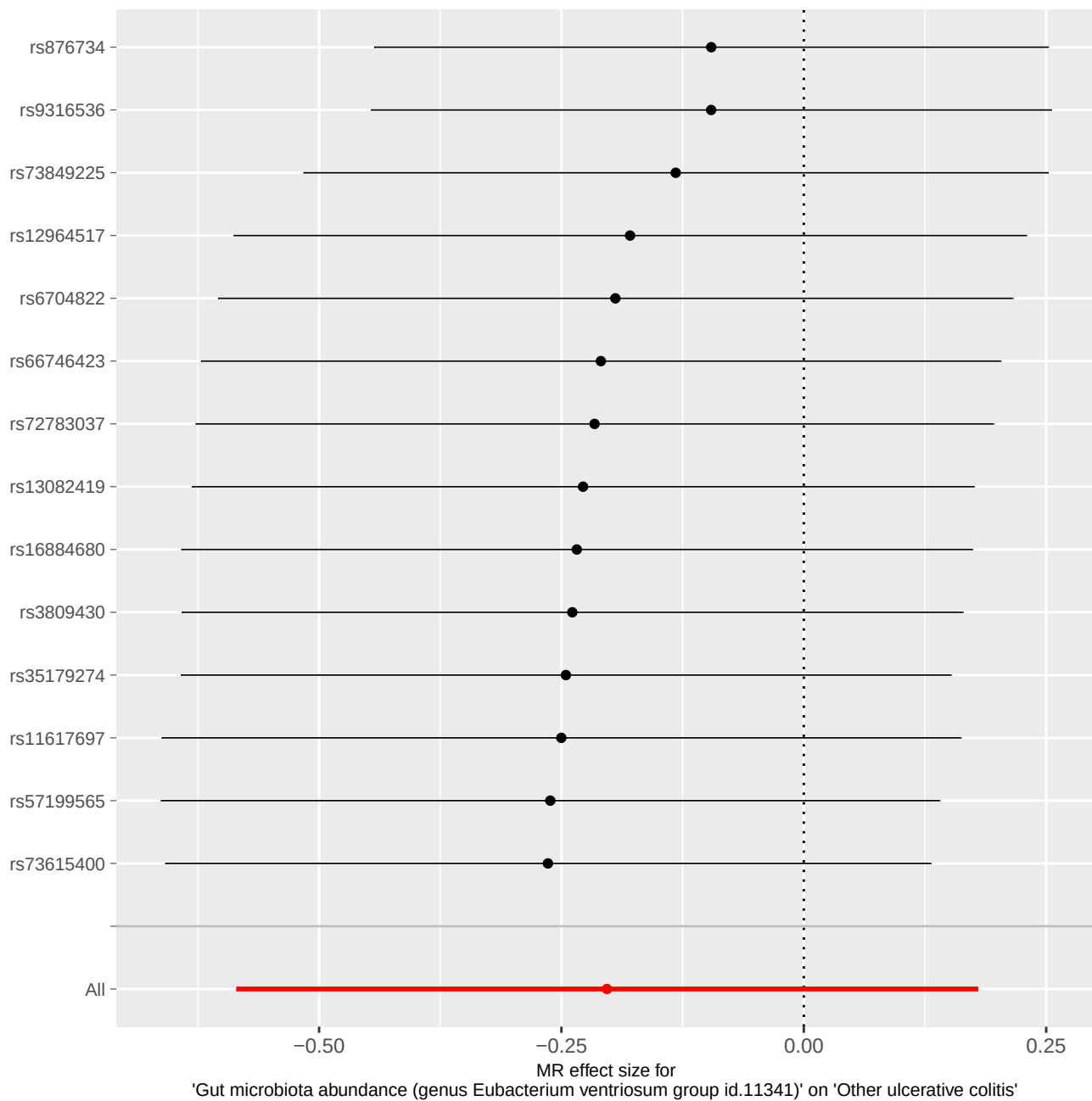
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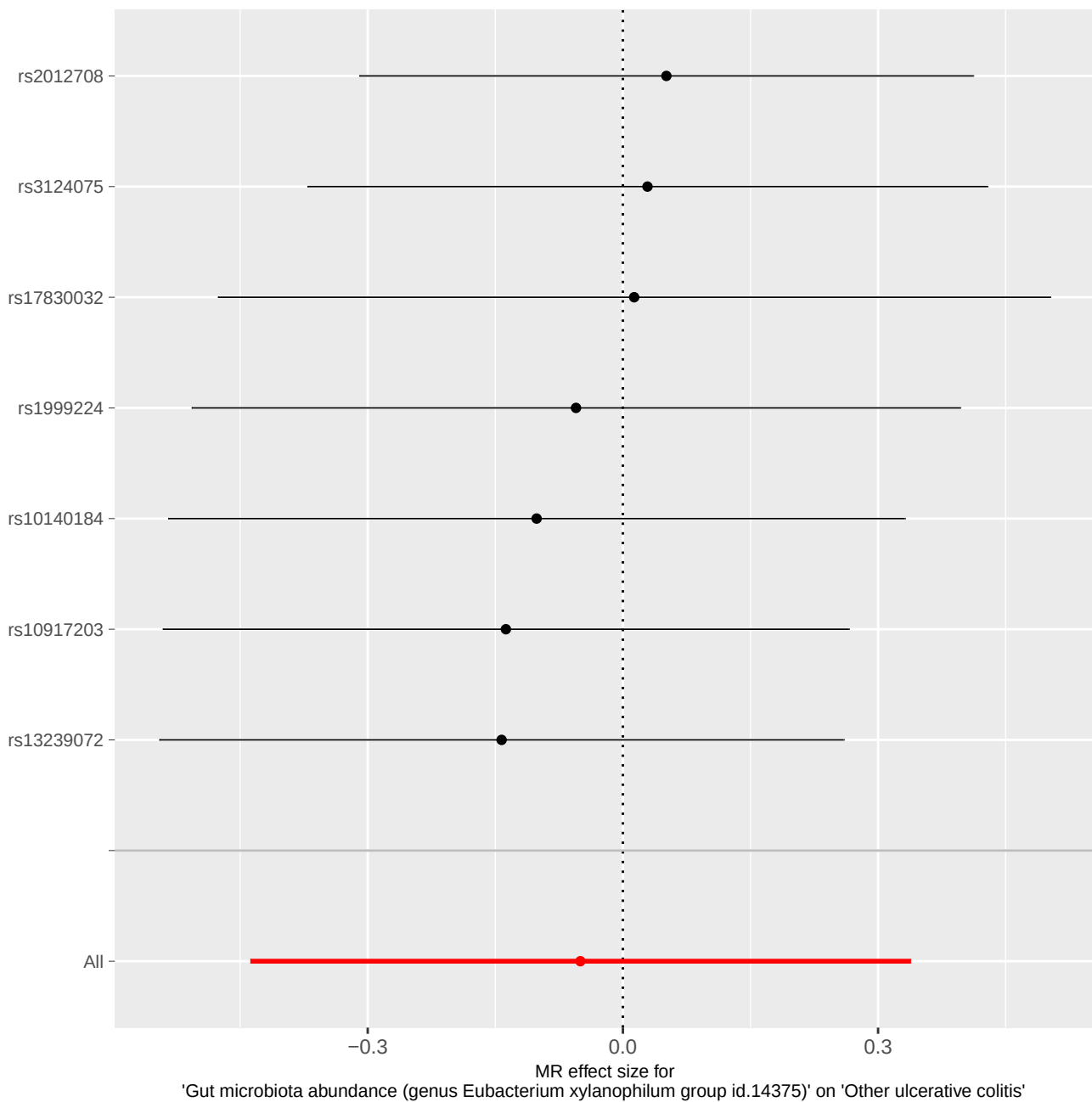
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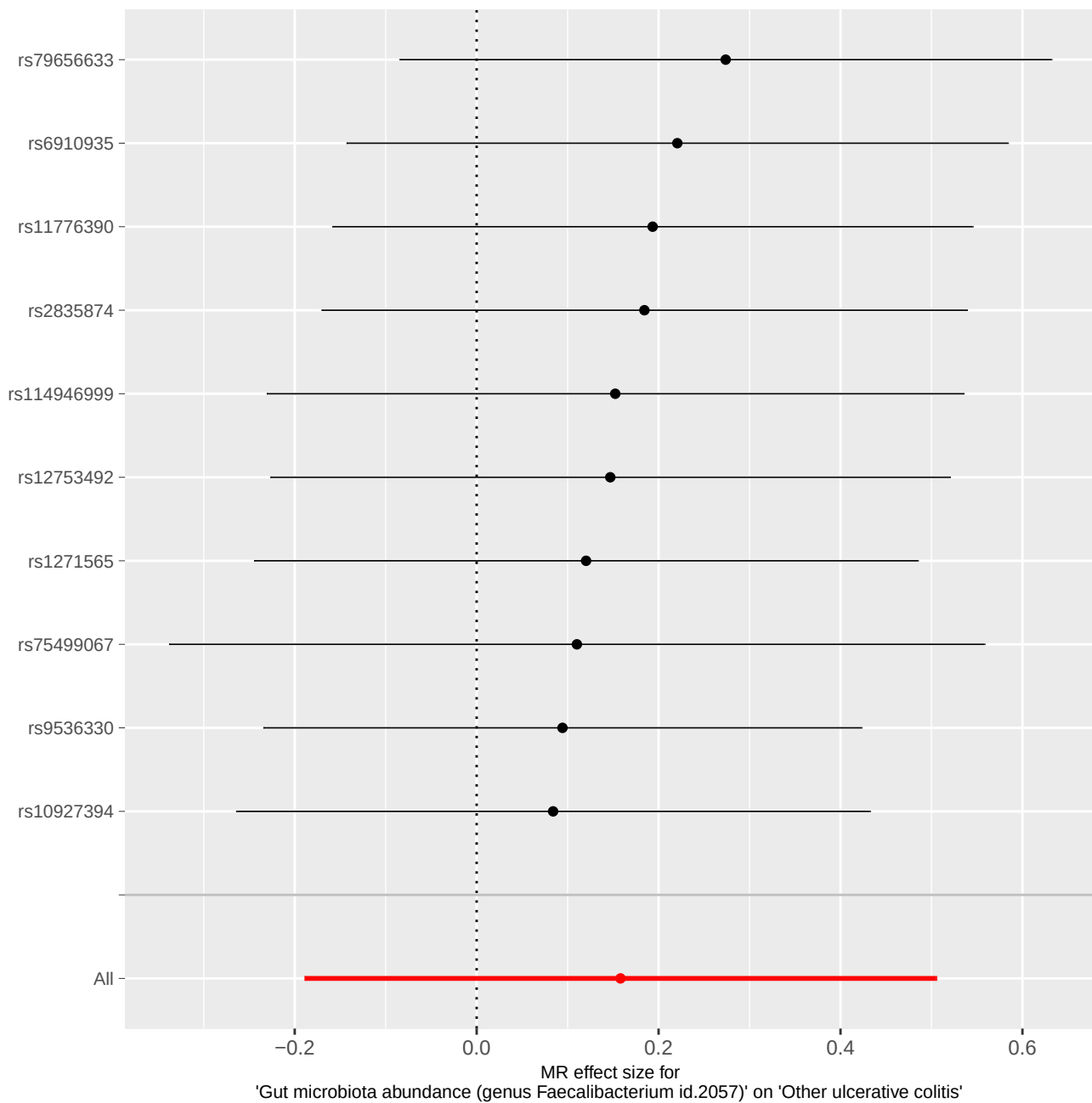
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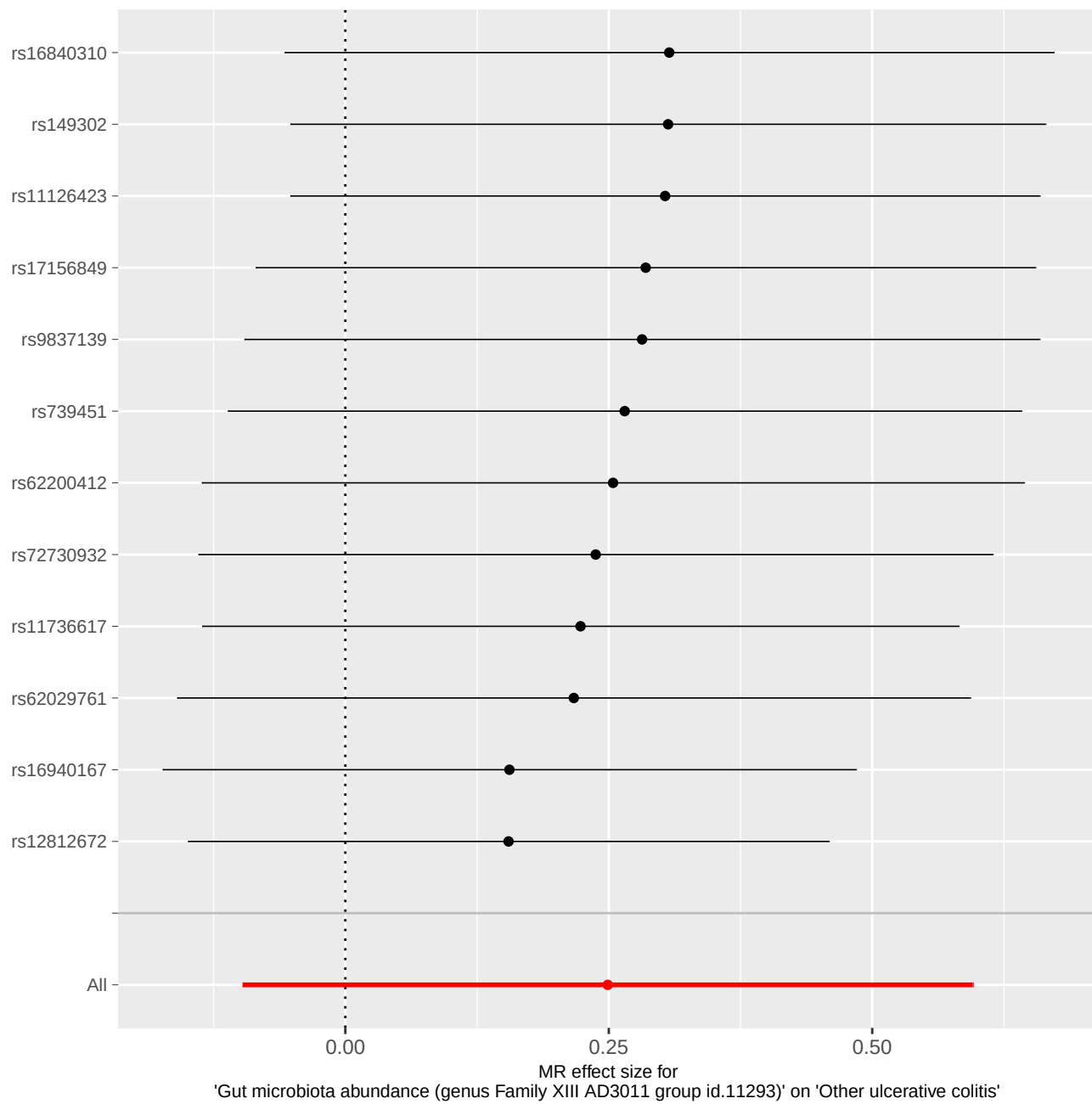
MR effect size for

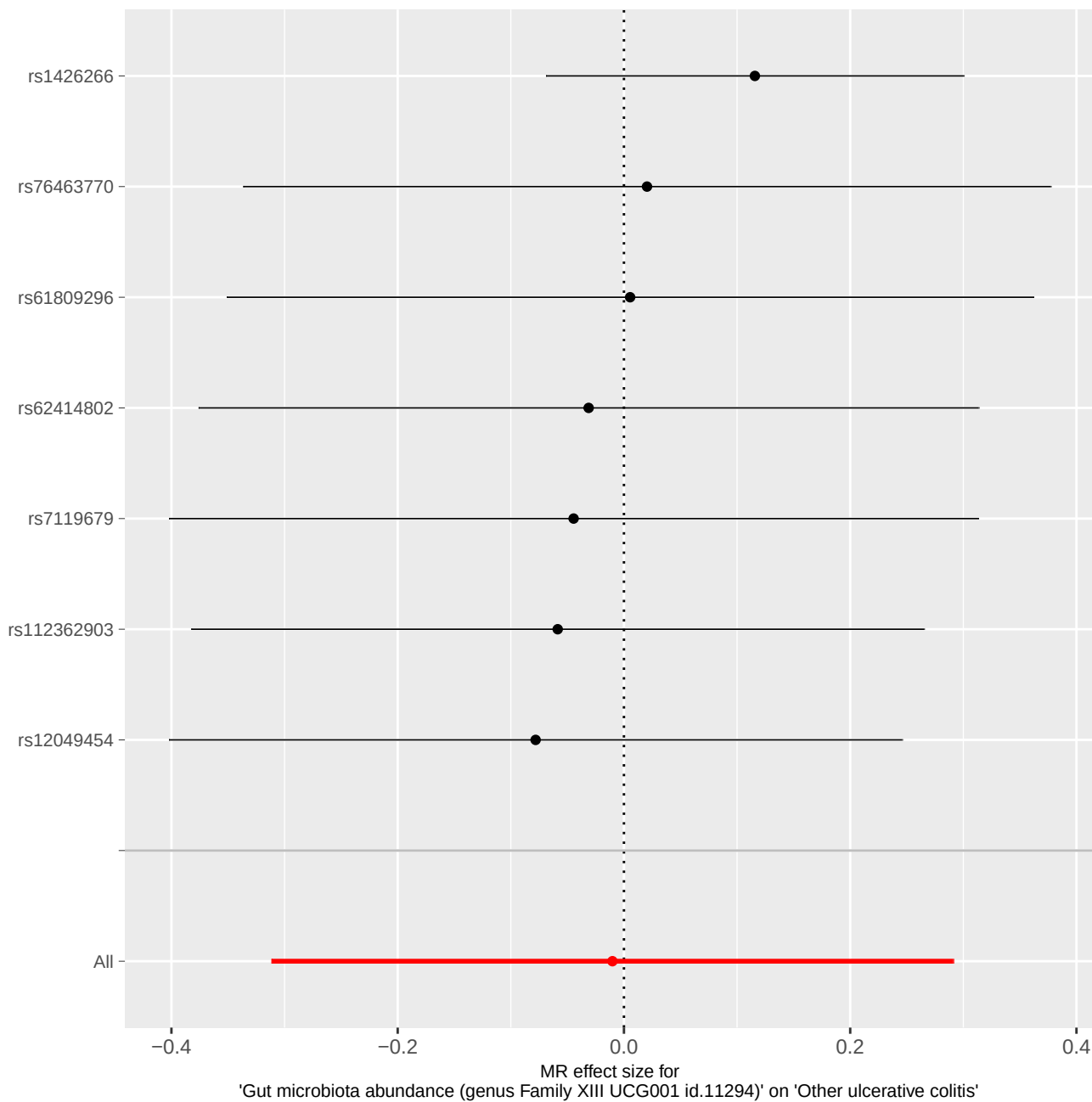
'Gut microbiota abundance (genus Eubacterium ruminantium group id.11340)' on 'Other ulcerative colitis'

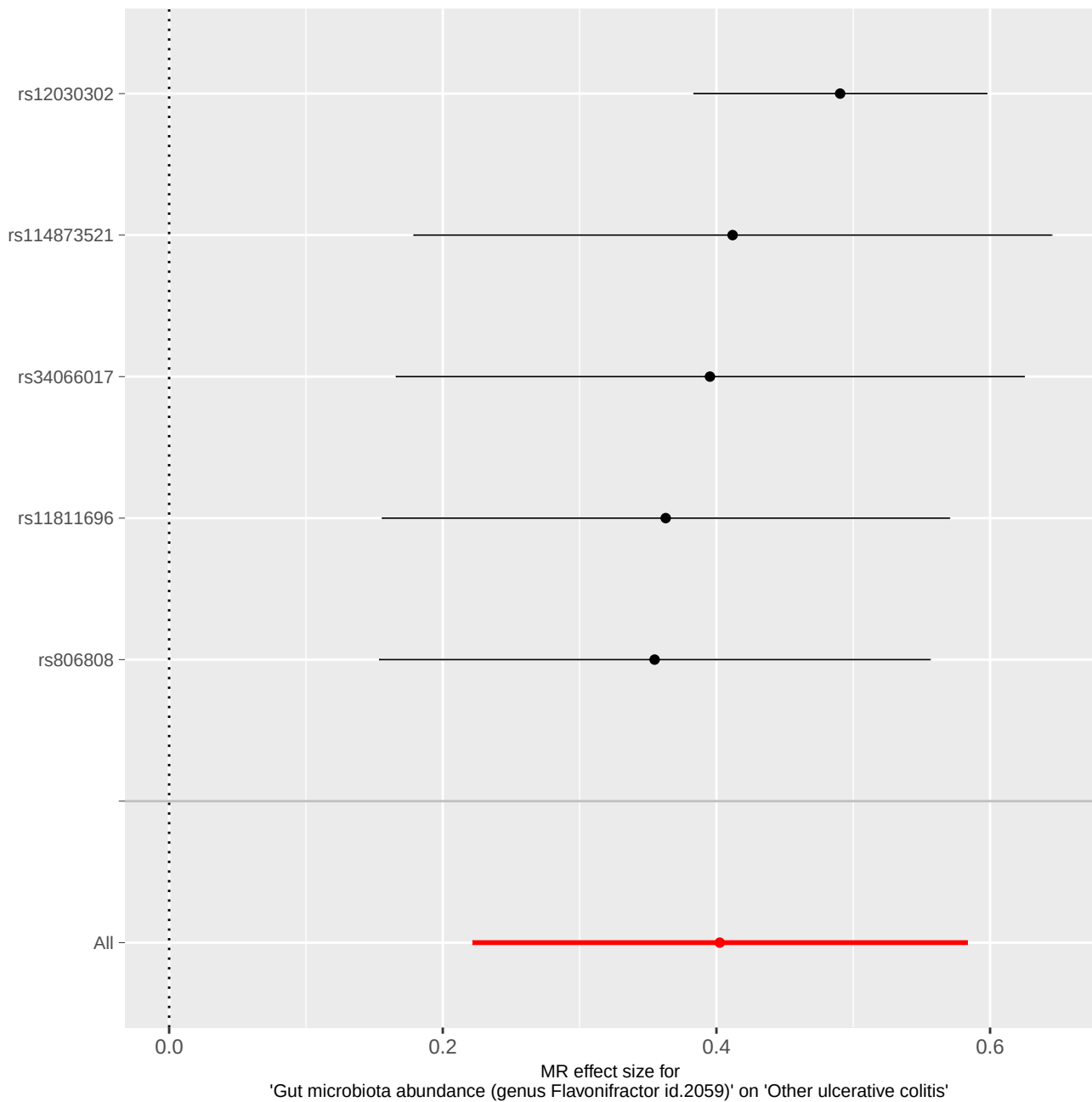




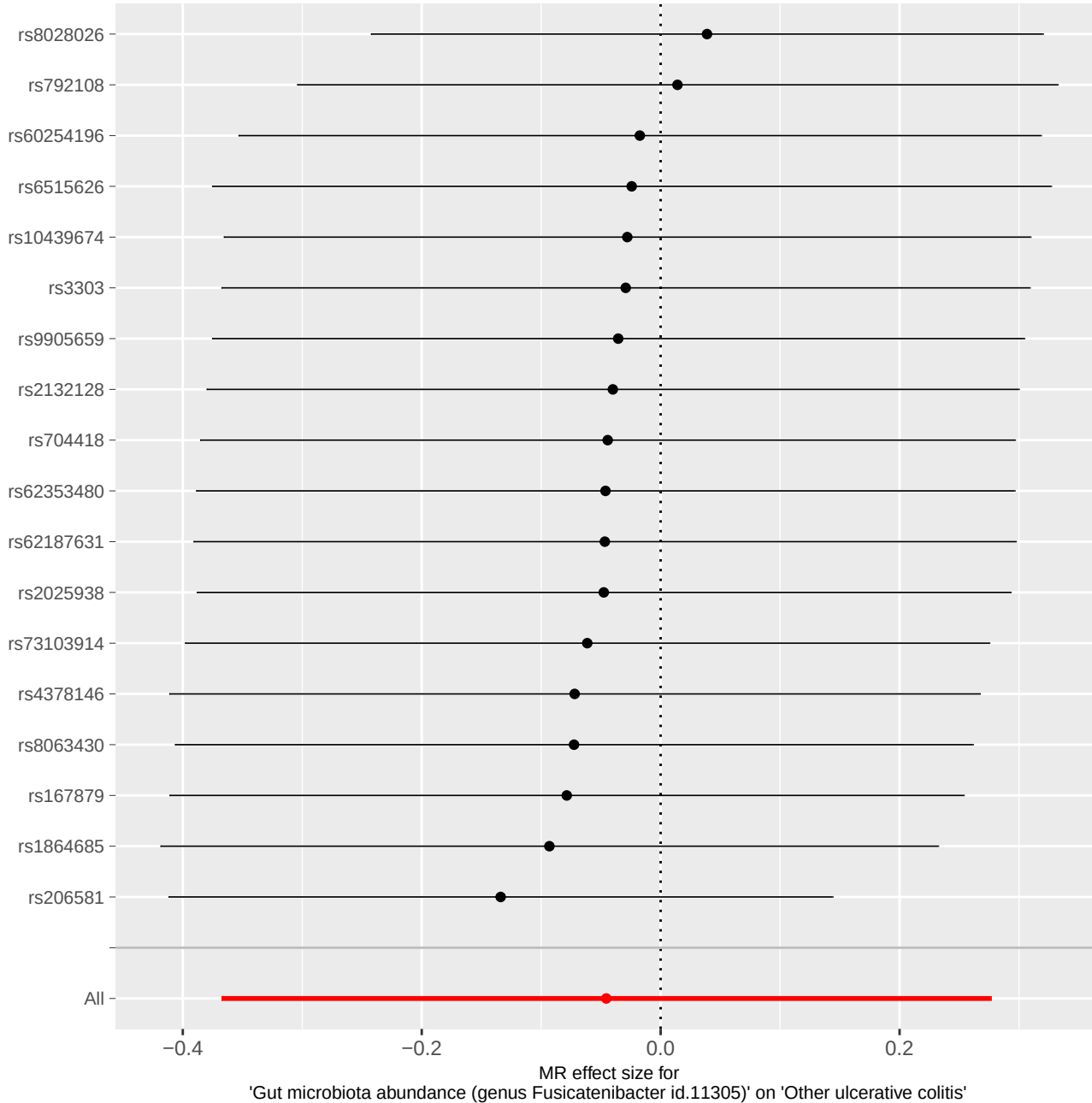


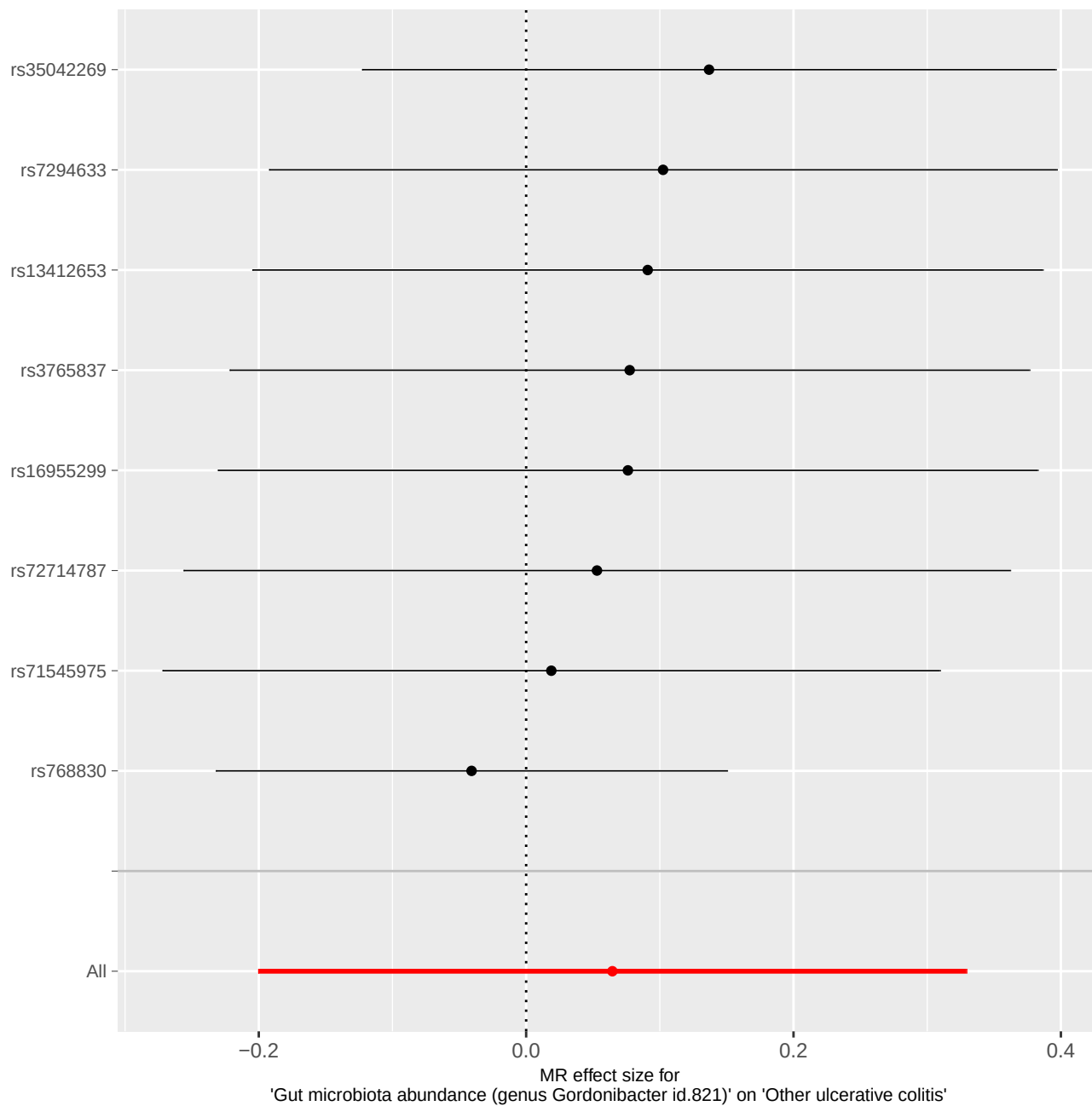


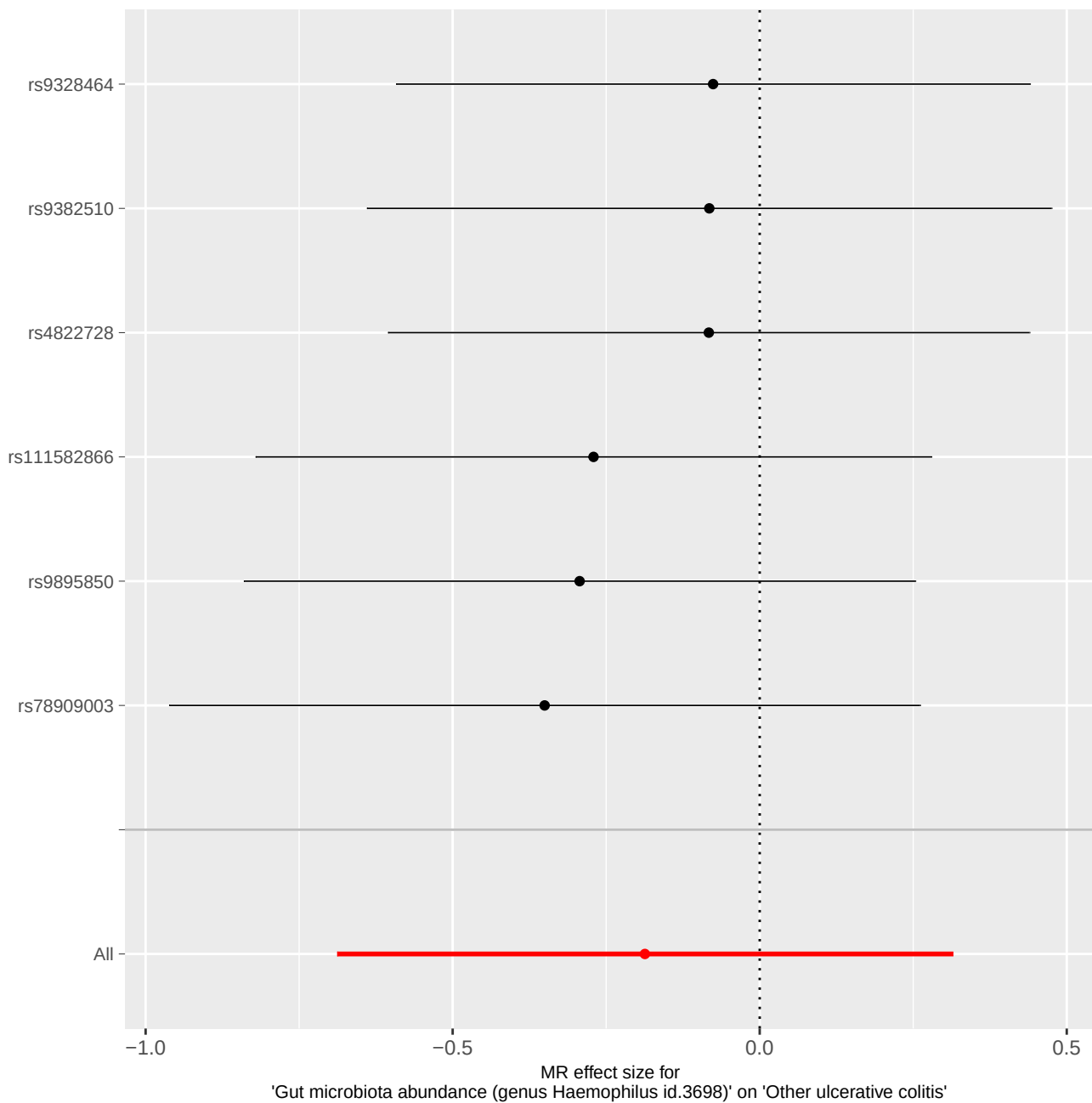


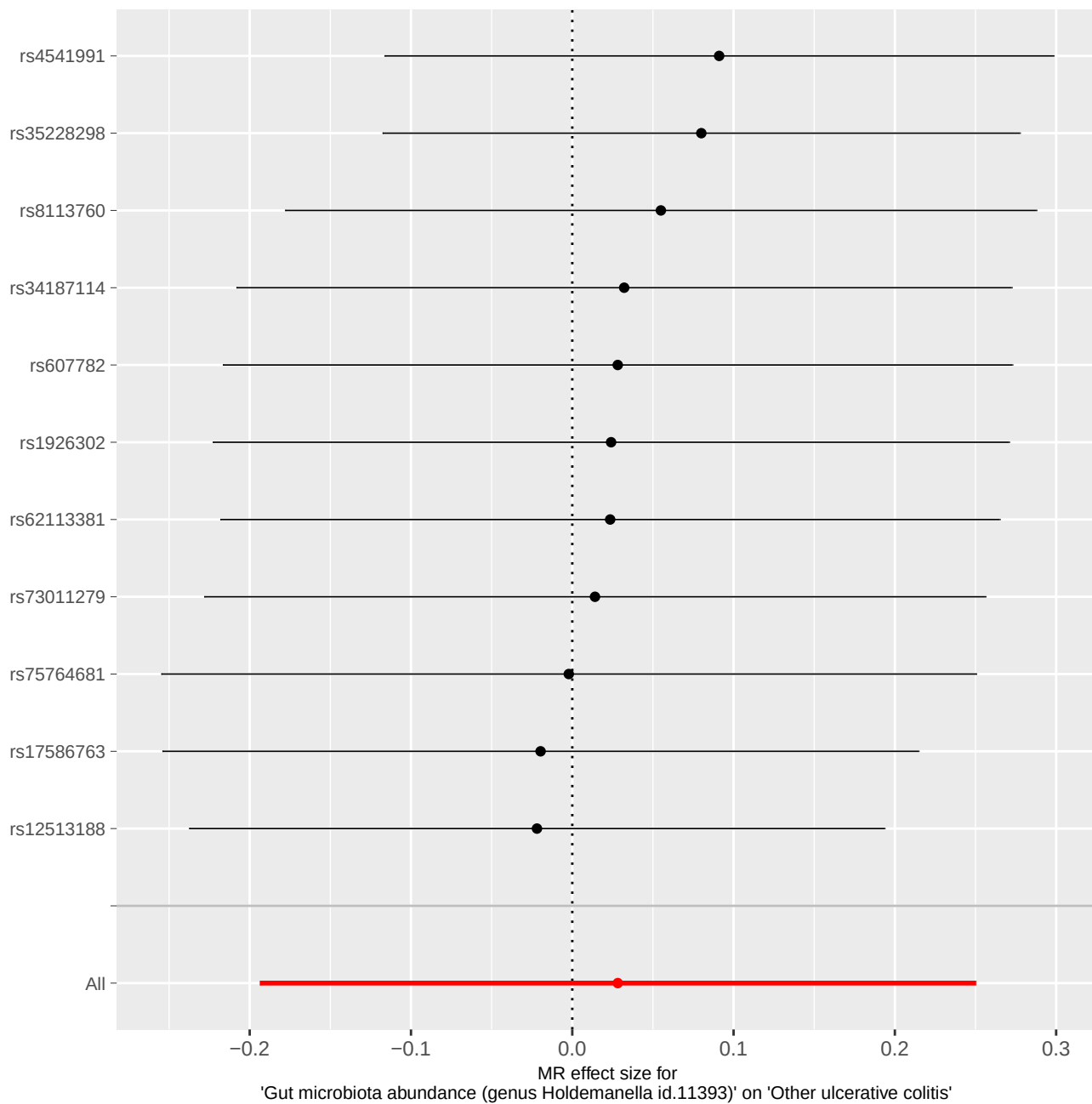


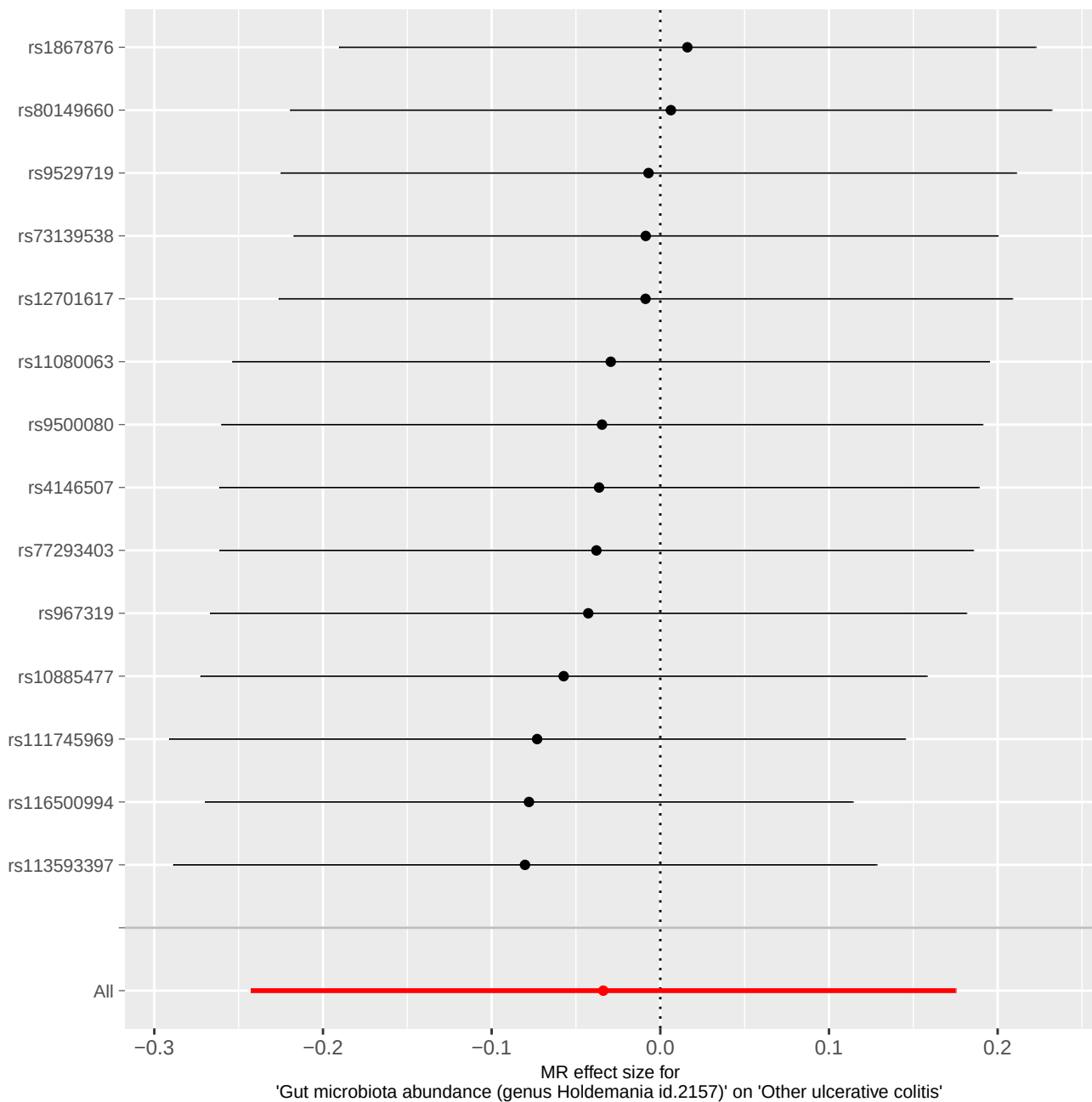
Batch 1285 : Gut microbiota abundance (genus Fusicatenibacter id.11305) on Other ulcerative colitis

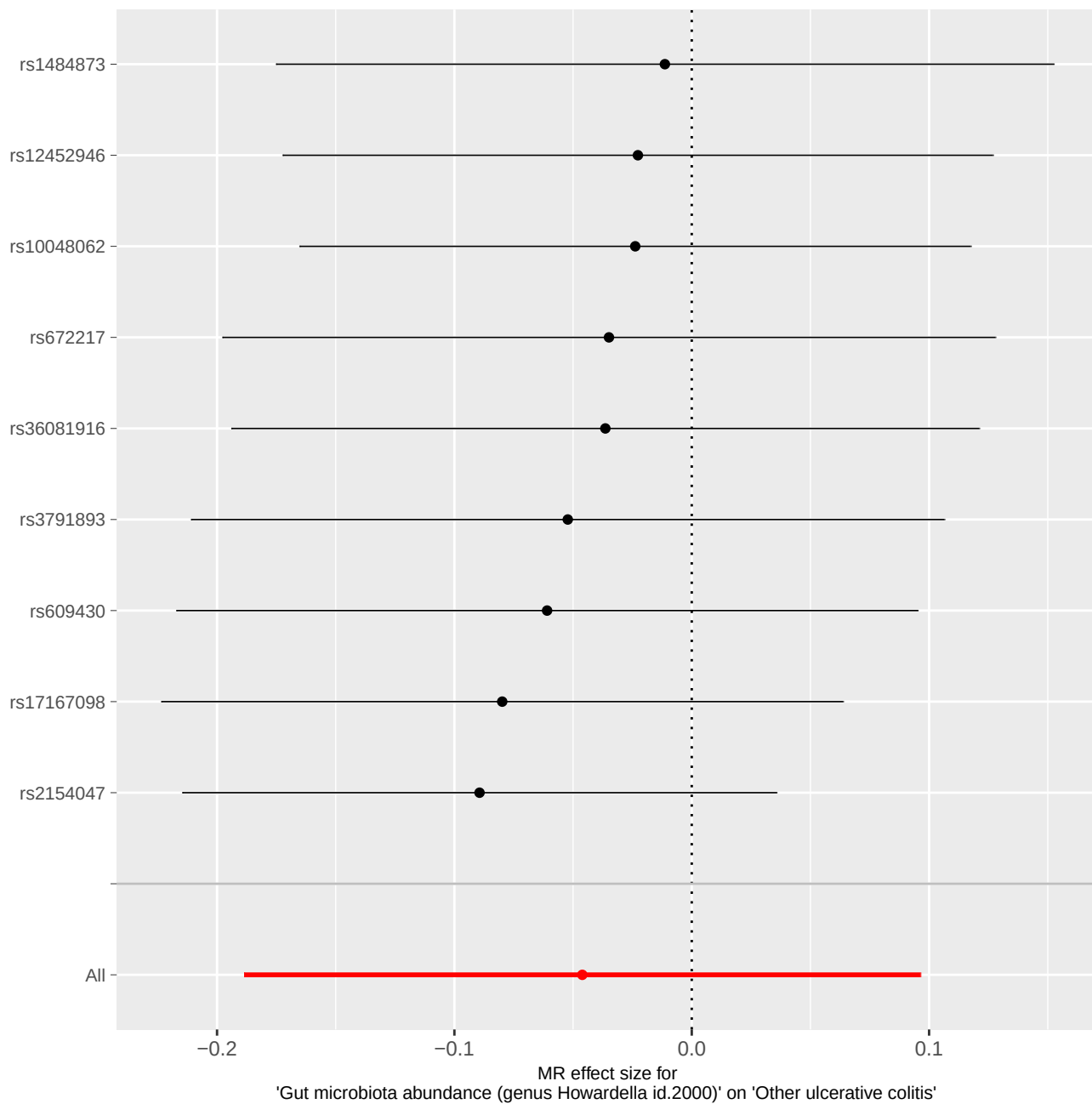




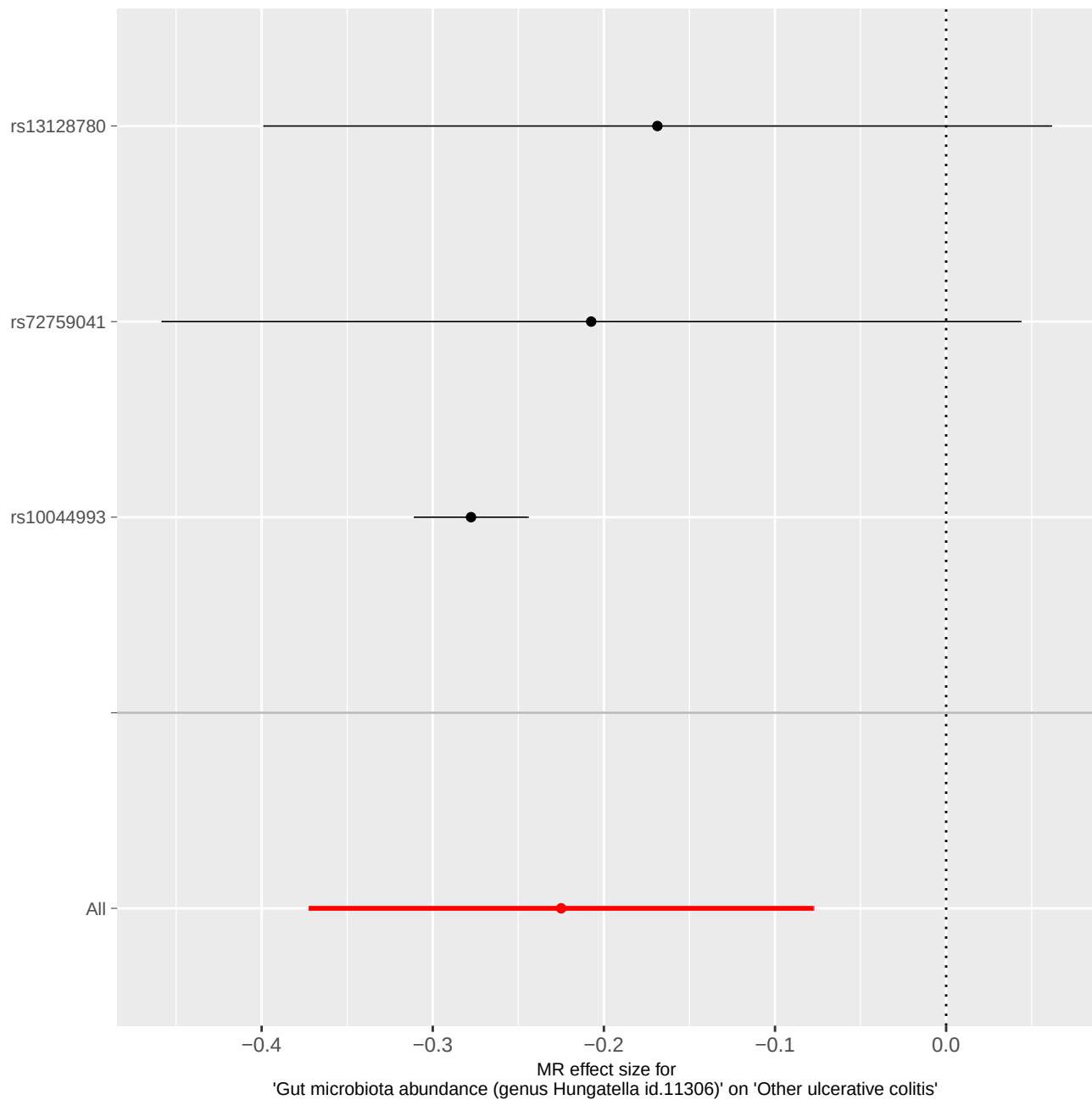


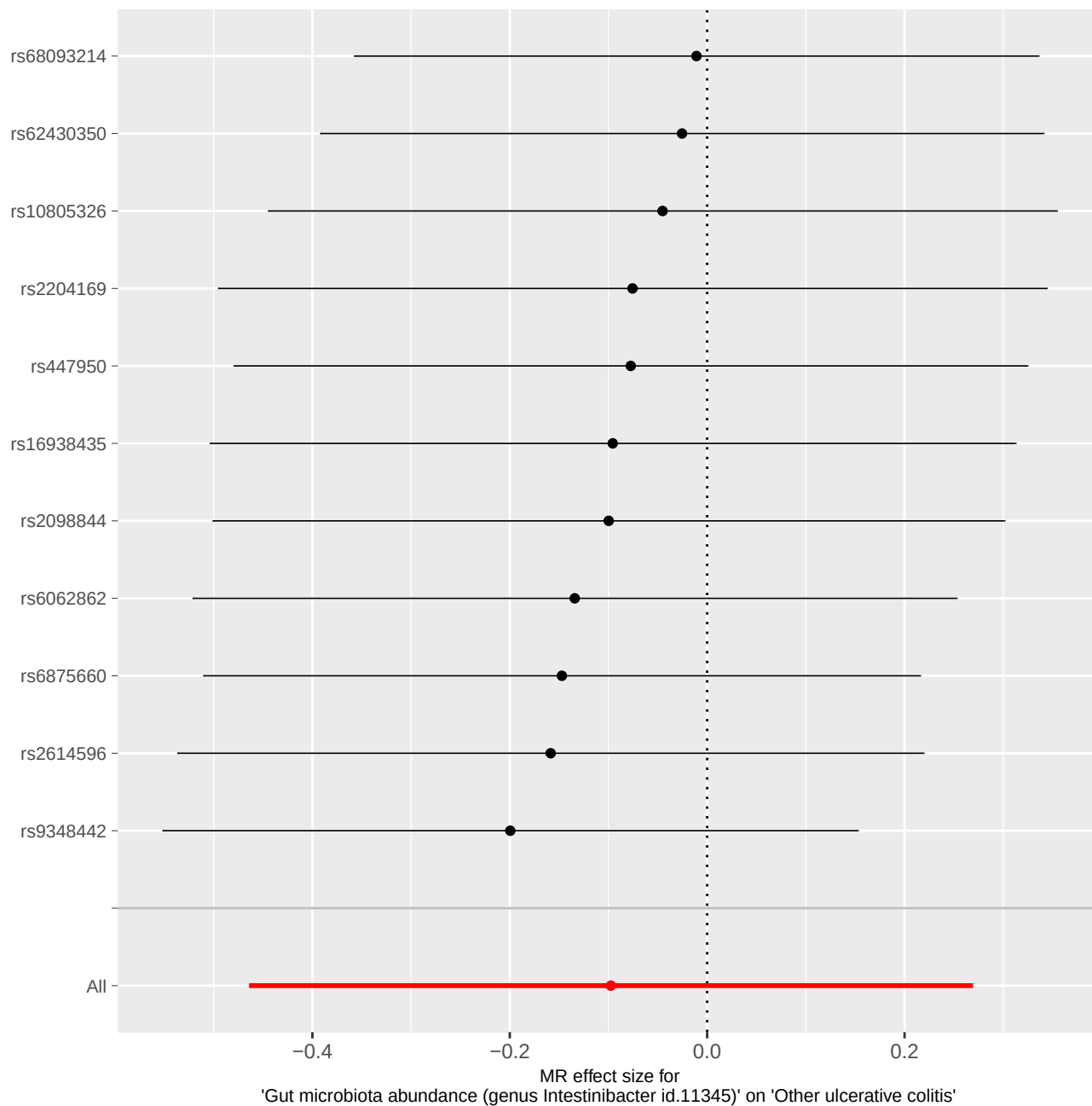


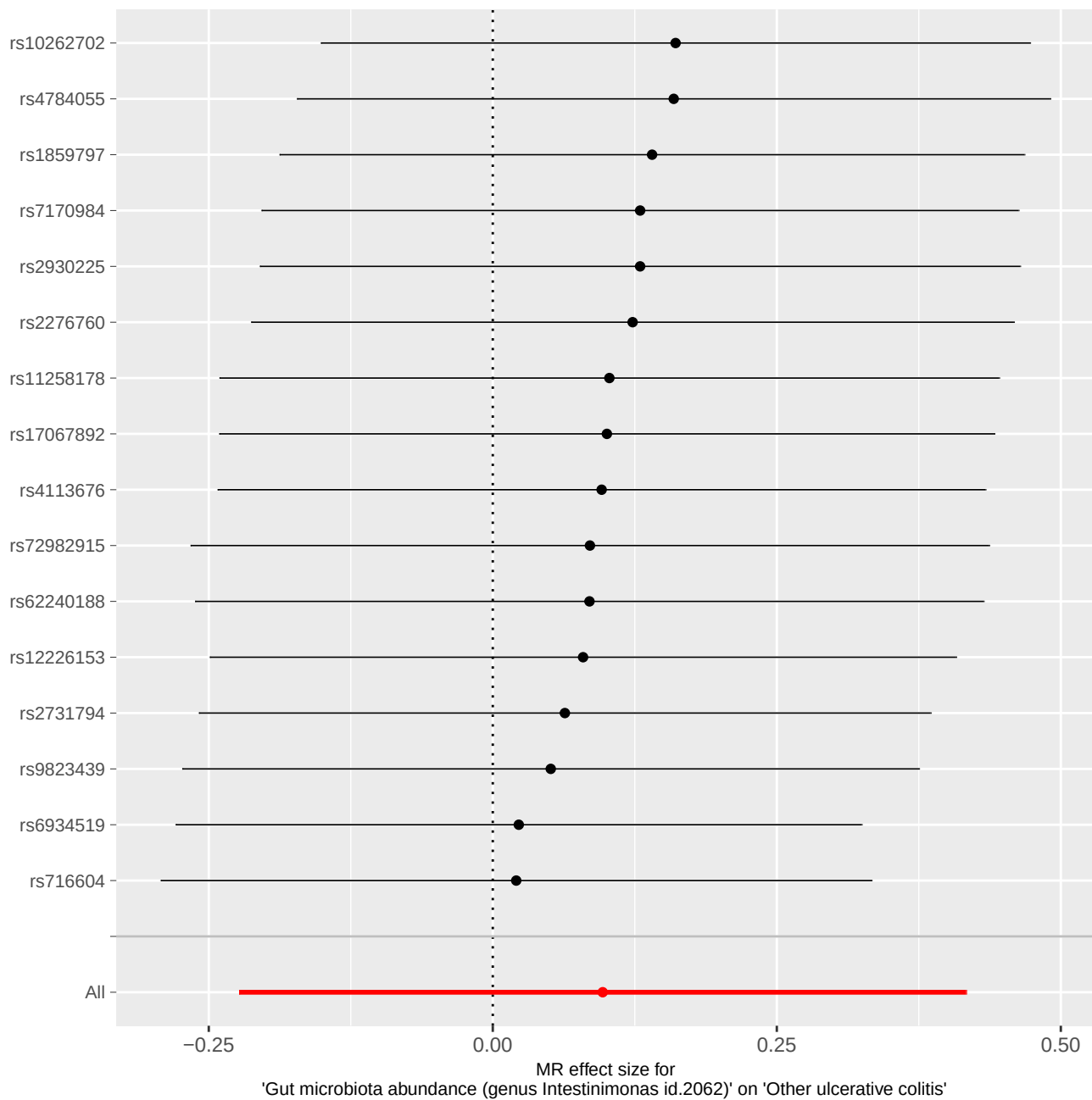


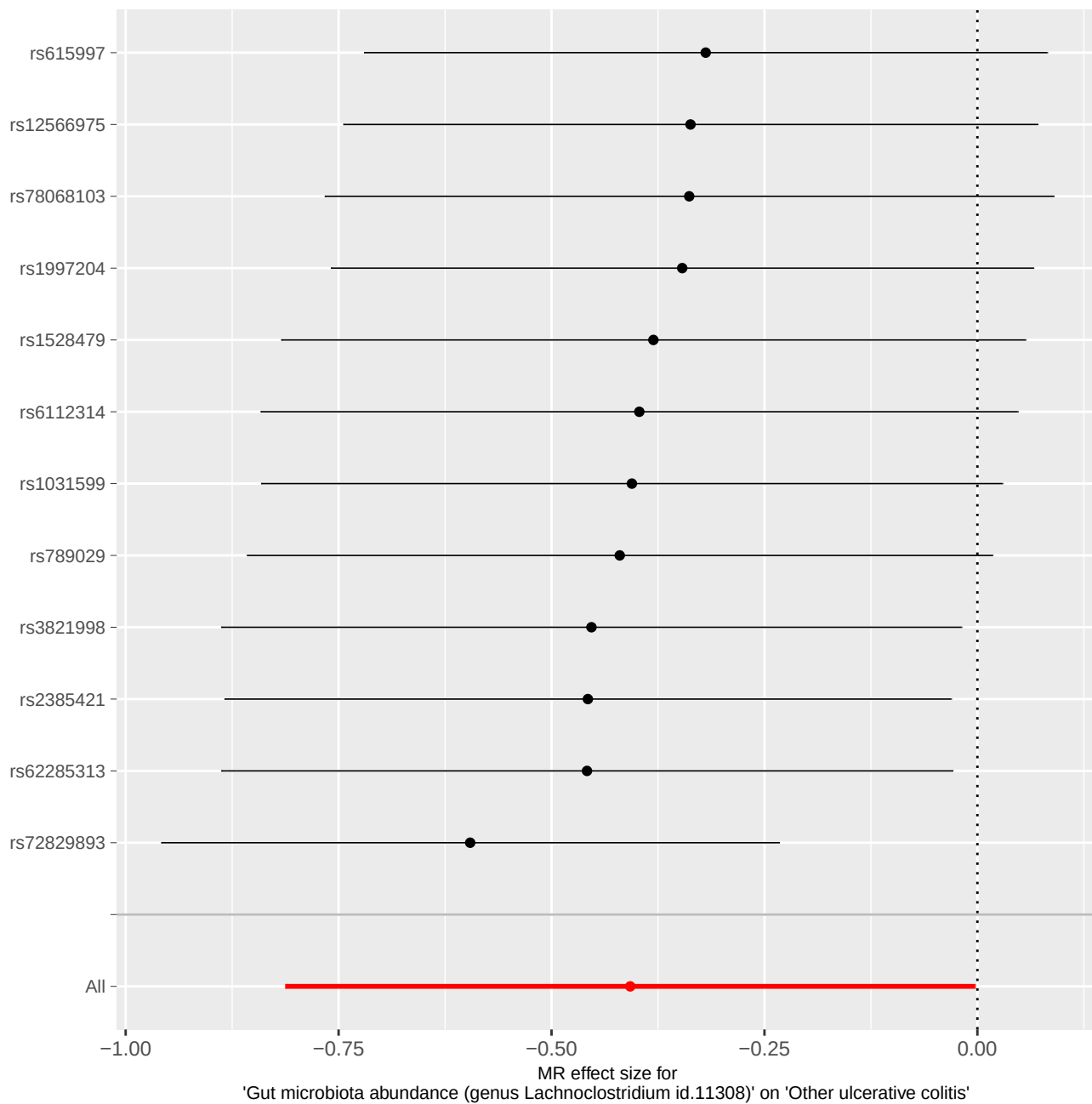


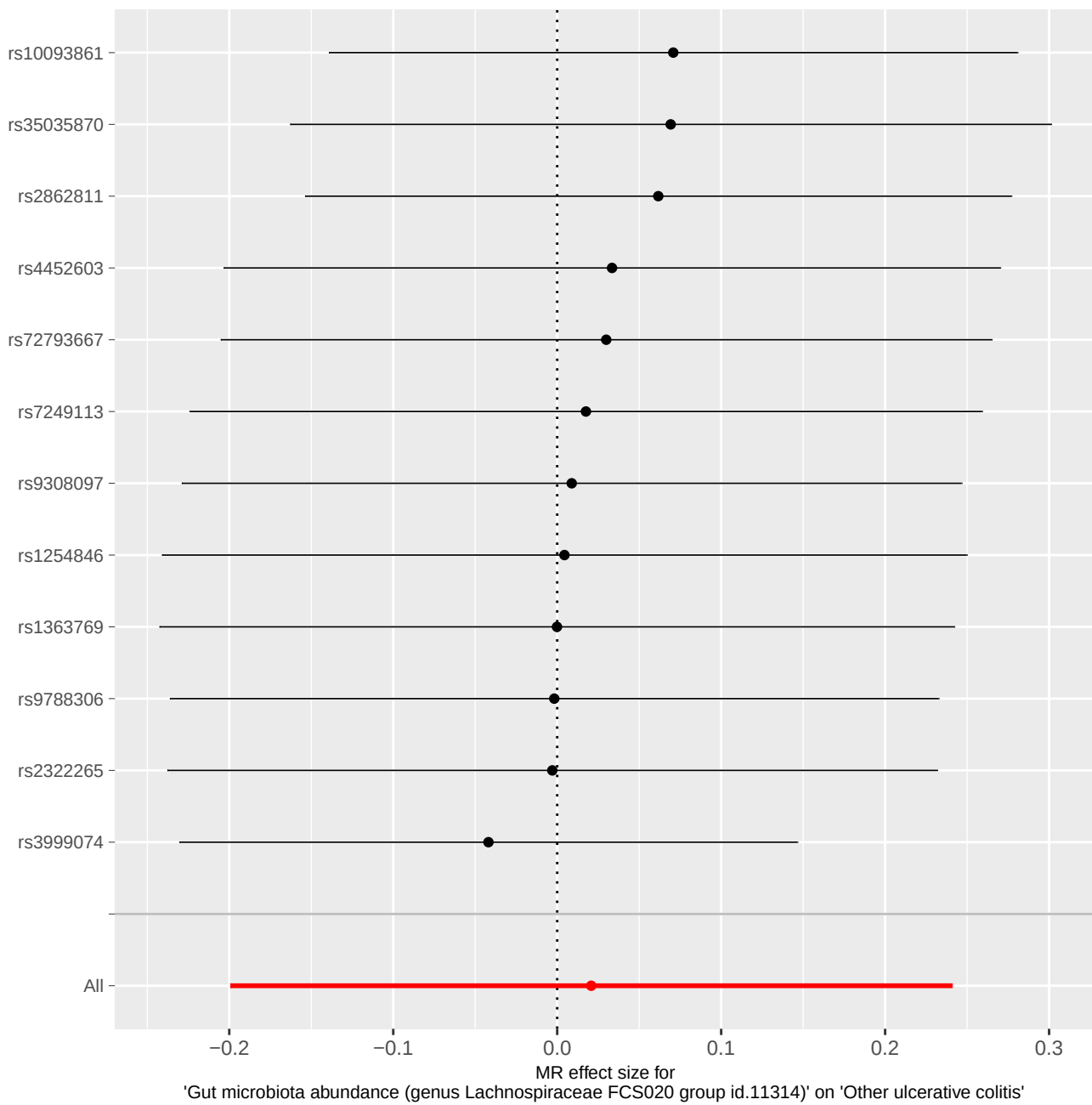
MR effect size for
'Gut microbiota abundance (genus Howardella id.2000)' on 'Other ulcerative colitis'

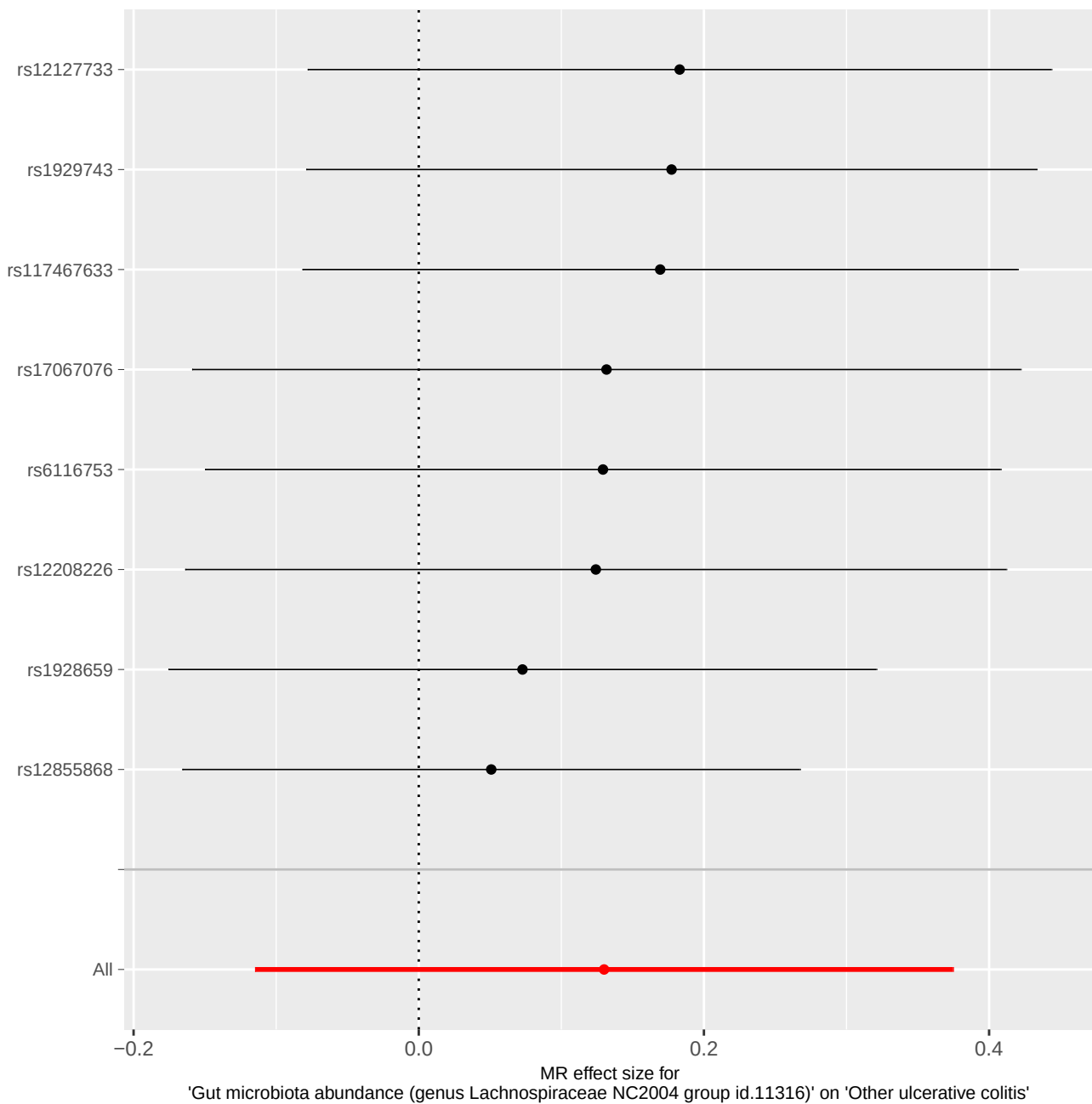


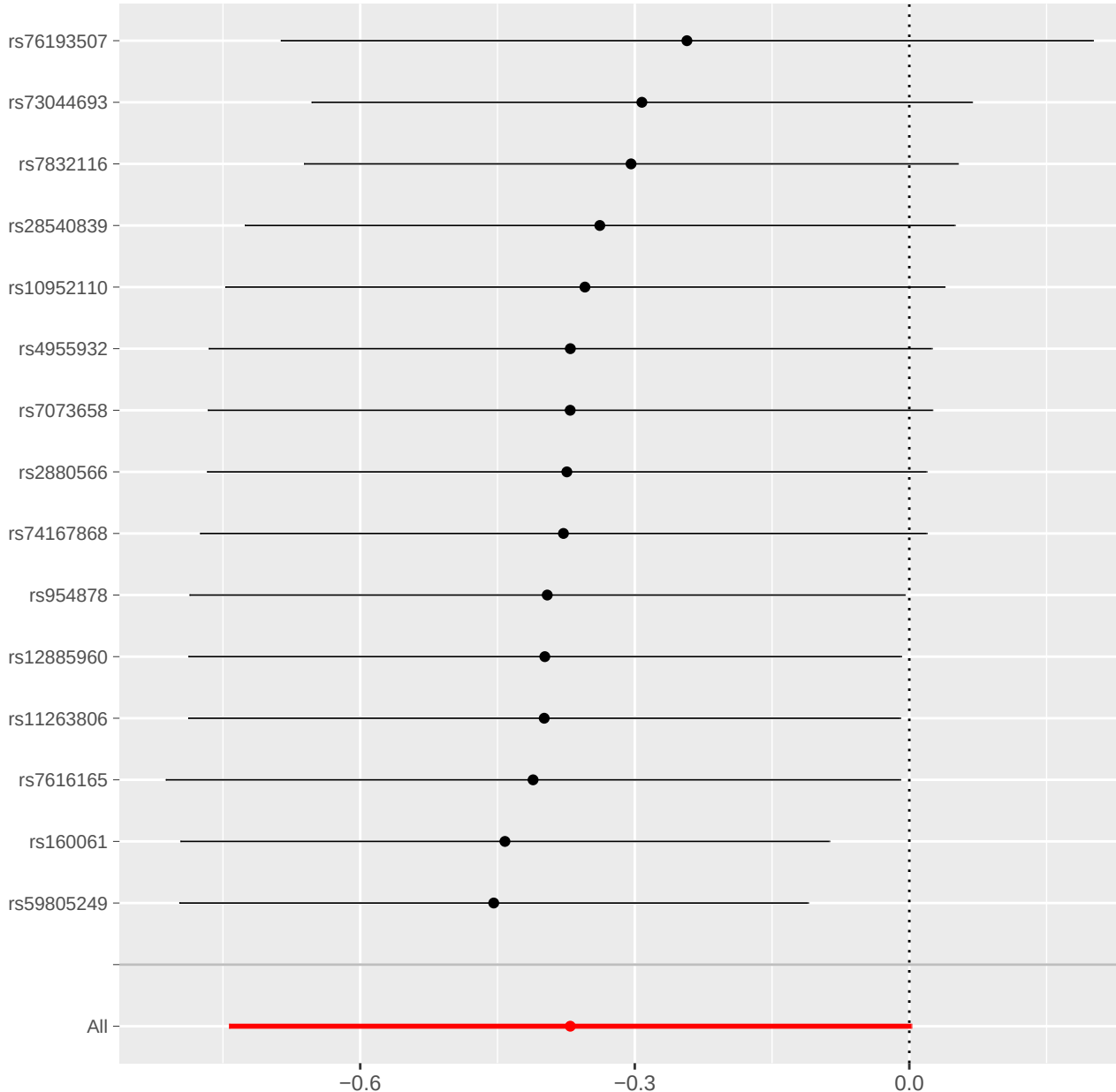






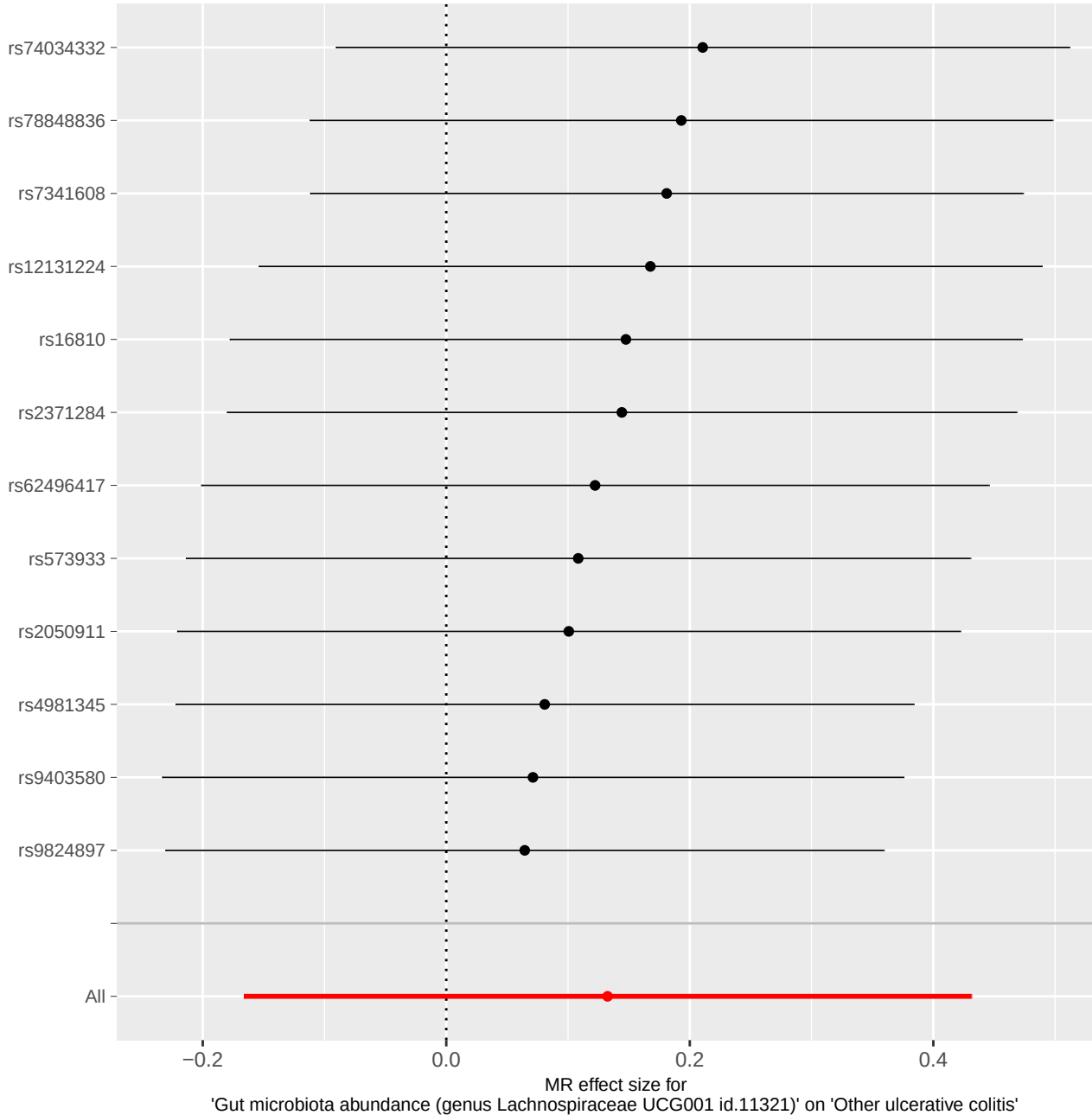


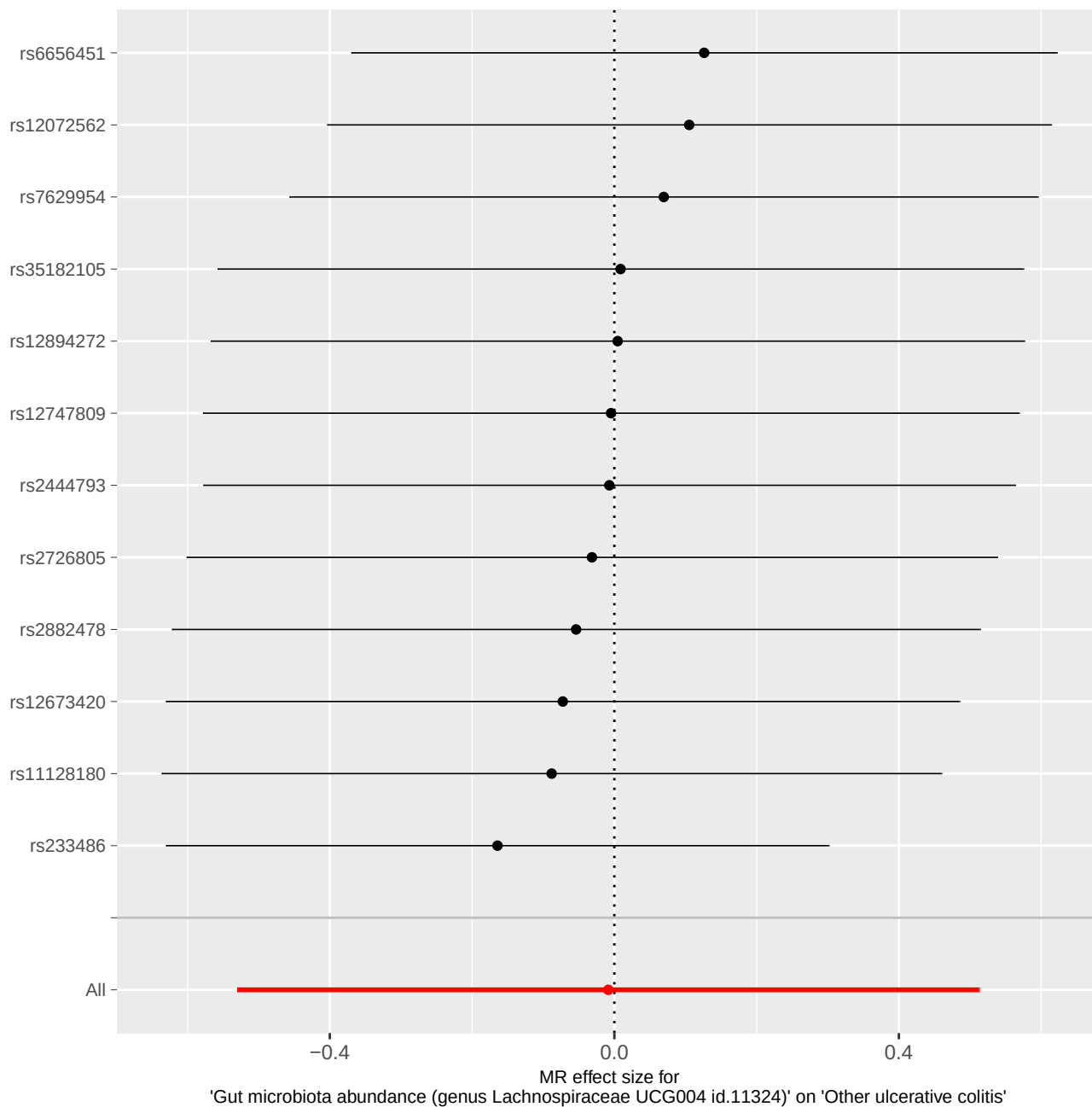


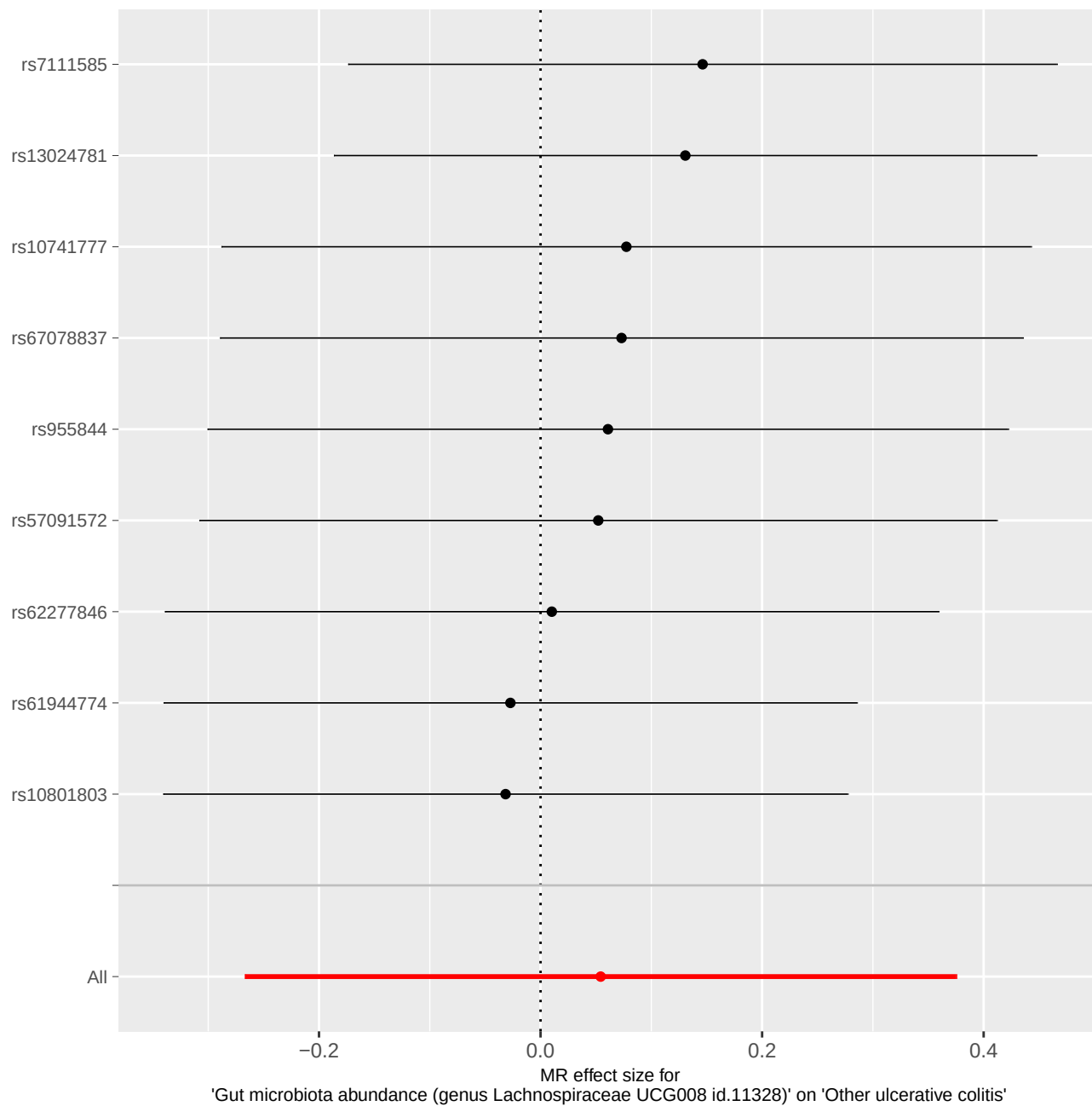


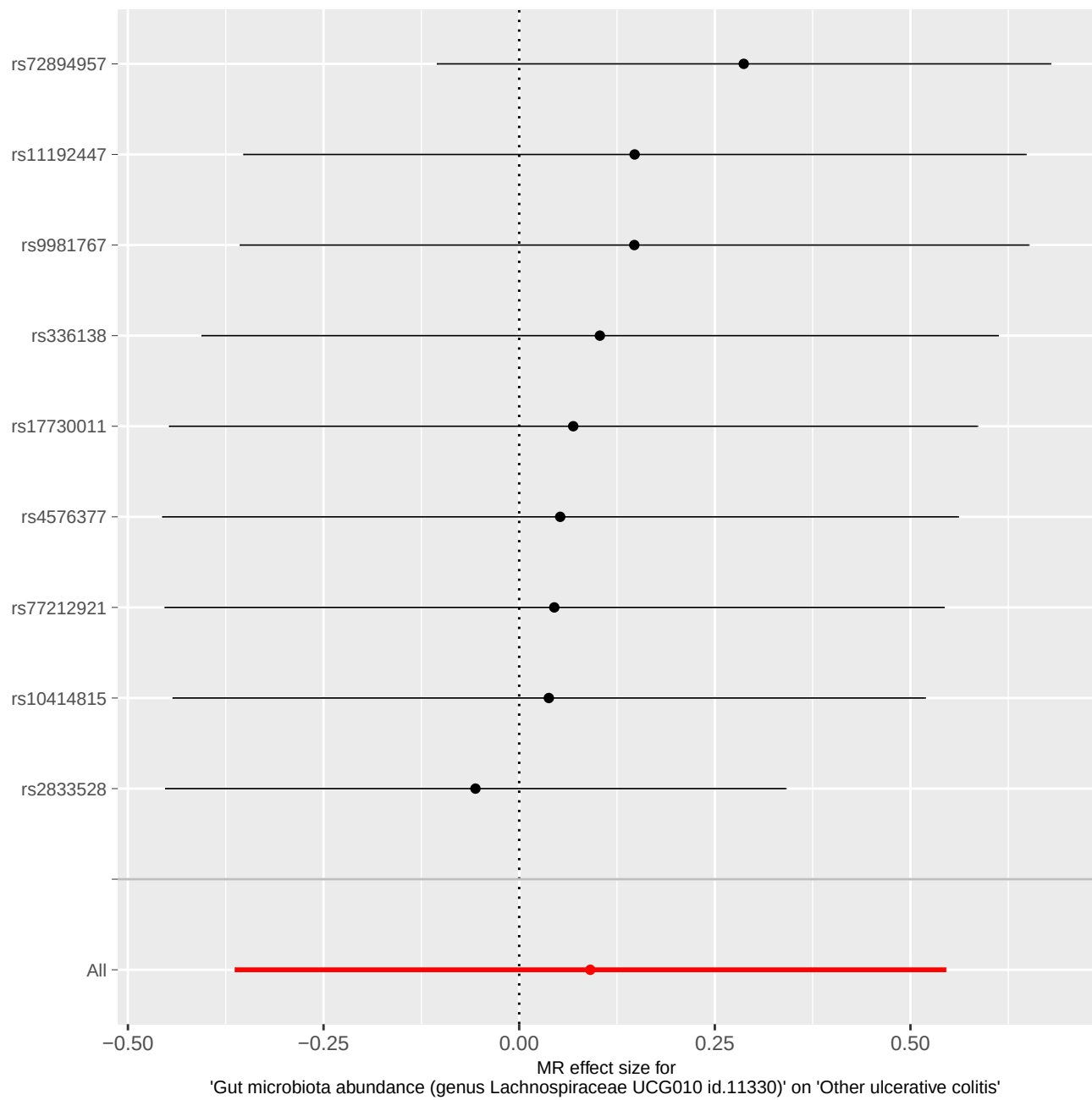
MR effect size for
'Gut microbiota abundance (genus Lachnospiraceae NK4A136 group id.11319)' on 'Other ulcerative colitis'

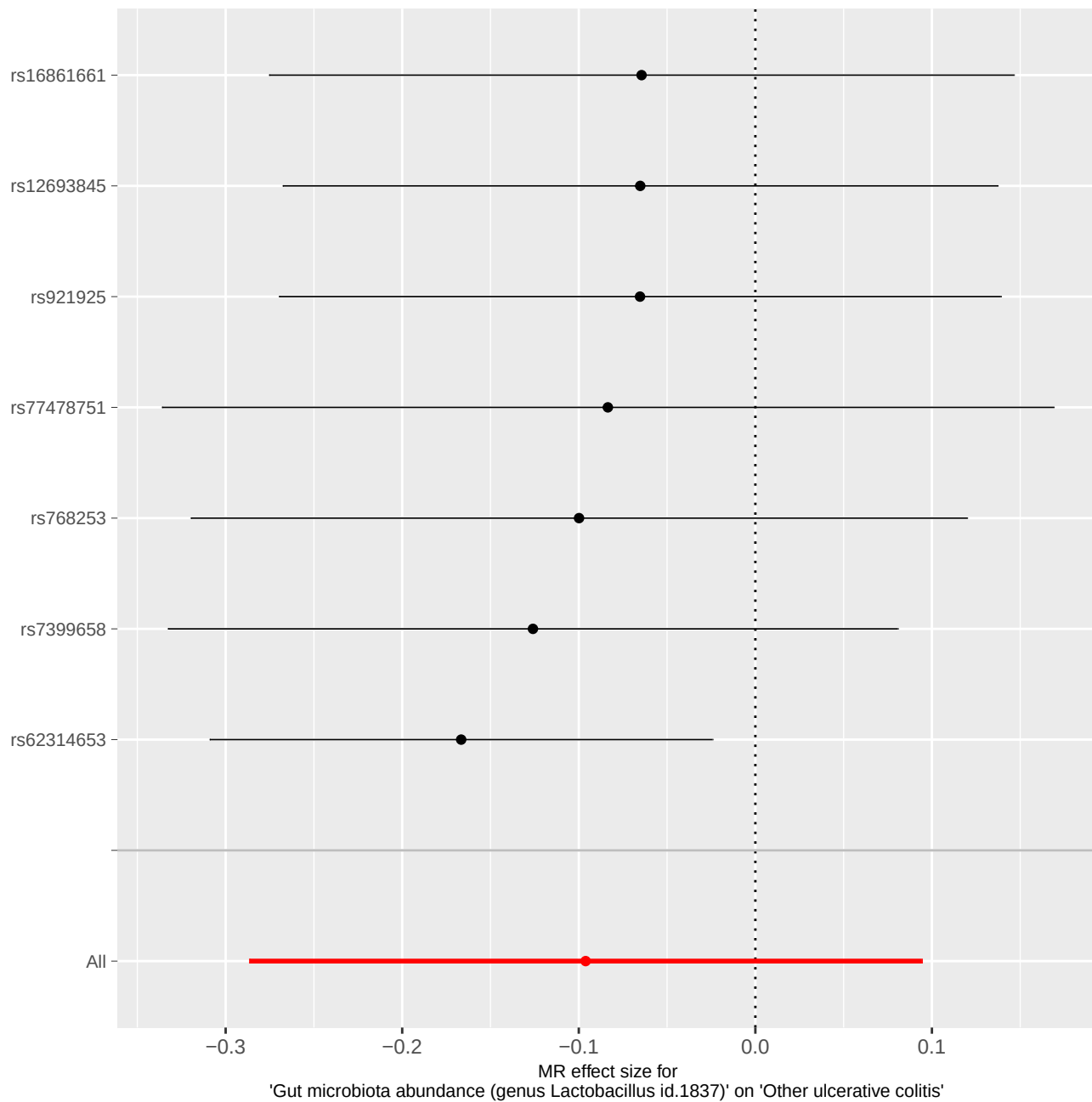
Batch 1299 : Gut microbiota abundance (genus Lachnospiraceae UCG001 id.11321) on Other ulcerative colitis



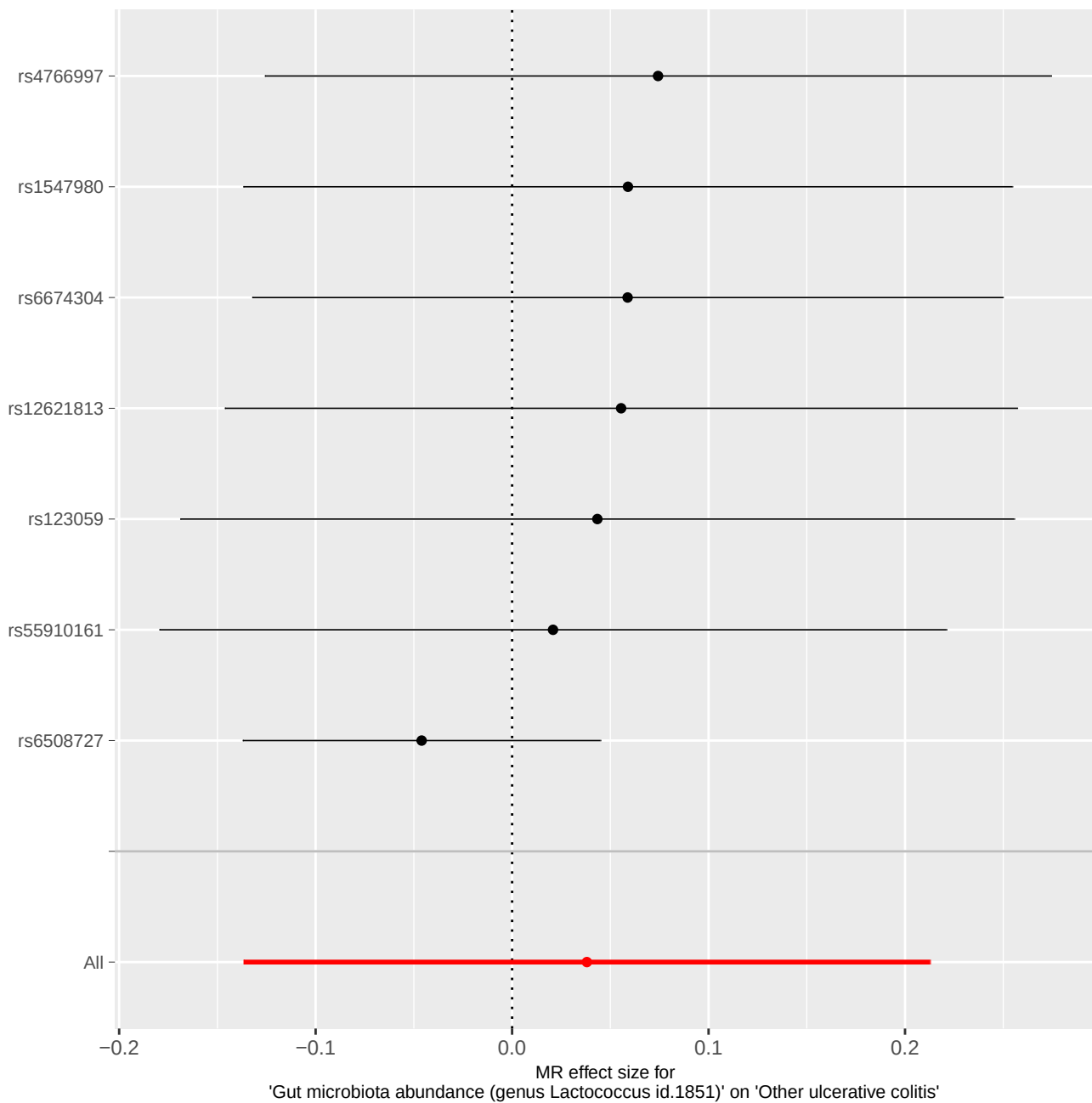


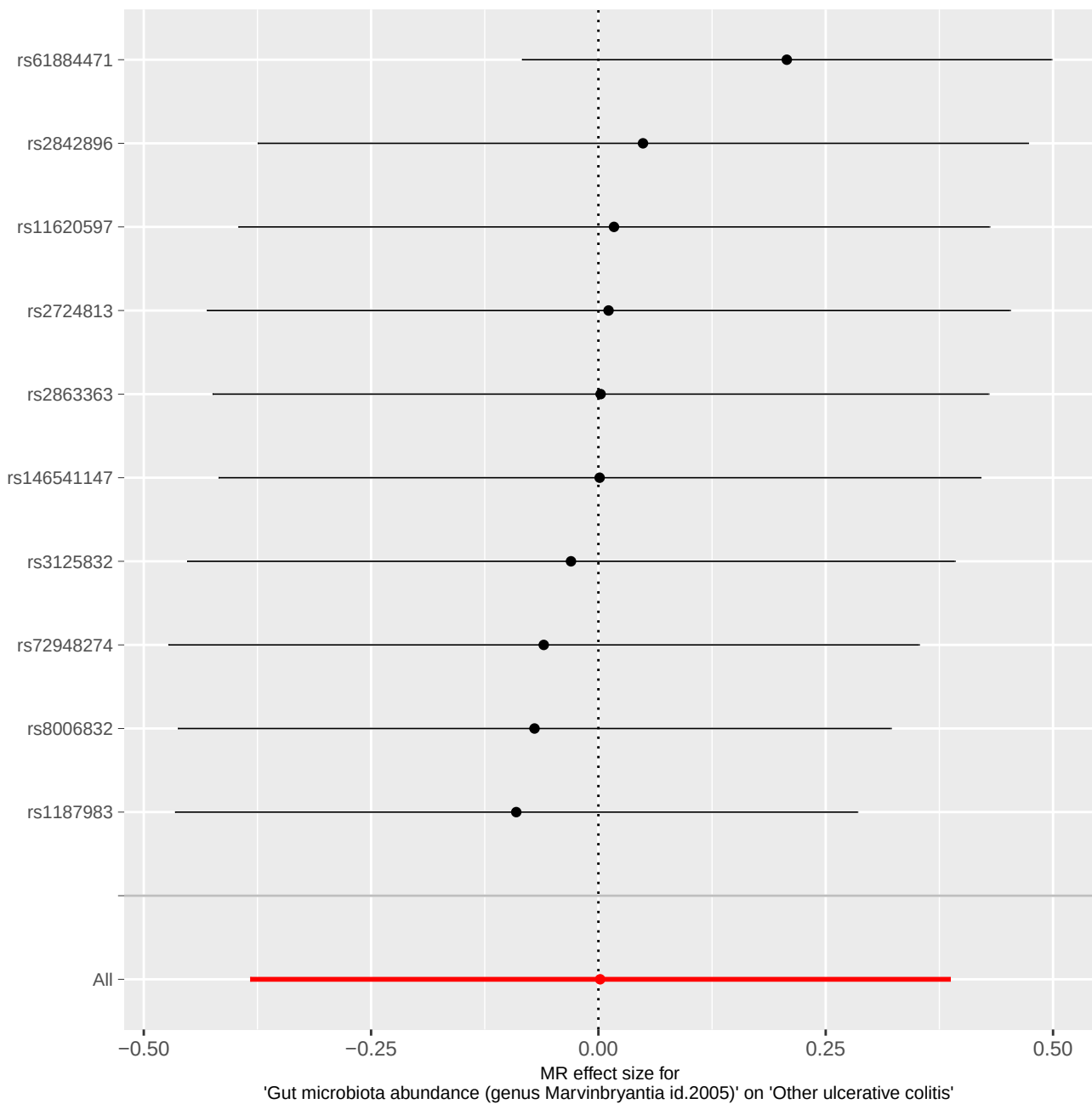


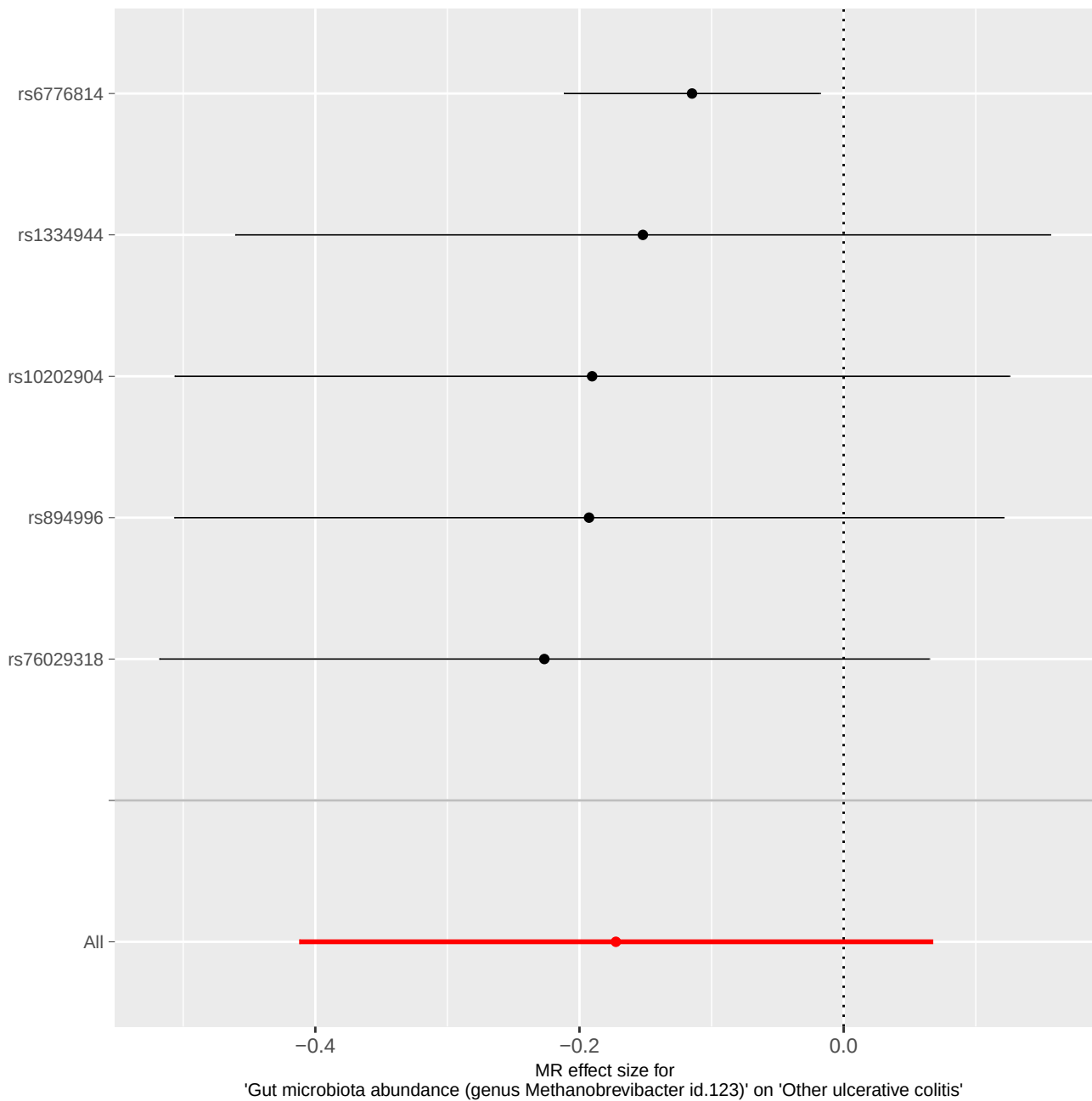


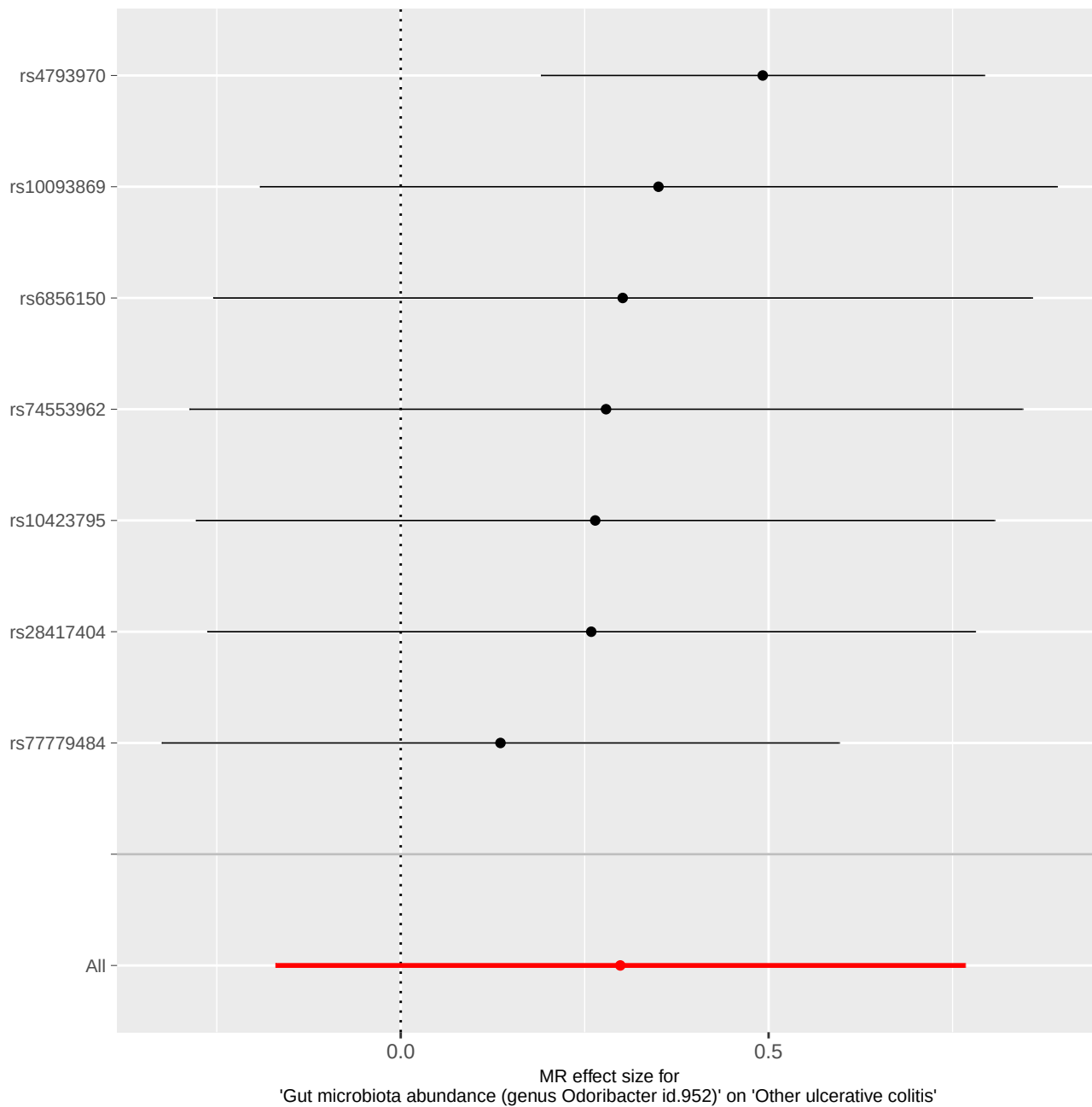


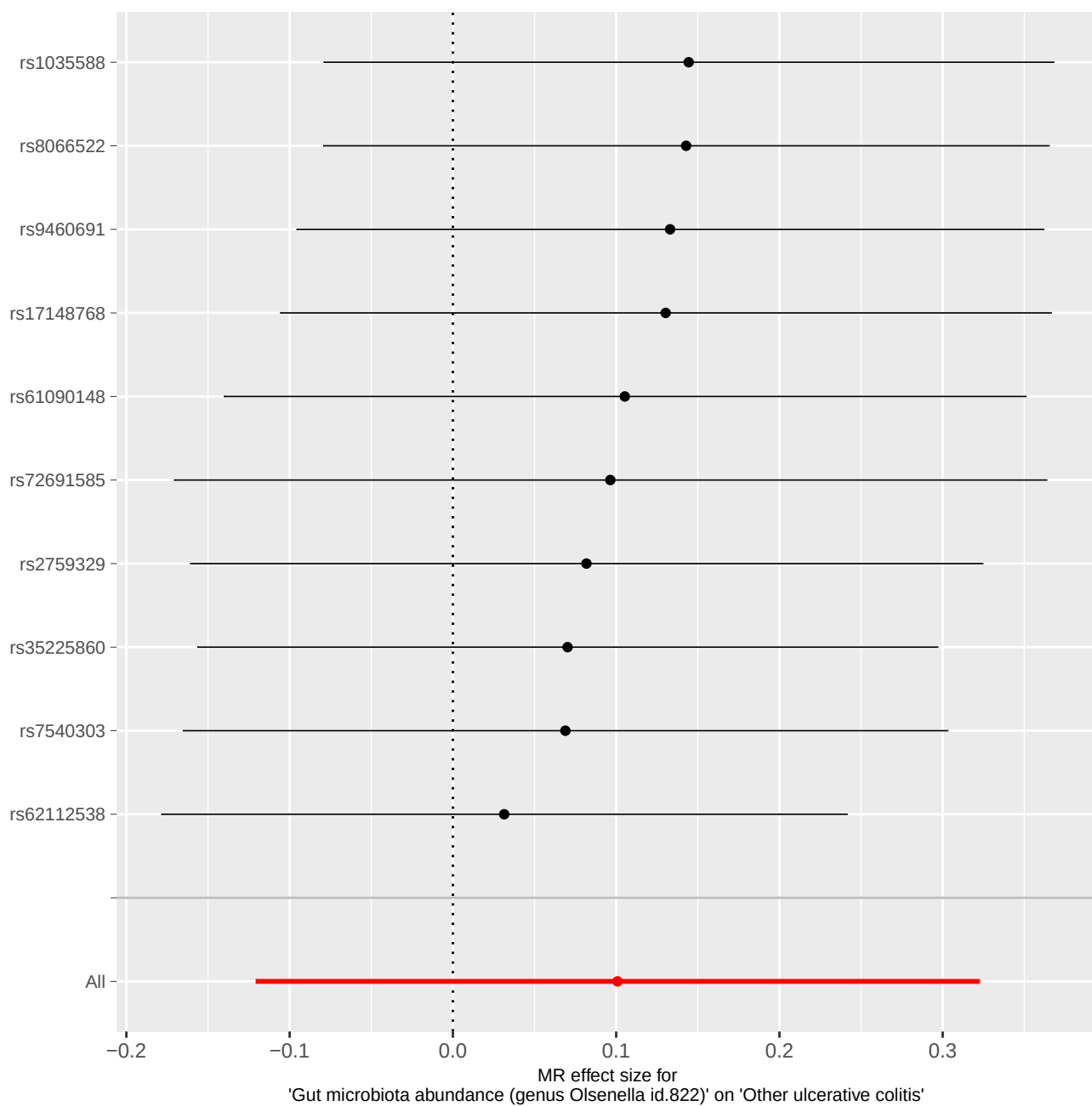
Batch 1305 : Gut microbiota abundance (genus Lactococcus id.1851) on Other ulcerative colitis

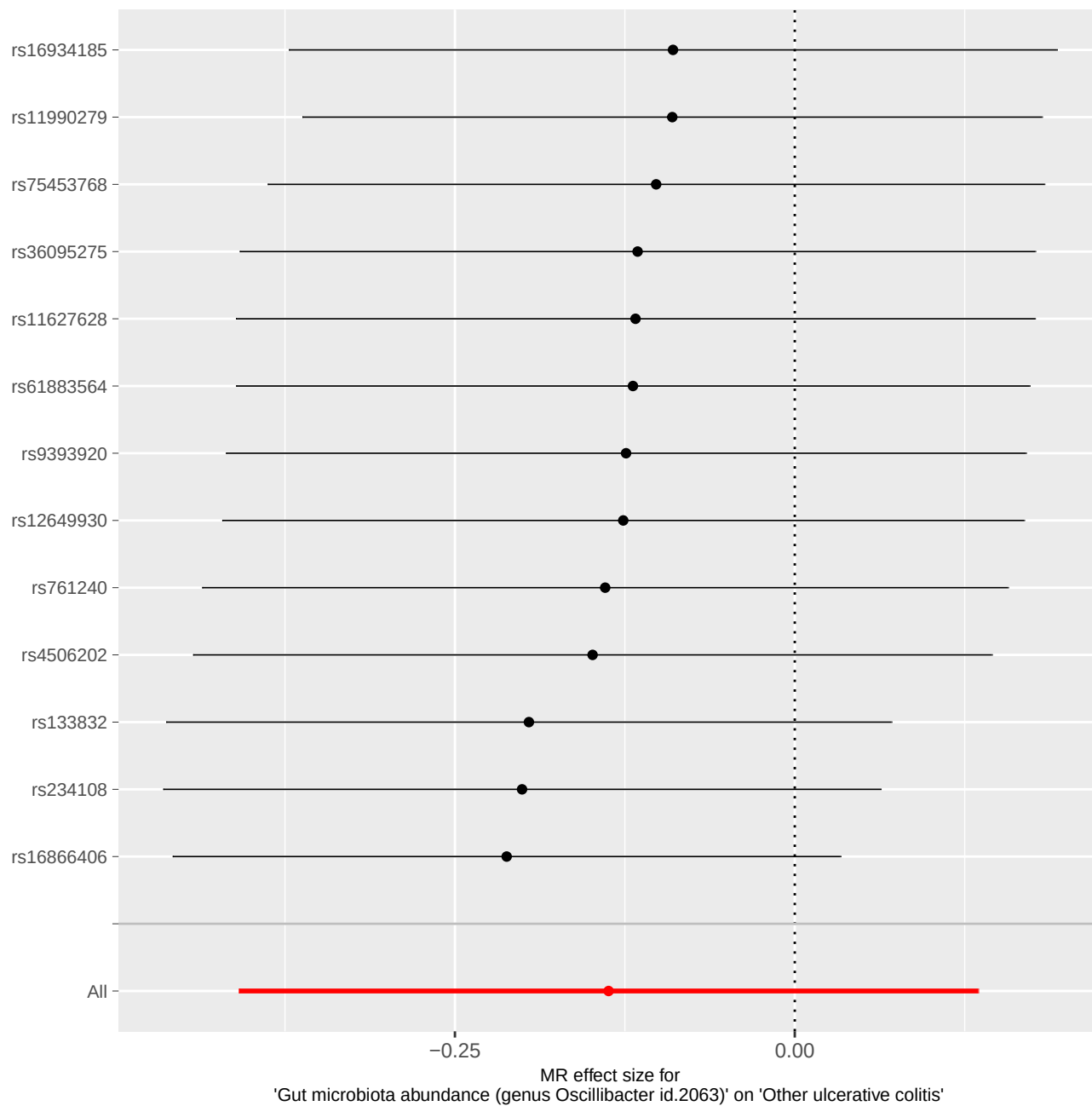


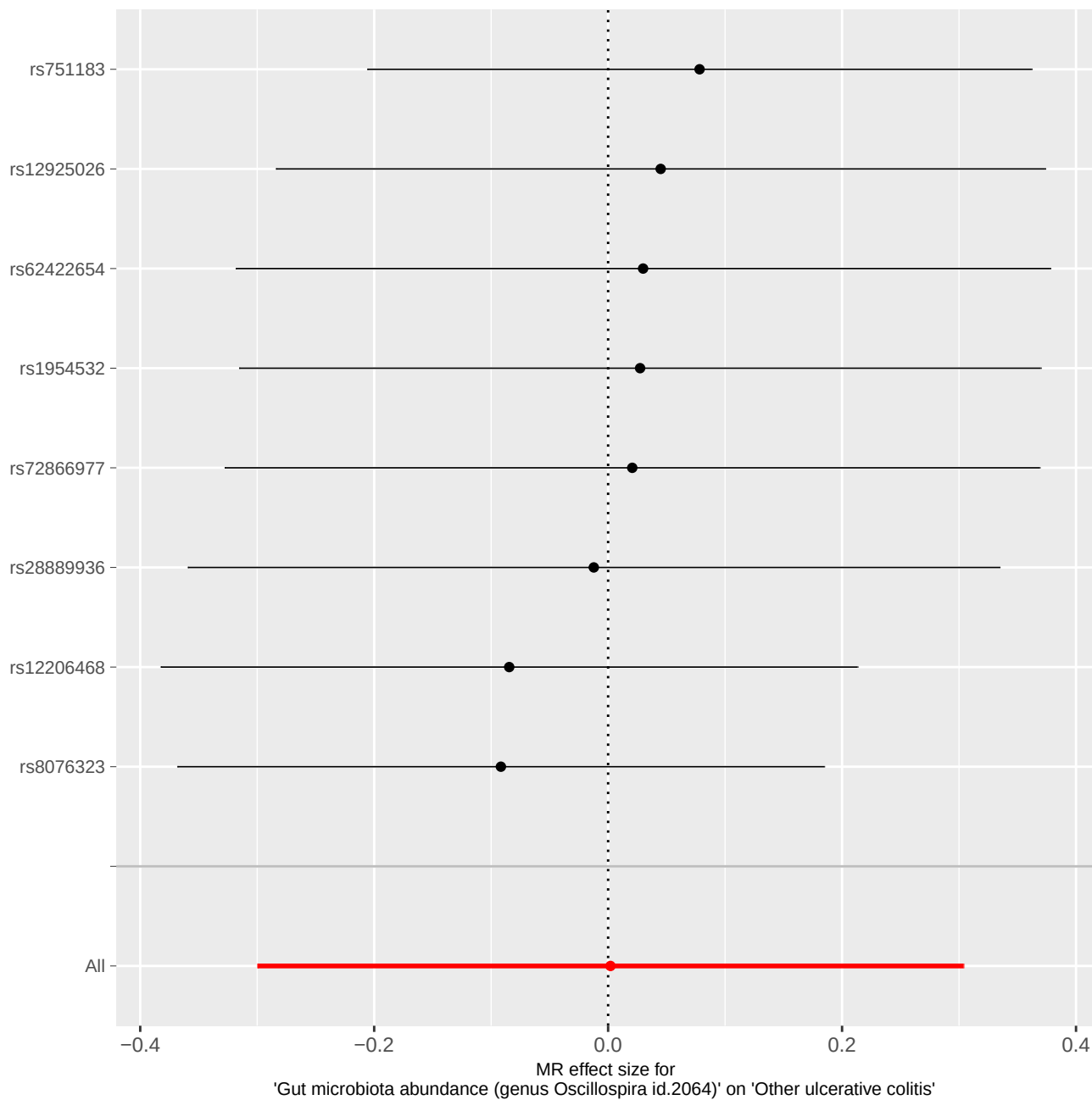


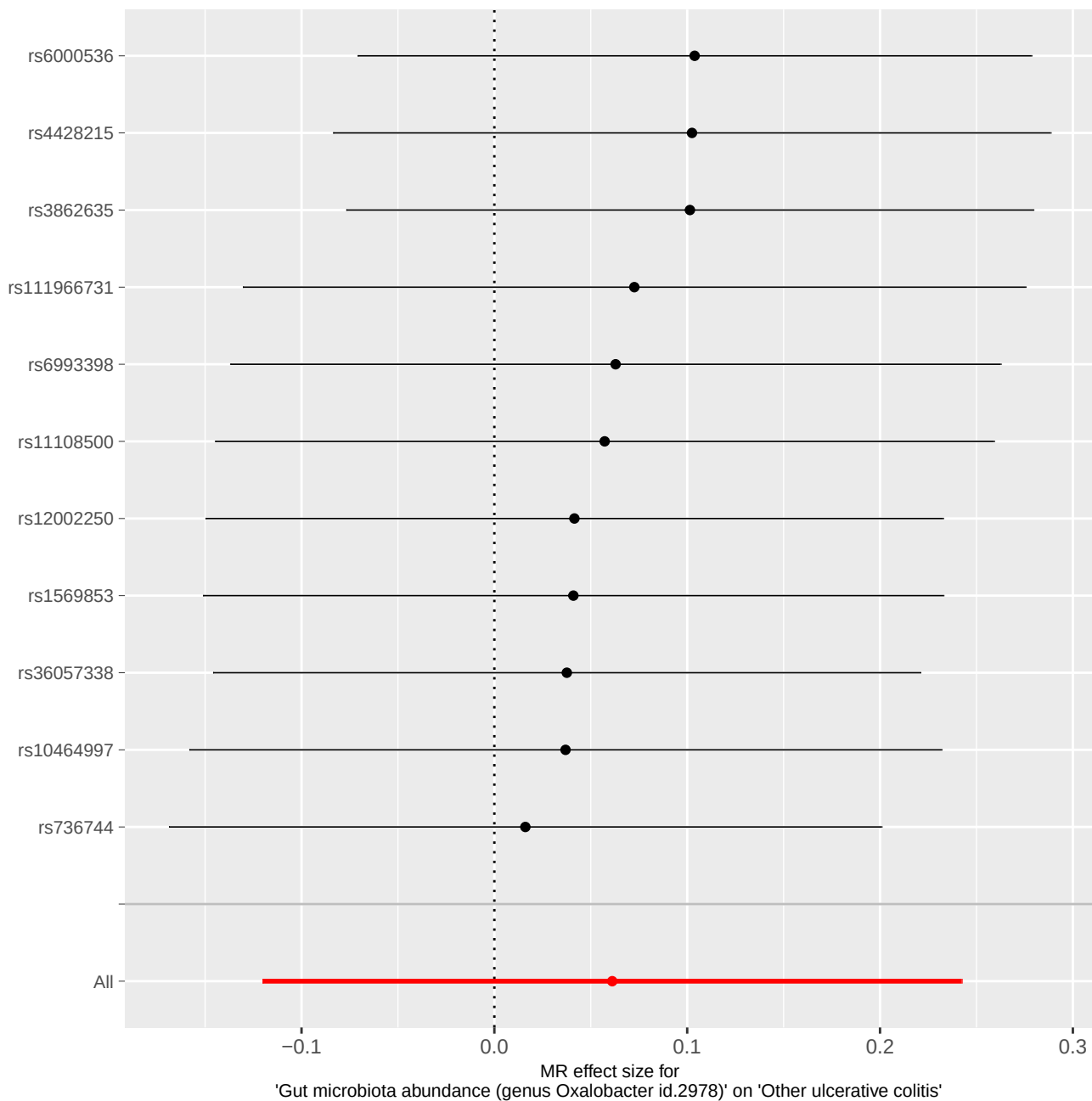


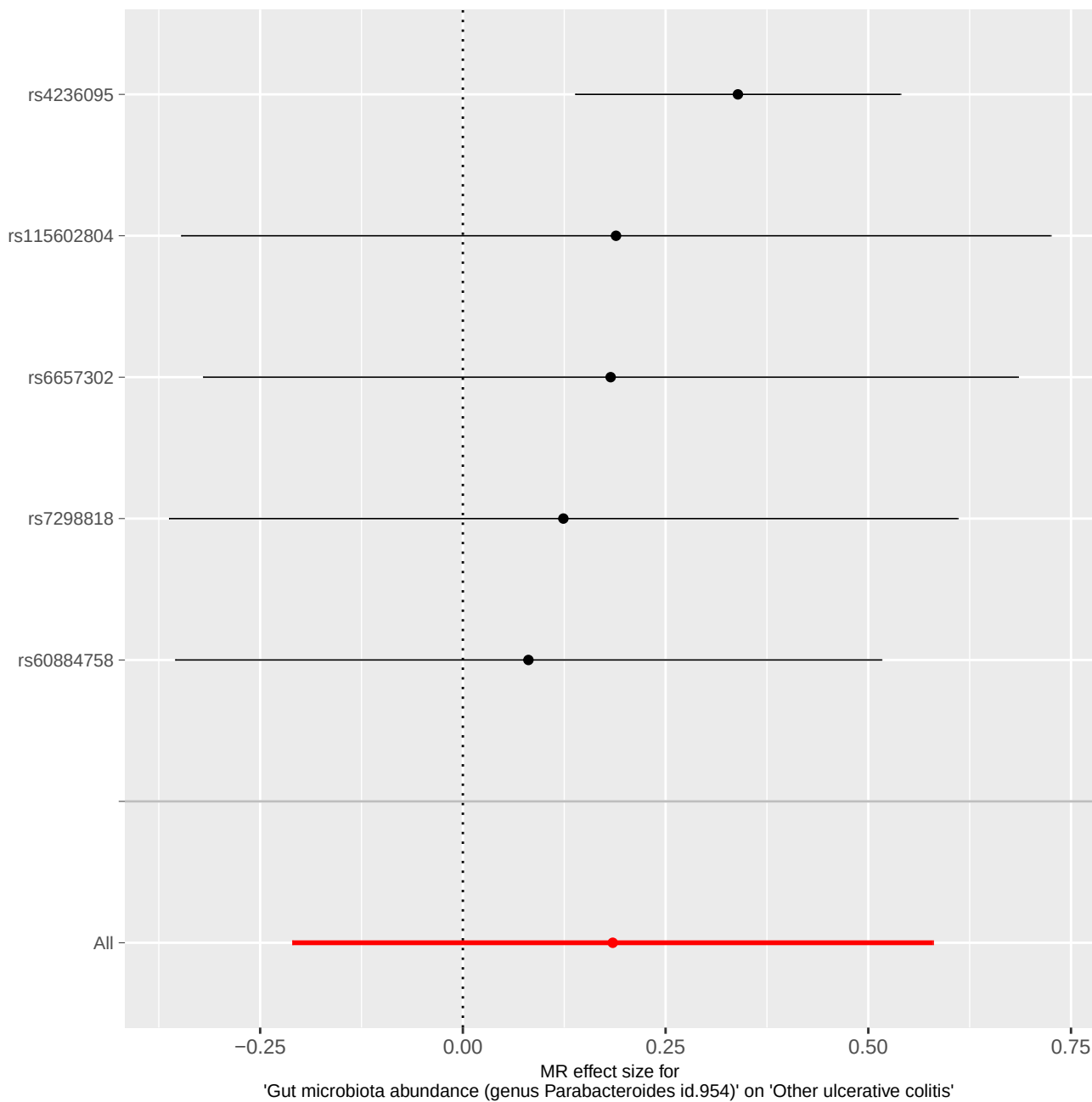


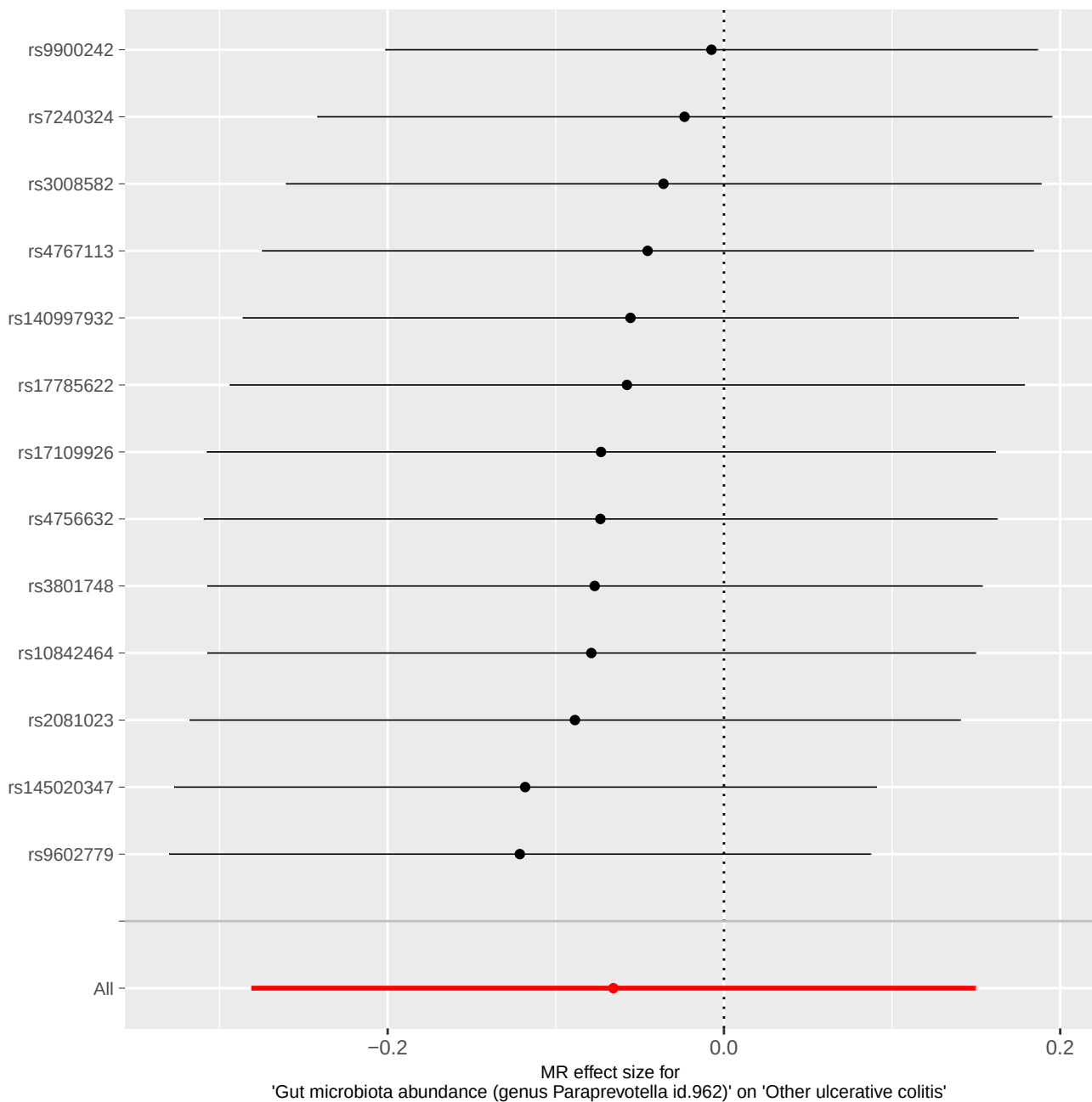


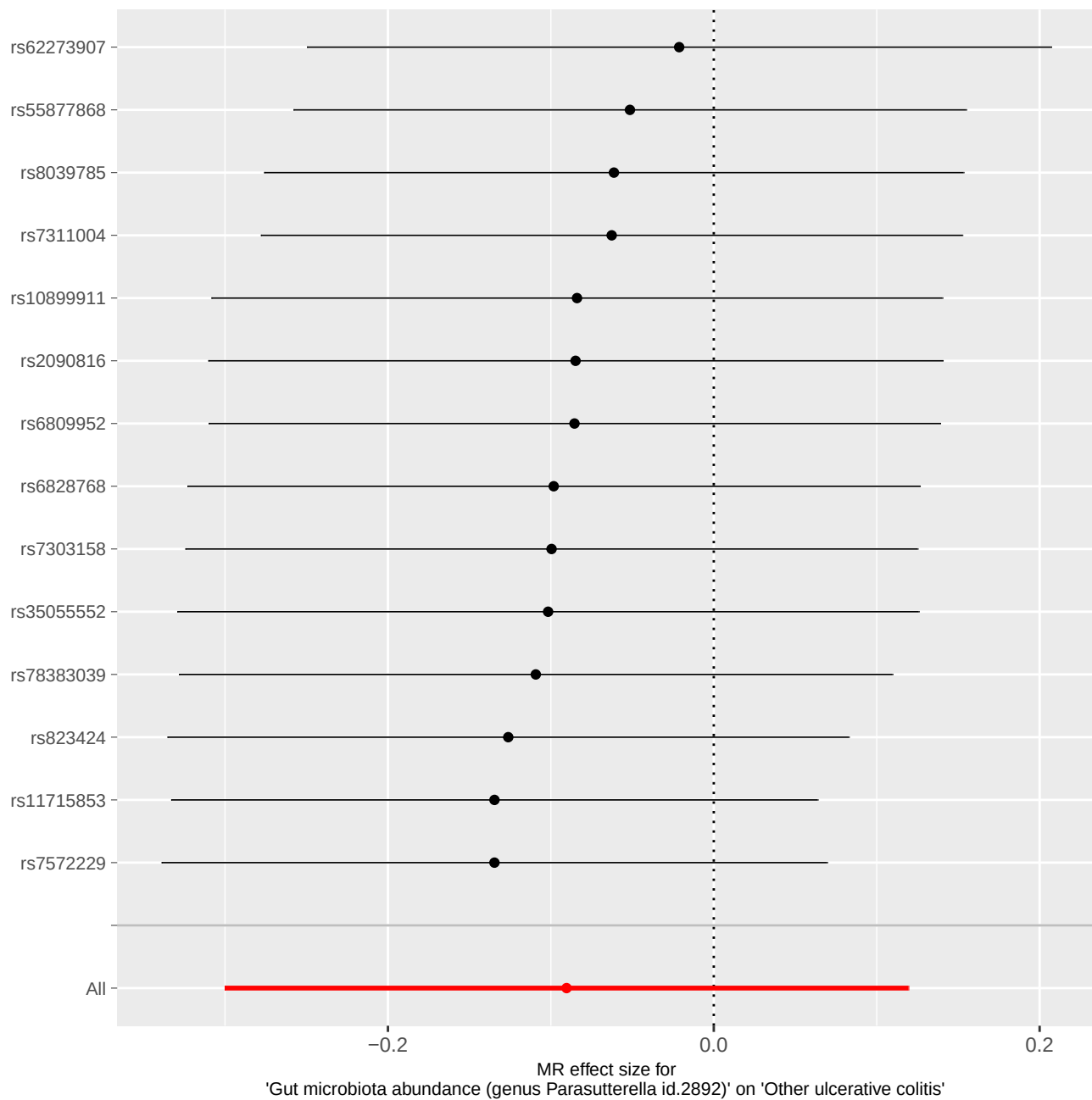


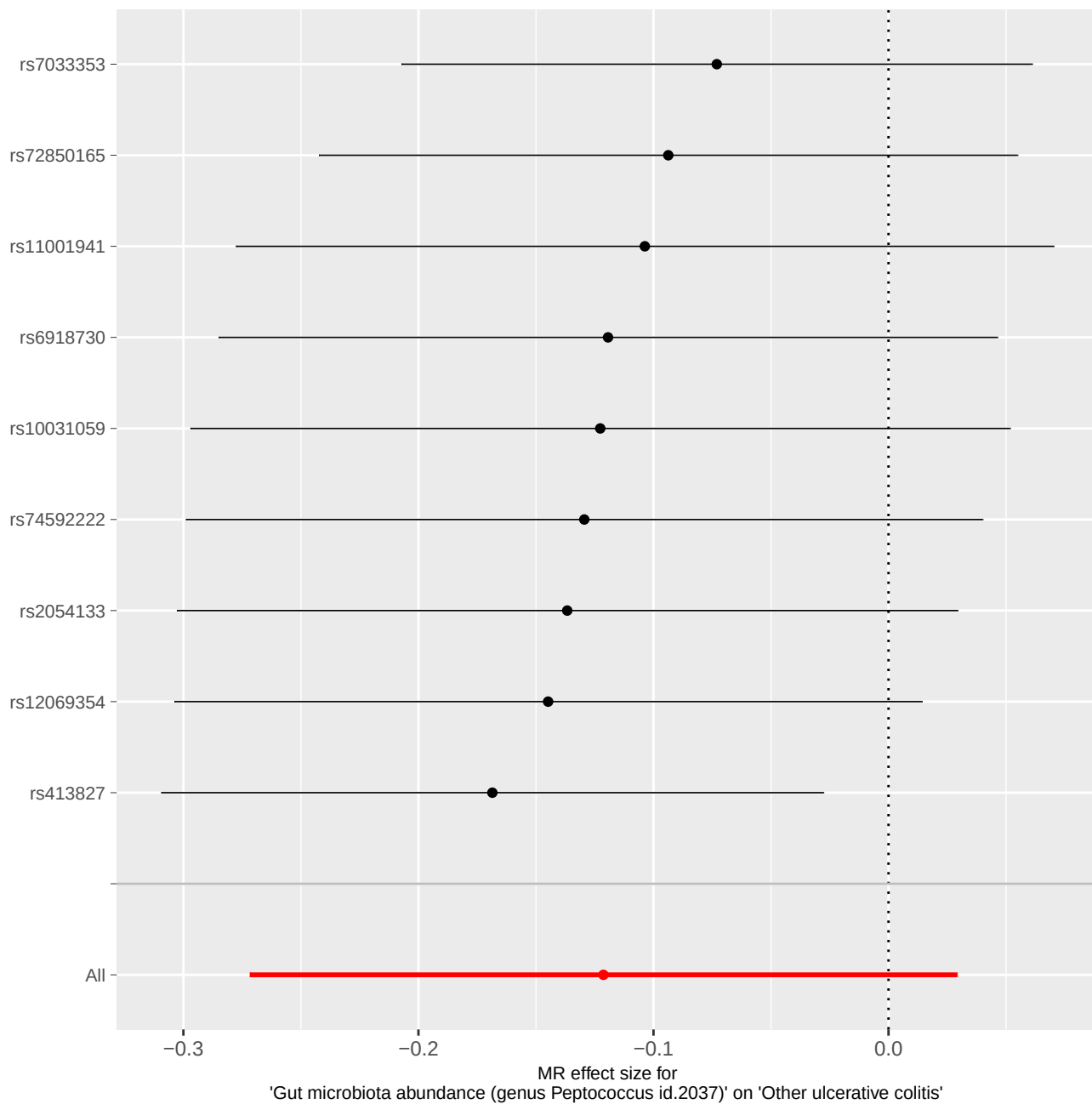


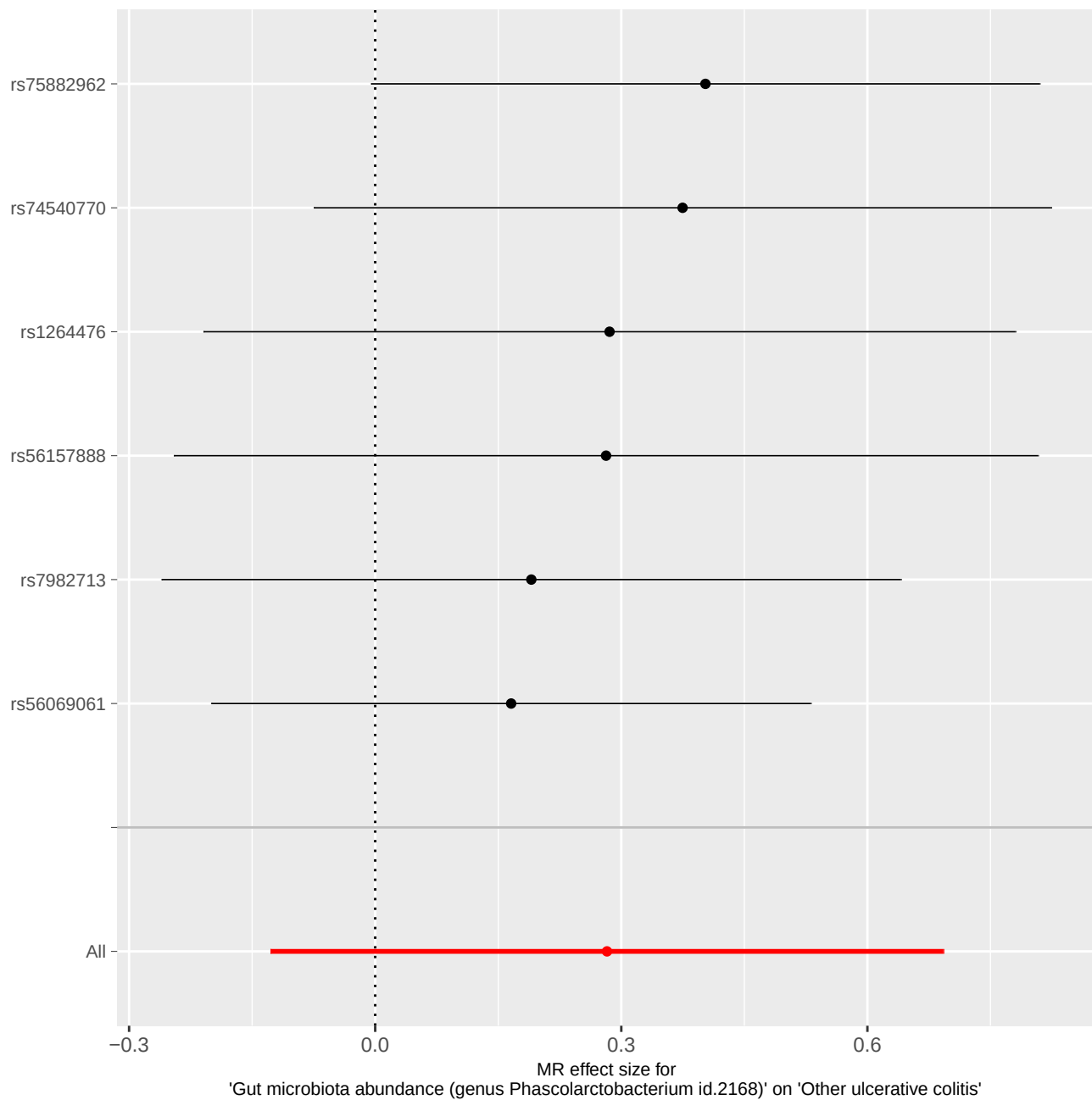


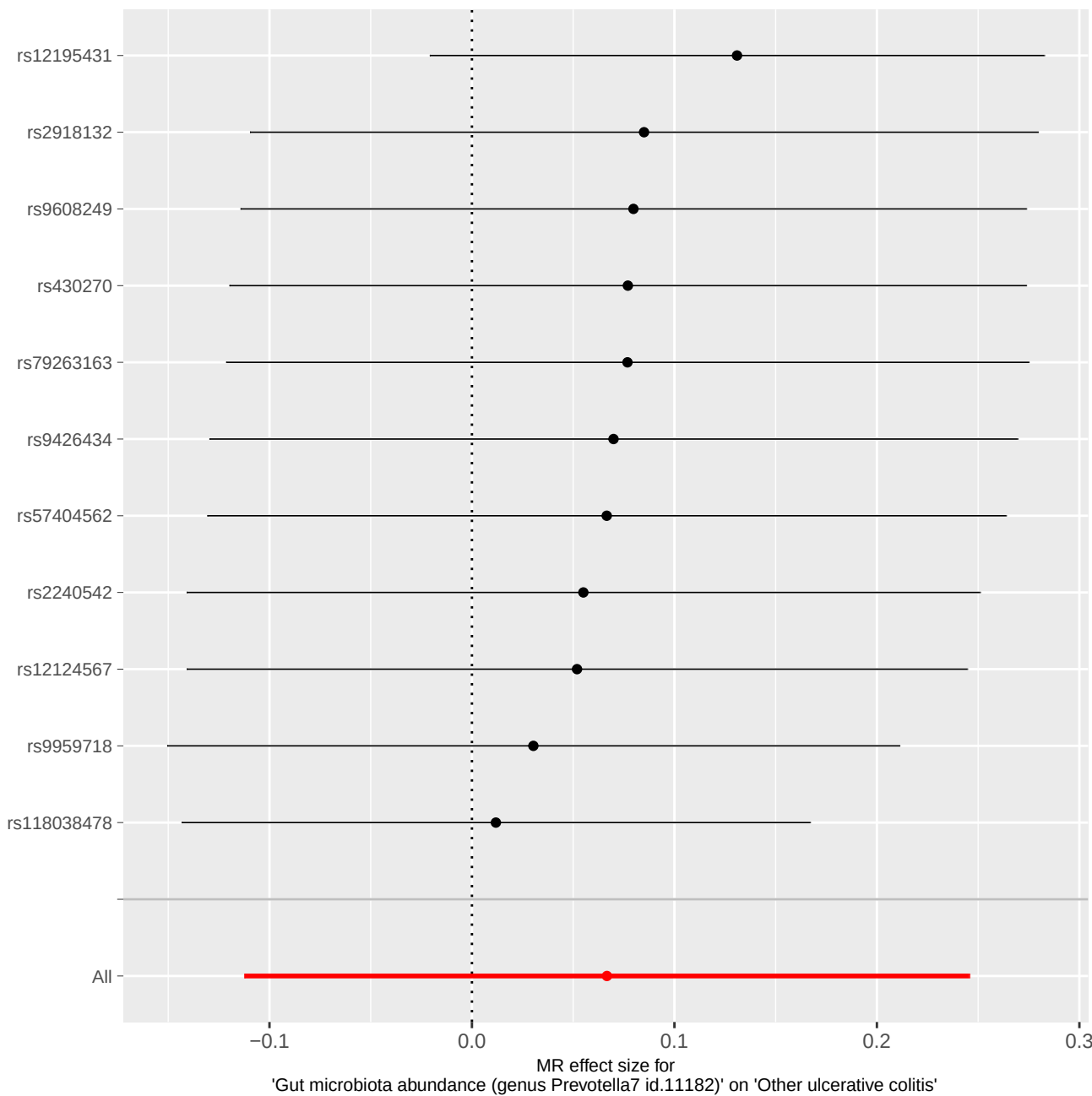


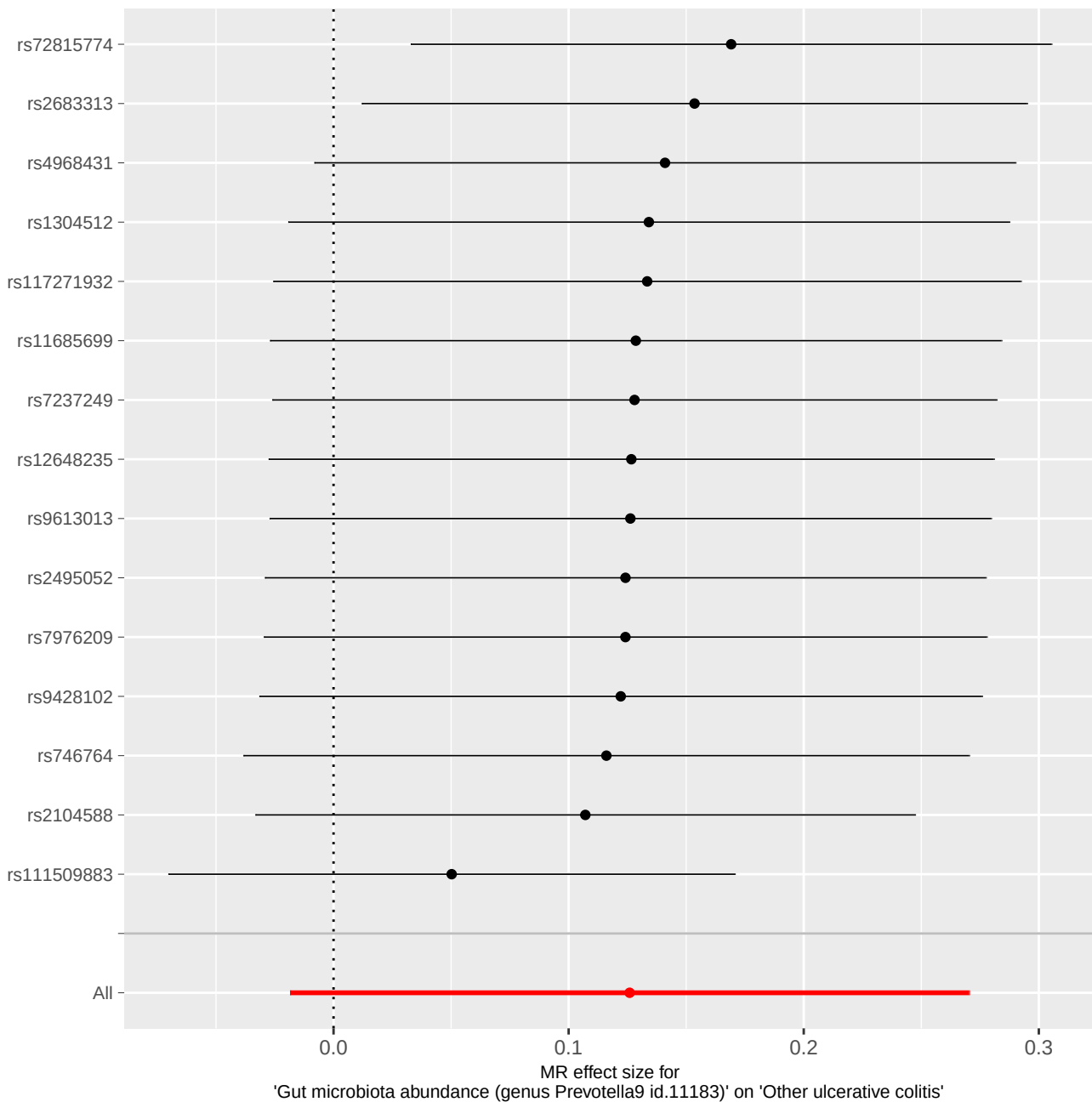


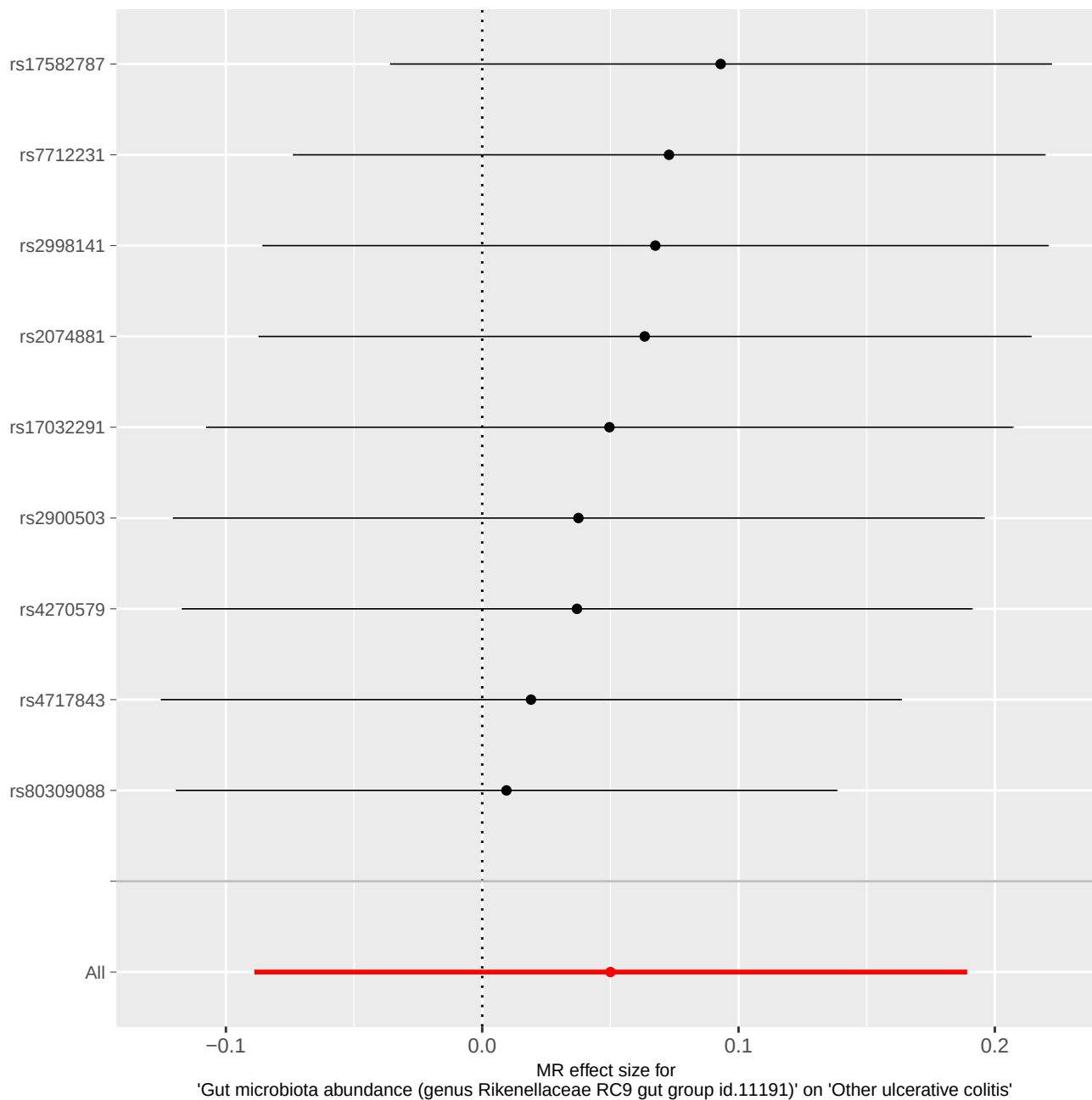


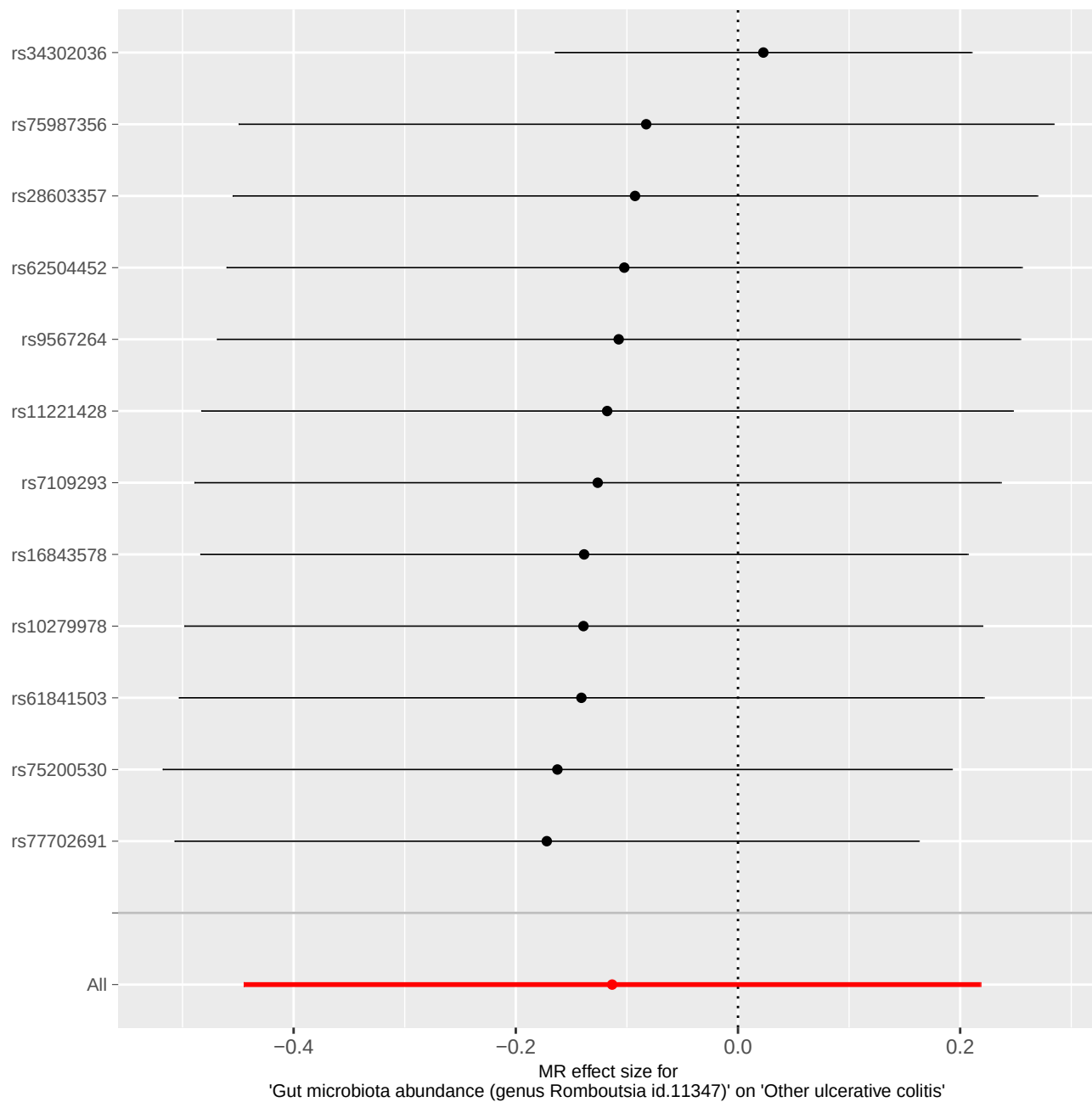


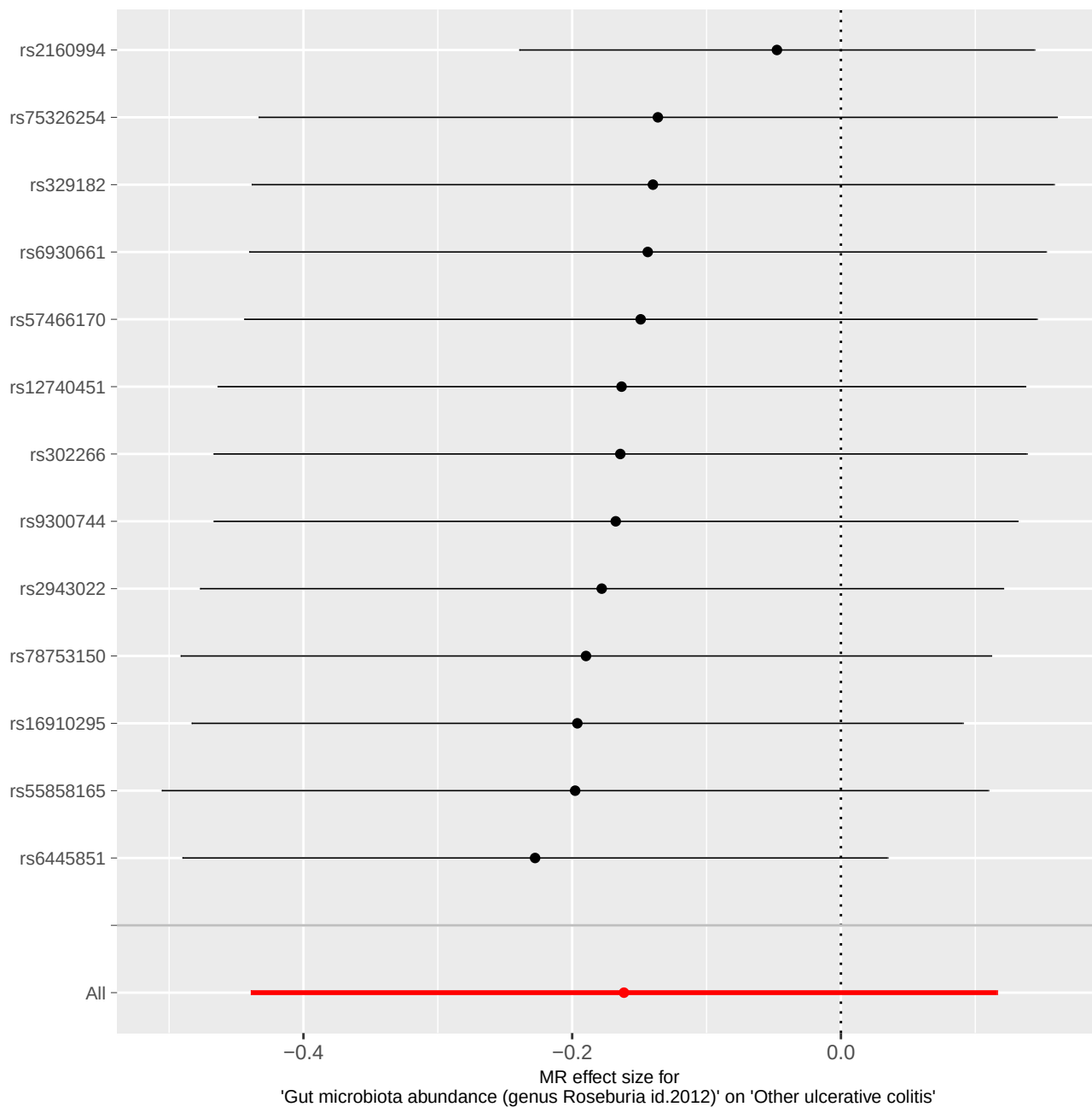


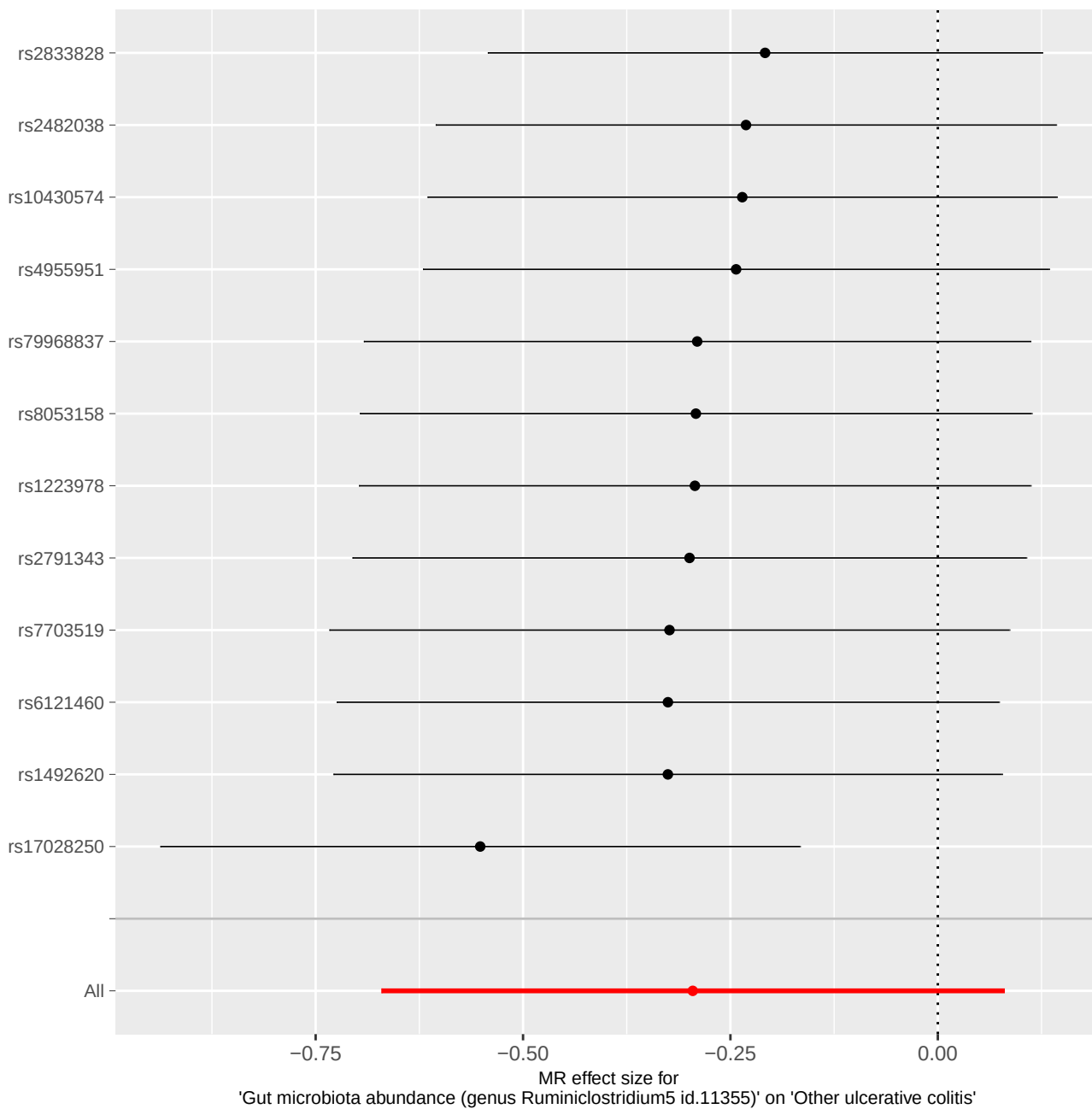


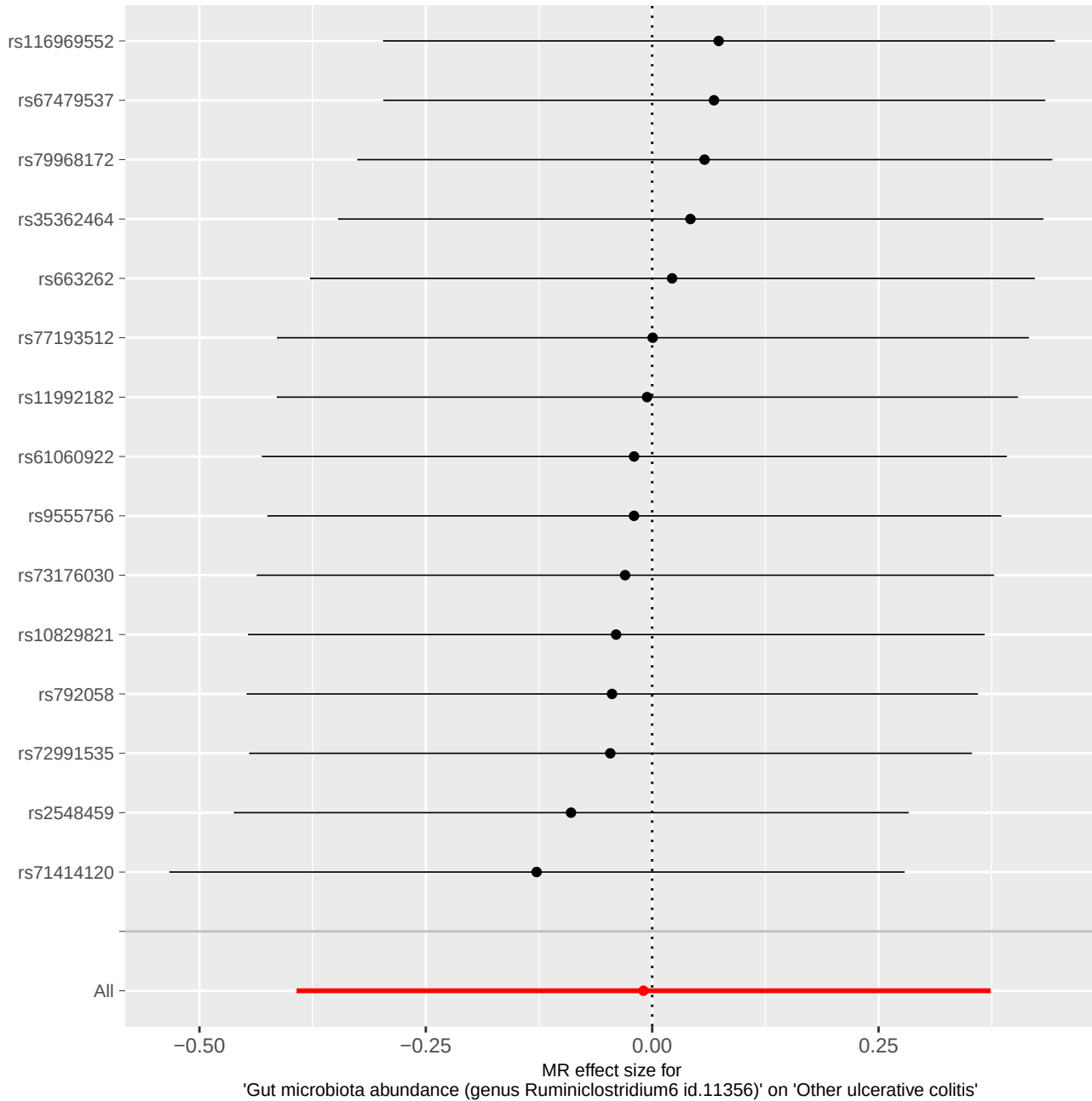


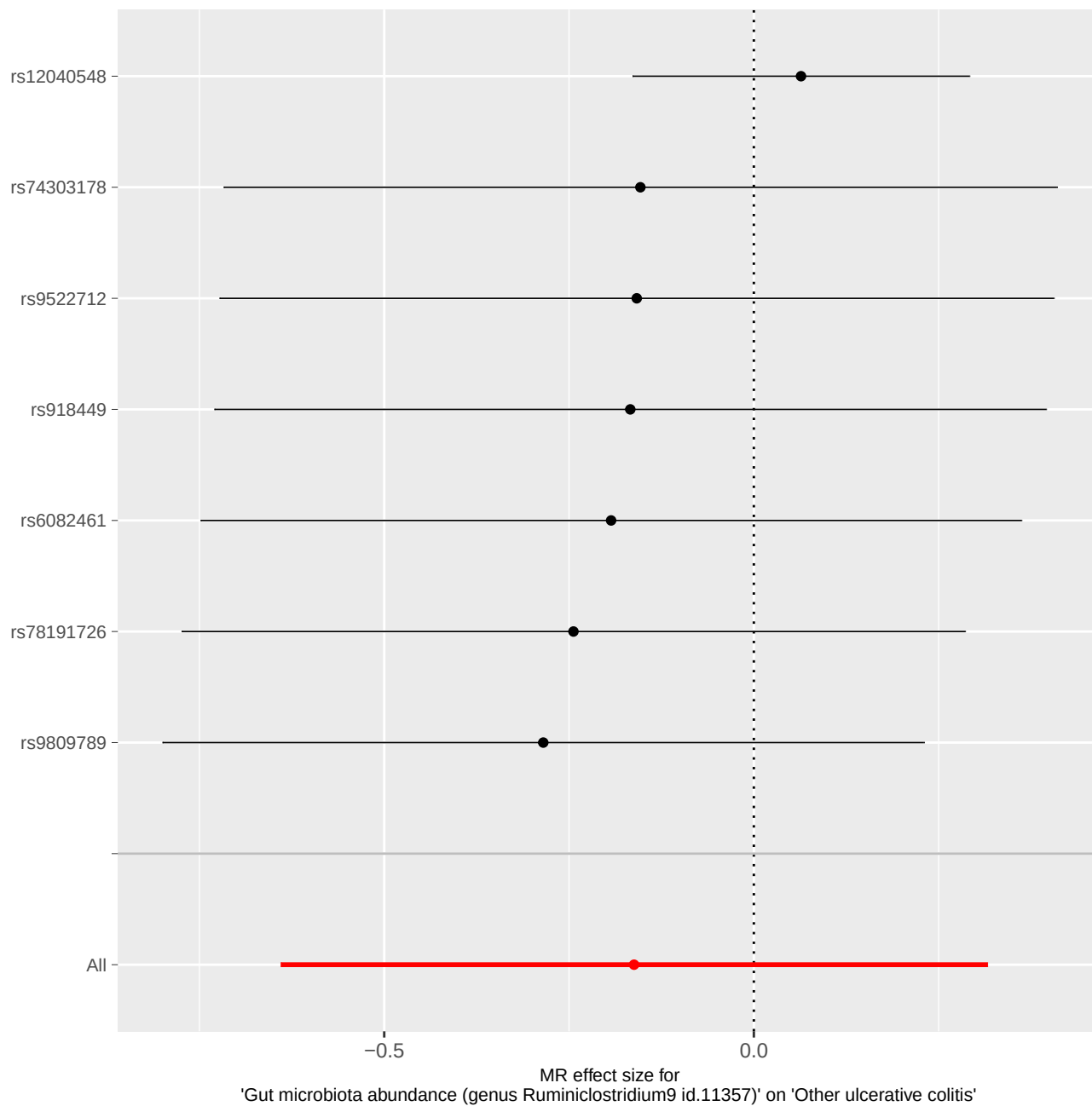


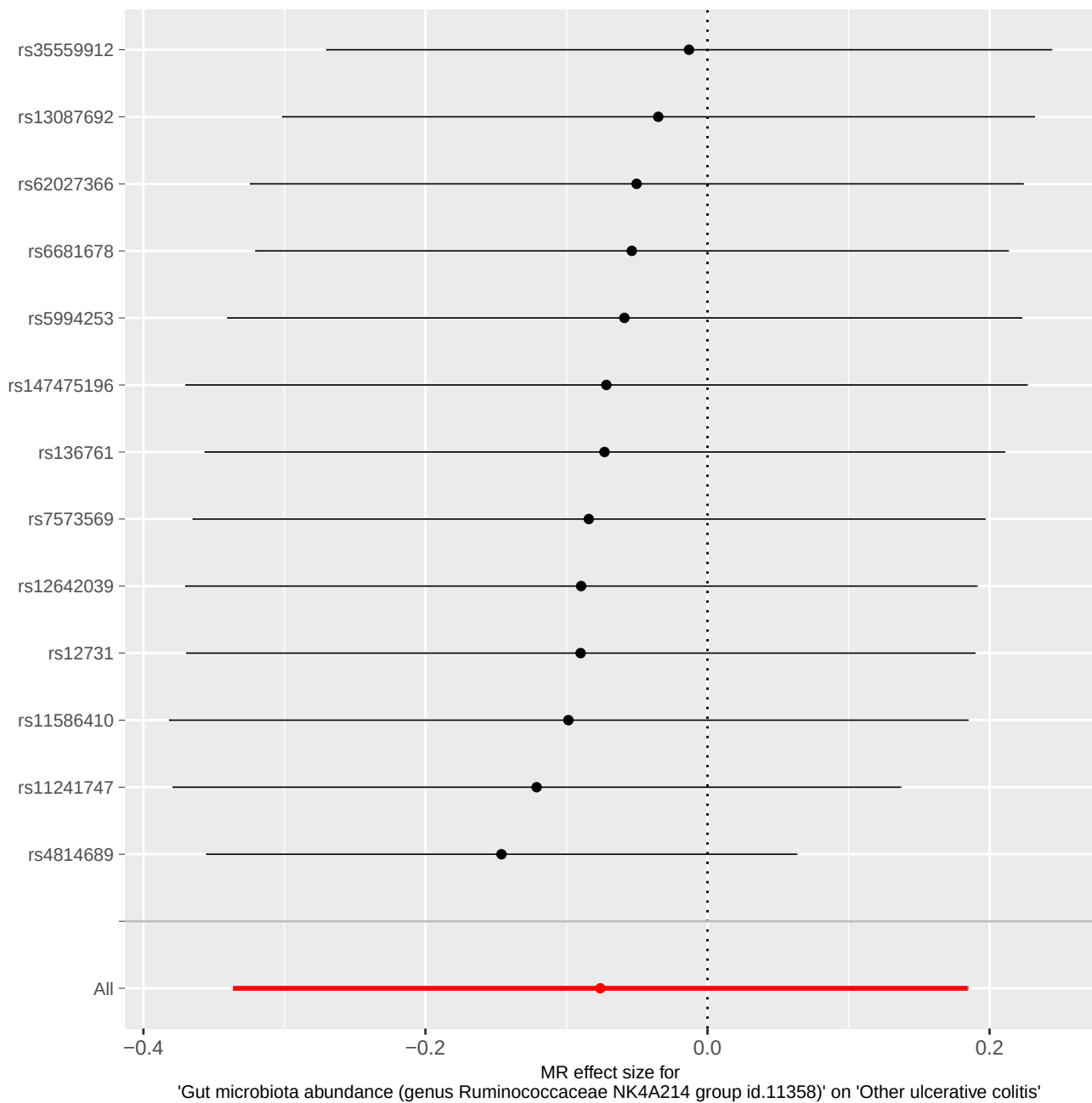




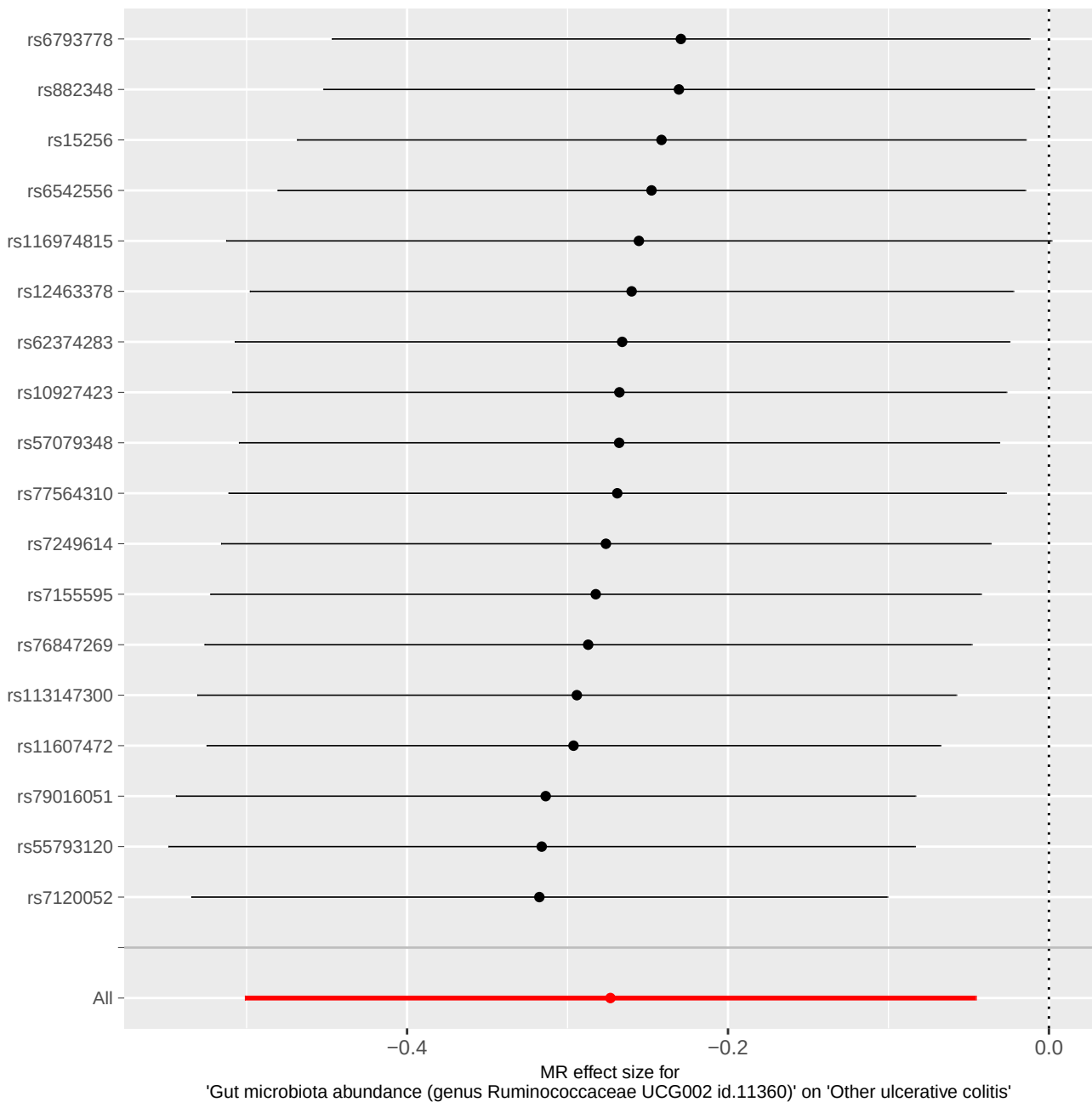


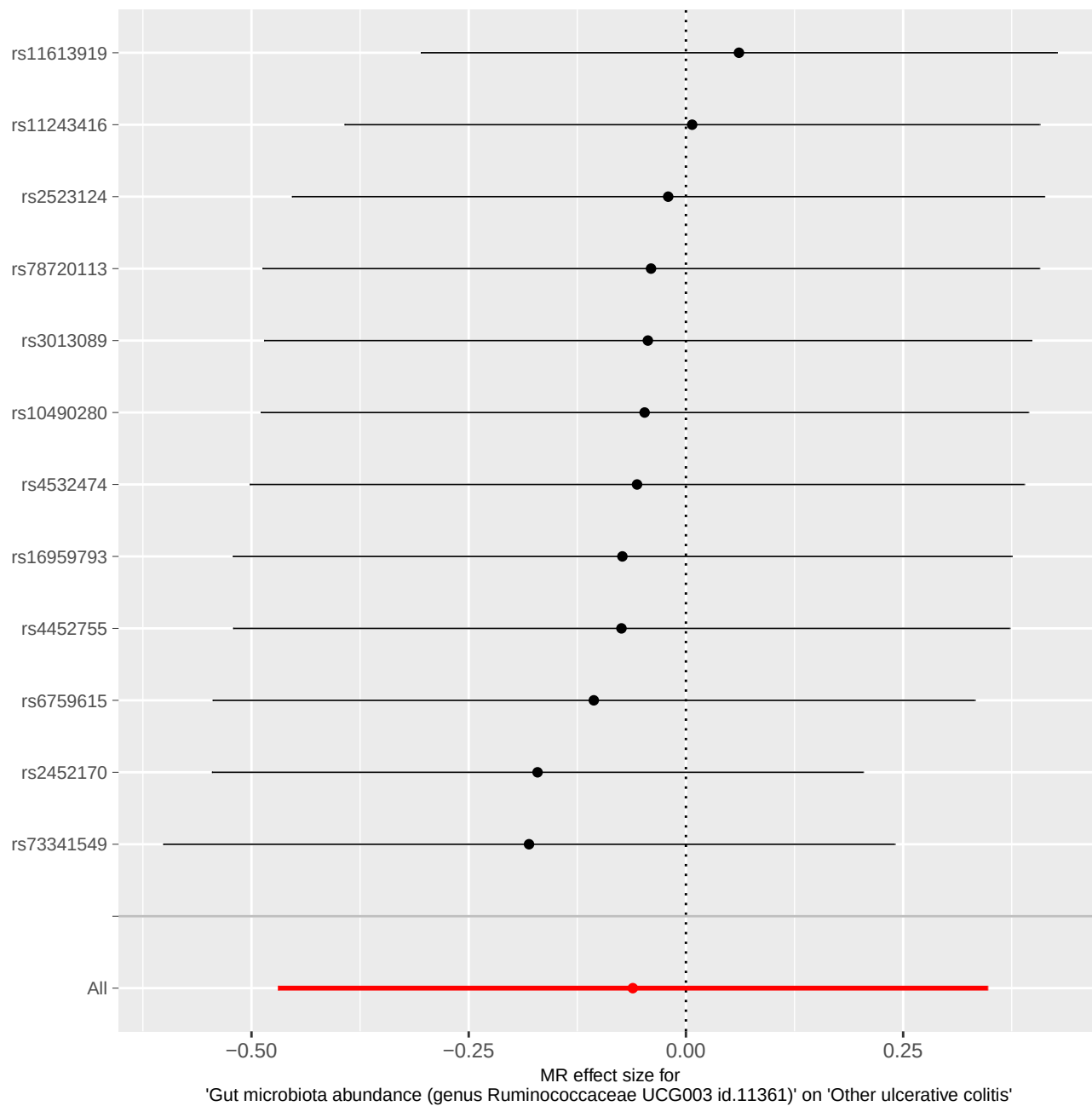




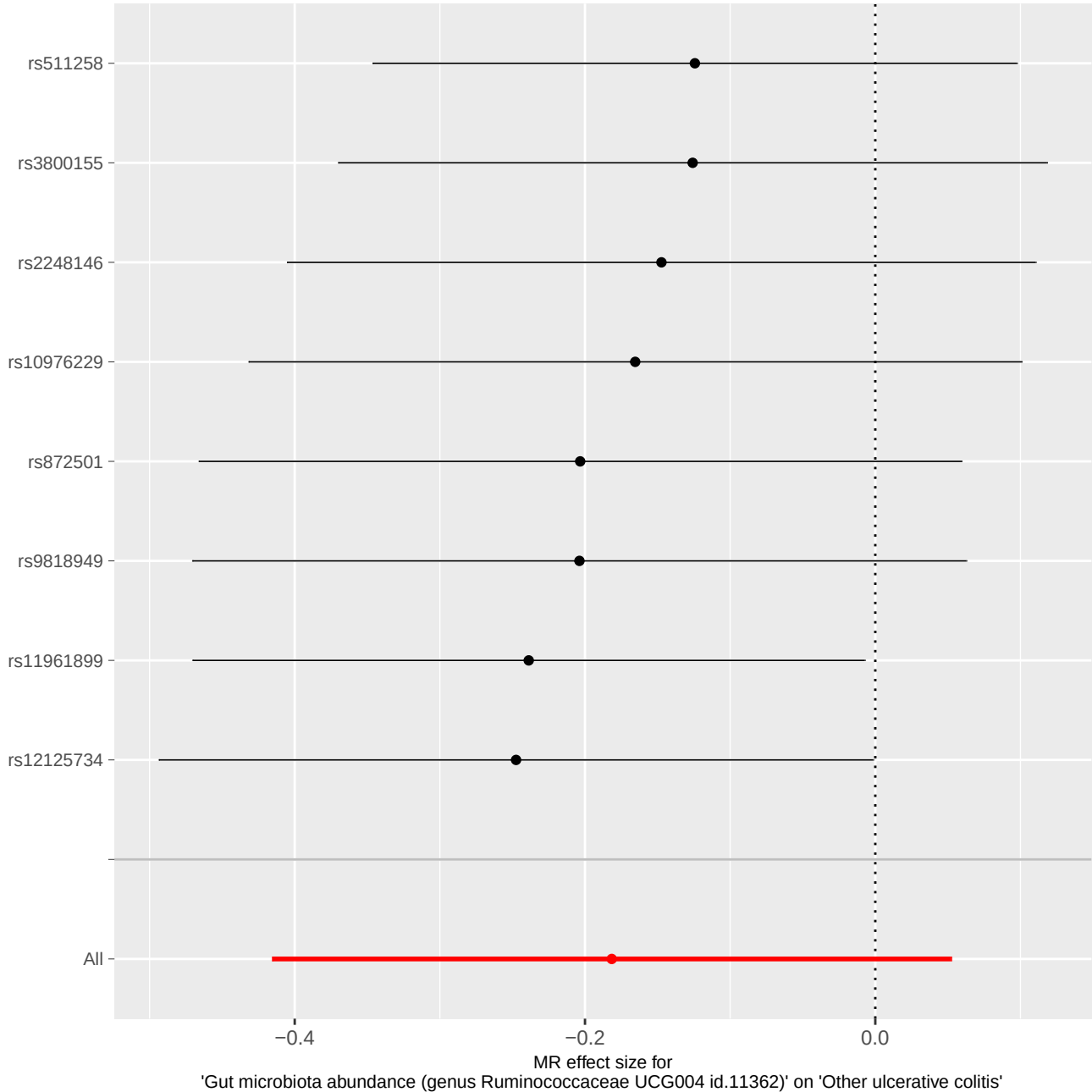


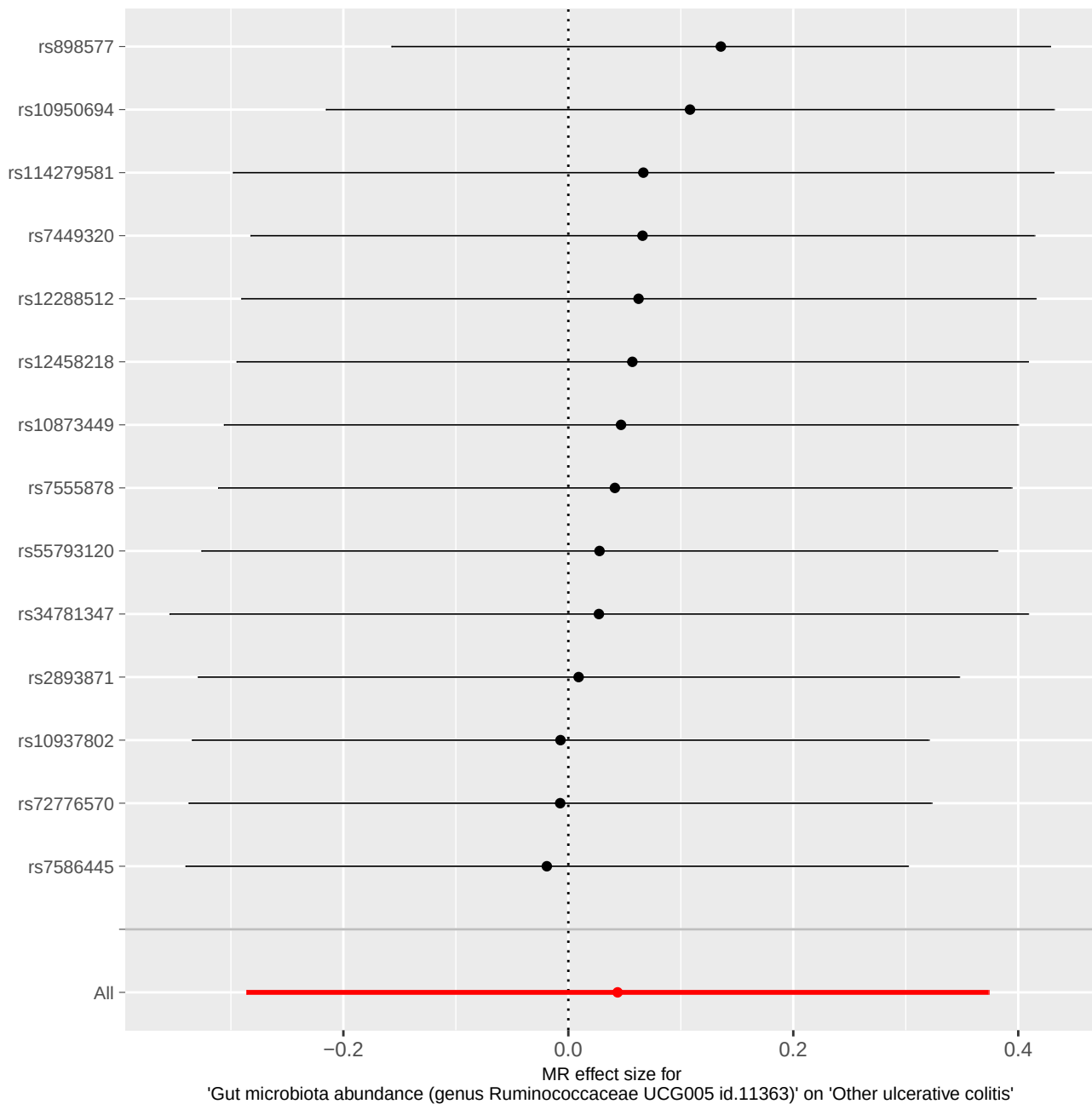
MR effect size for
'Gut microbiota abundance (genus Ruminococcaceae NK4A214 group id.11358)' on 'Other ulcerative colitis'

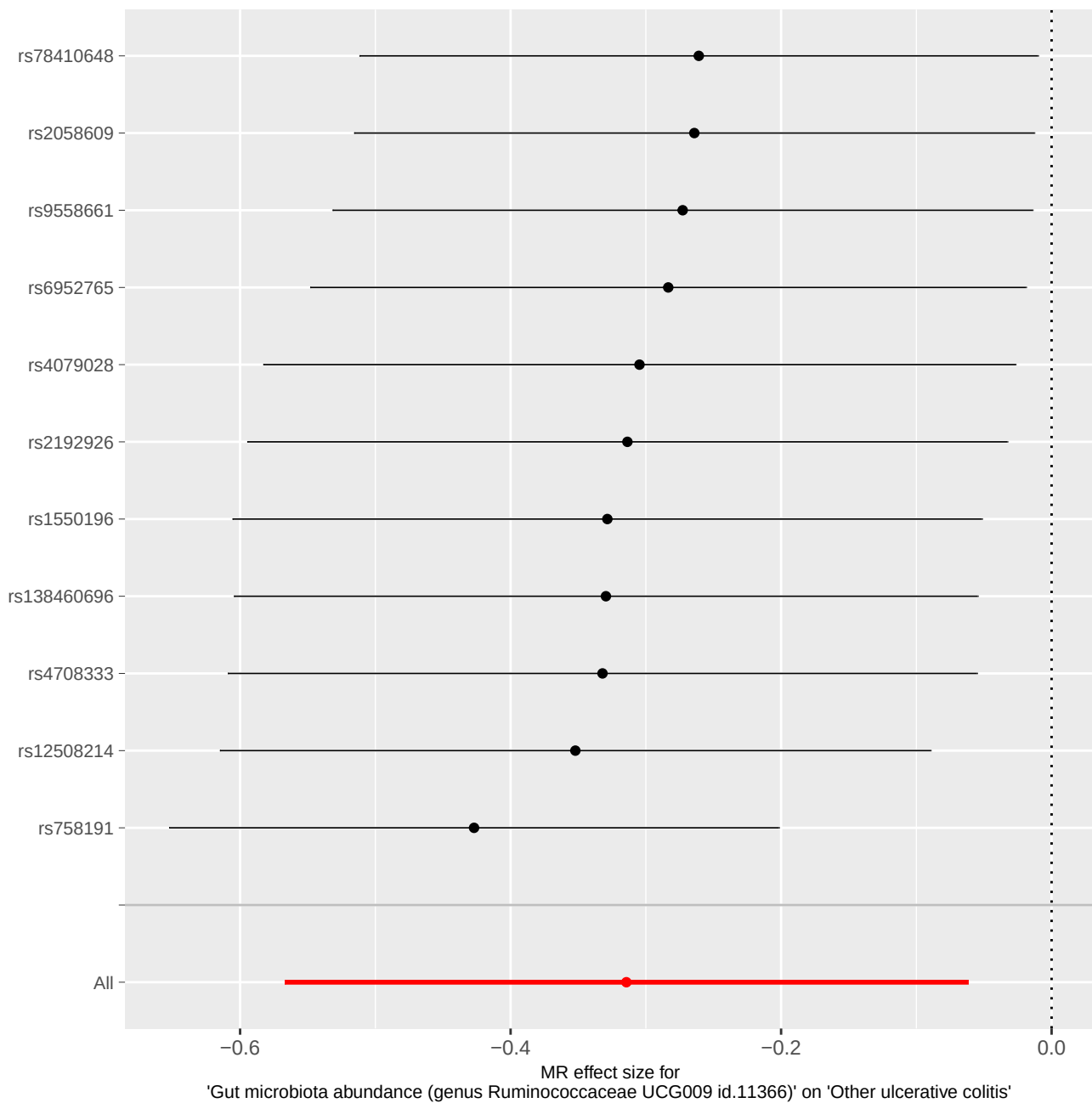


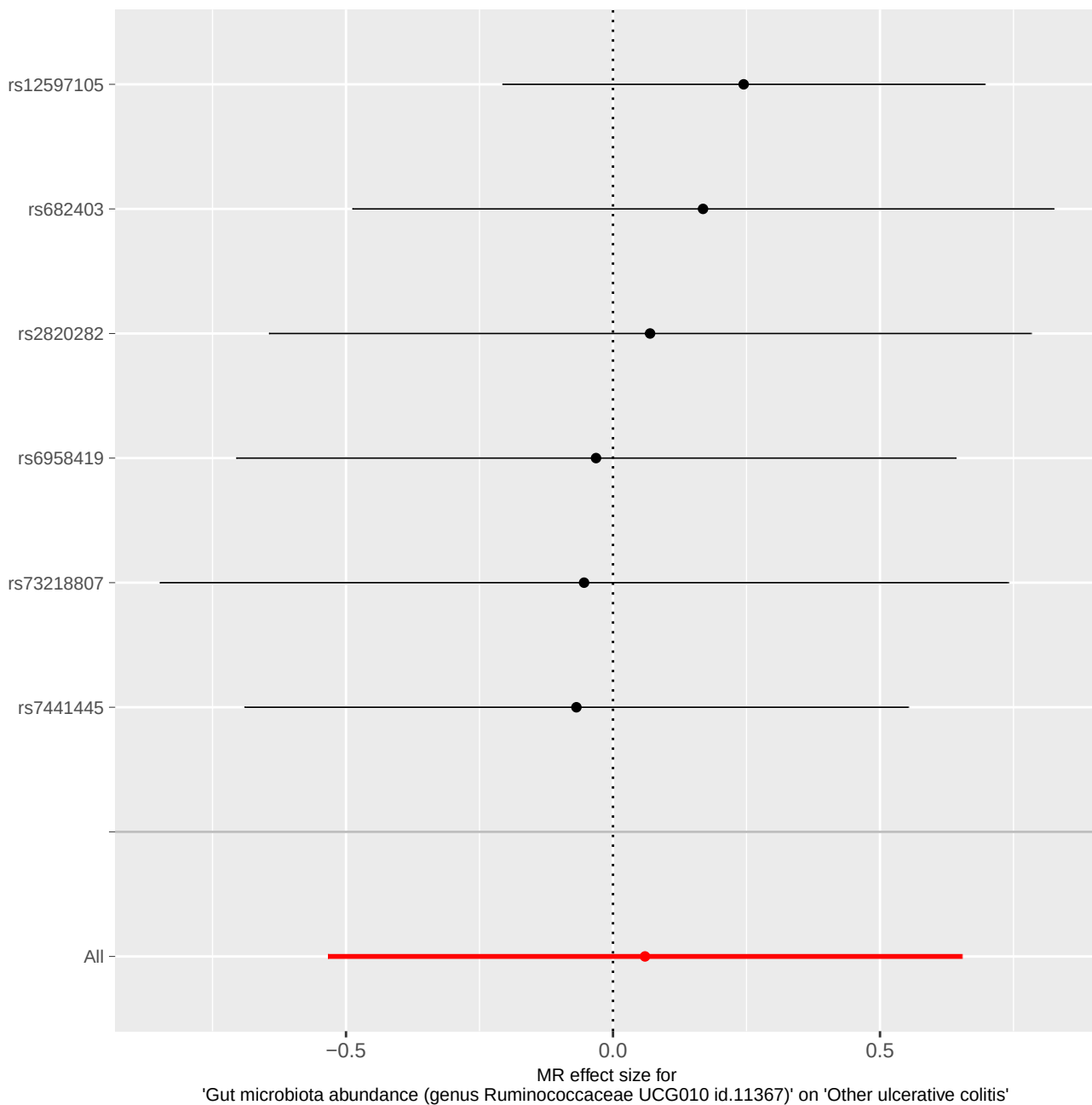


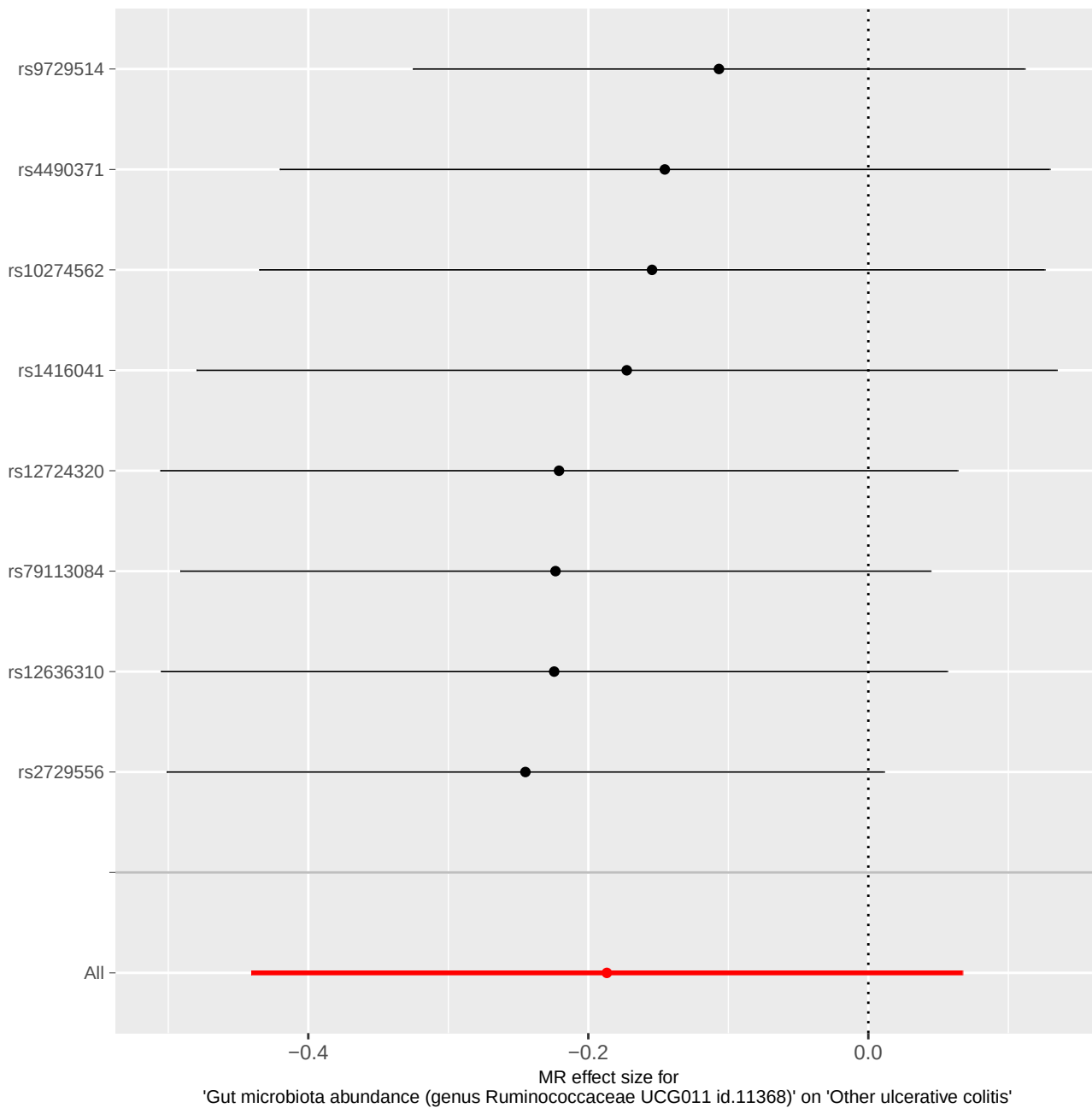
Batch 1329 : Gut microbiota abundance (genus Ruminococcaceae UCG004 id.11362) on Other ulcerative colitis

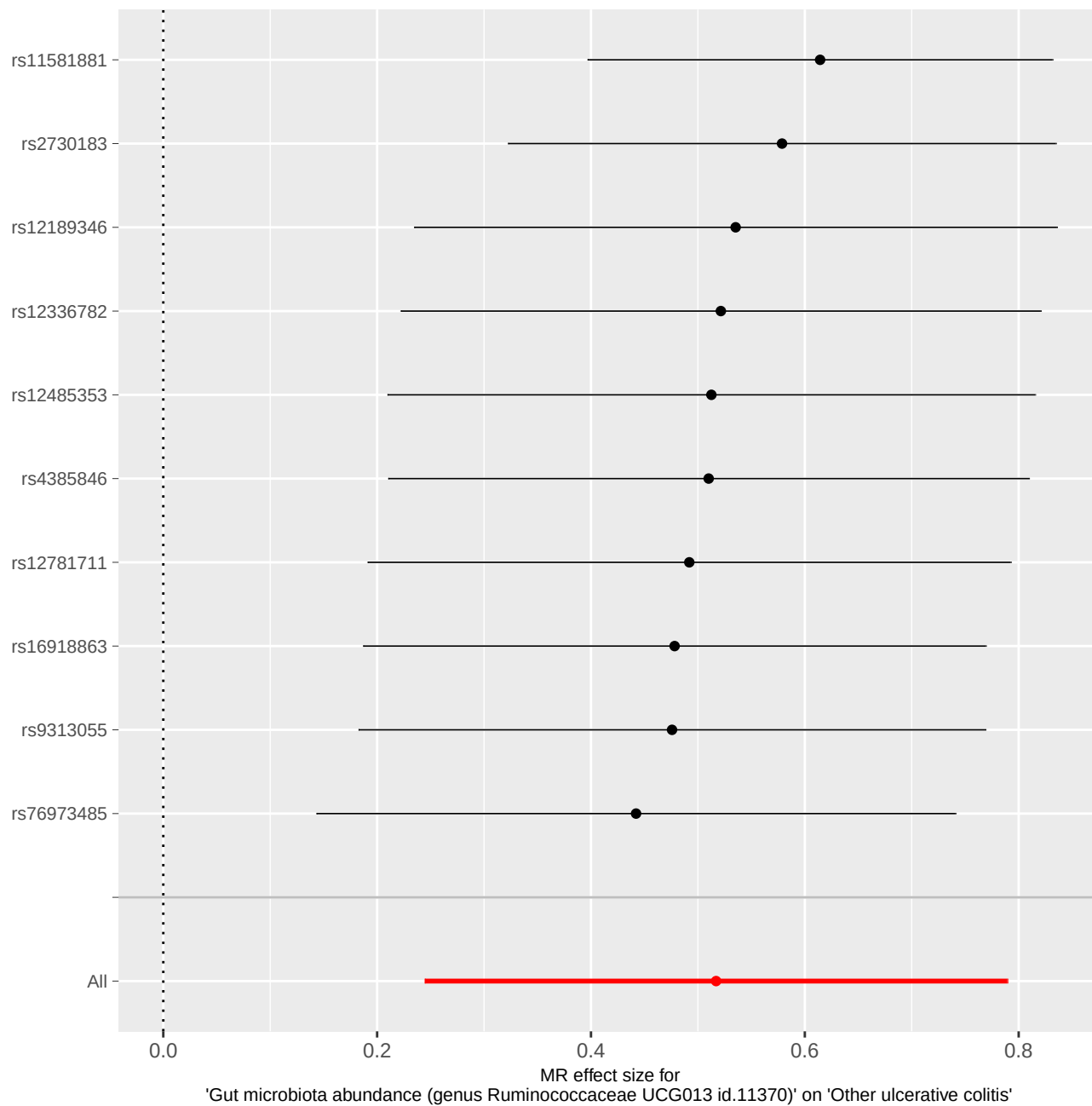


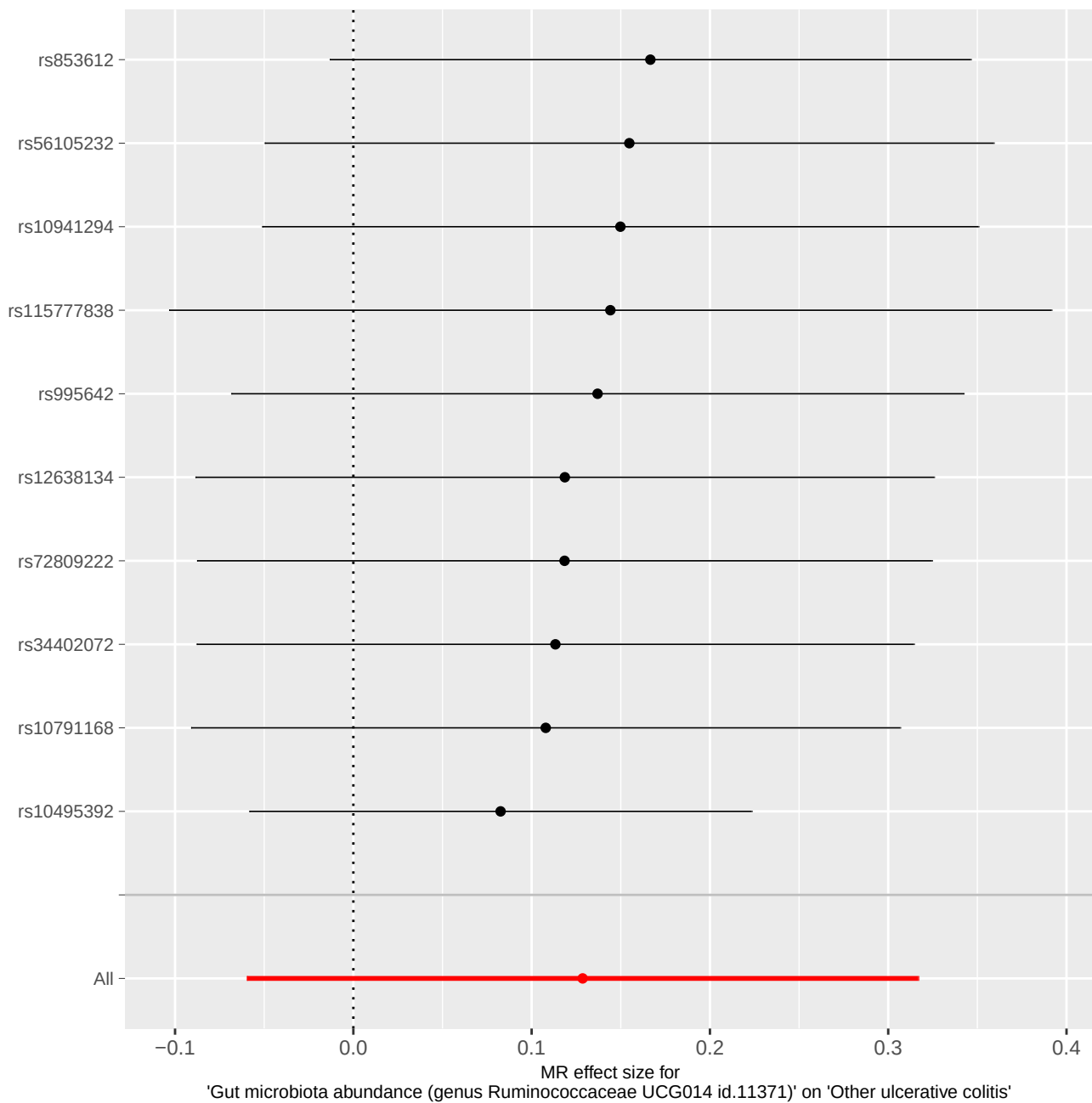




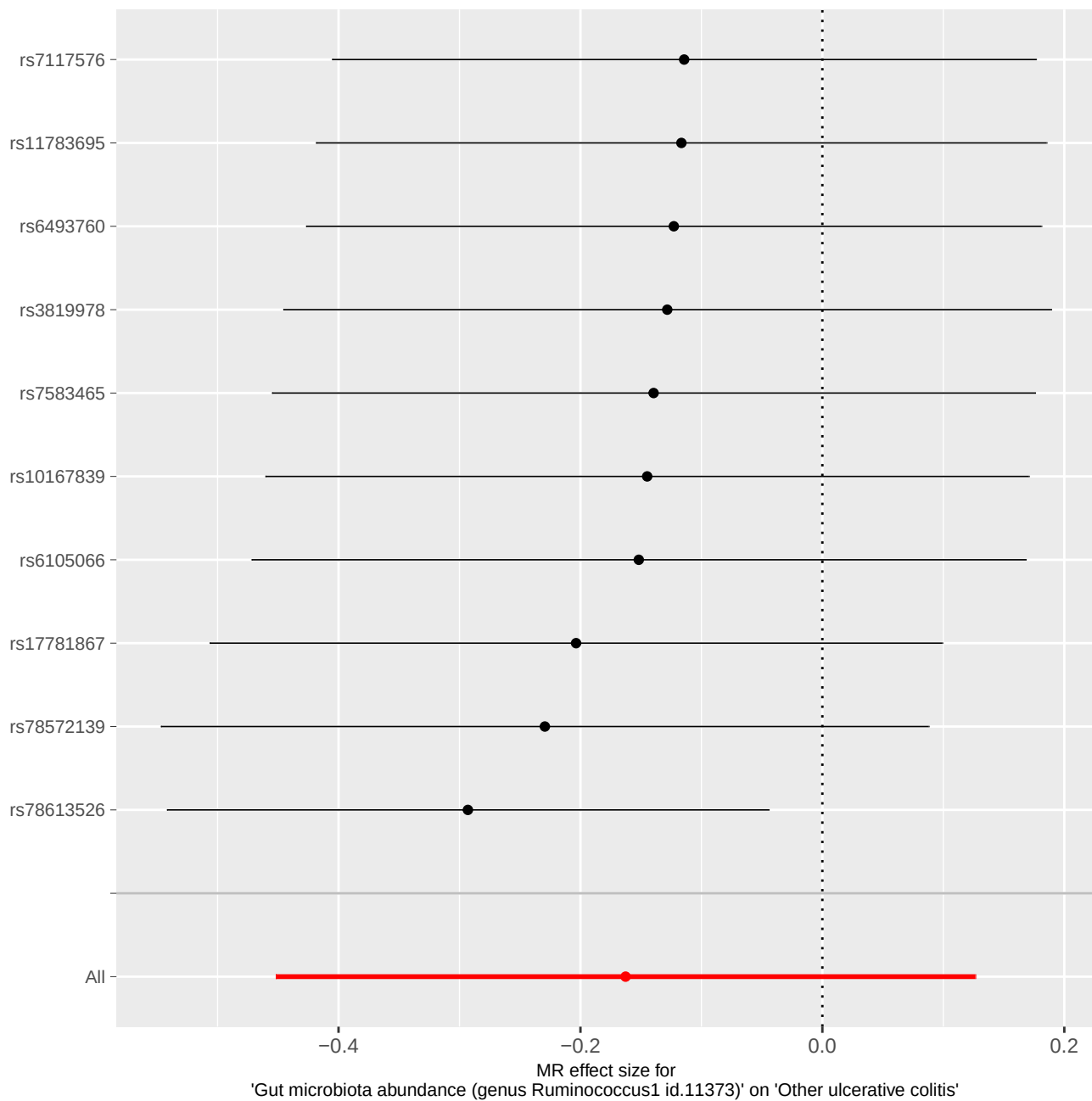




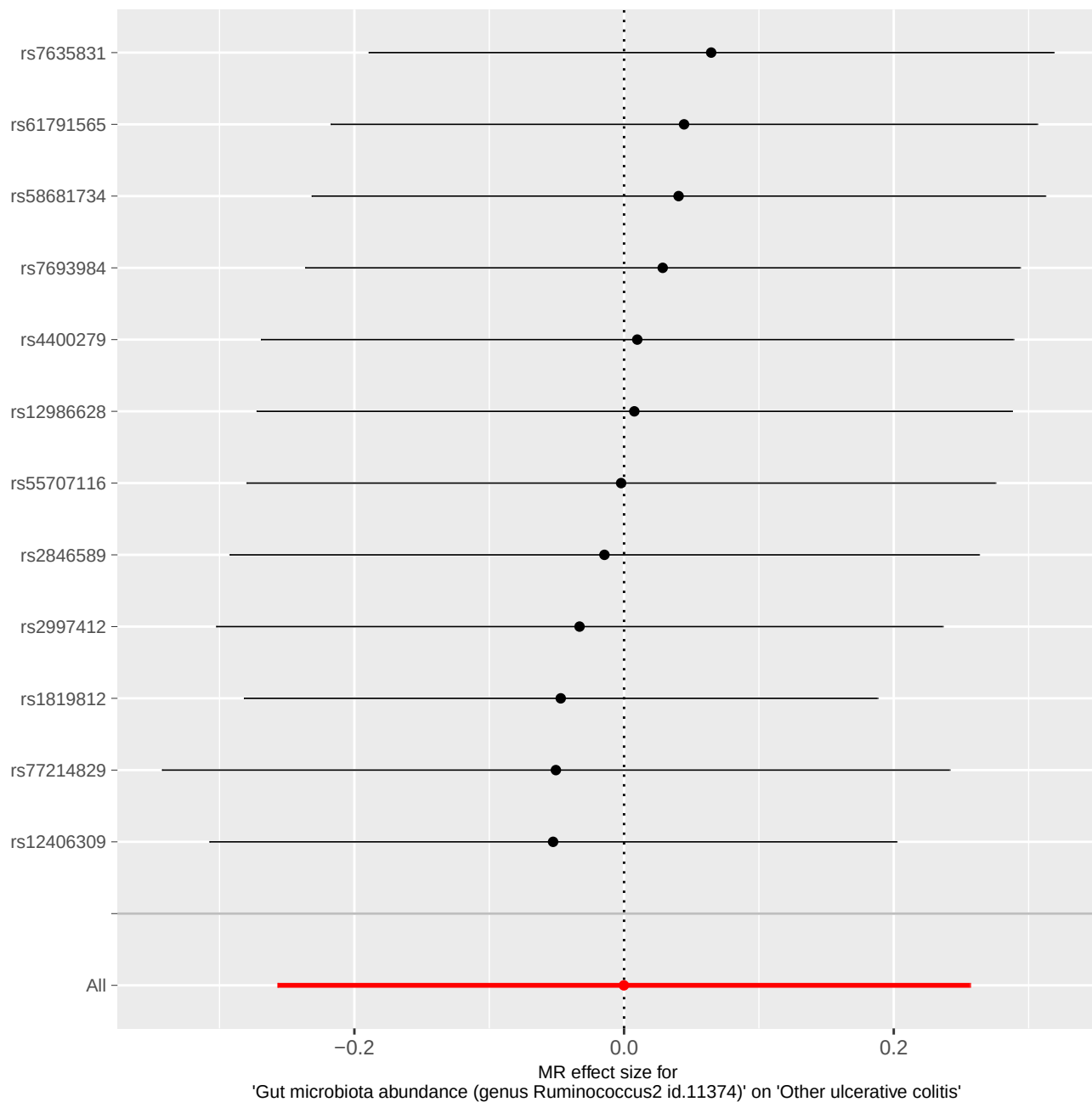


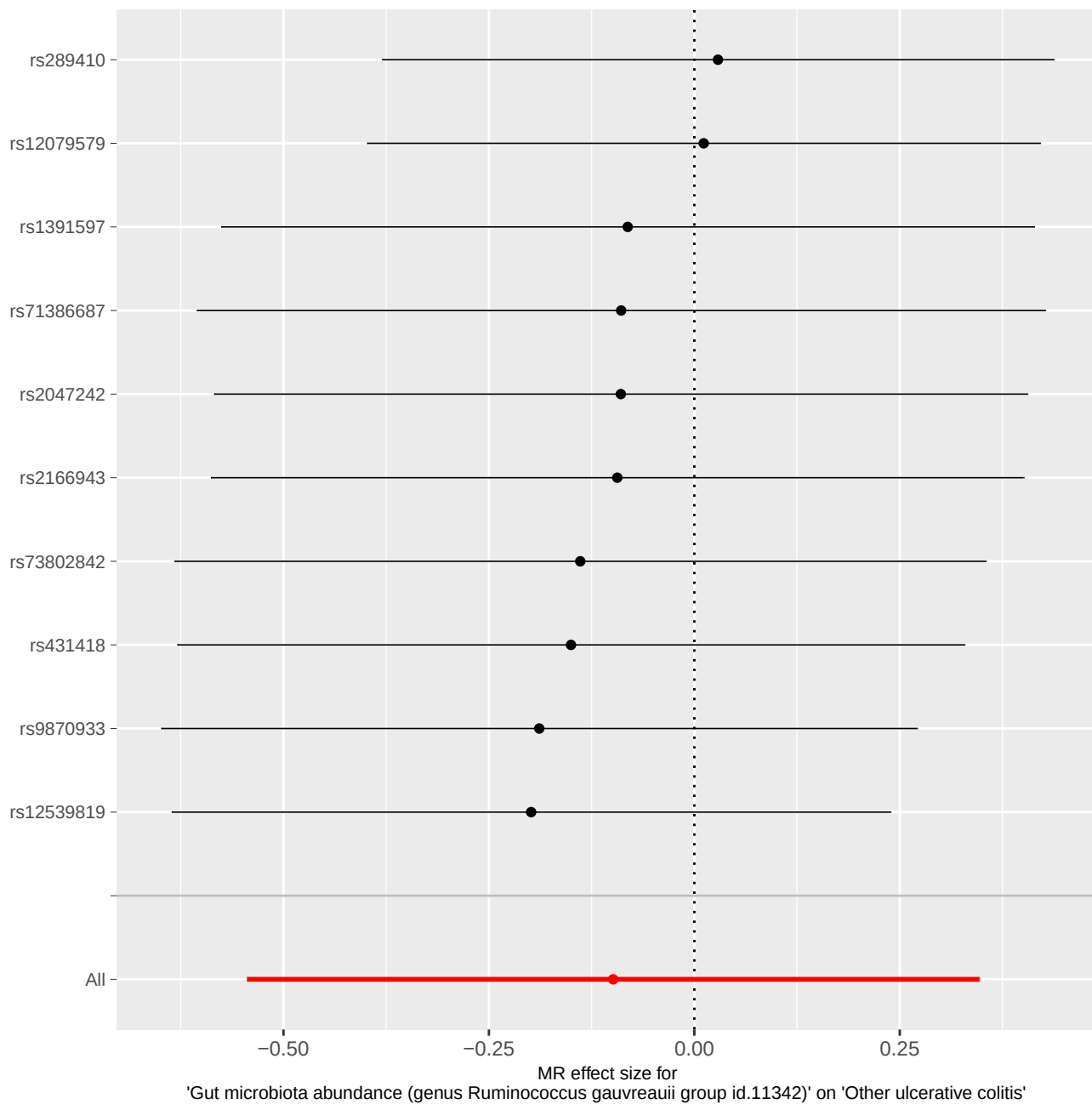


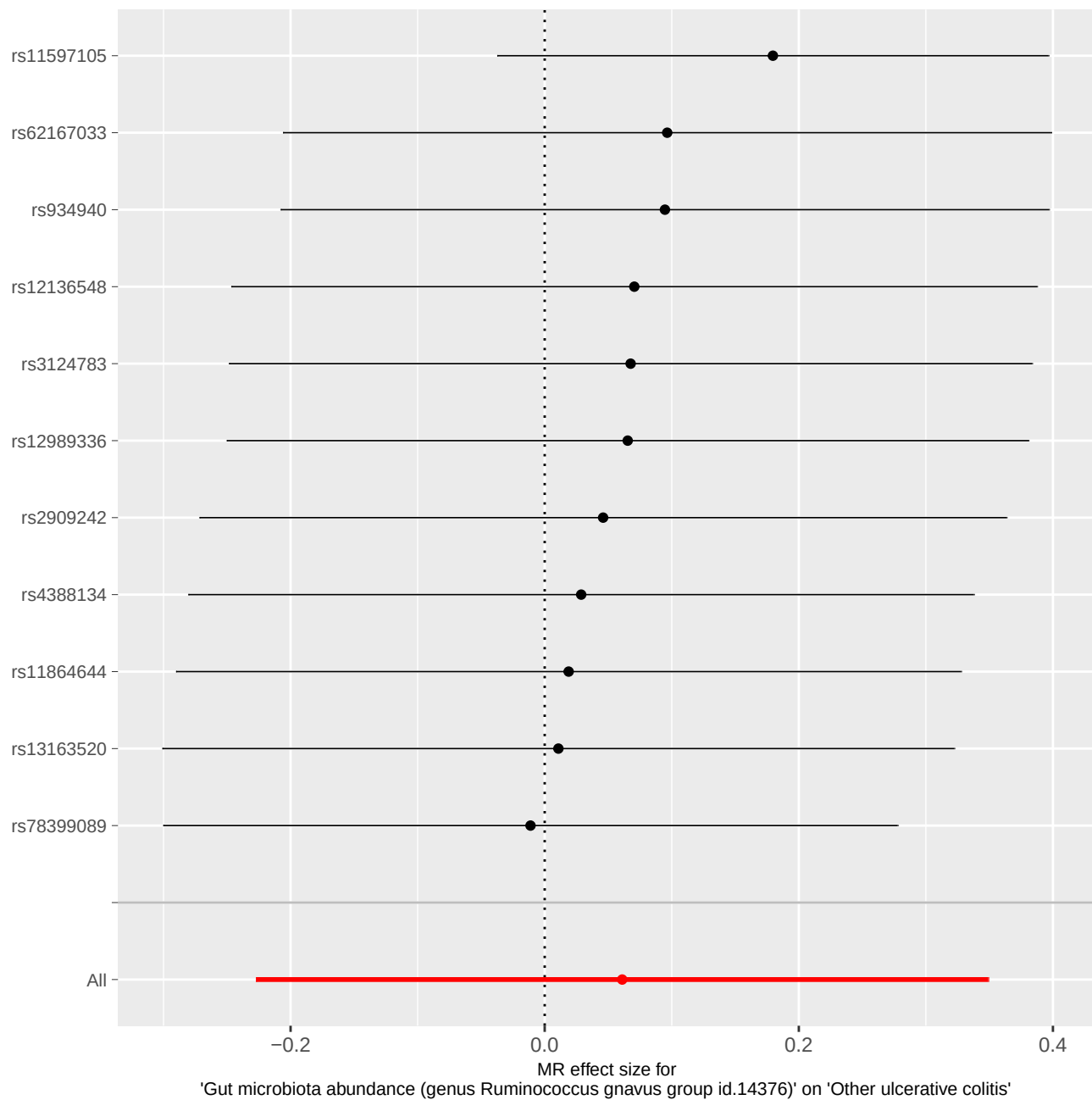
Batch 1336 : Gut microbiota abundance (genus Ruminococcus1 id.11373) on Other ulcerative colitis



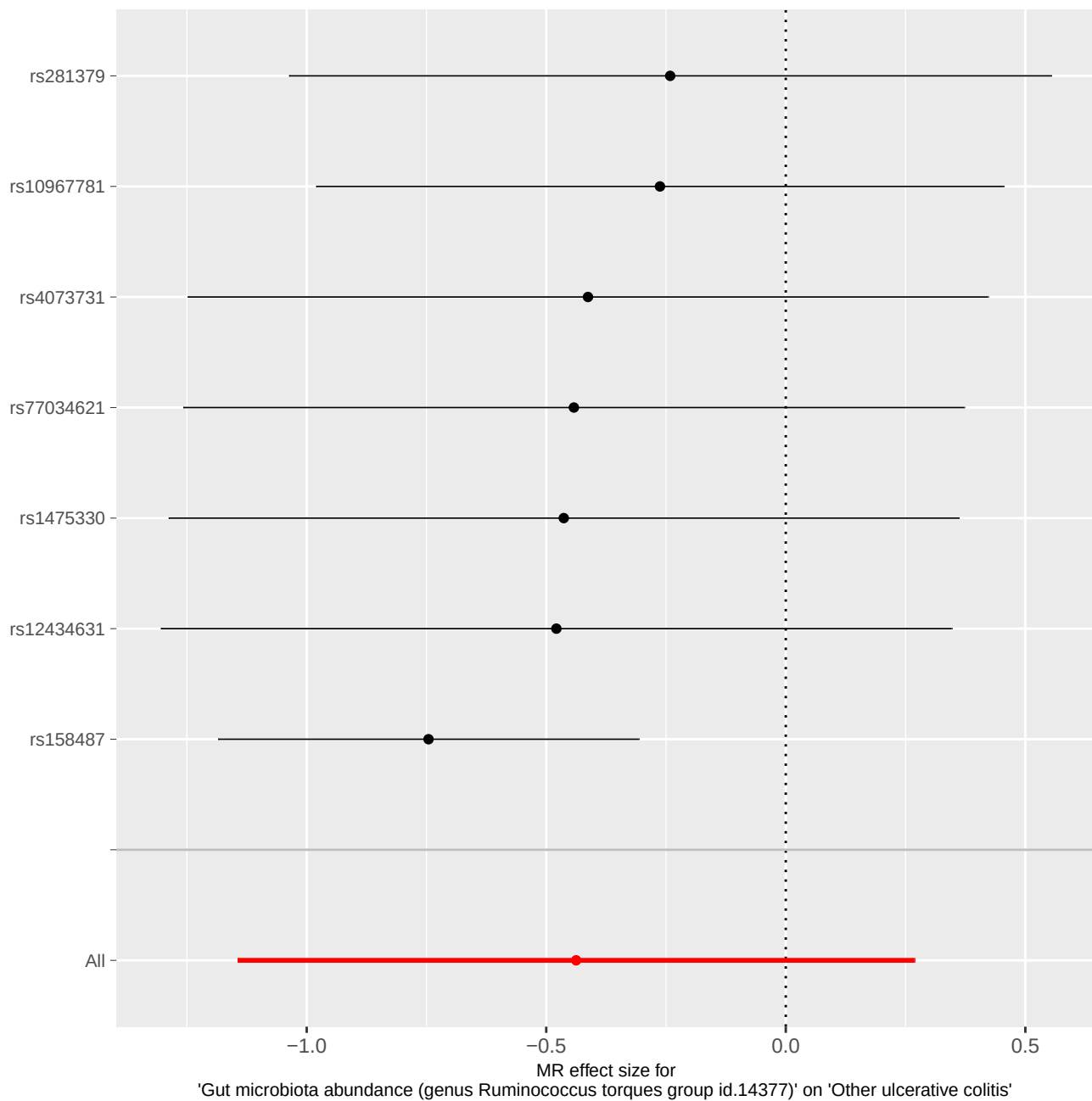
Batch 1337 : Gut microbiota abundance (genus Ruminococcus2 id.11374) on Other ulcerative colitis

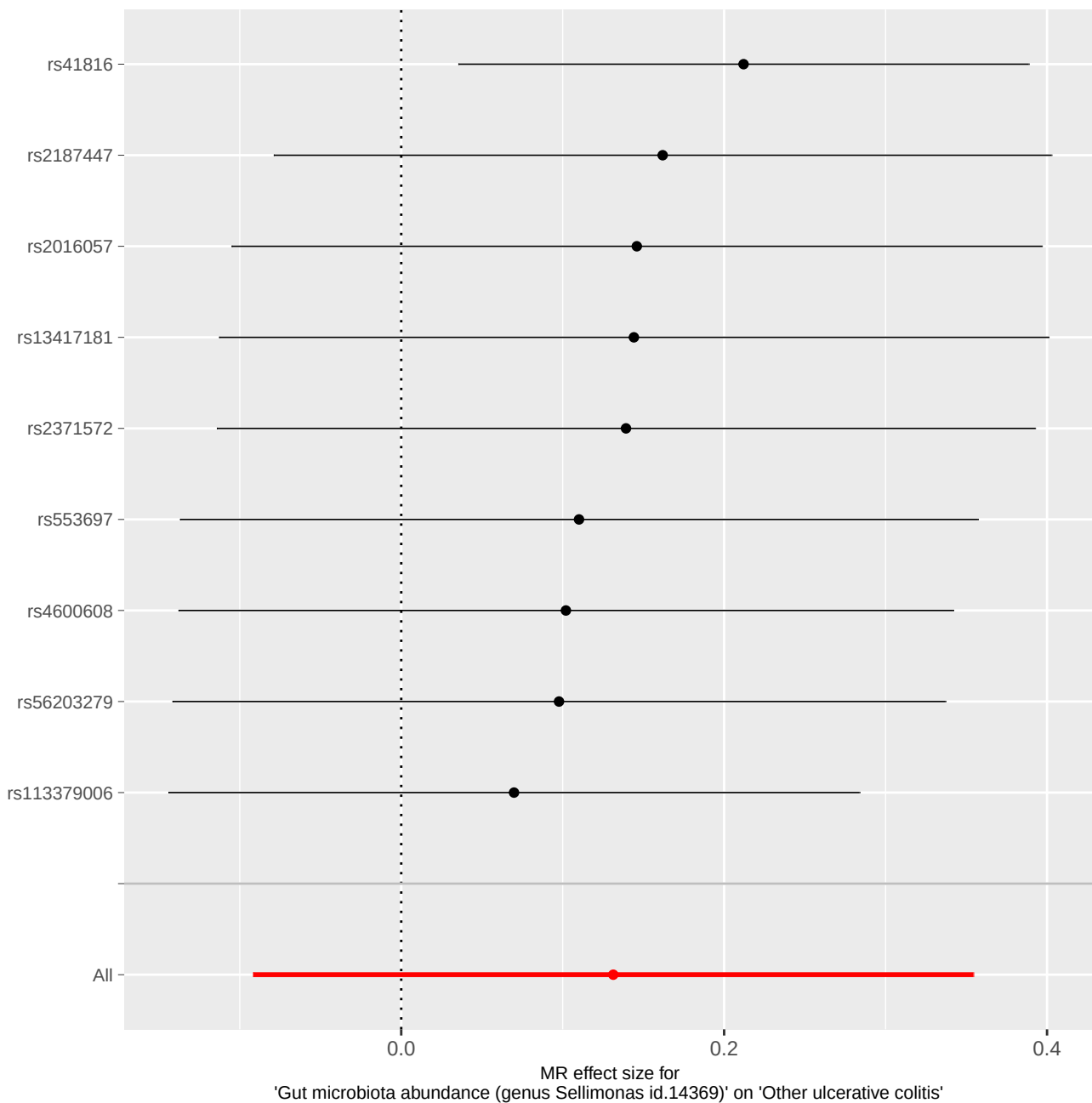


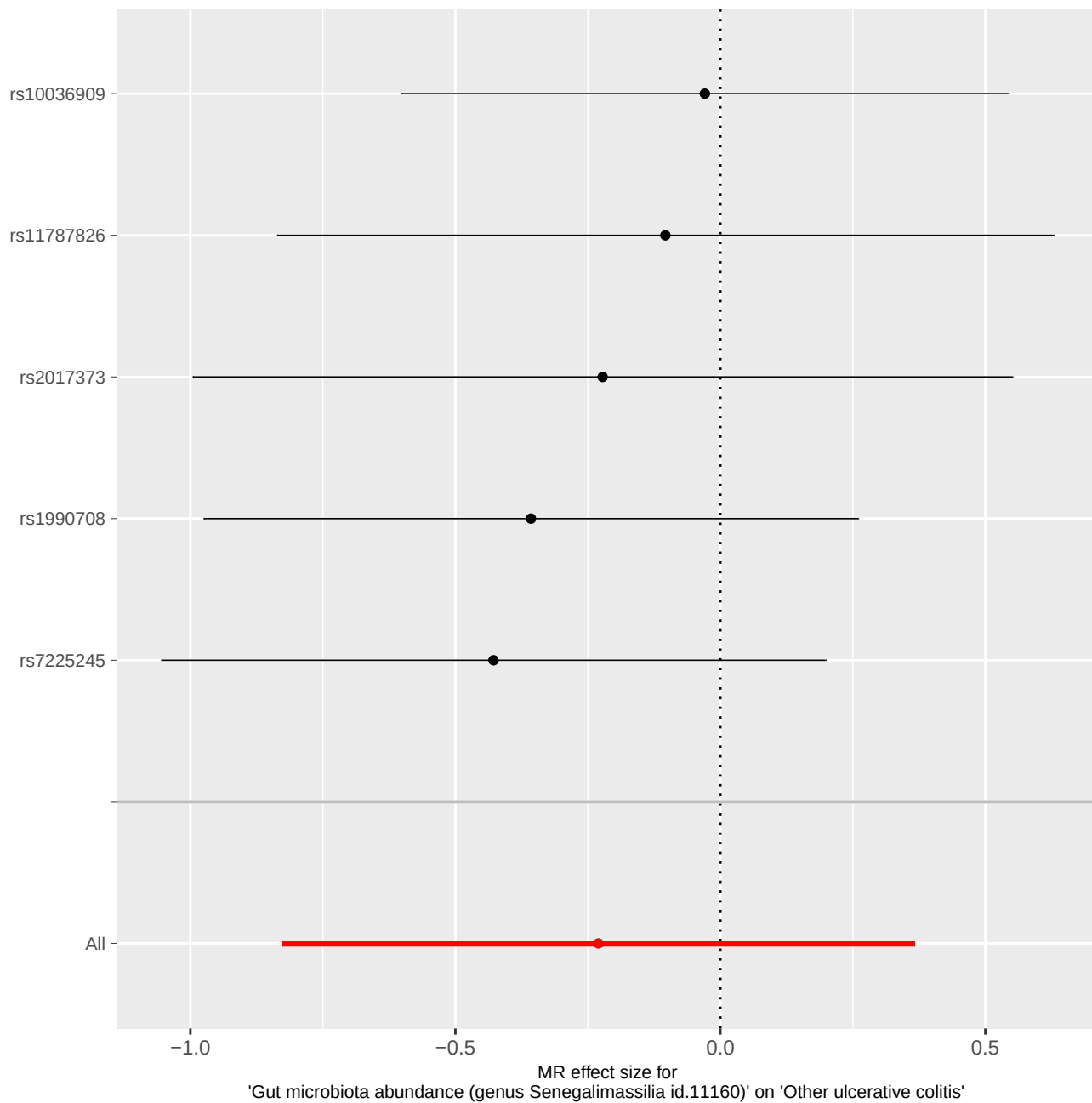


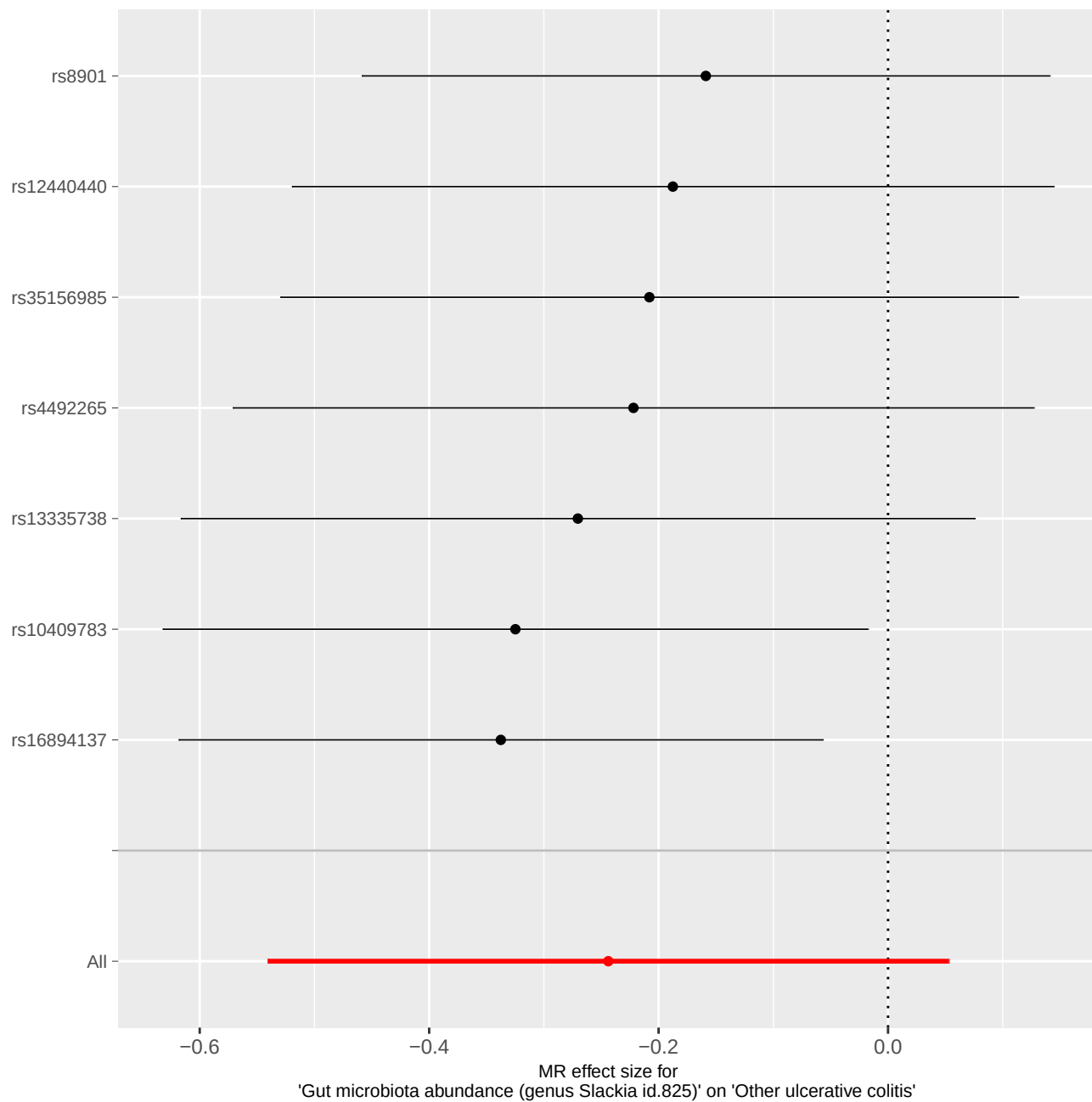


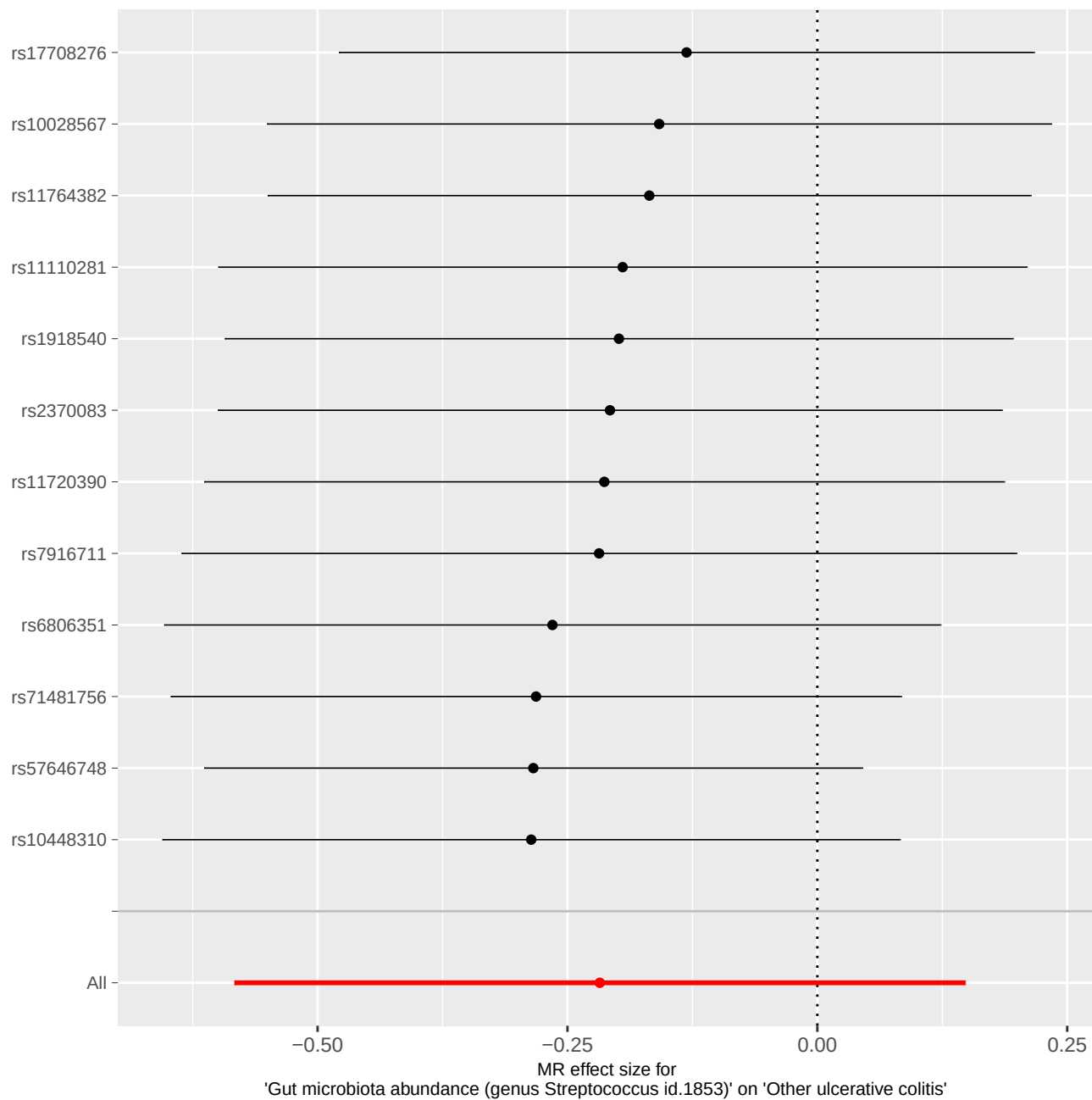
MR effect size for
'Gut microbiota abundance (genus Ruminococcus gnavus group id.14376)' on 'Other ulcerative colitis'

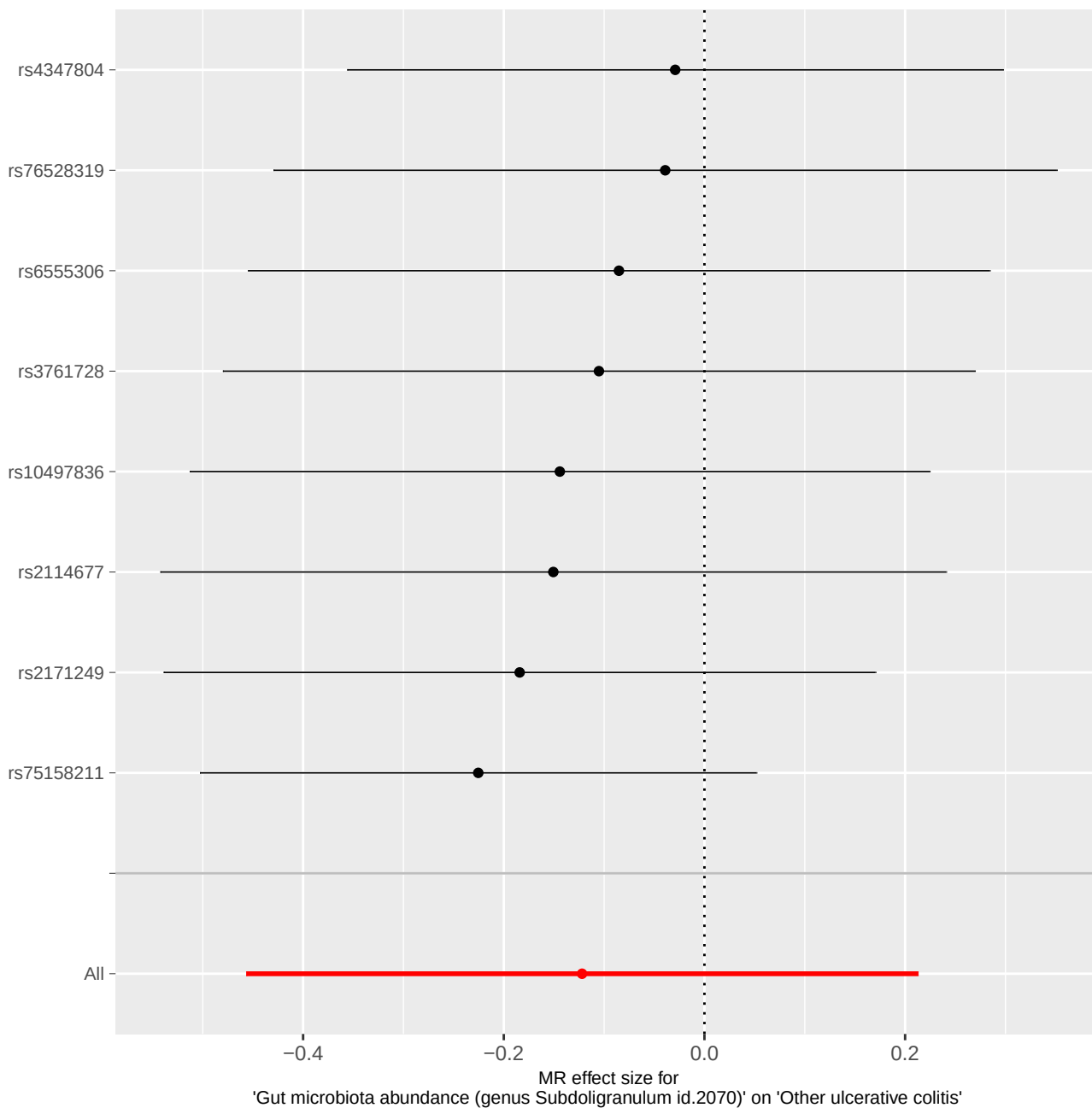


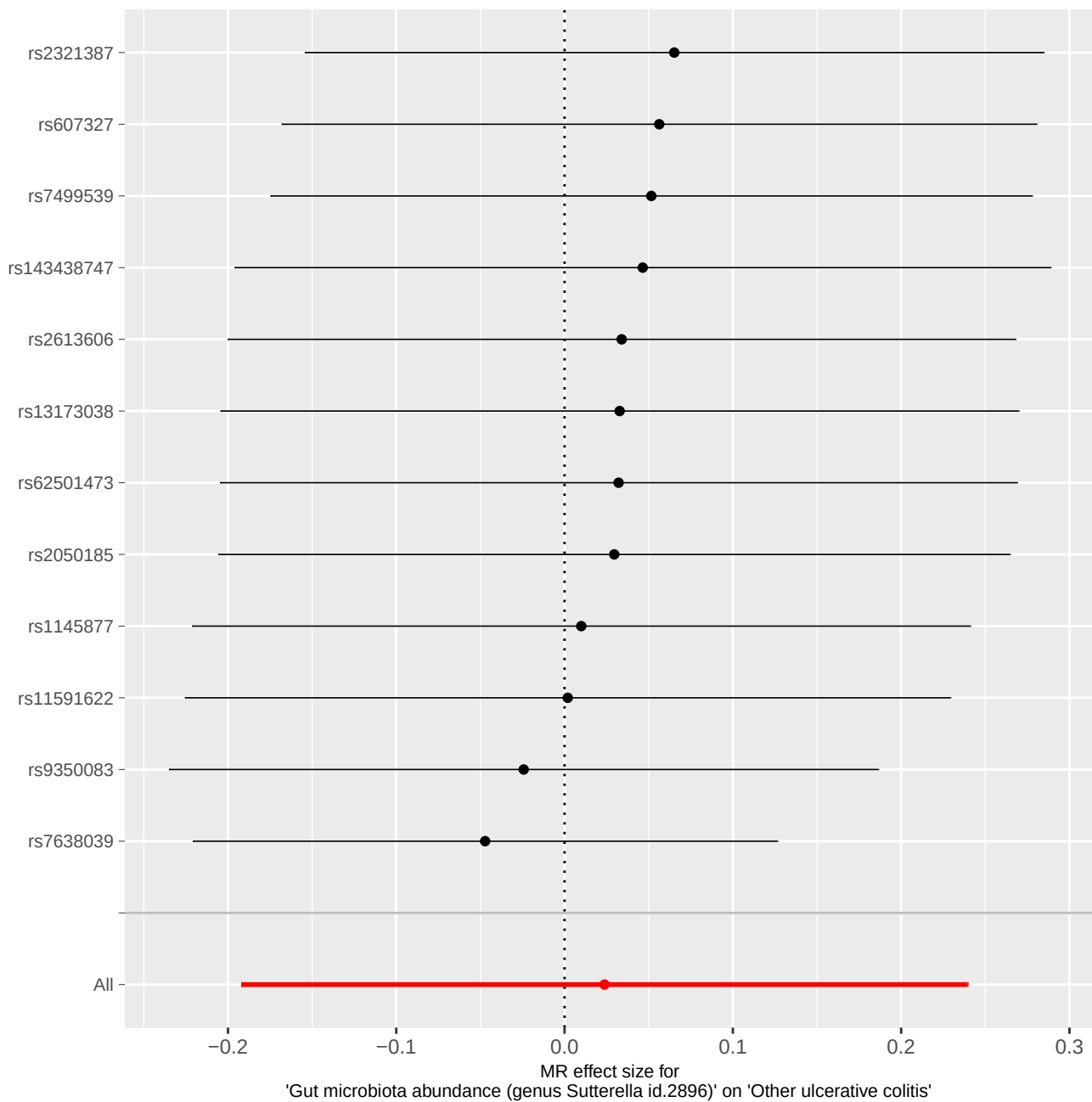


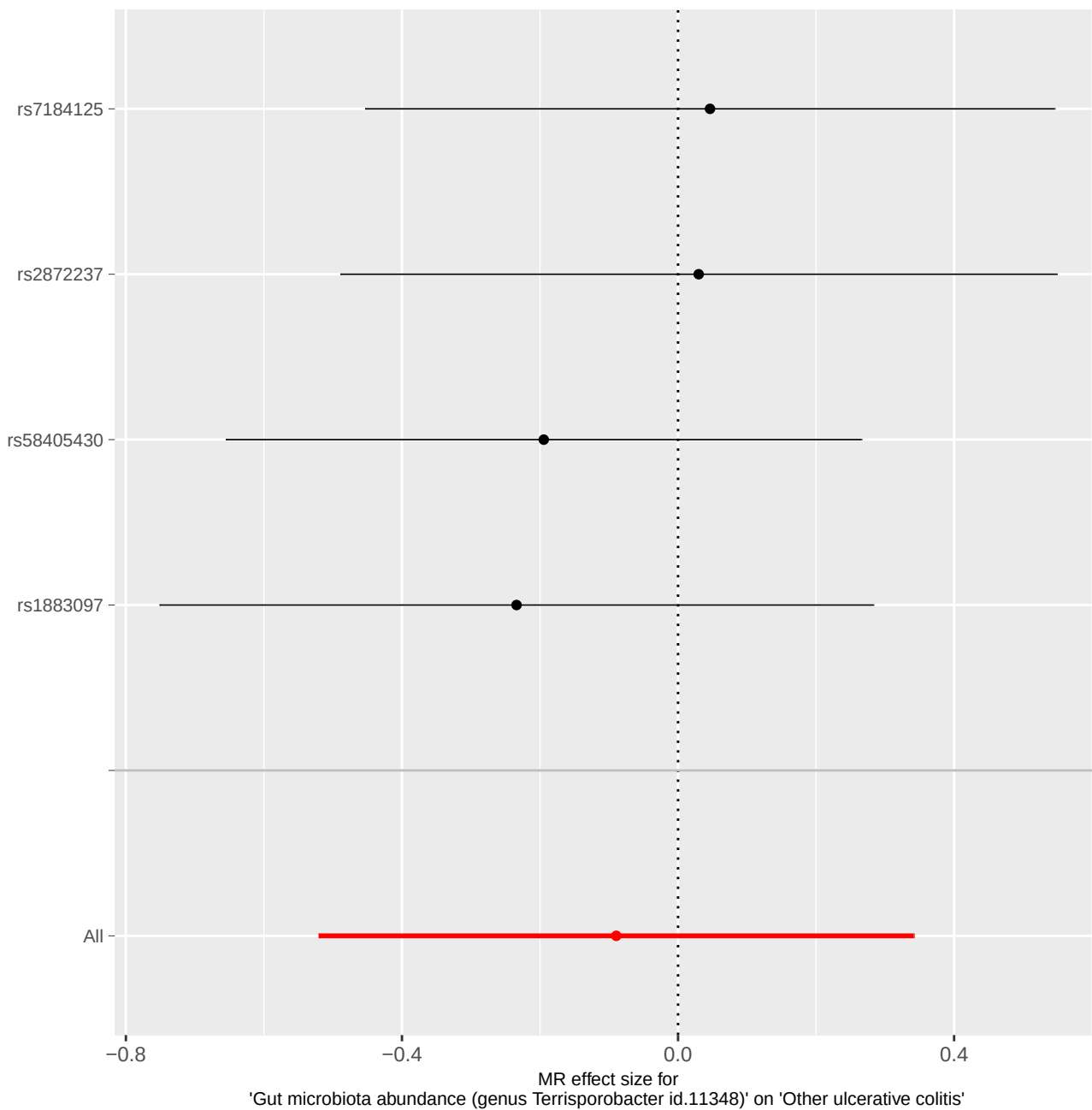


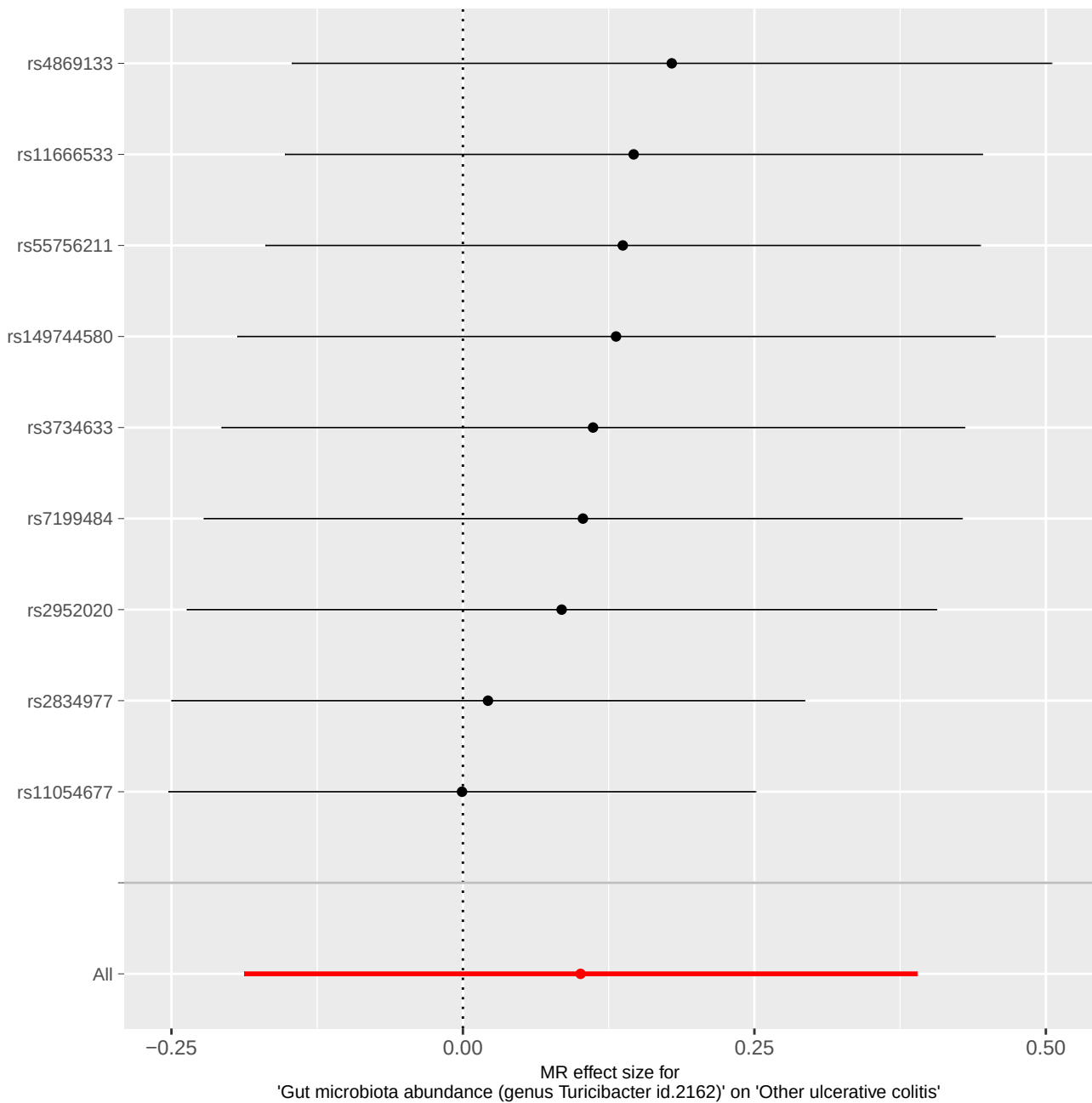


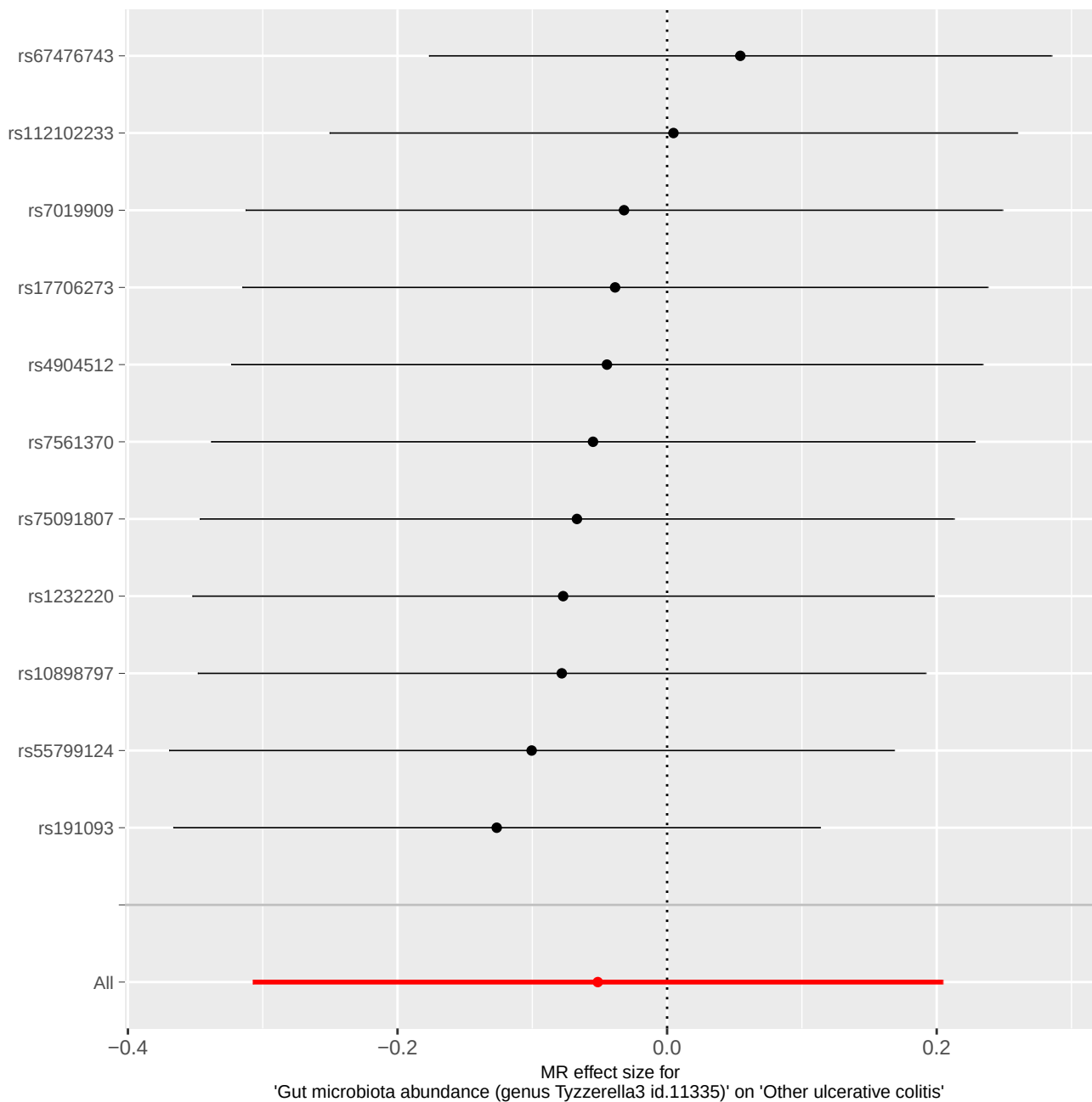


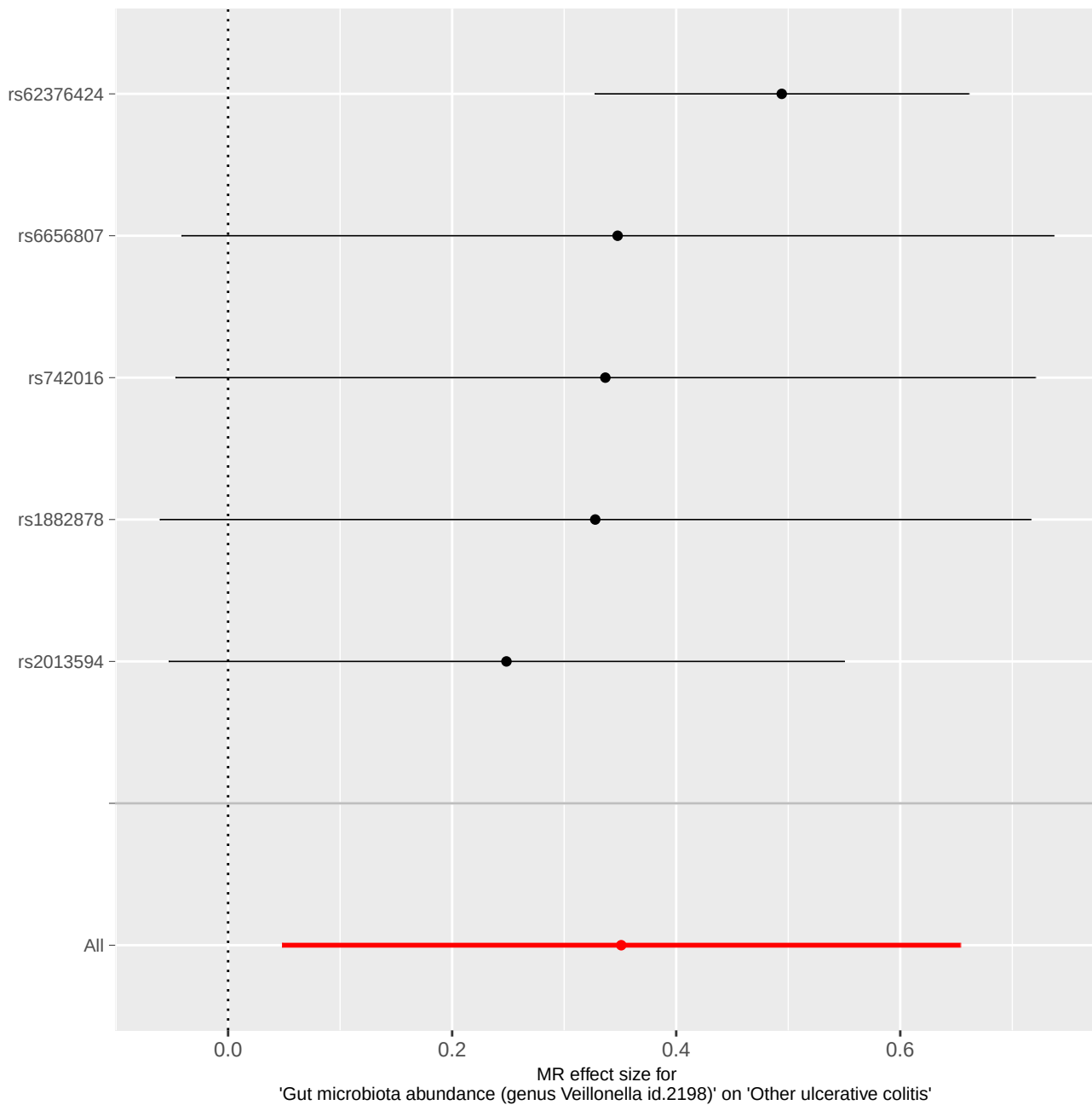


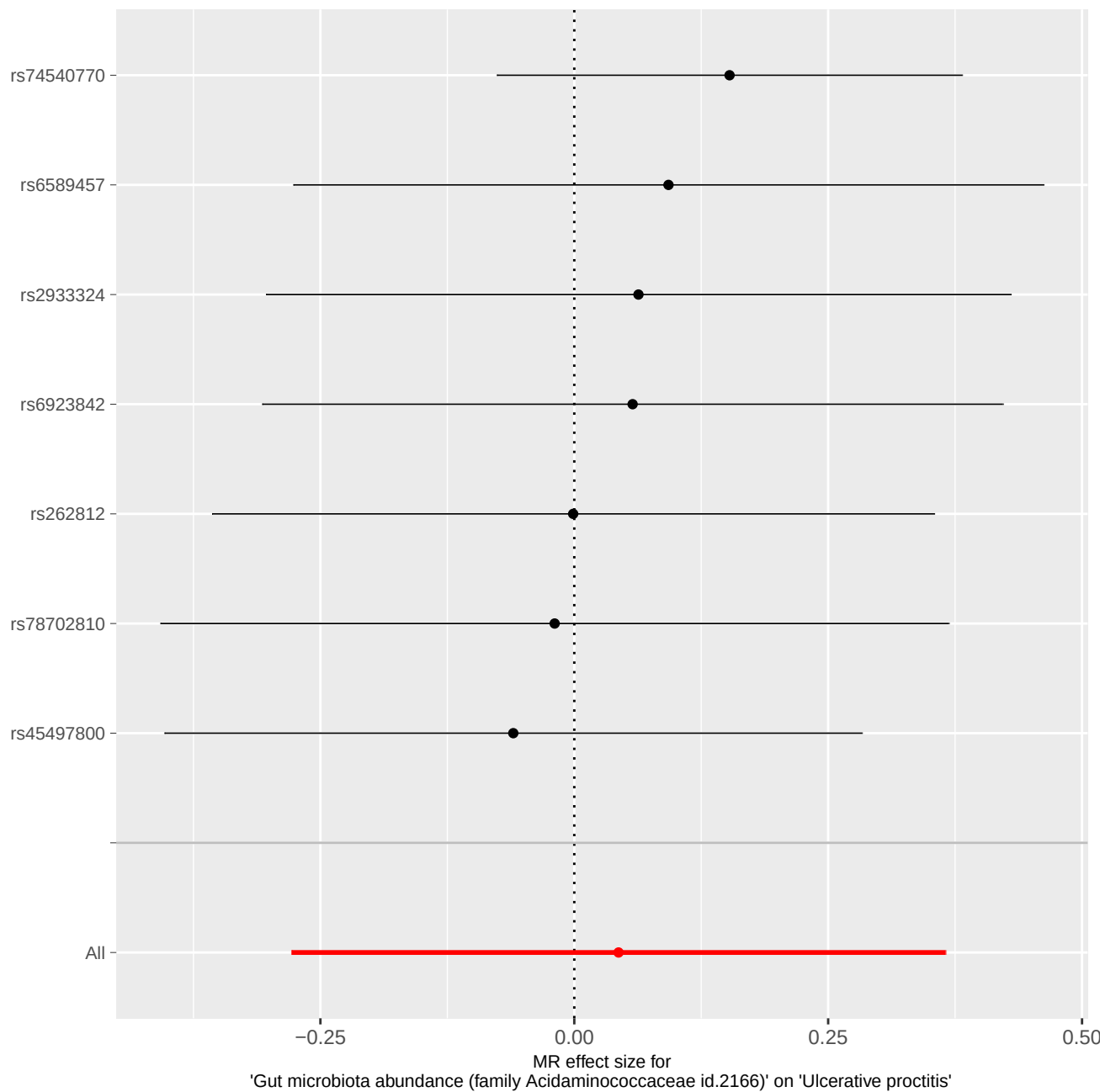




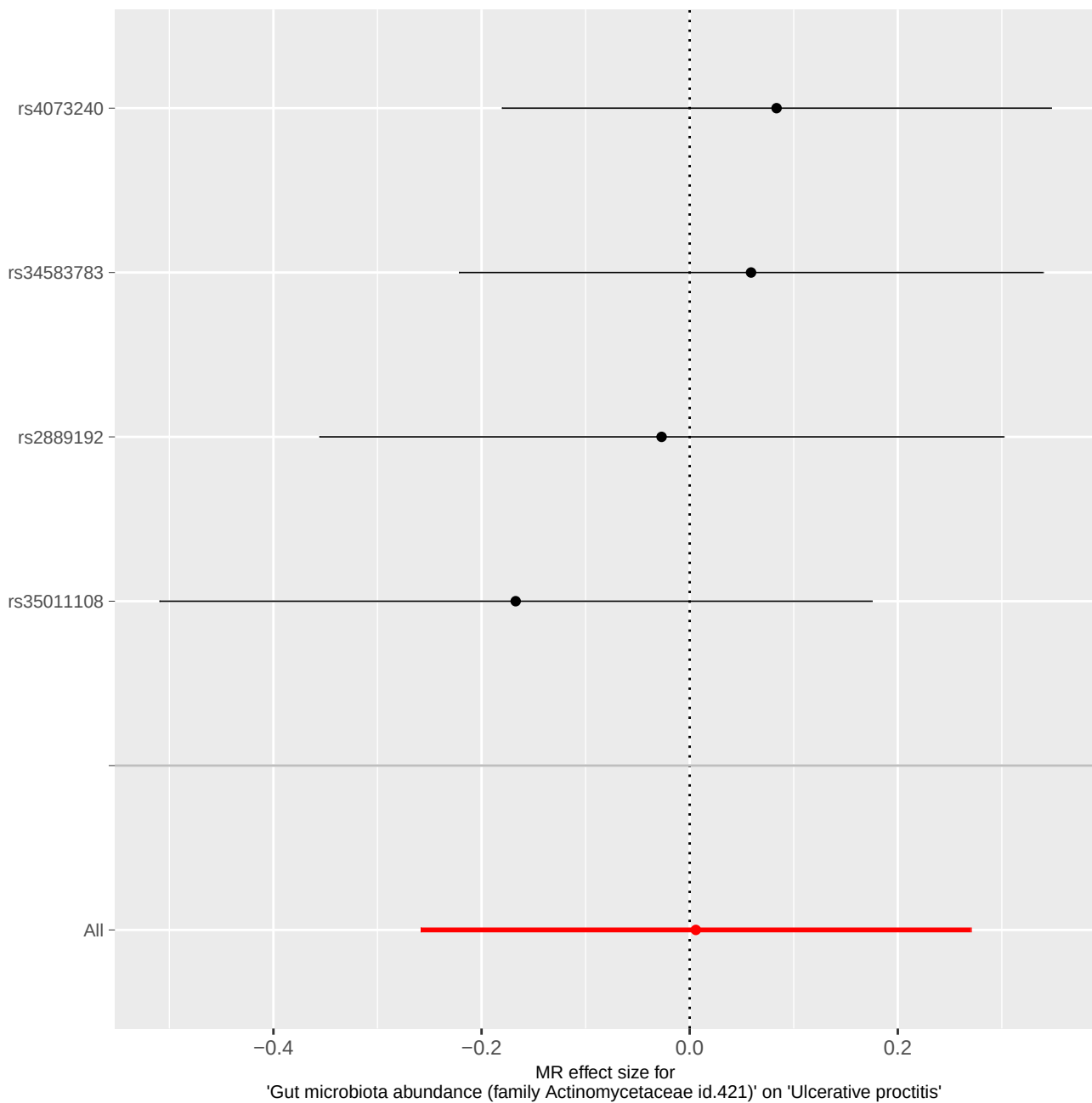


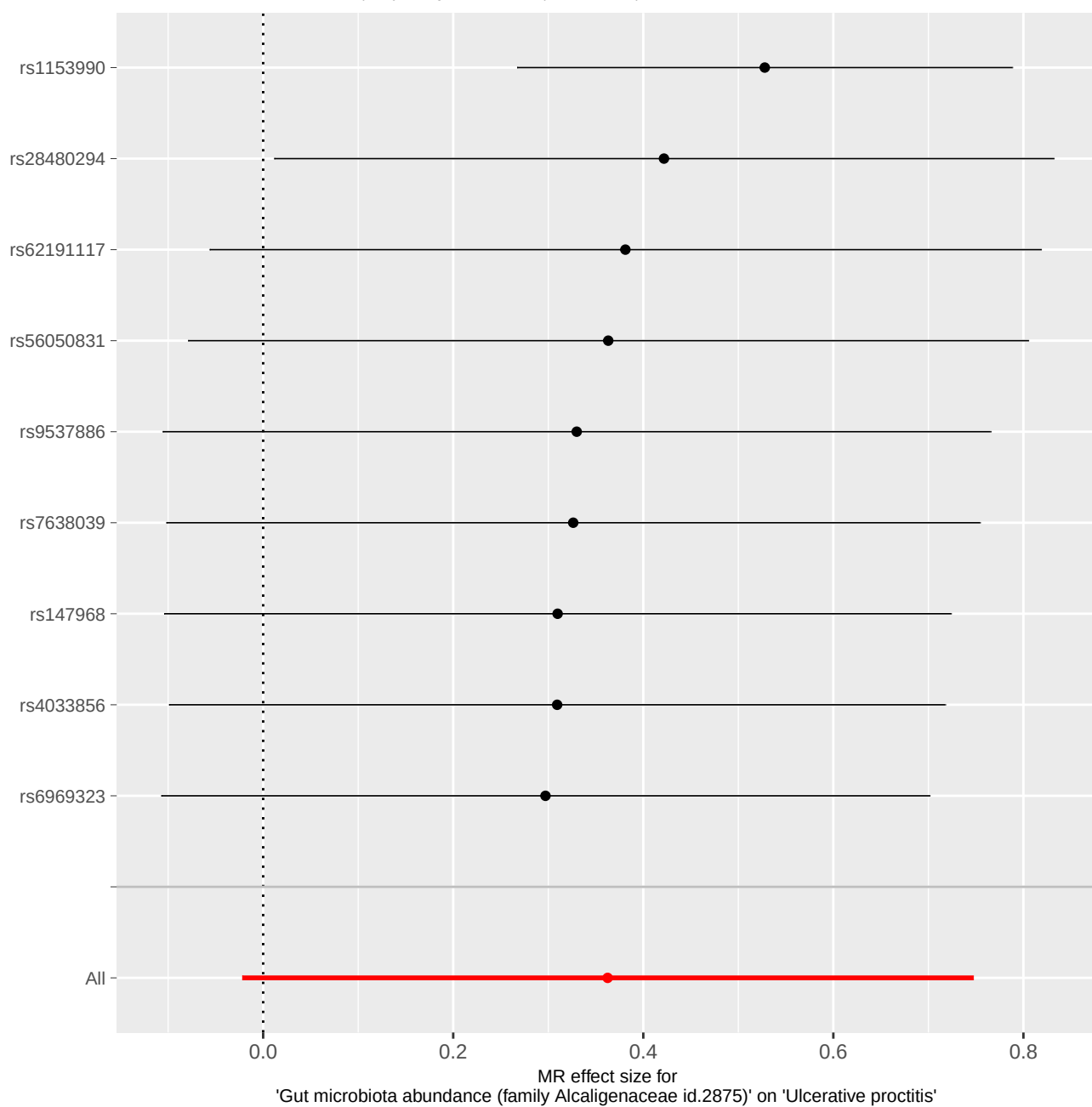


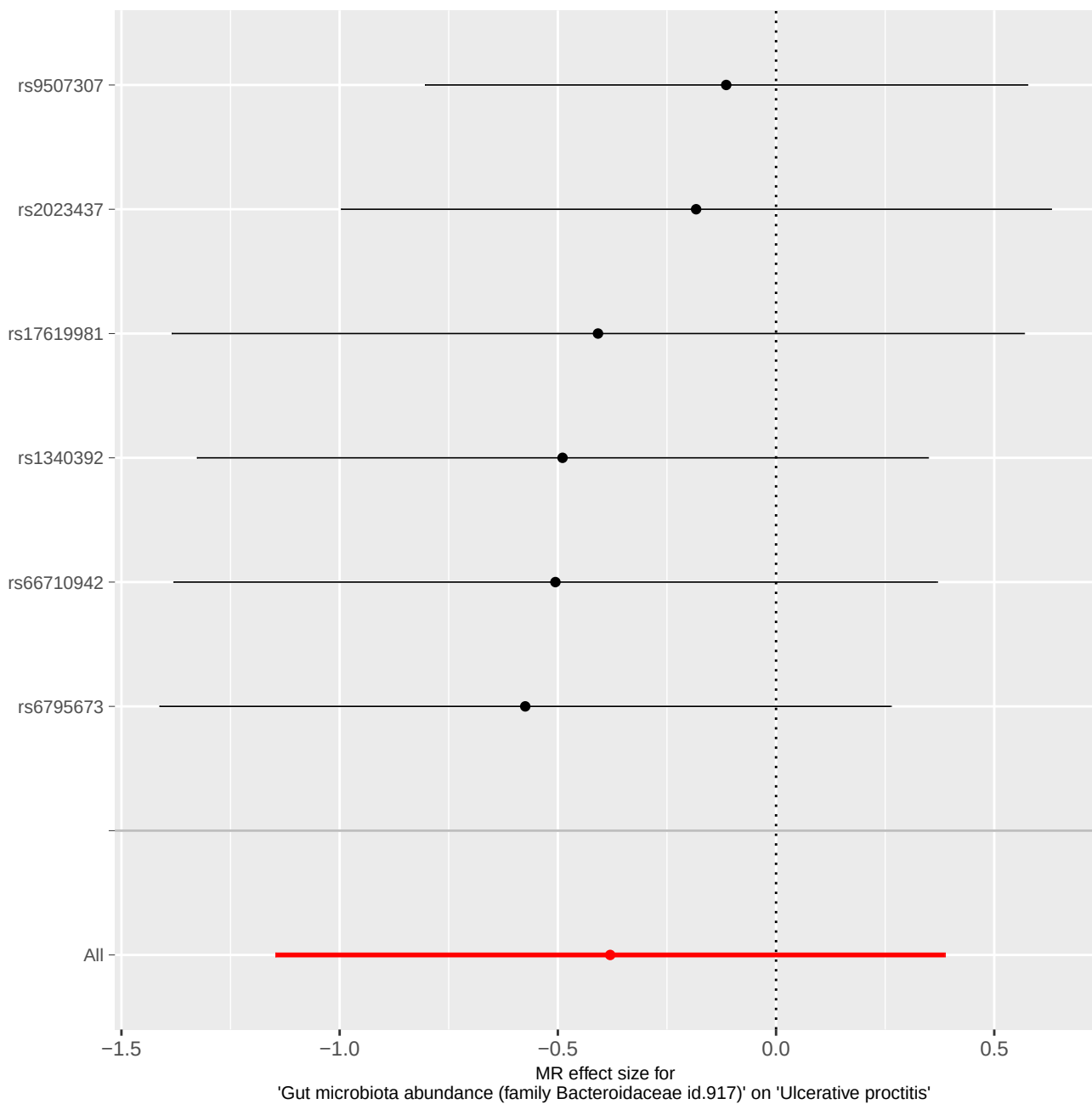


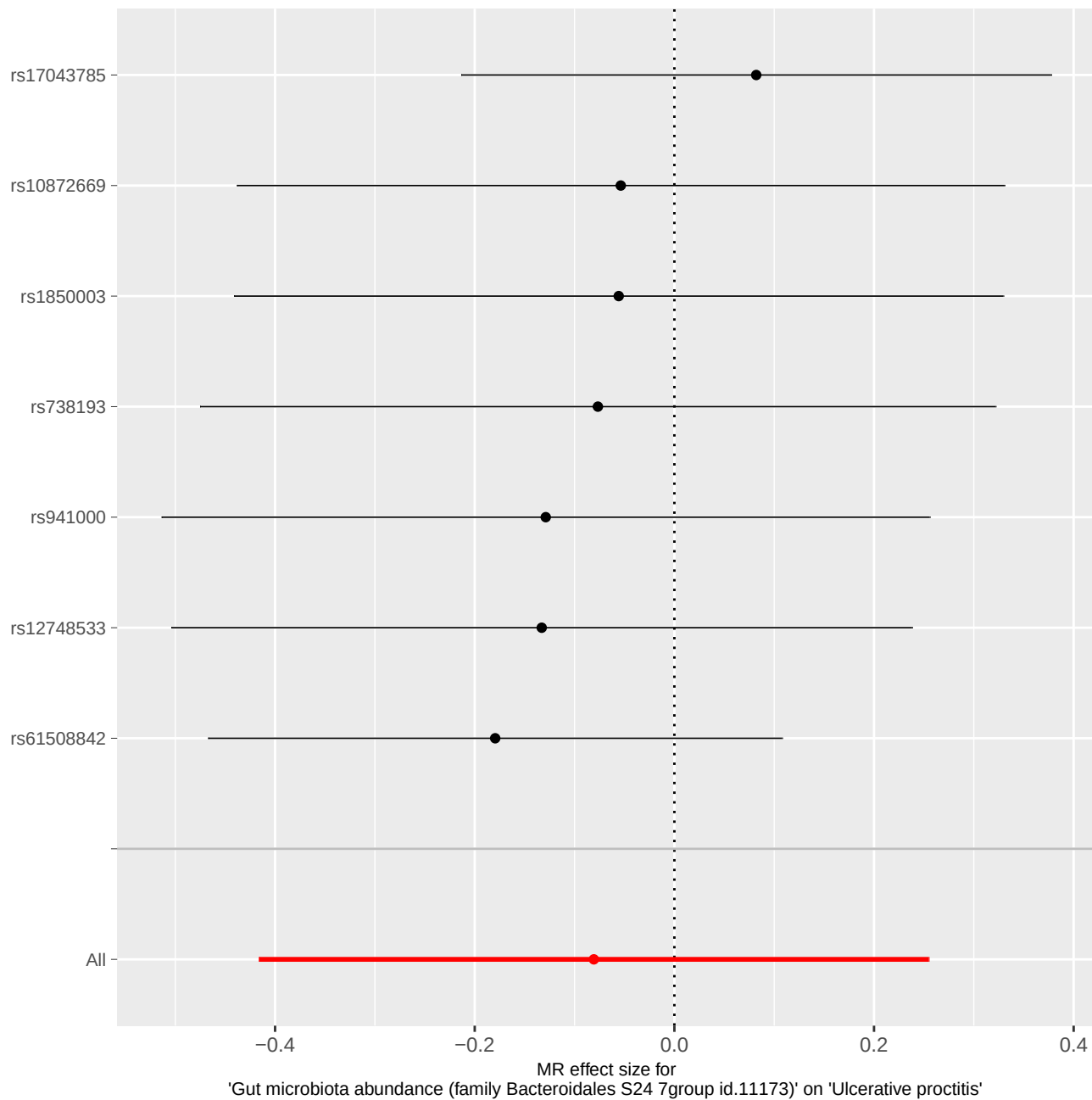


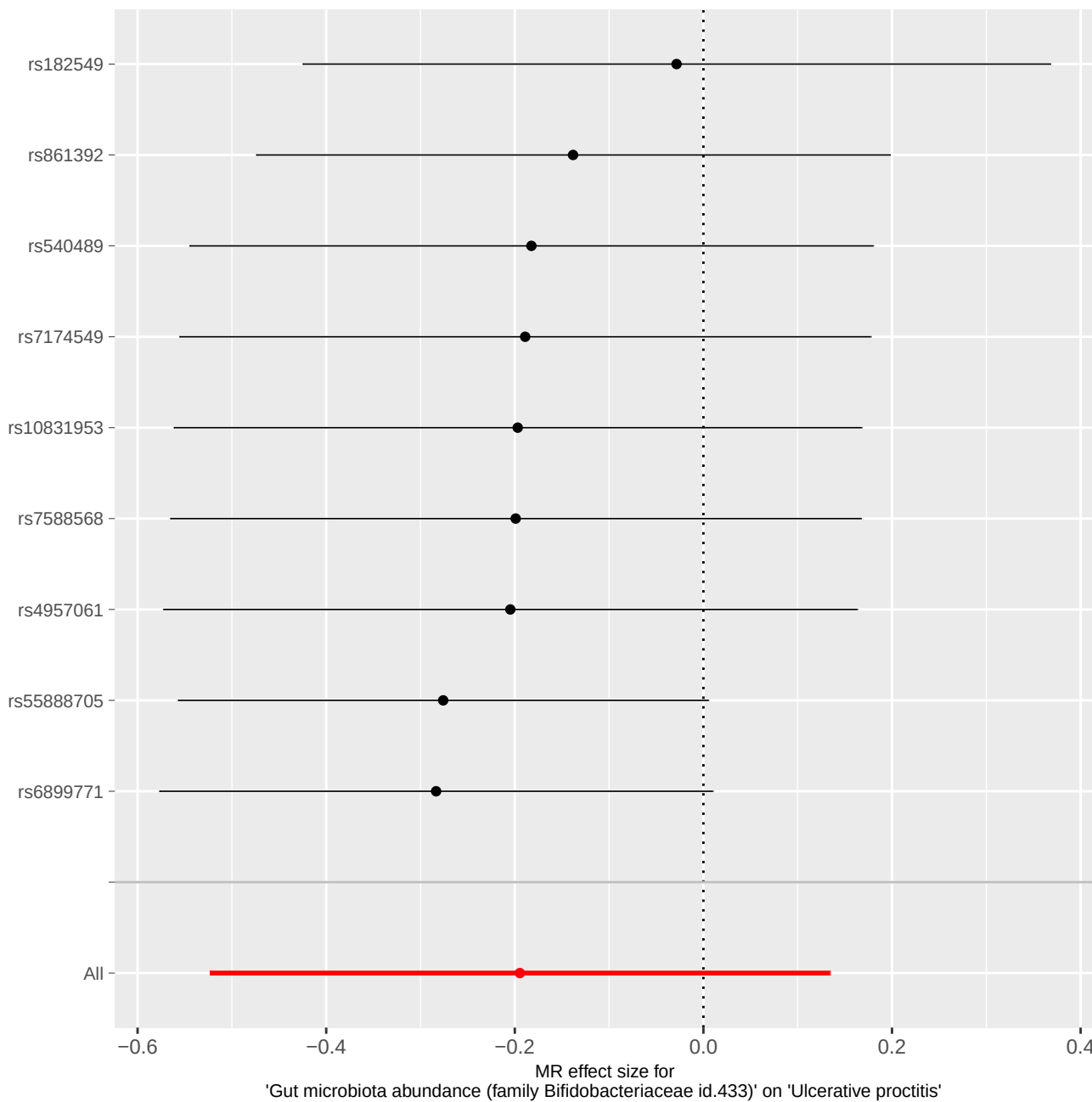
MR effect size for
'Gut microbiota abundance (family Acidaminococcaceae id.2166)' on 'Ulcerative proctitis'

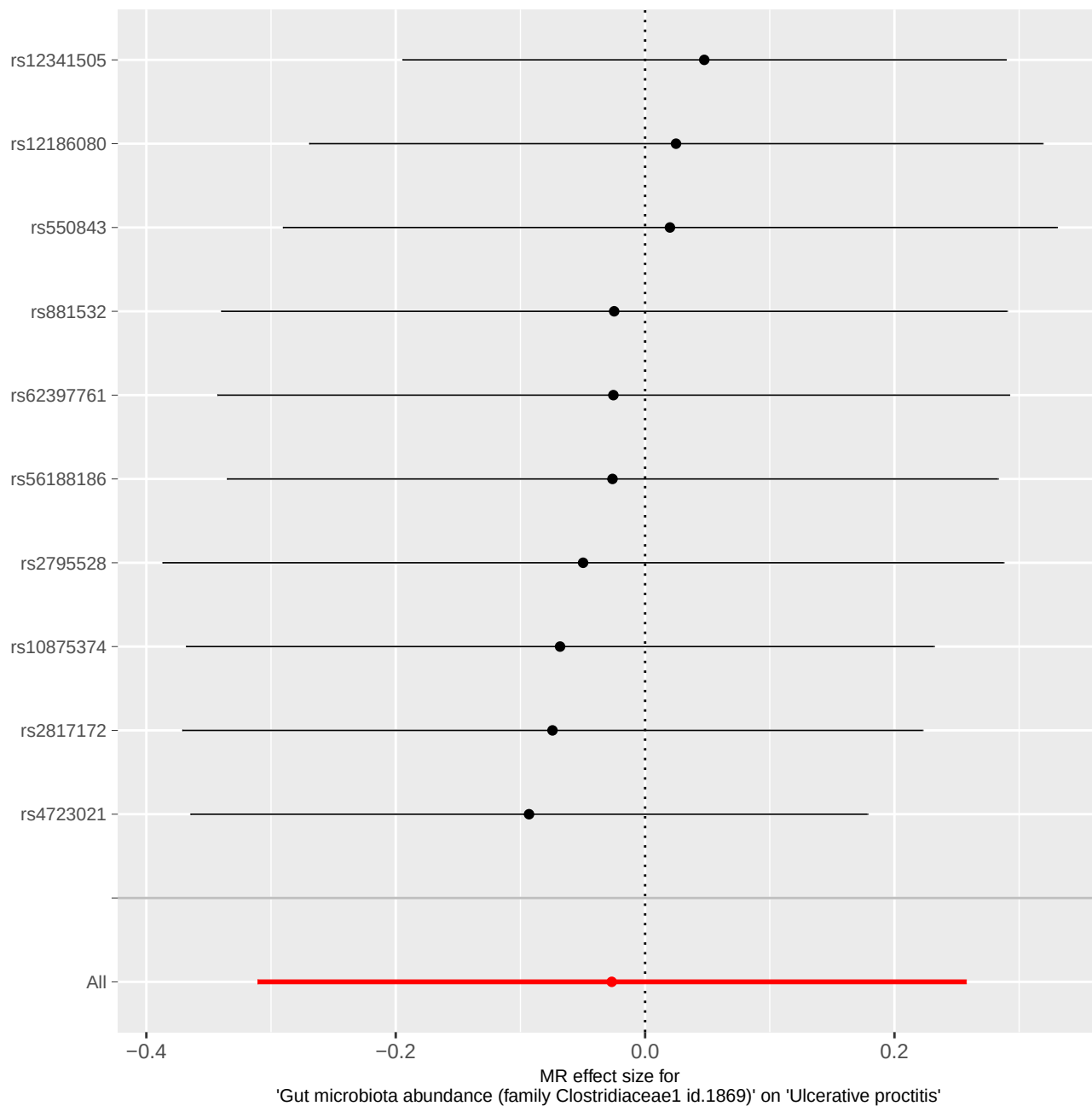


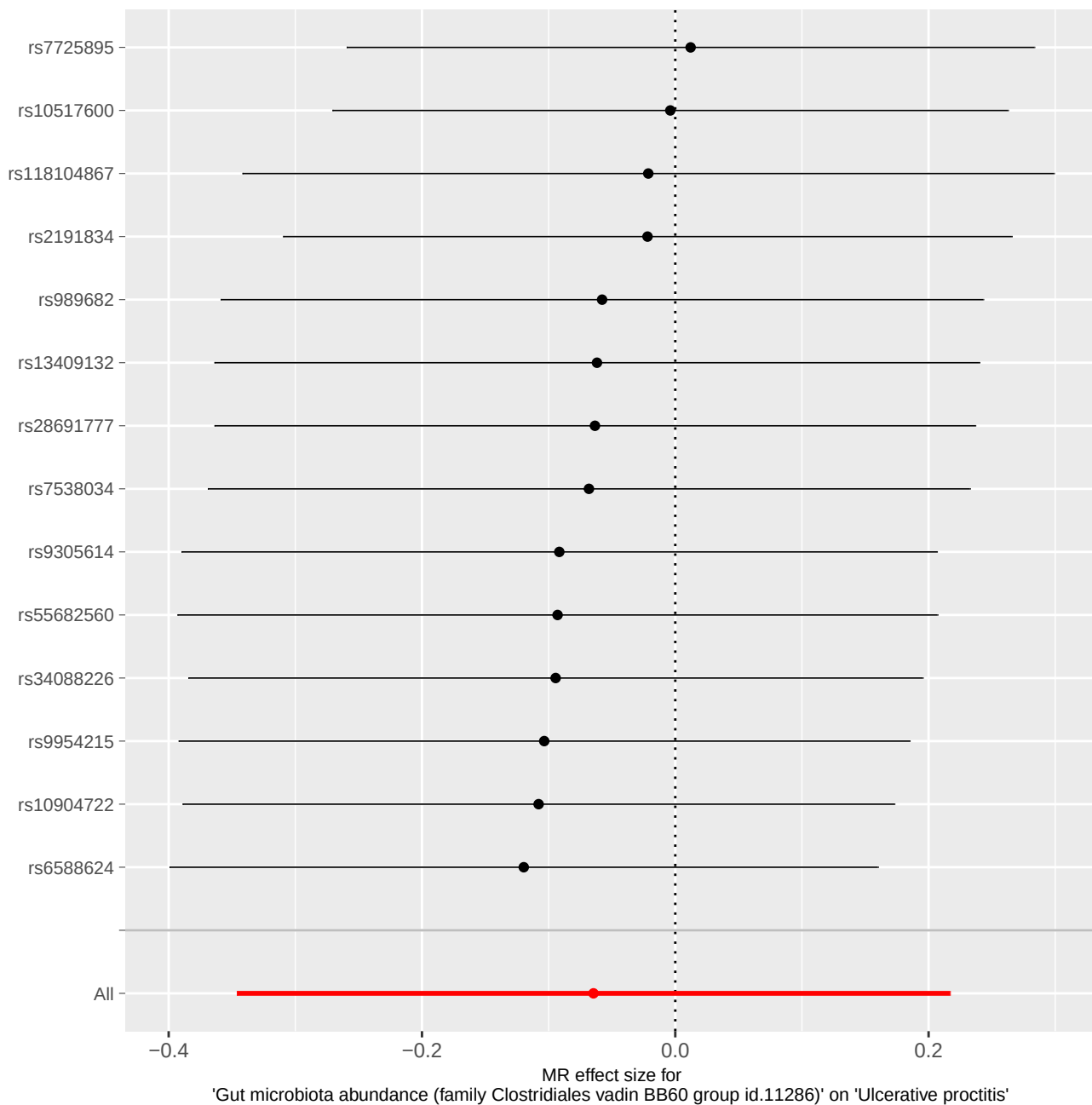


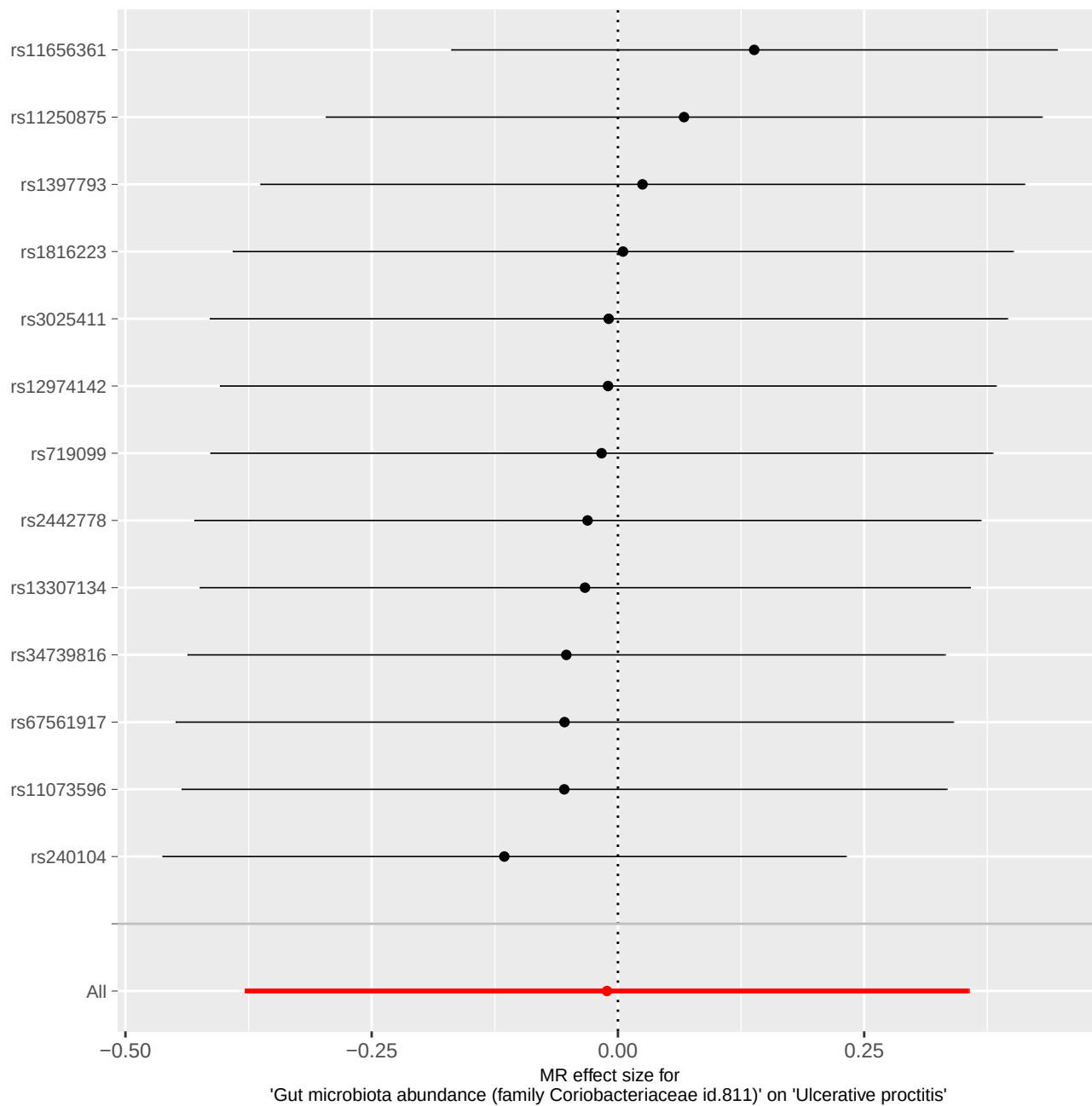


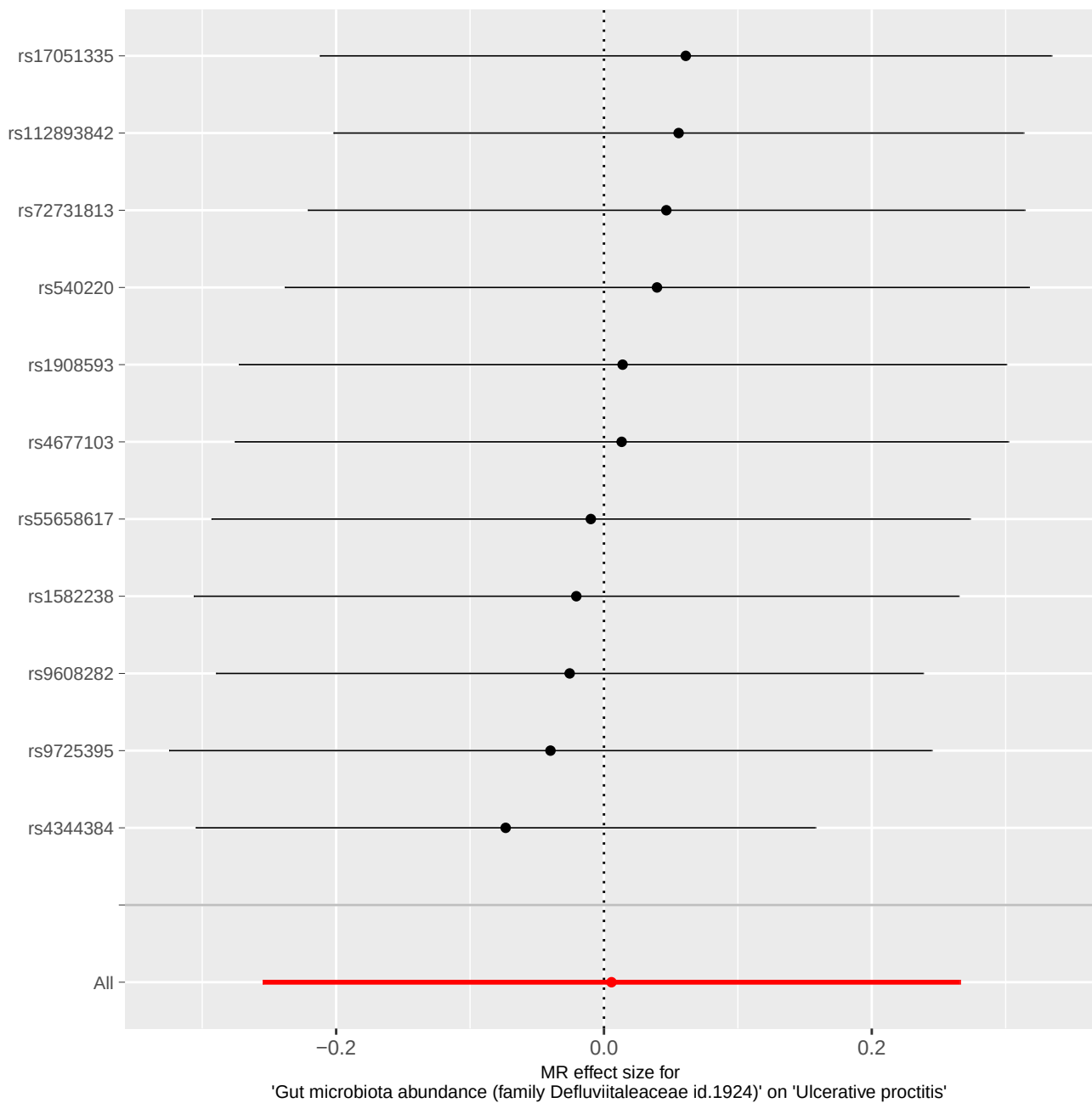


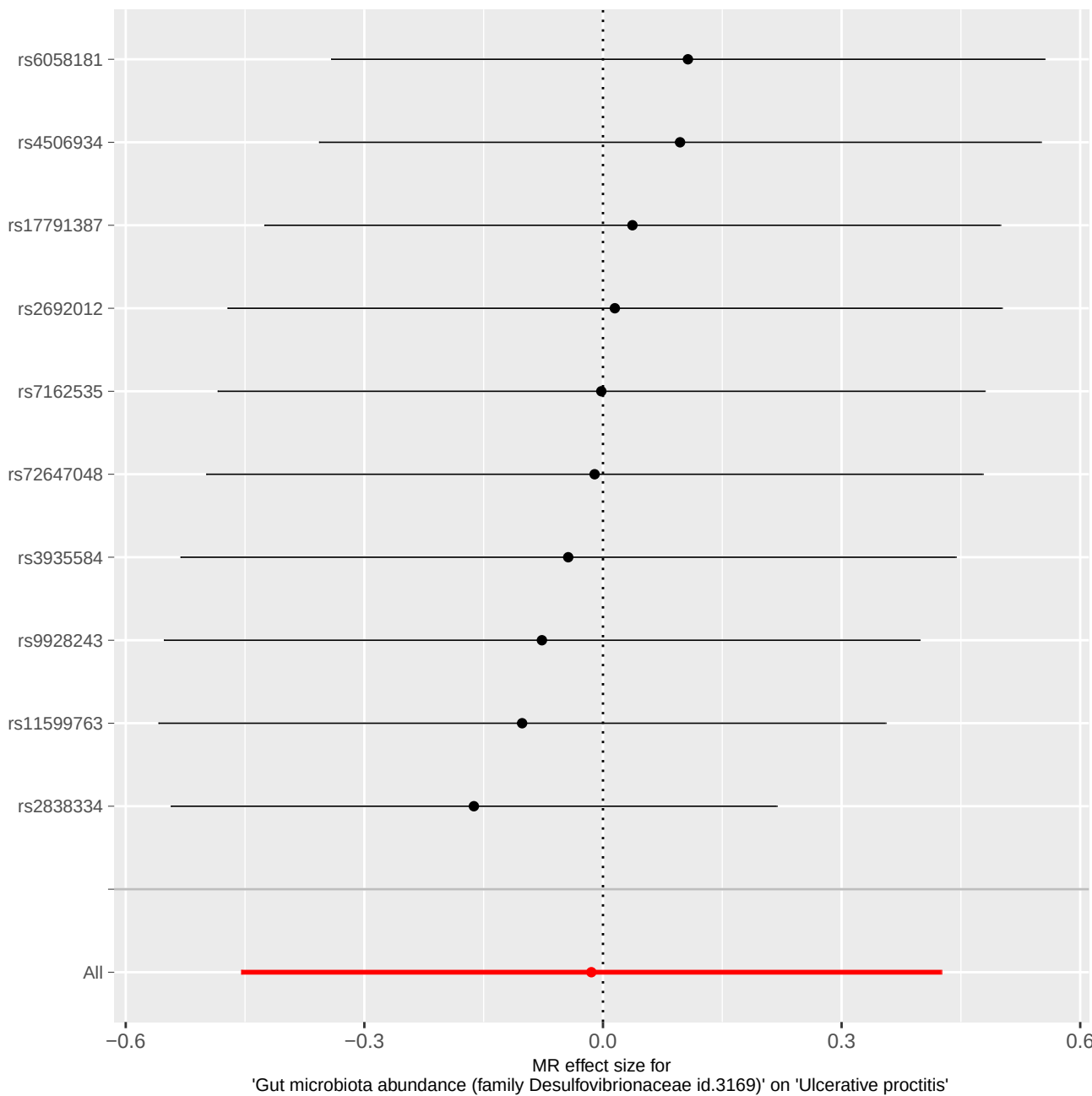




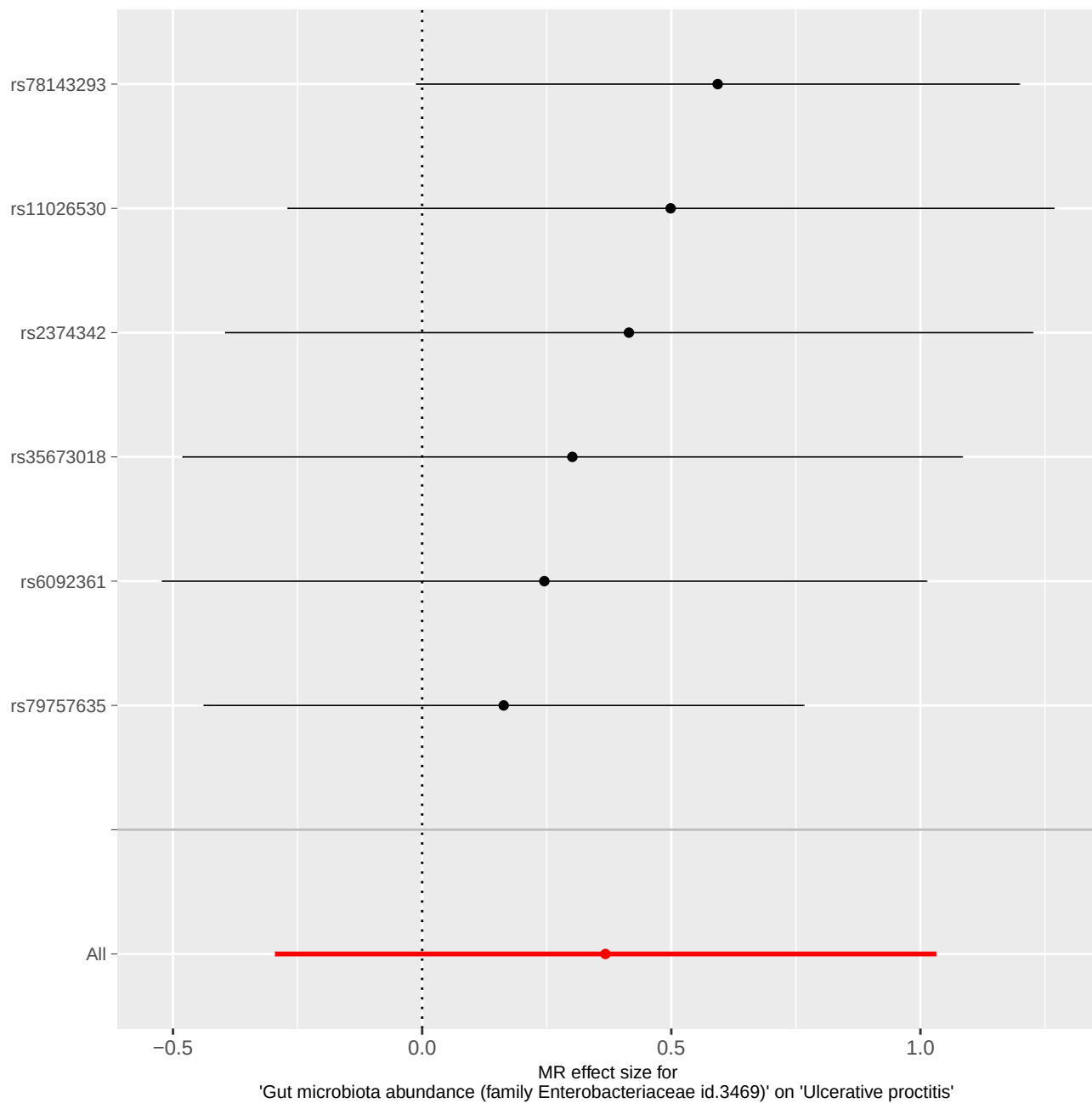


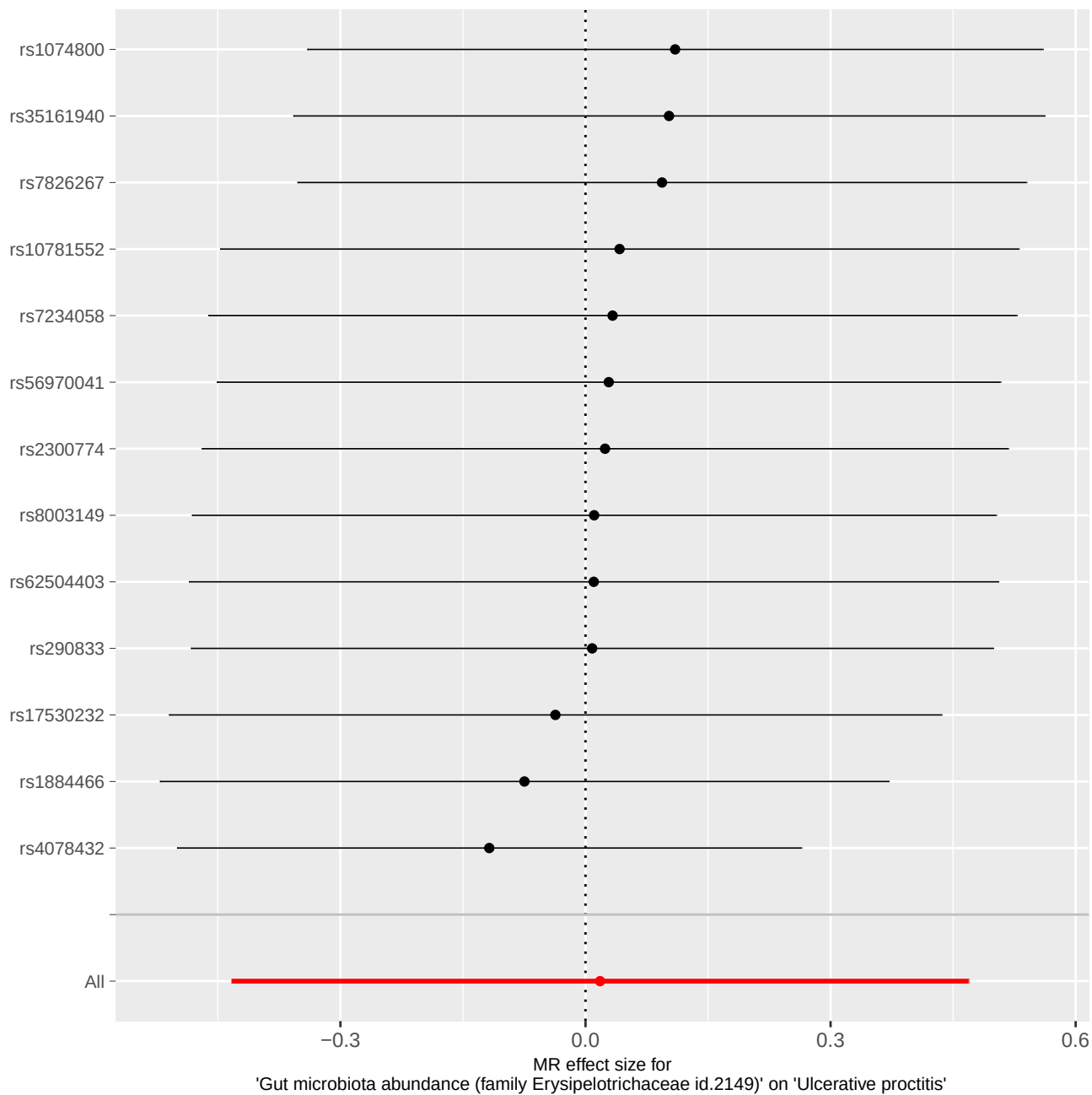


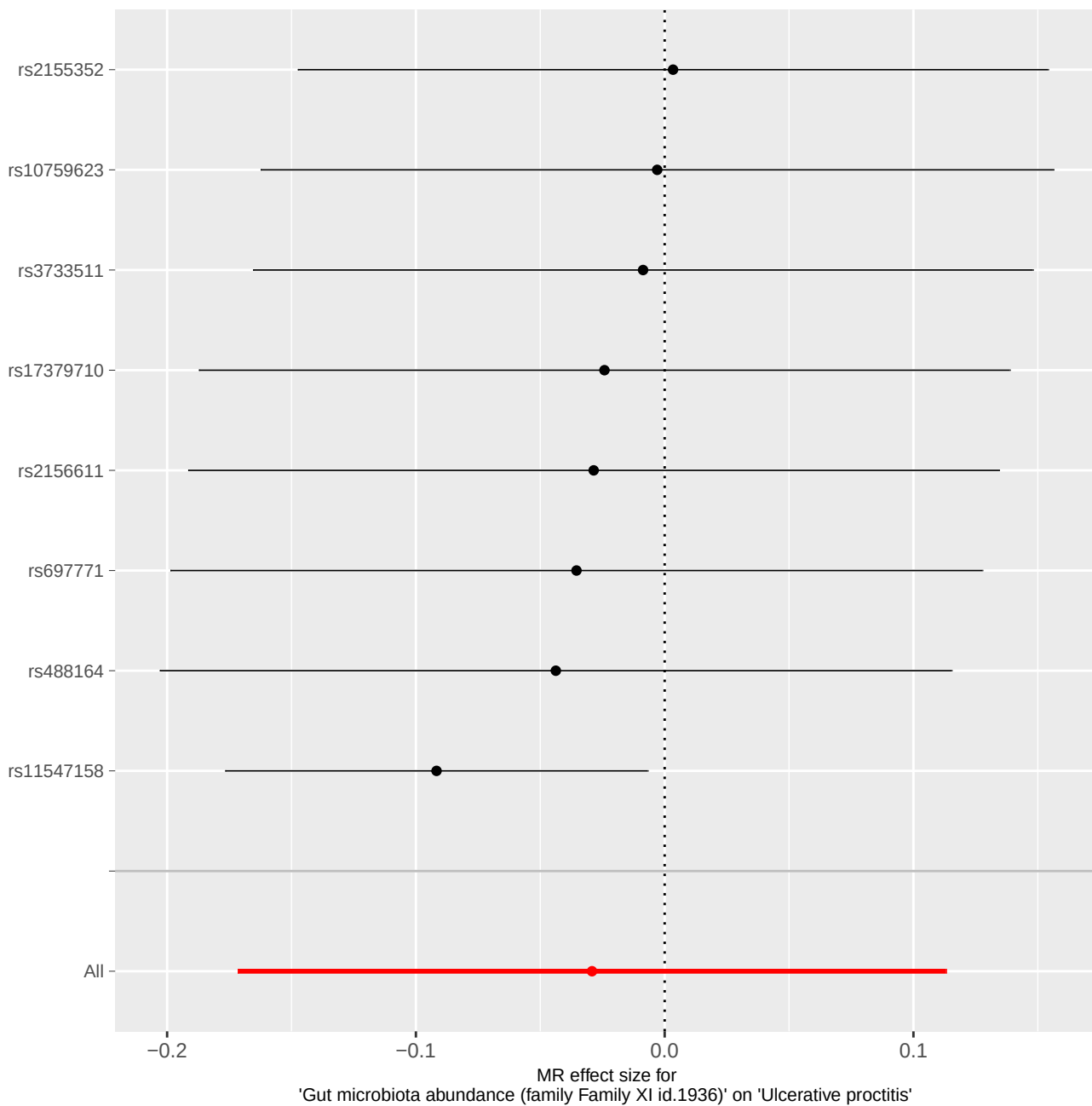




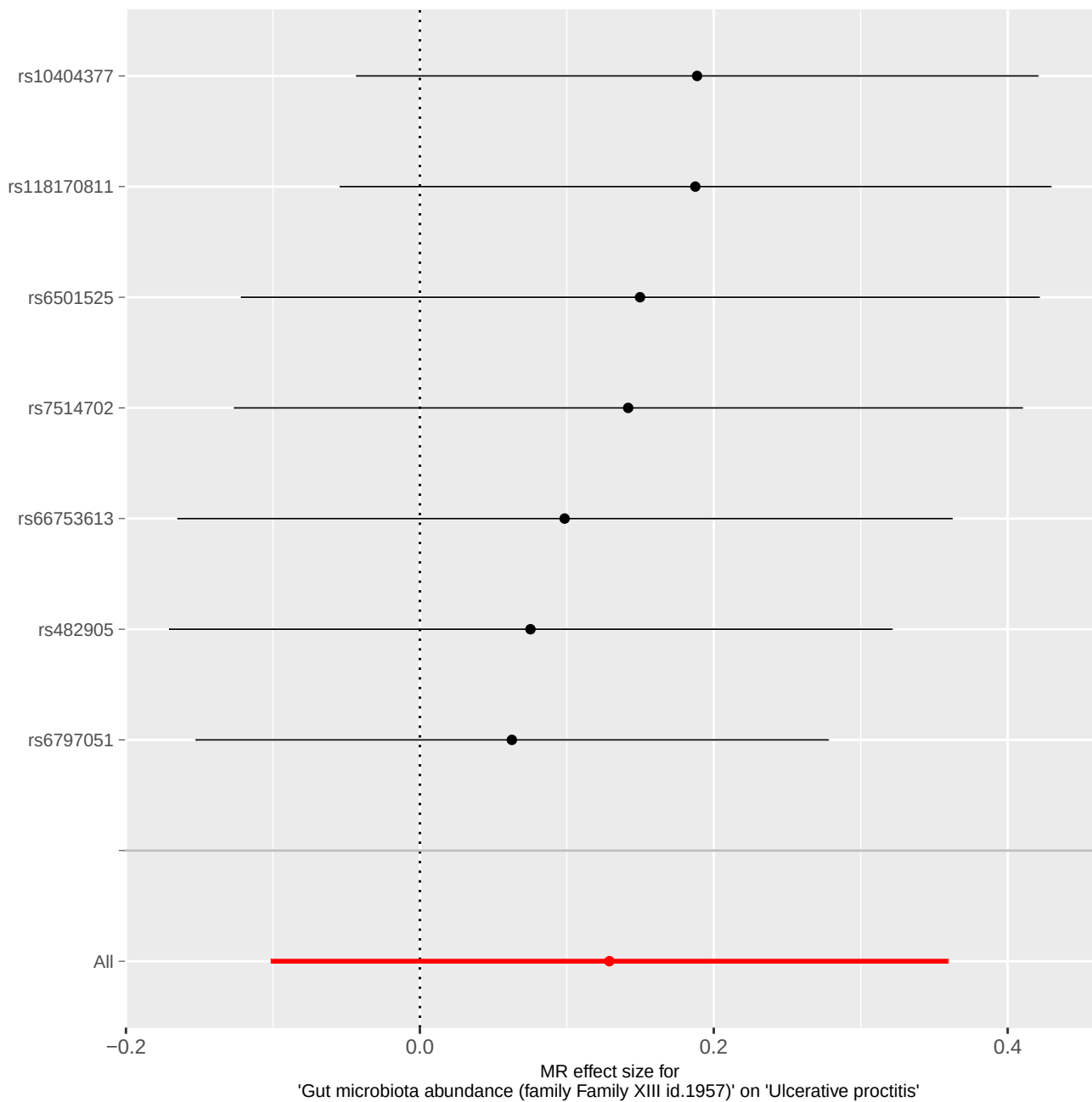
MR effect size for
'Gut microbiota abundance (family Desulfovibrionaceae id.3169)' on 'Ulcerative proctitis'



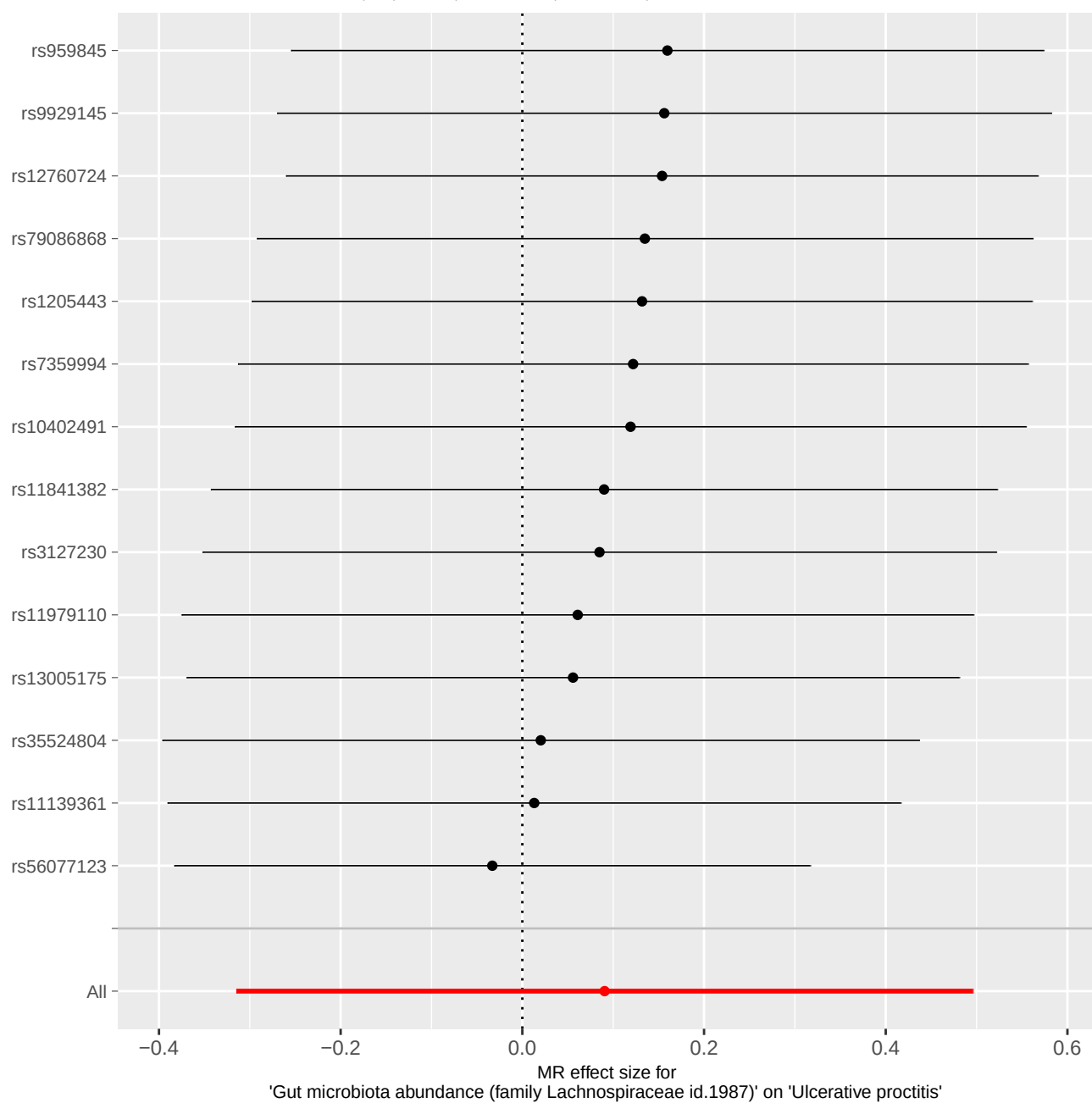


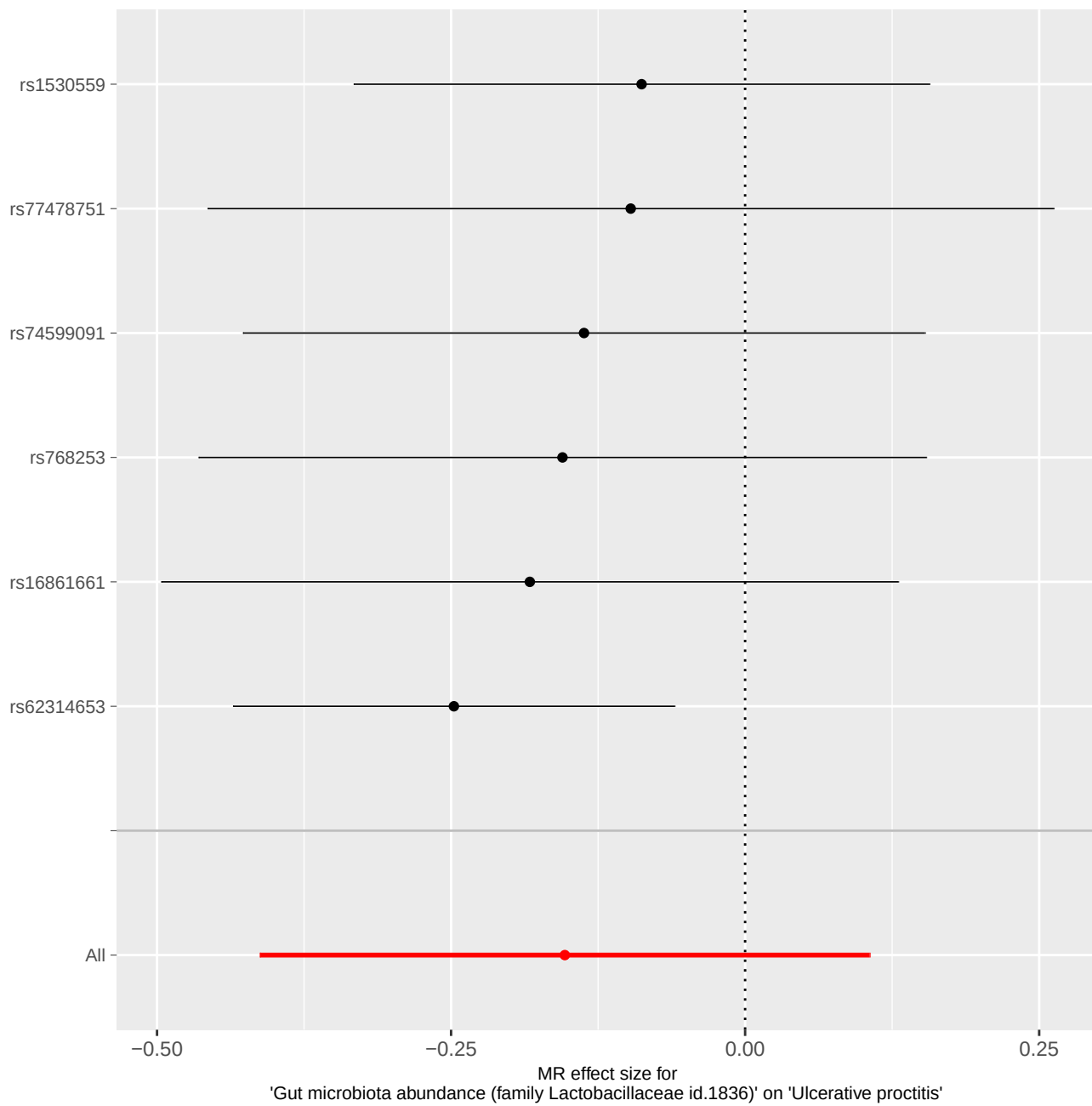


Batch 1366 : Gut microbiota abundance (family Family XIII id.1957) on Ulcerative proctitis

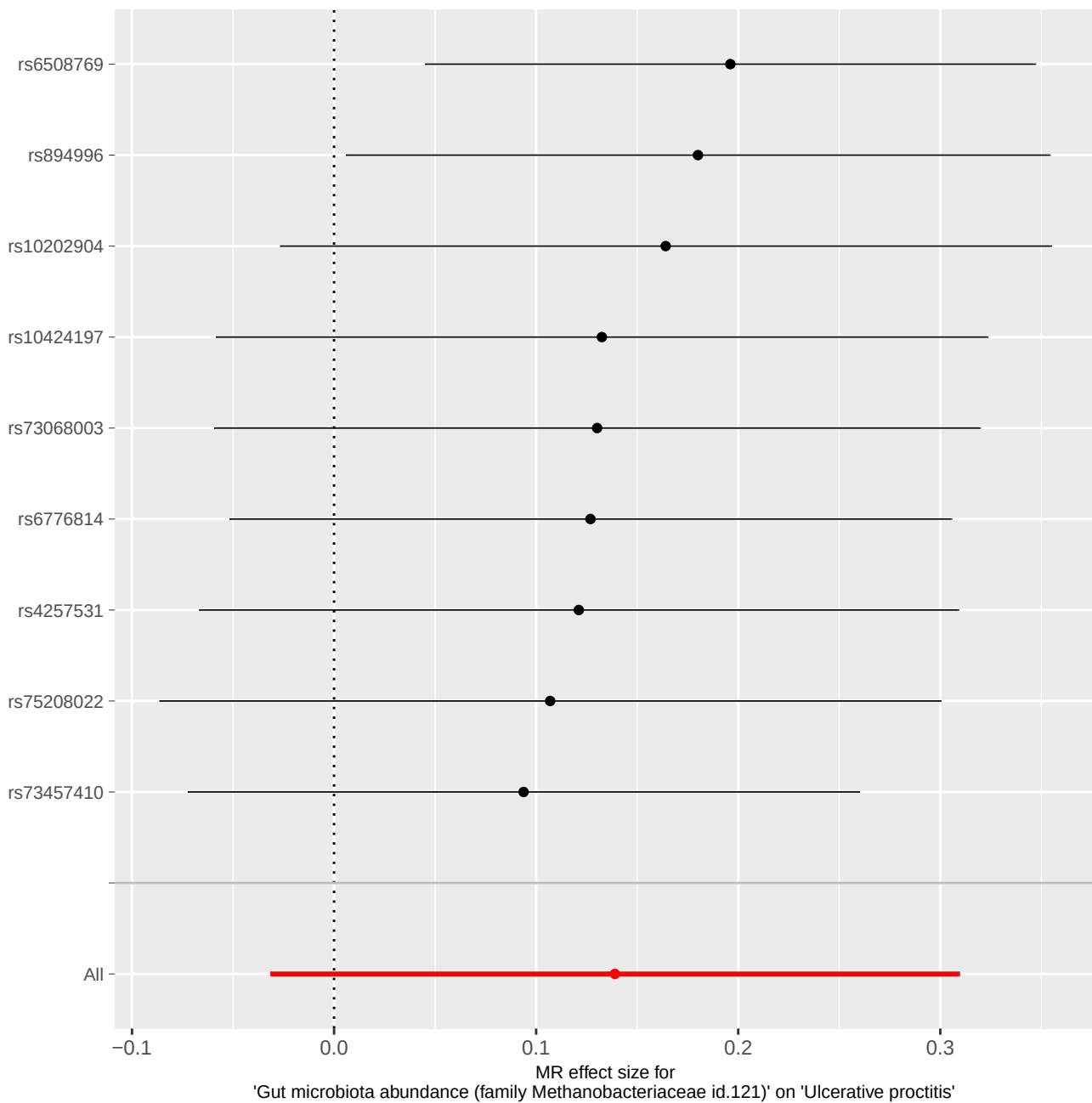


Batch 1367 : Gut microbiota abundance (family Lachnospiraceae id.1987) on Ulcerative proctitis

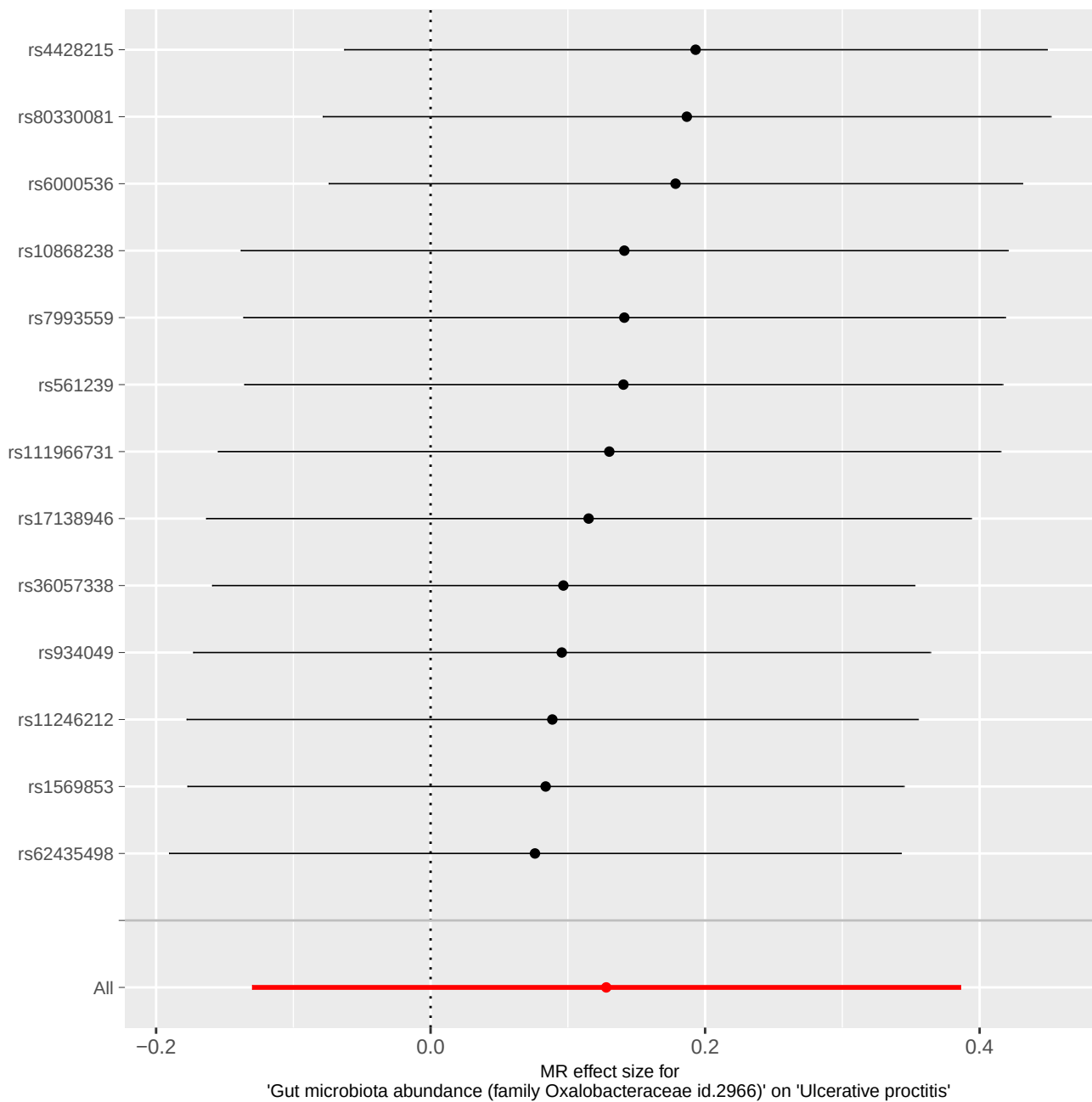


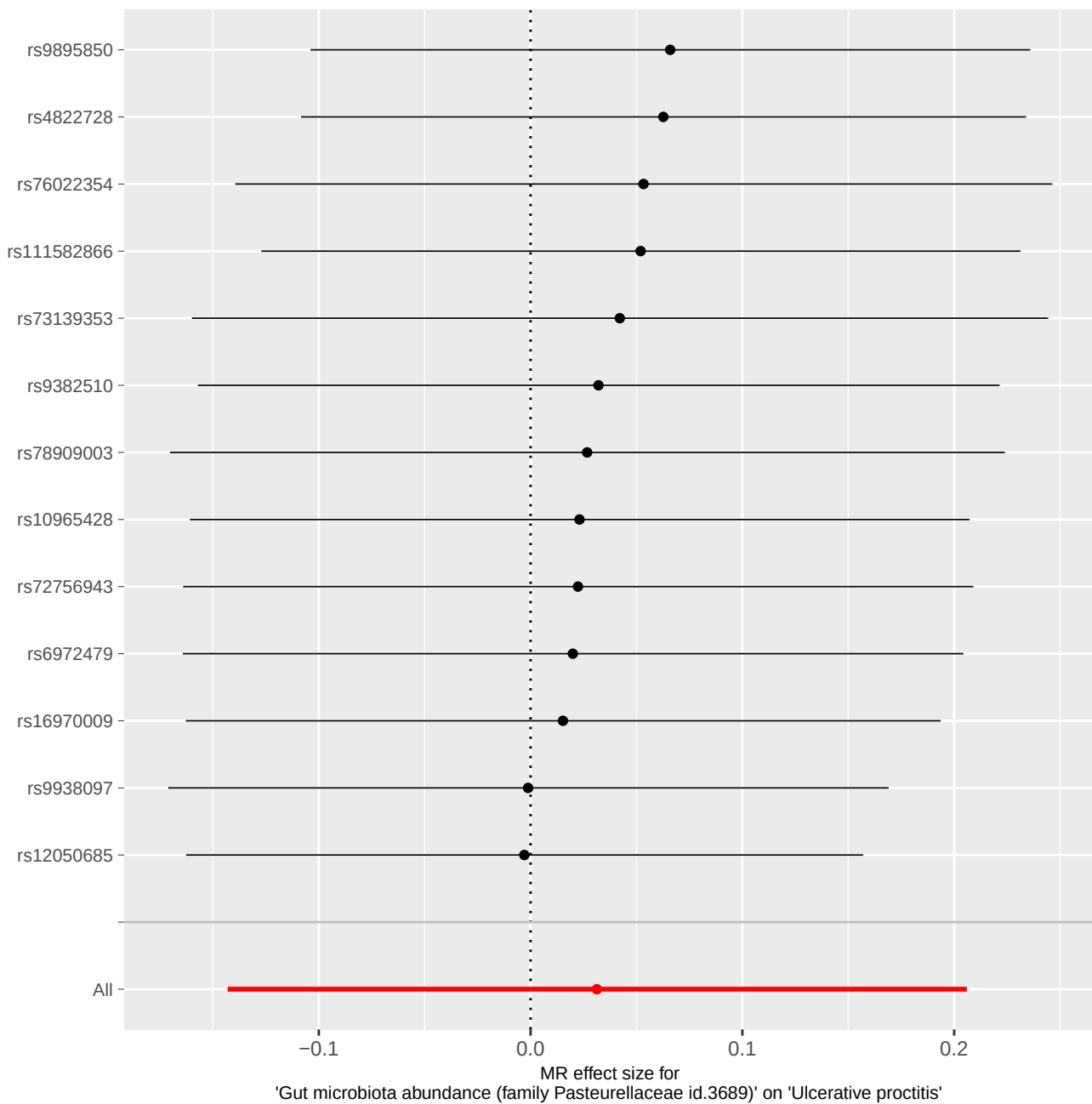


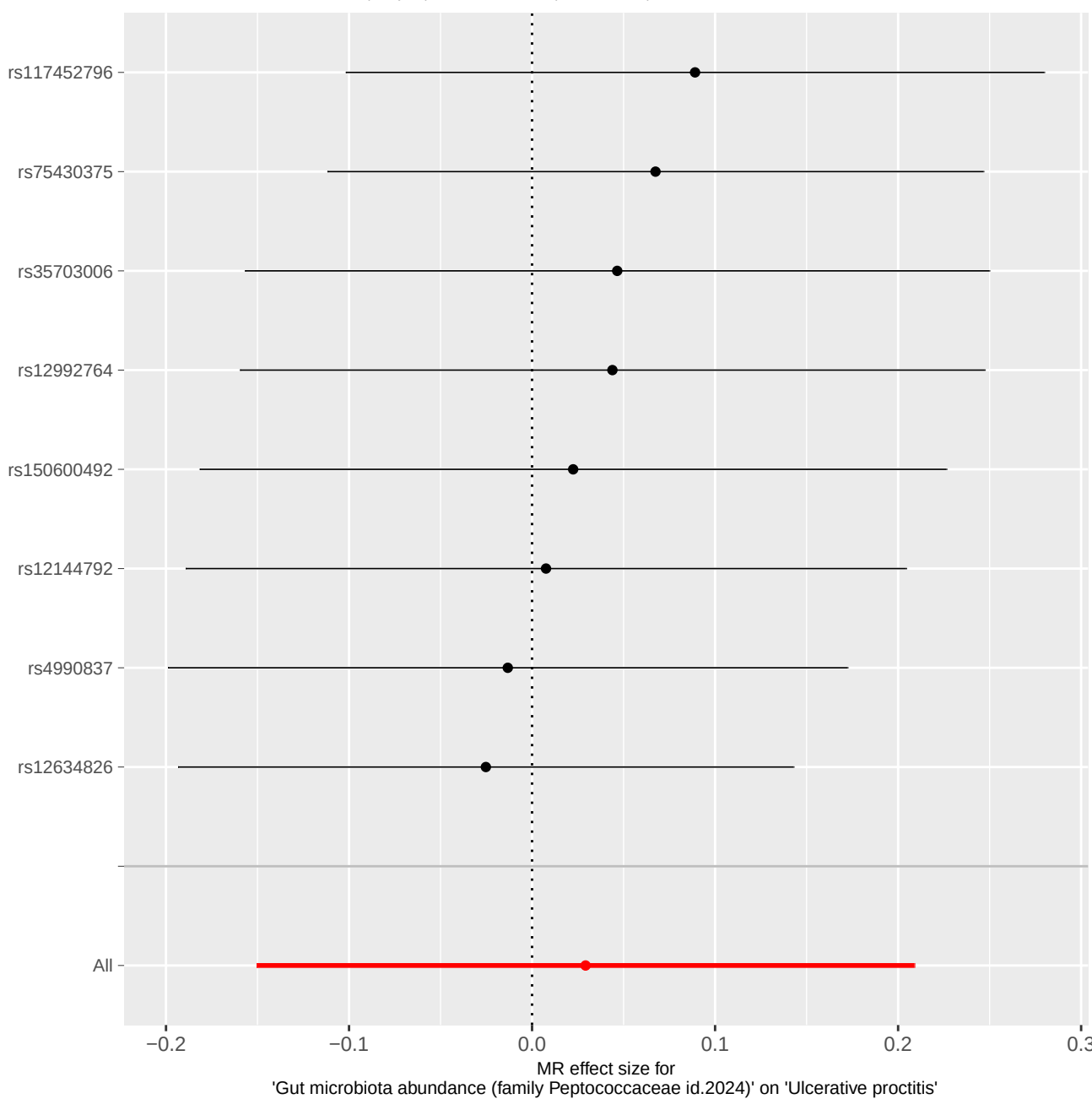
Batch 1369 : Gut microbiota abundance (family Methanobacteriaceae id.121) on Ulcerative proctitis

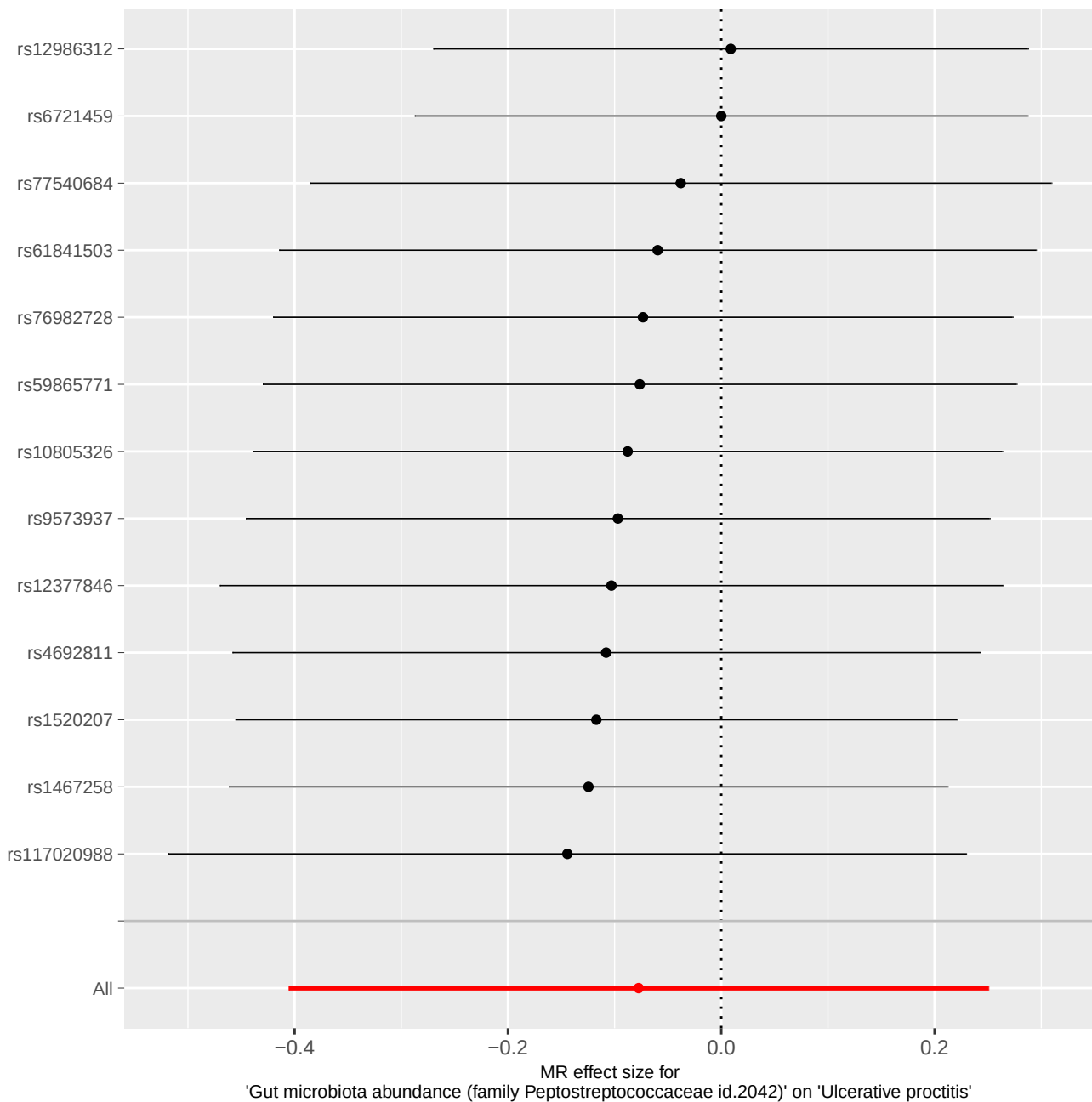


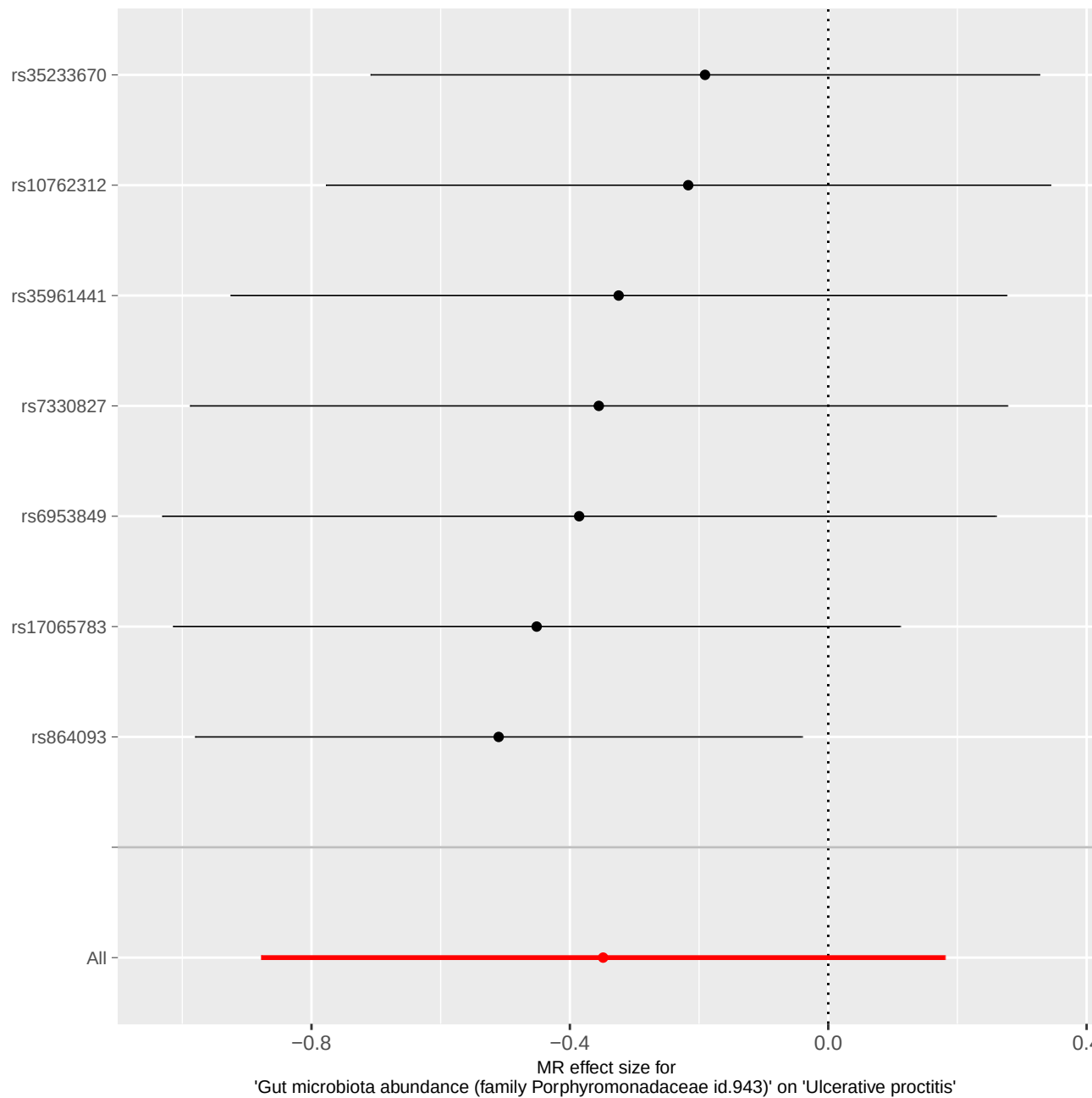
Batch 1370 : Gut microbiota abundance (family Oxalobacteraceae id.2966) on Ulcerative proctitis

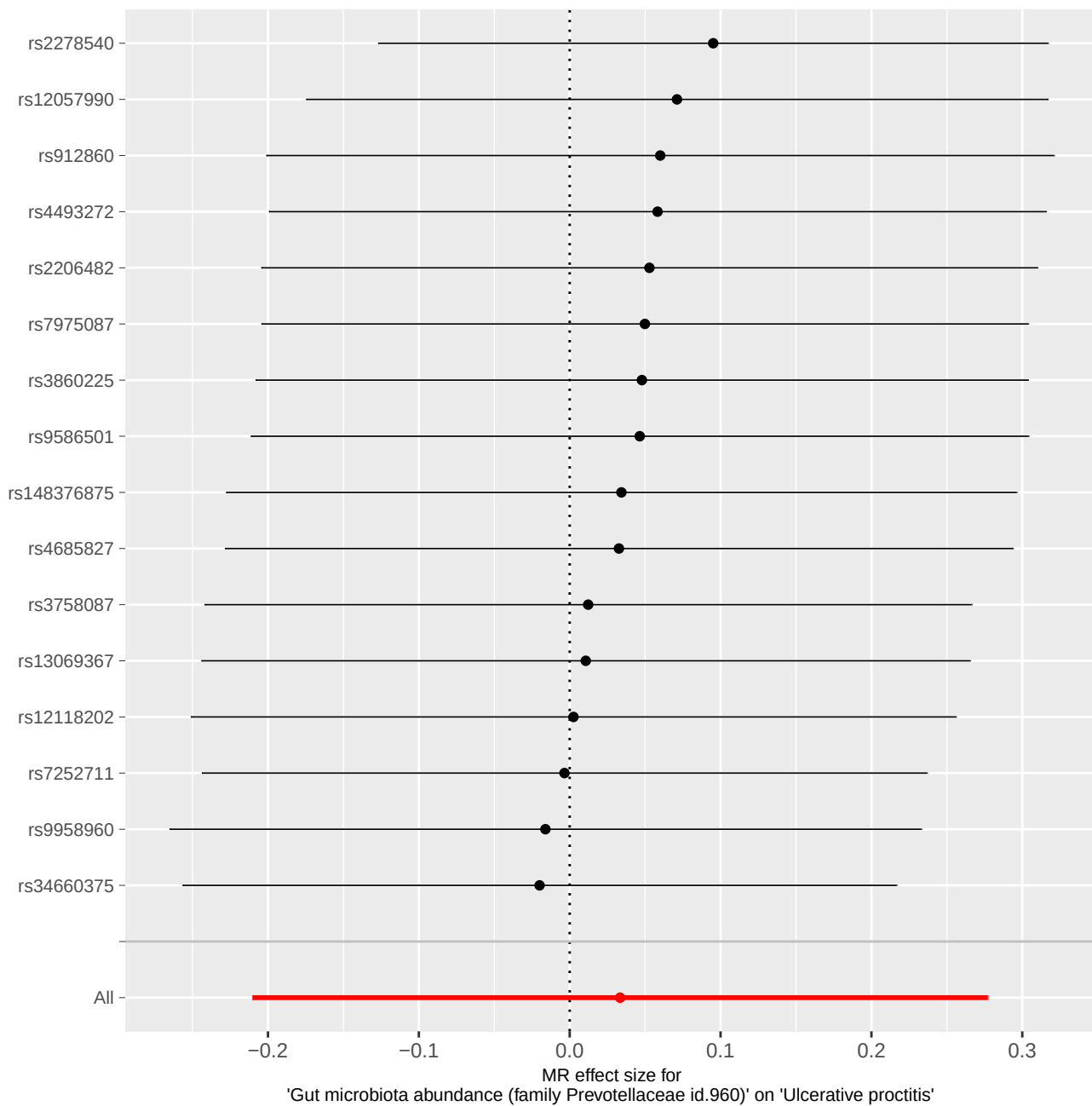


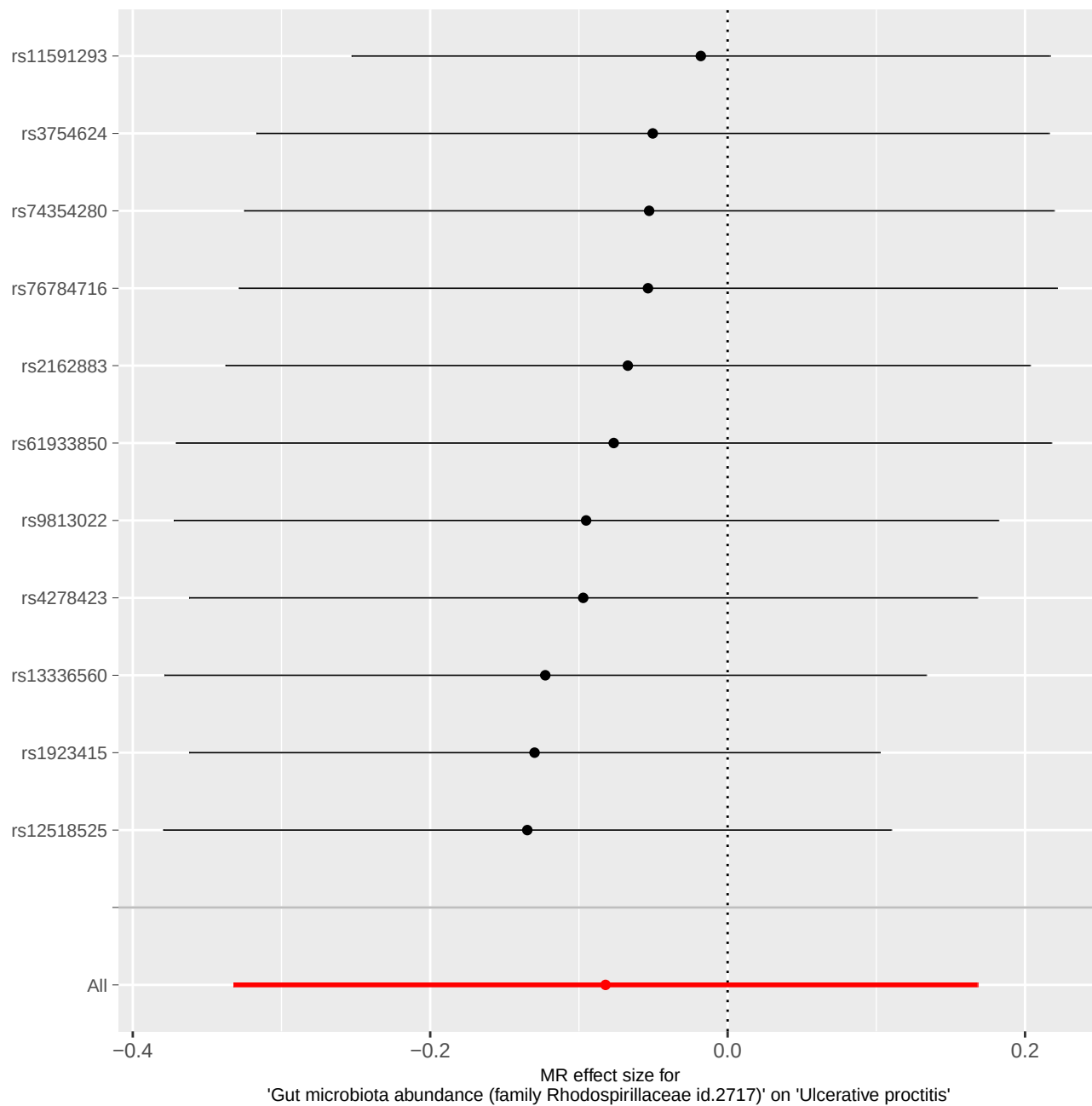




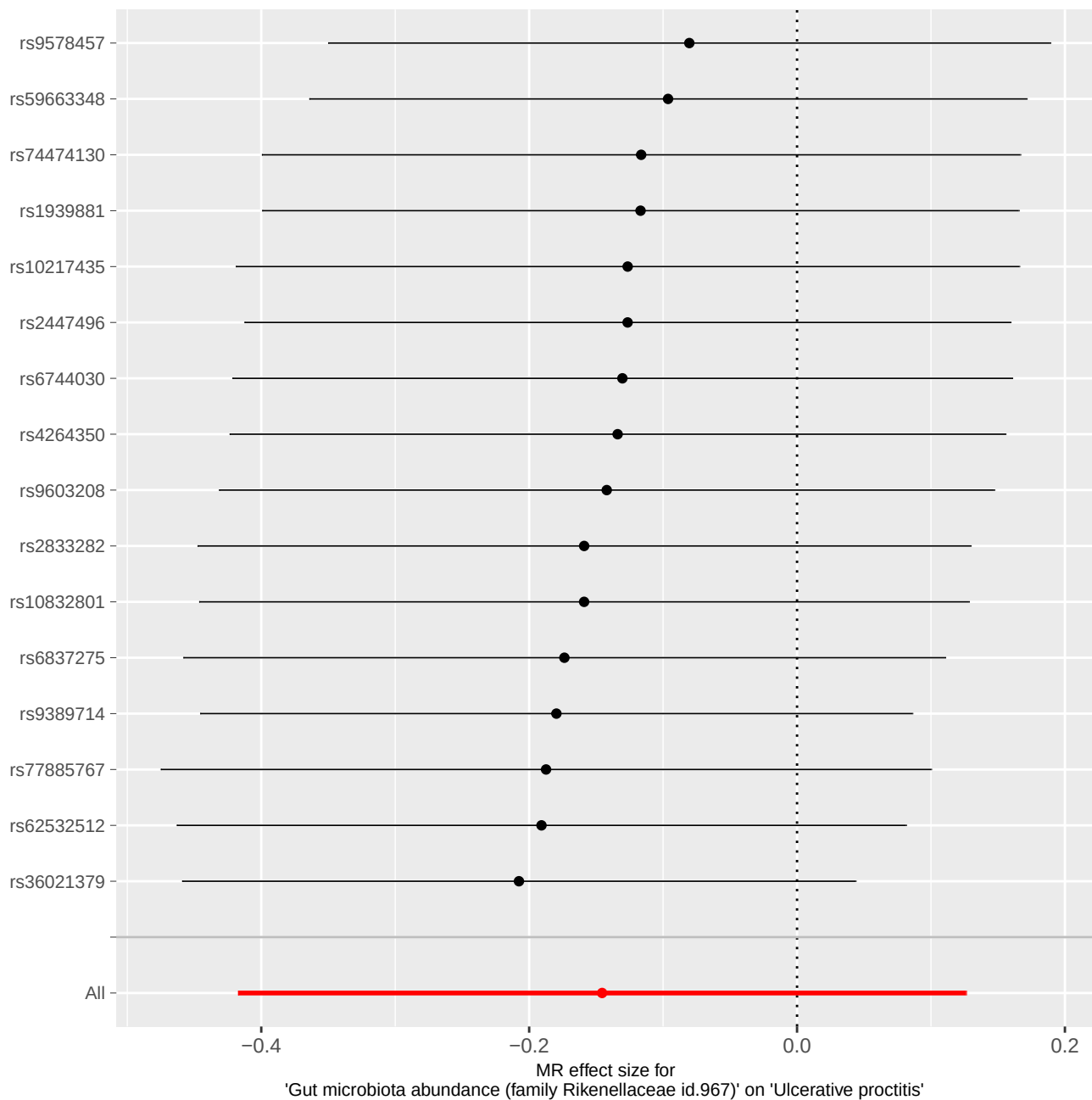


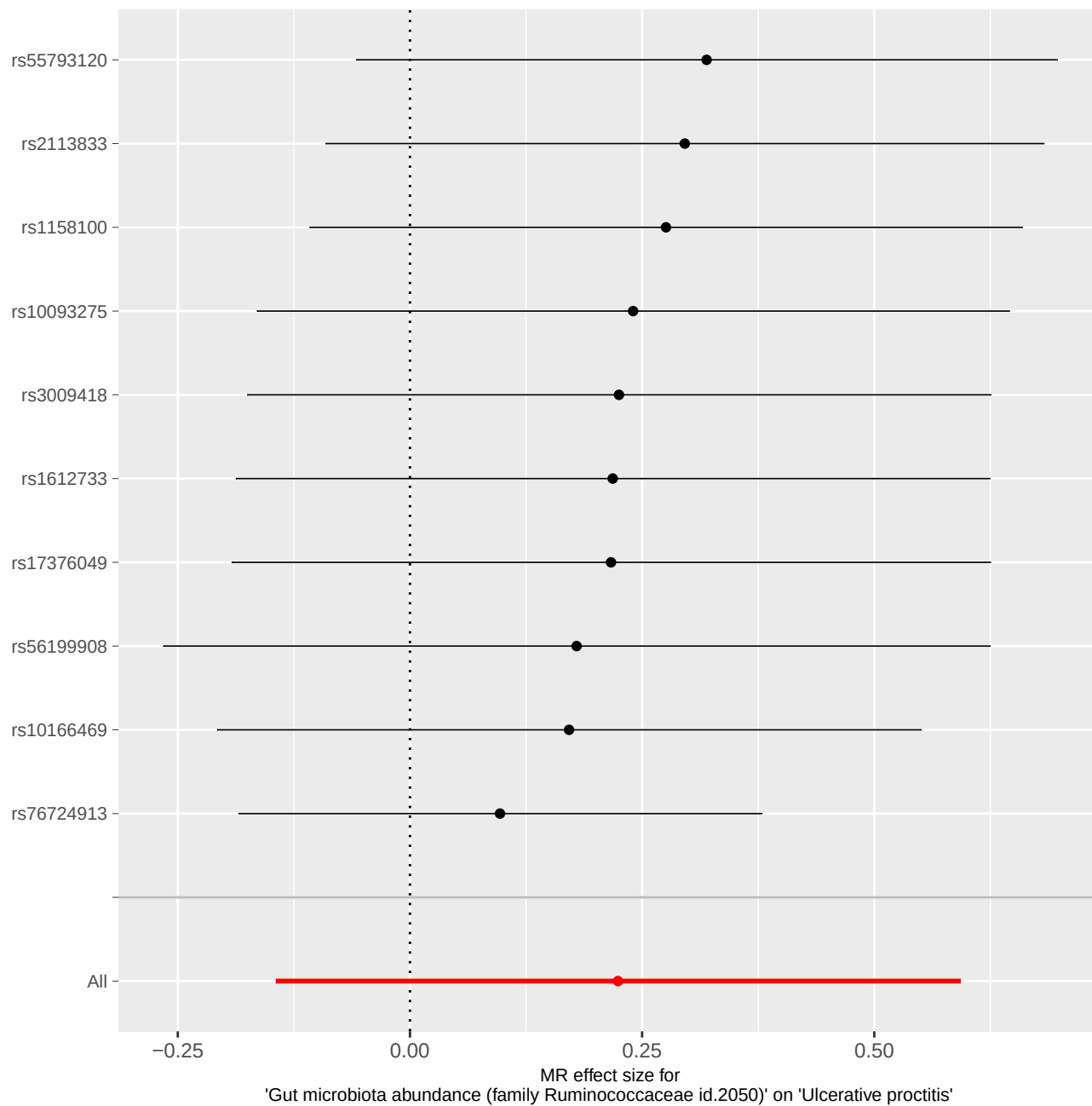


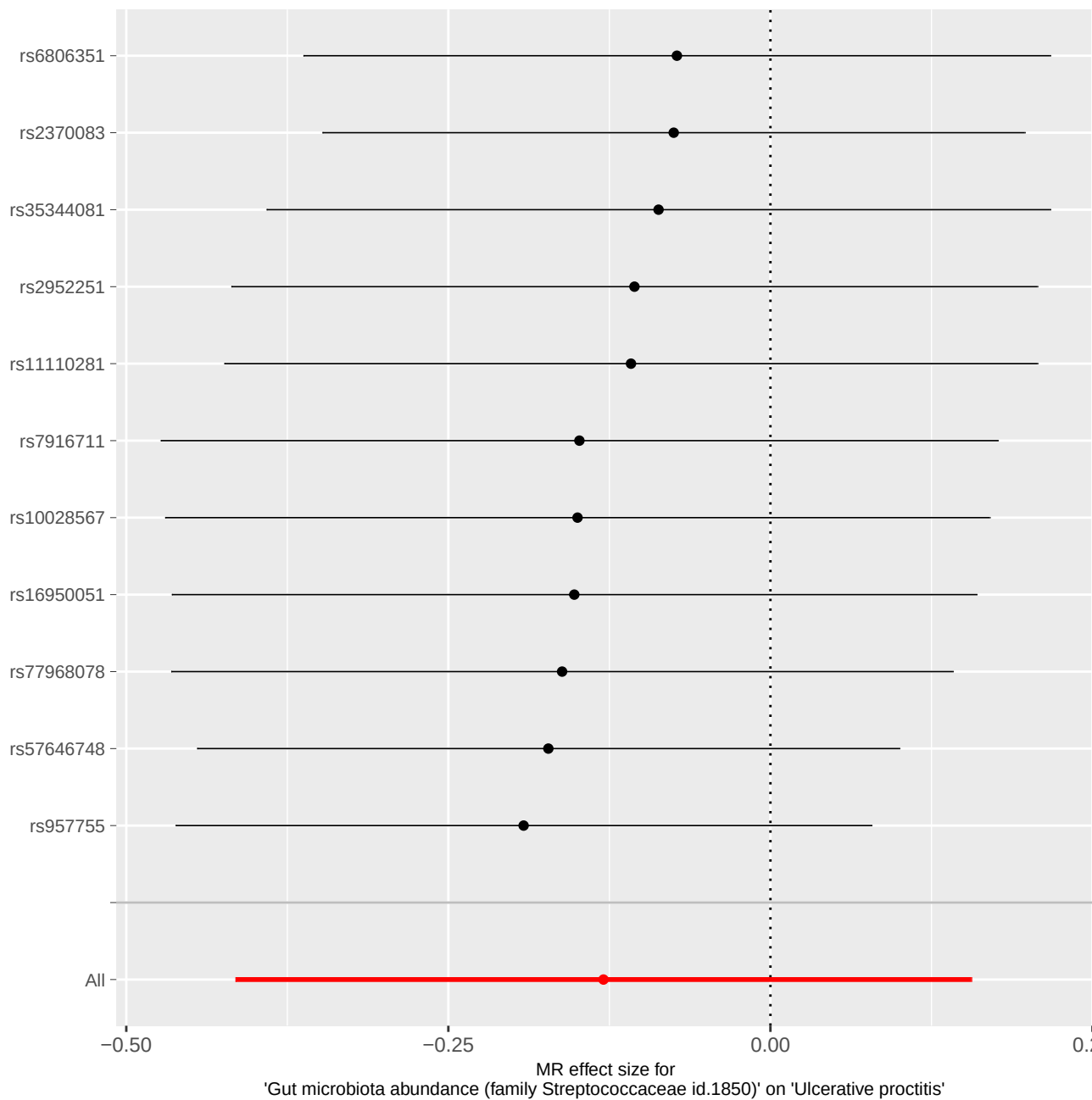


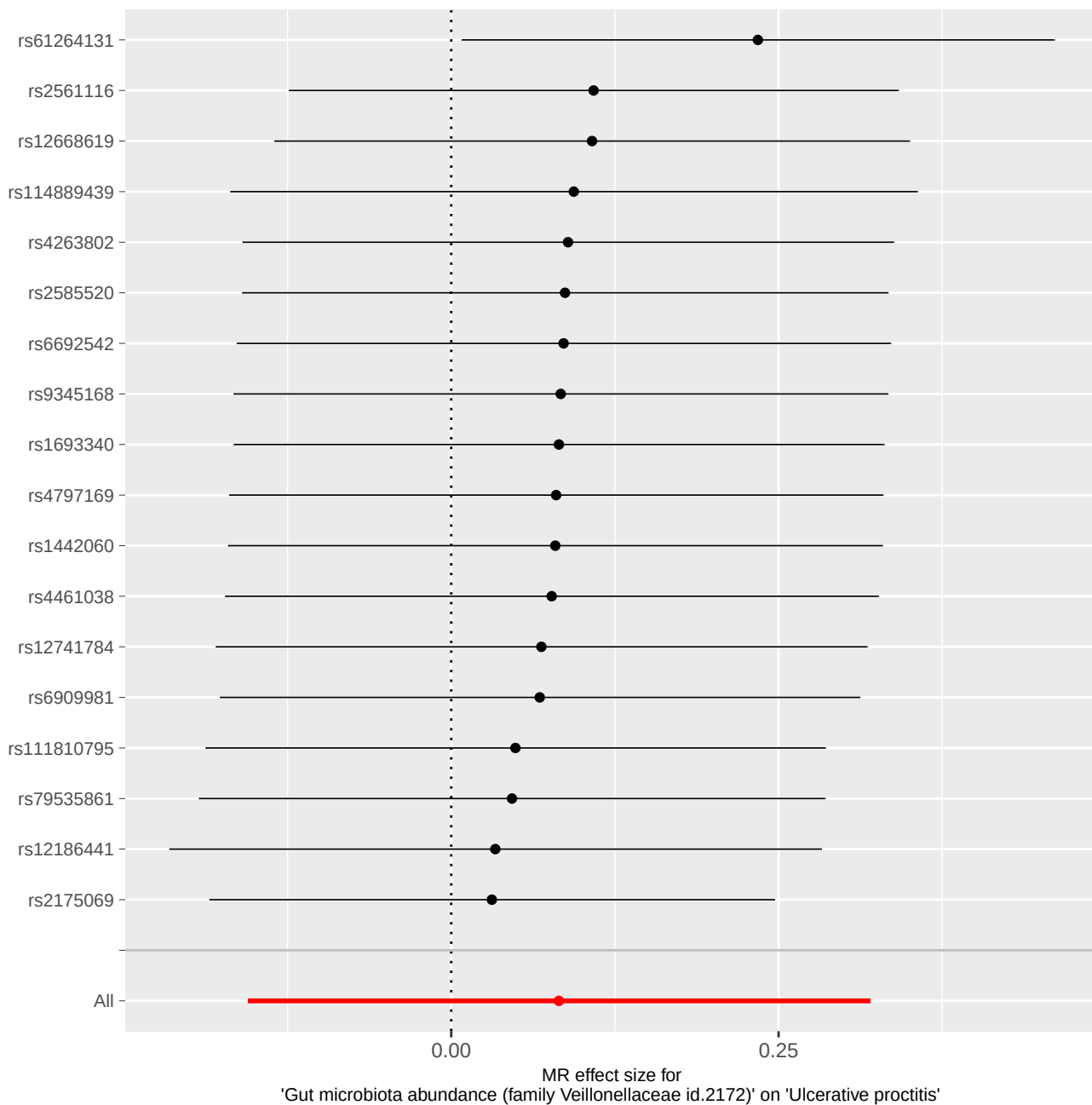


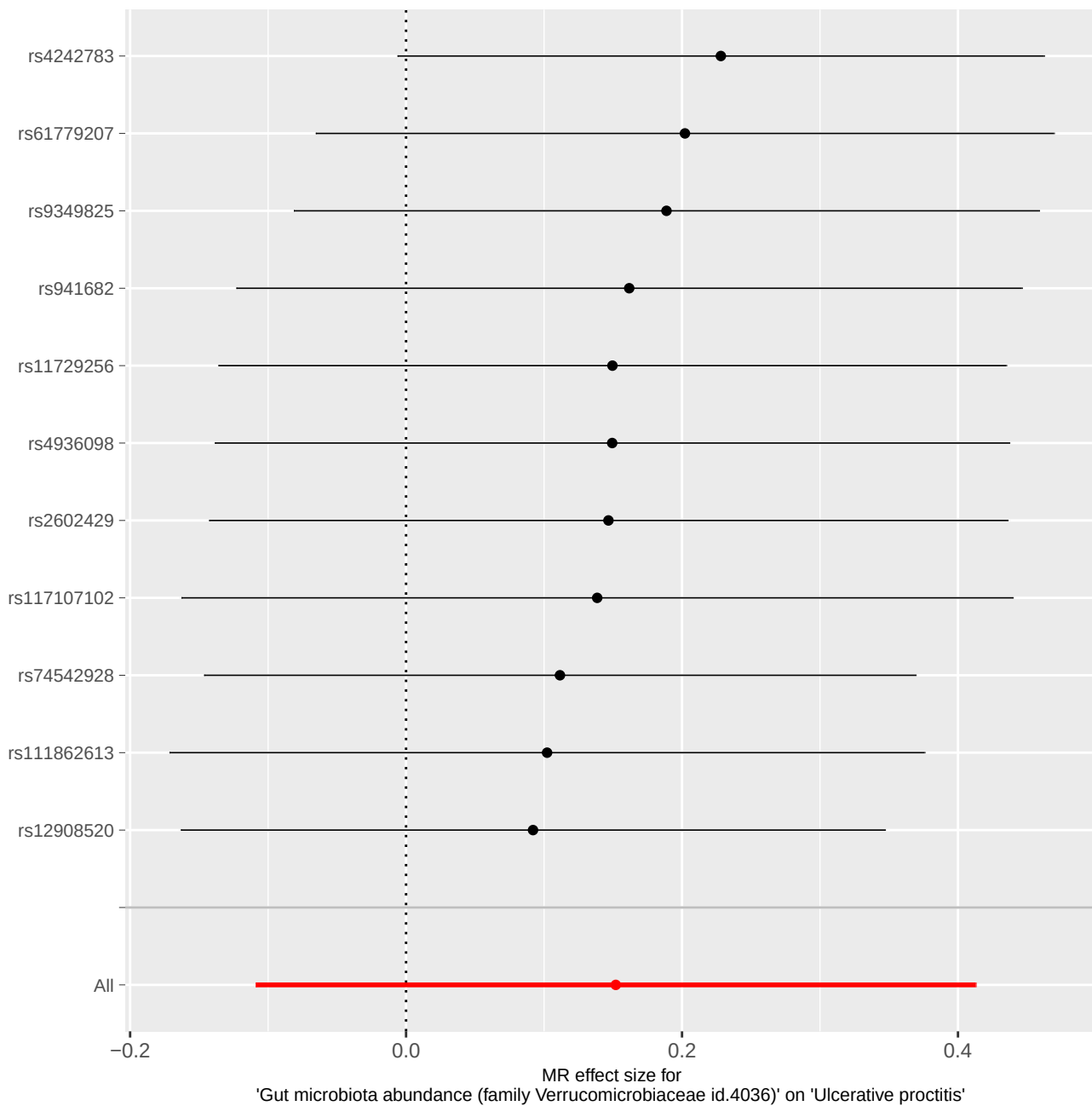
Batch 1377 : Gut microbiota abundance (family Rikenellaceae id.967) on Ulcerative proctitis

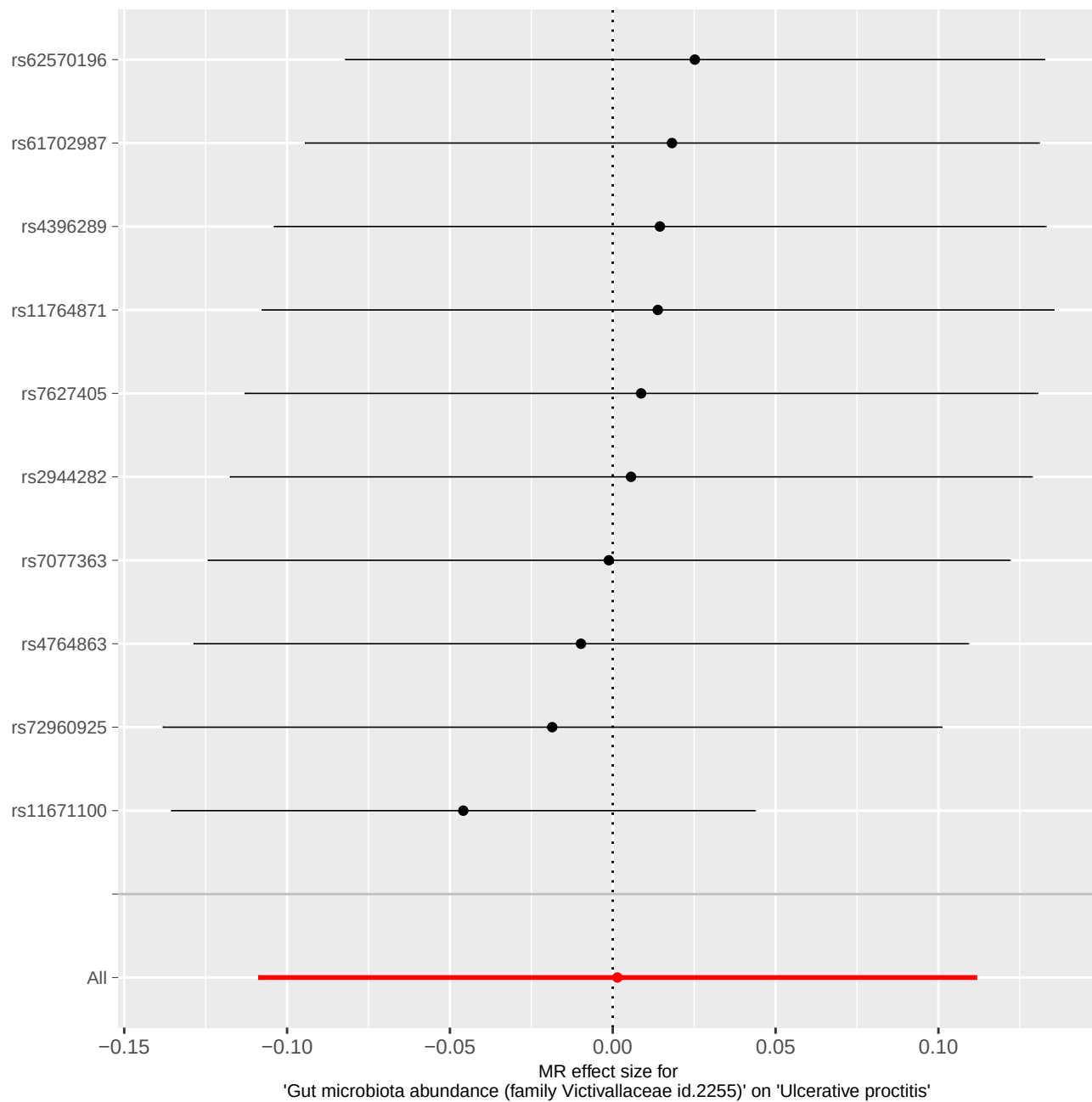


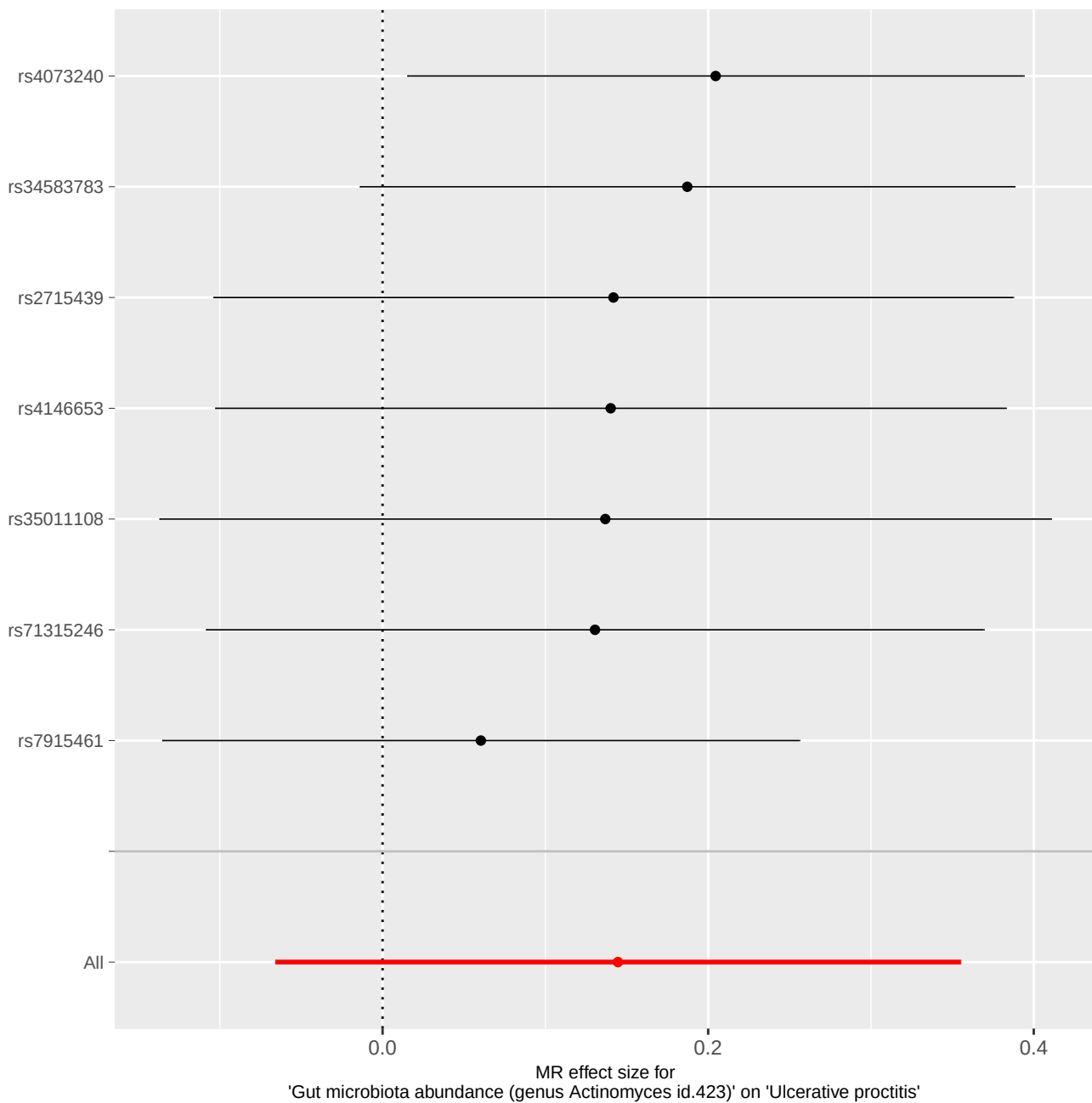


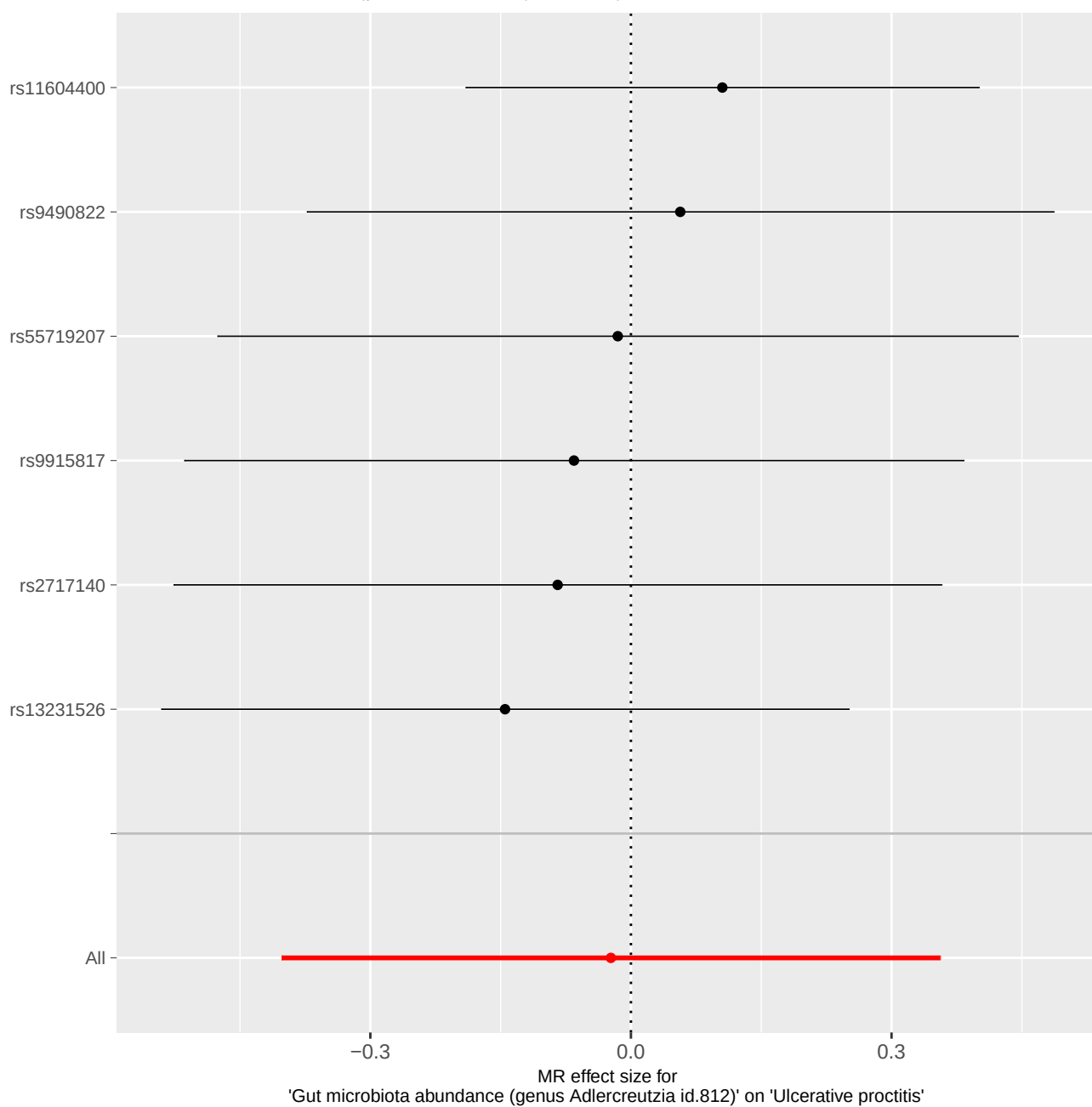


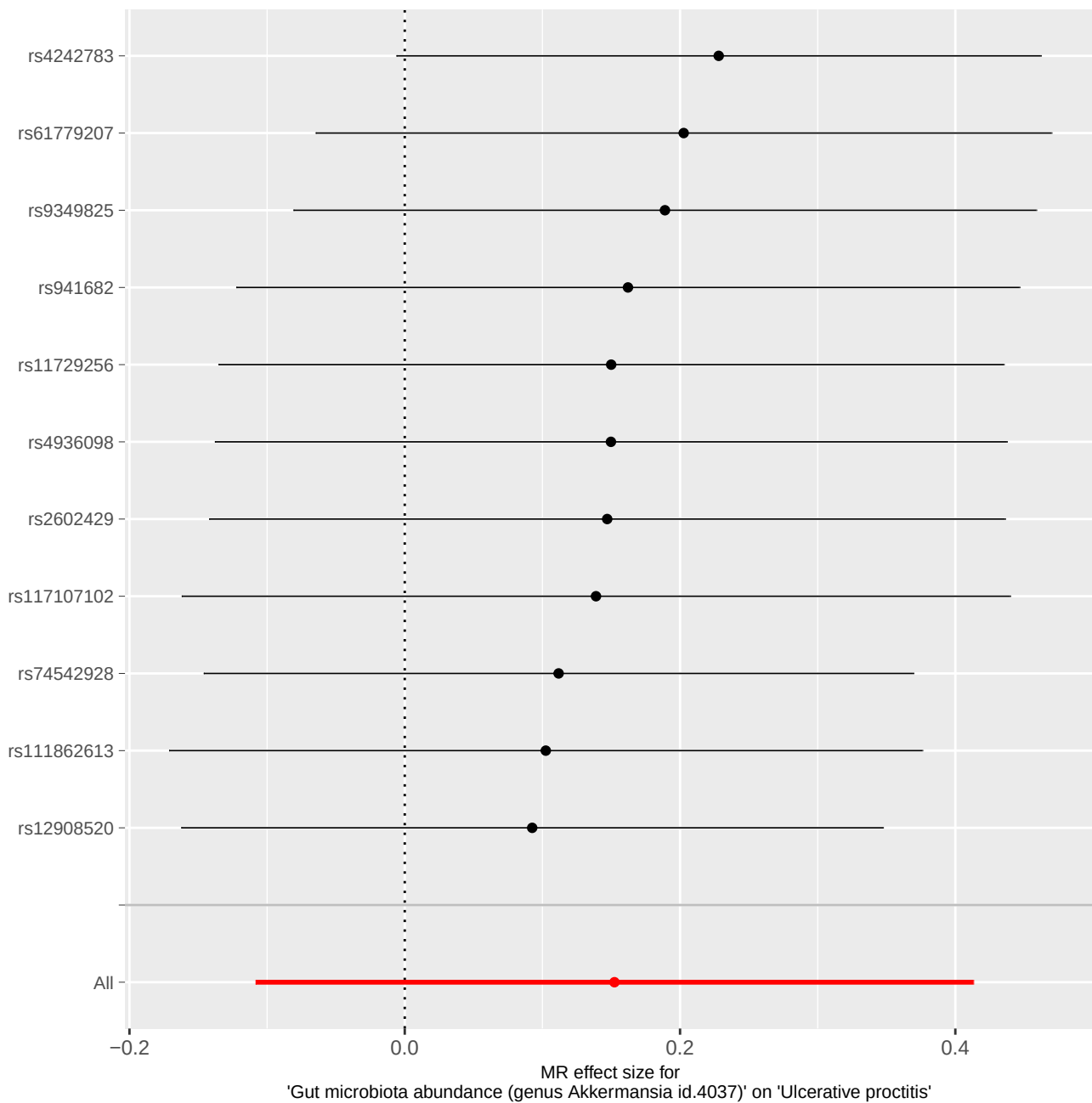


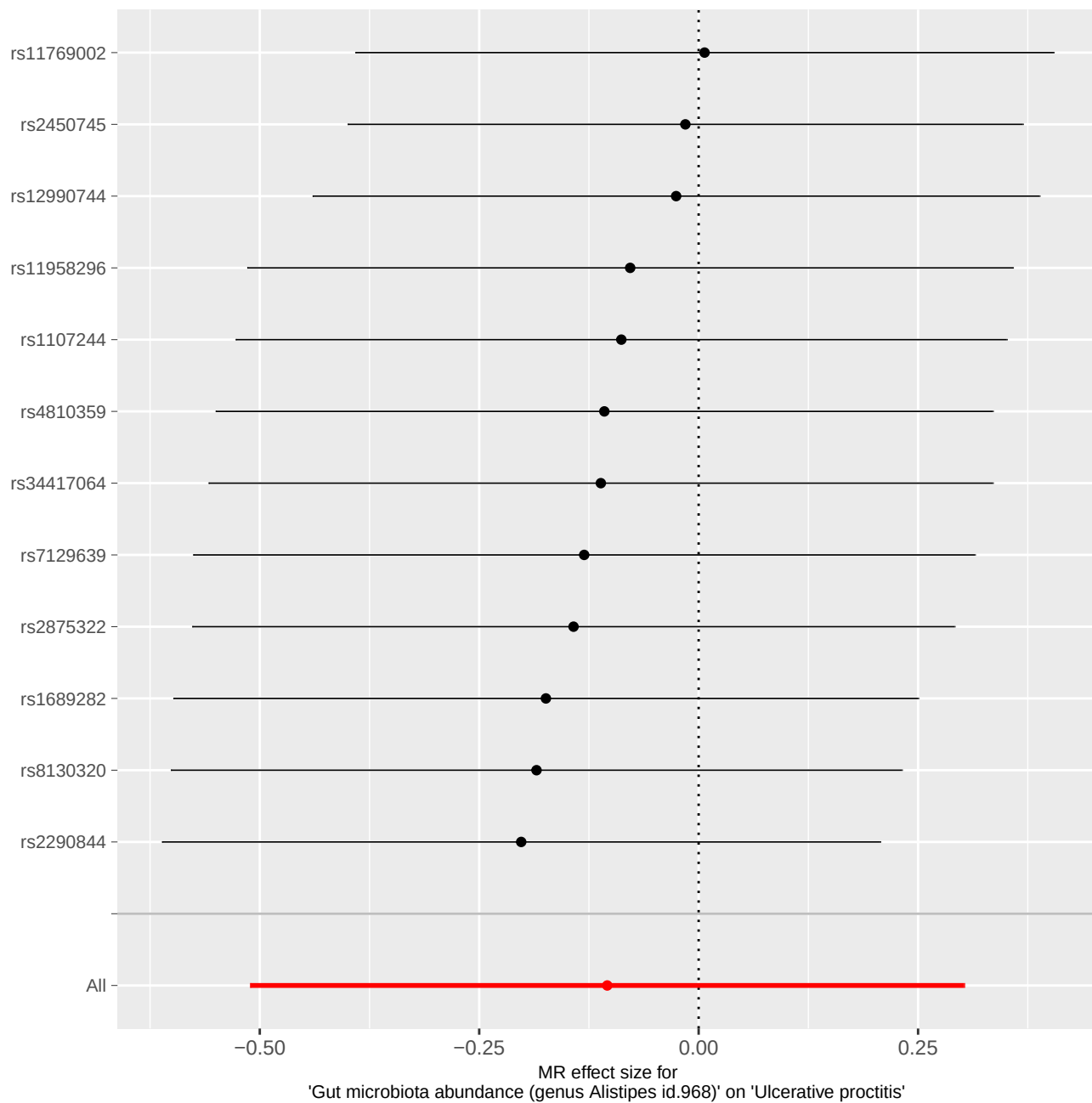




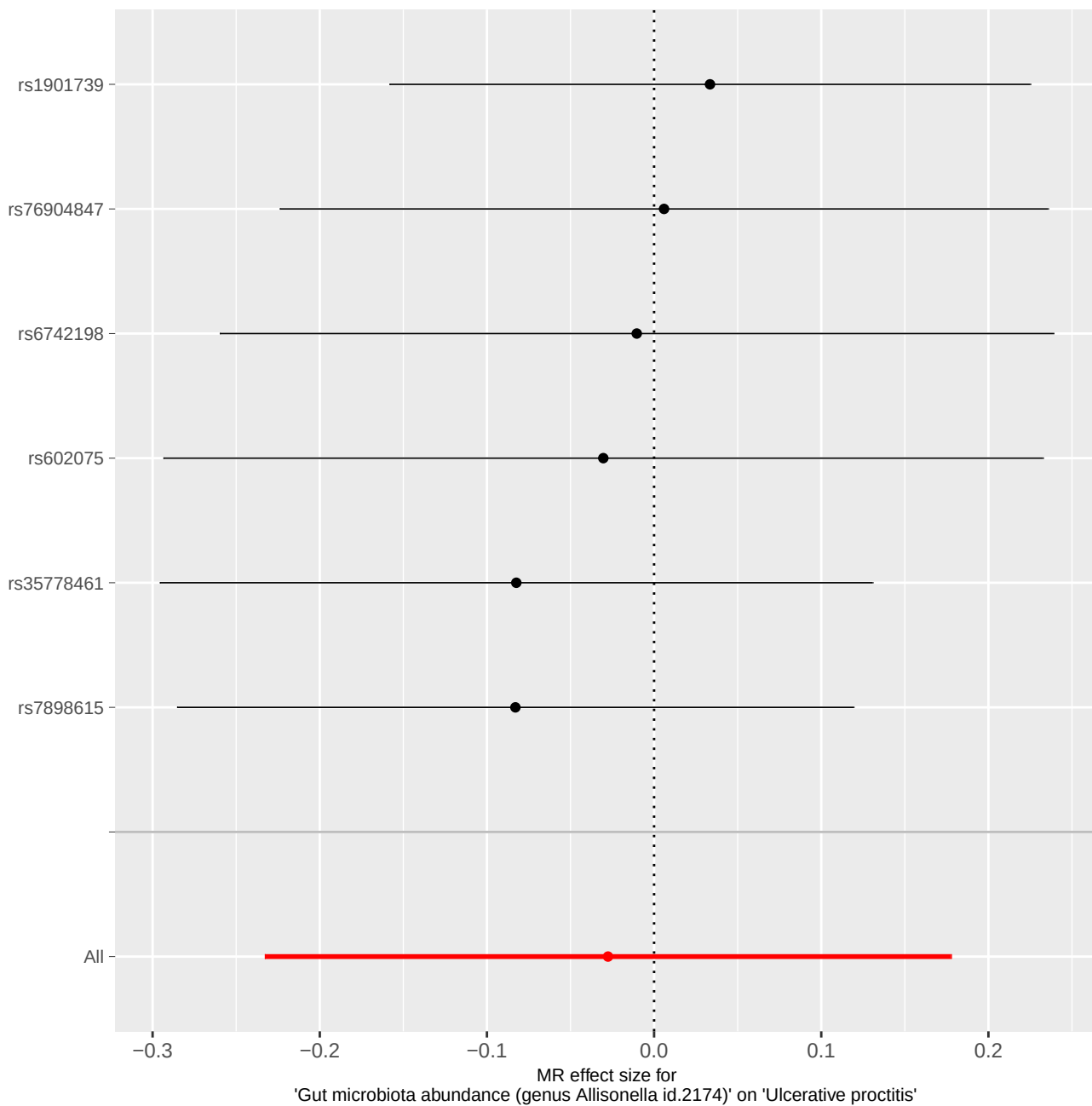


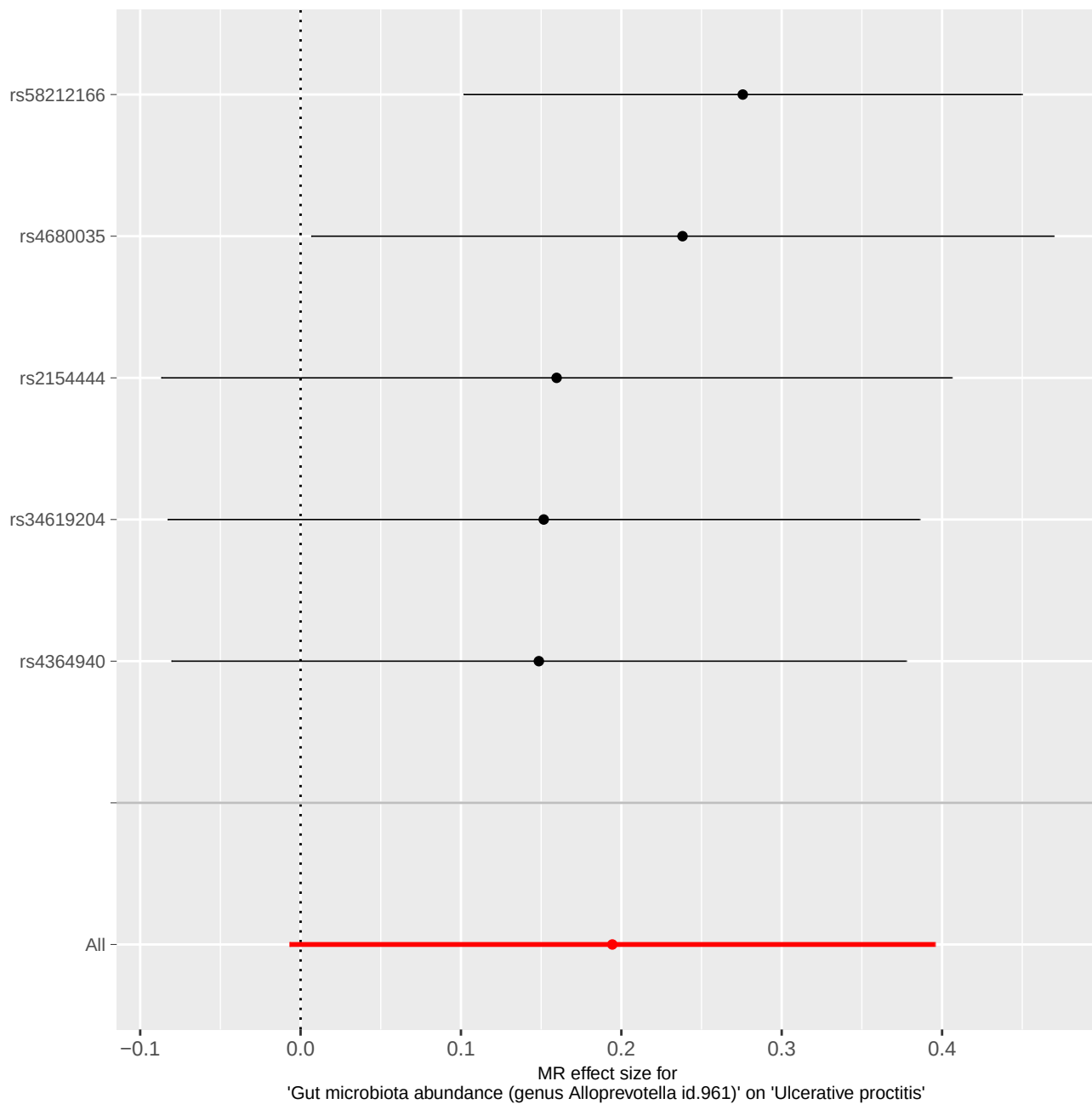


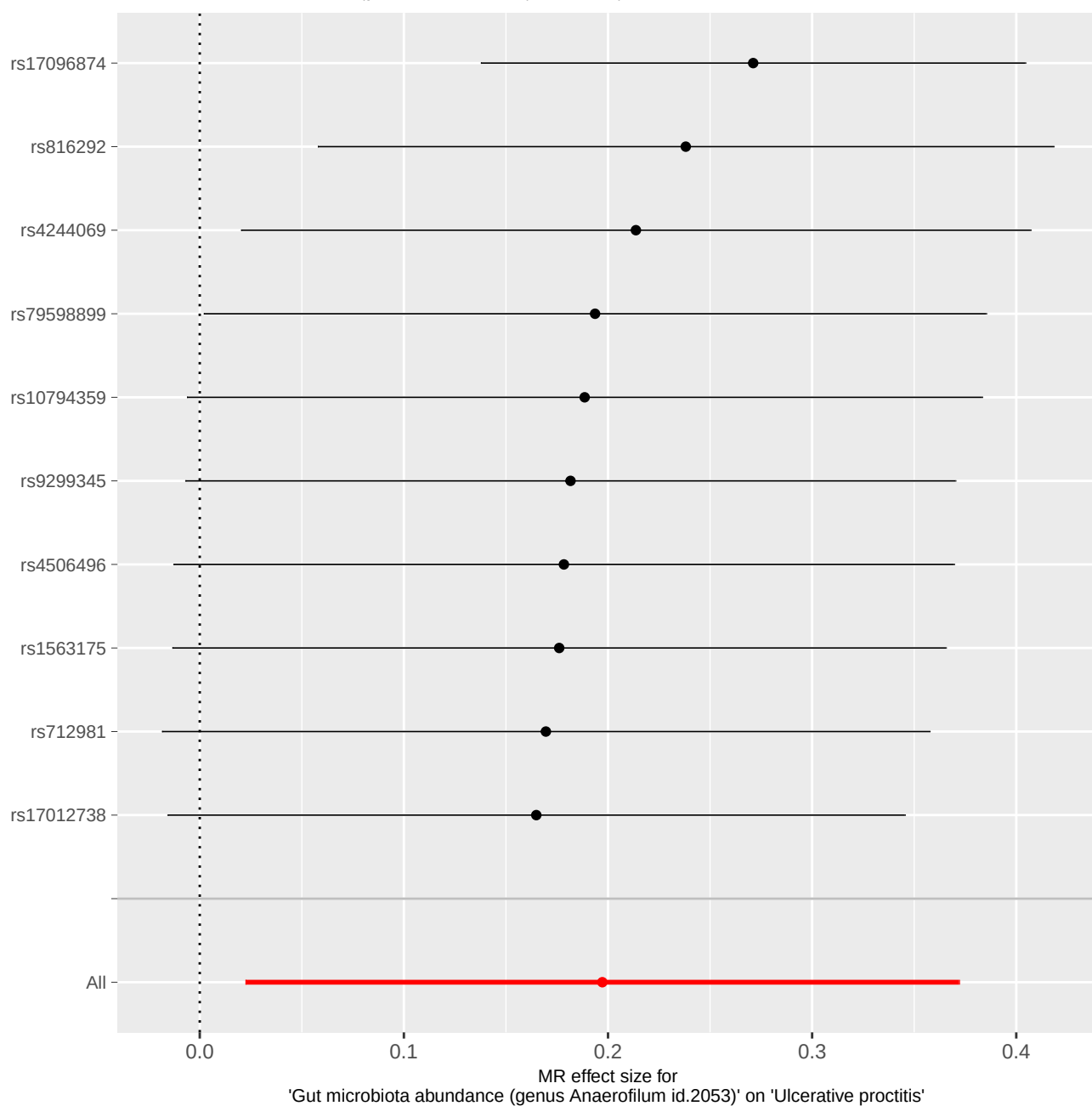




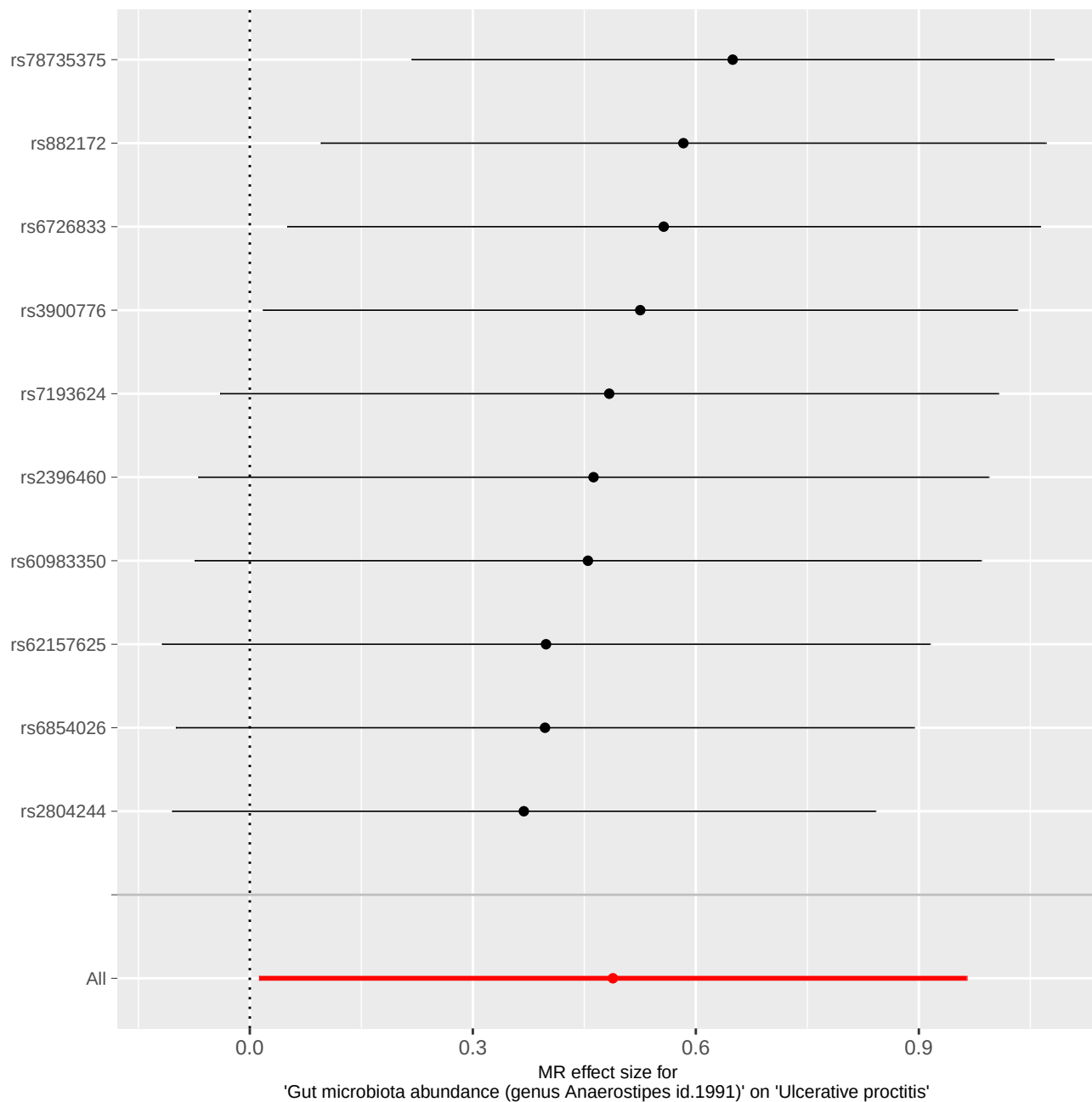
Batch 1387 : Gut microbiota abundance (genus Allisonella id.2174) on Ulcerative proctitis

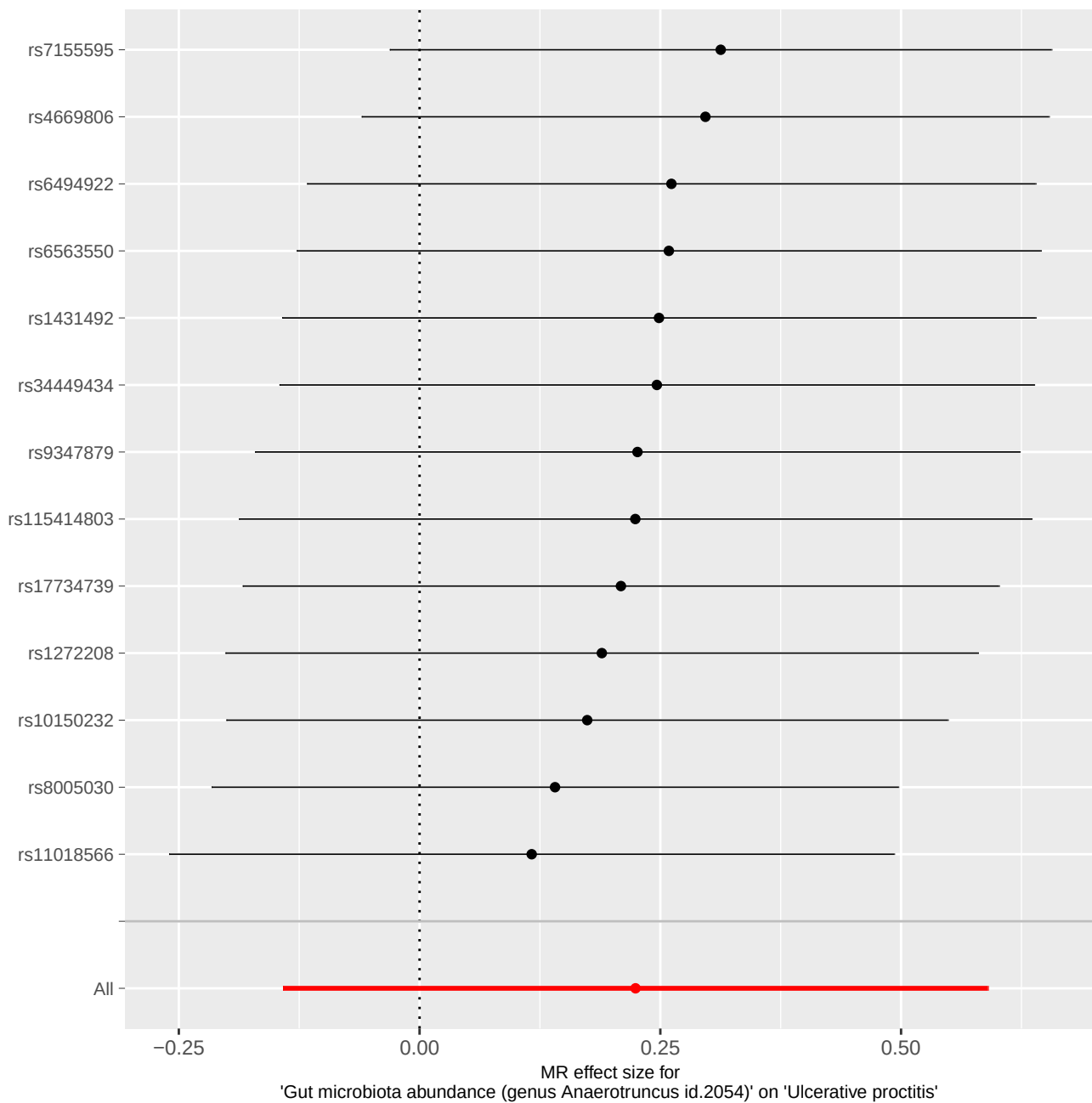


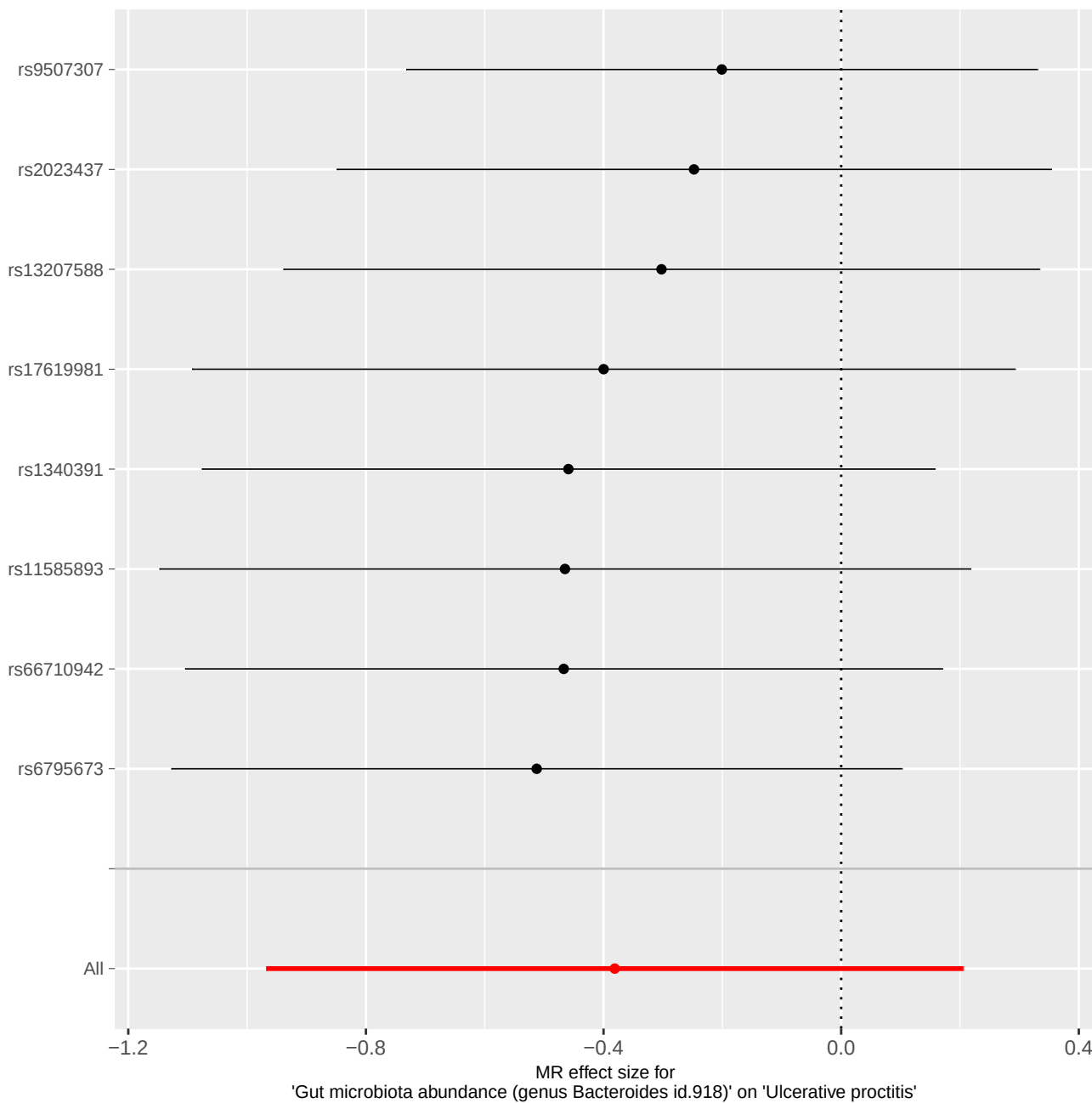




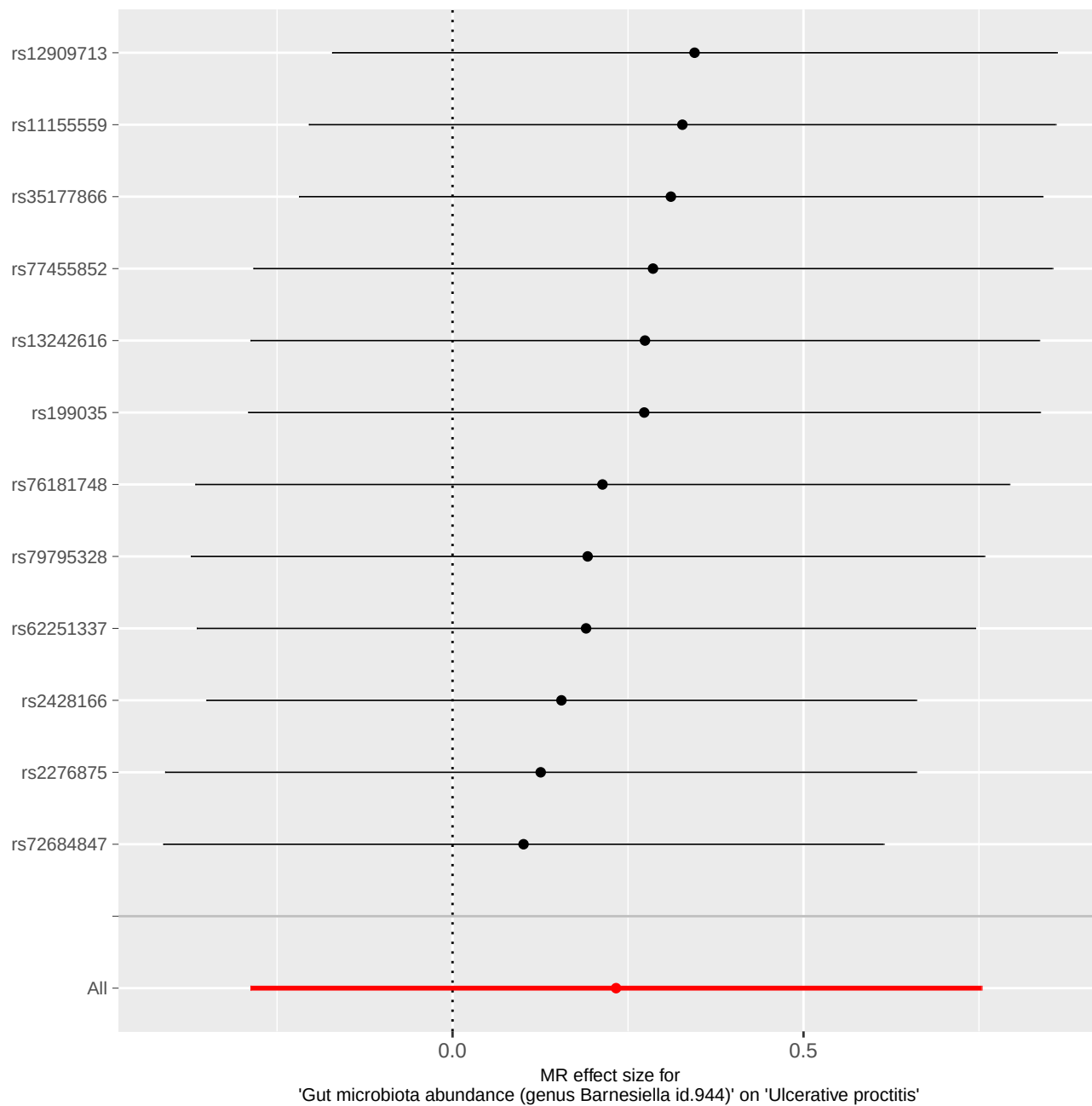
Batch 1390 : Gut microbiota abundance (genus Anaerostipes id.1991) on Ulcerative proctitis

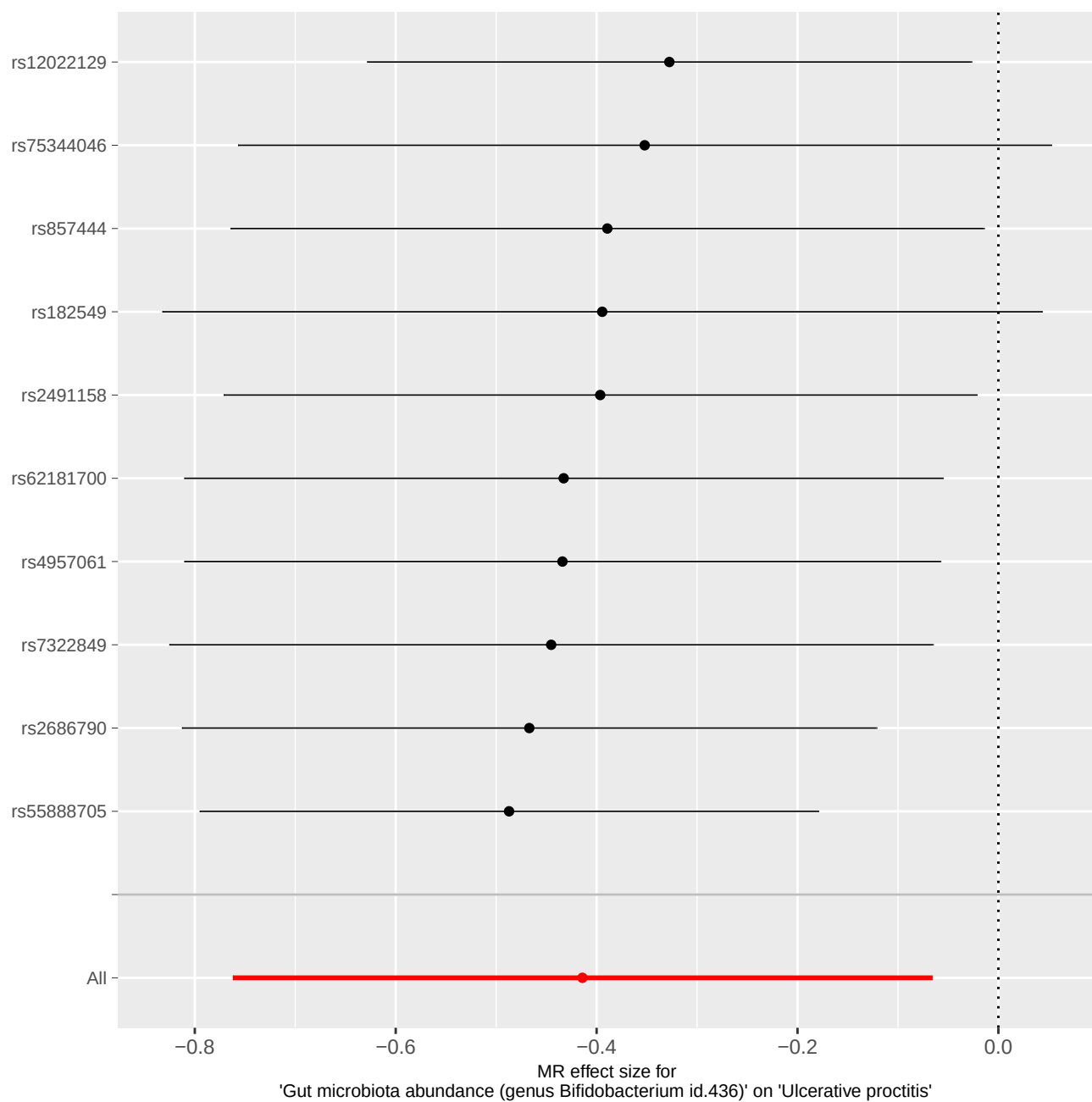


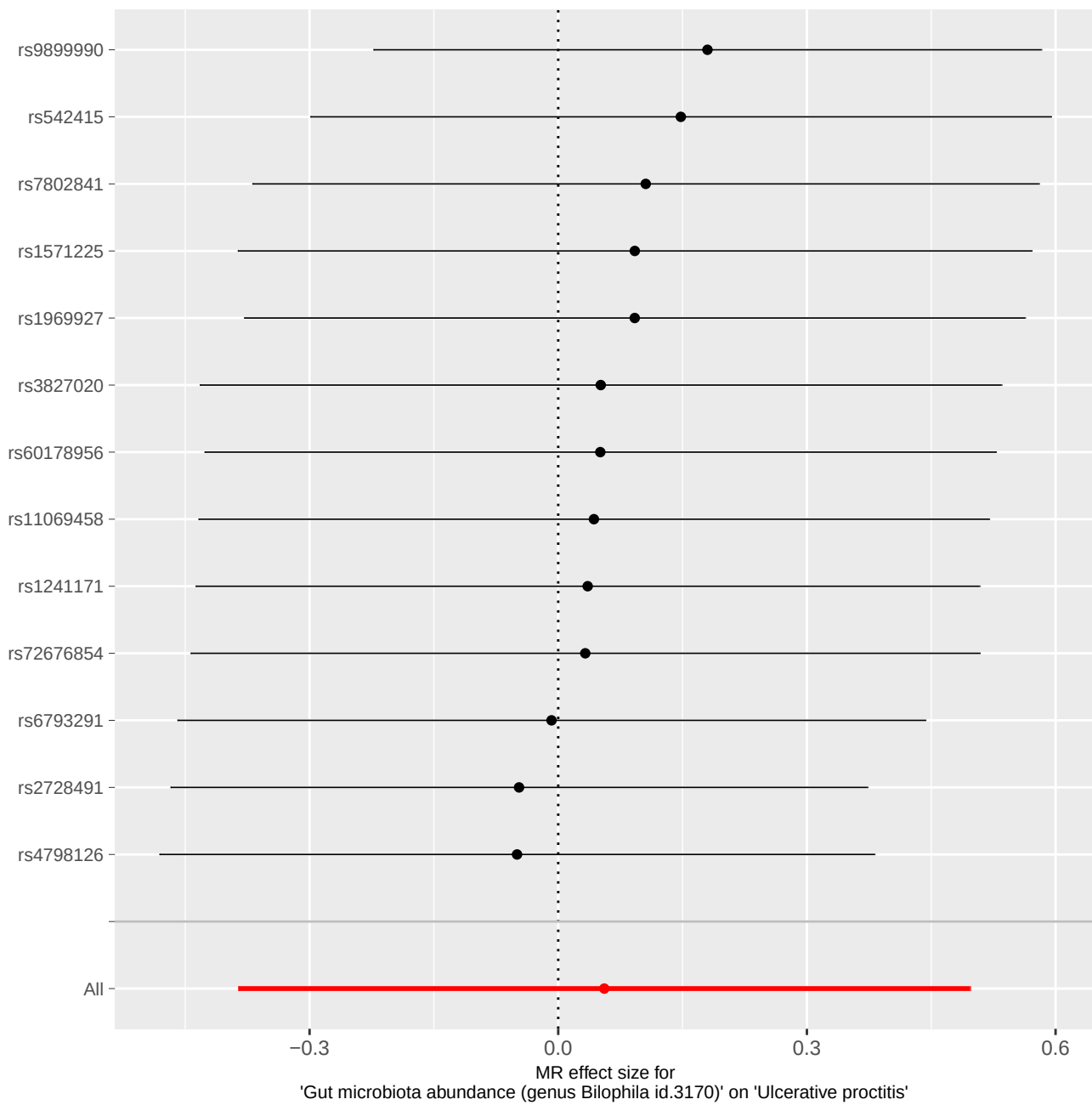


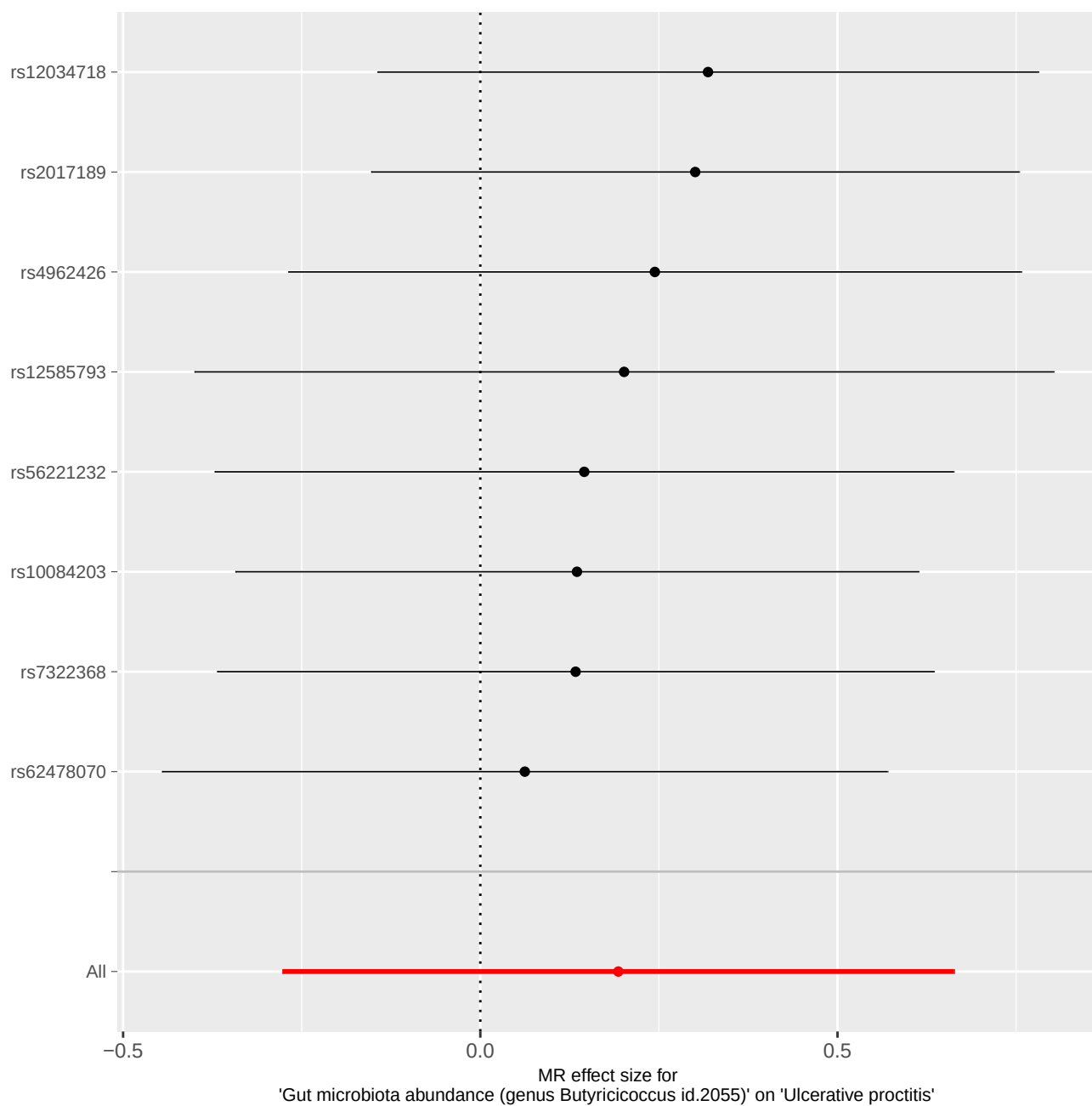


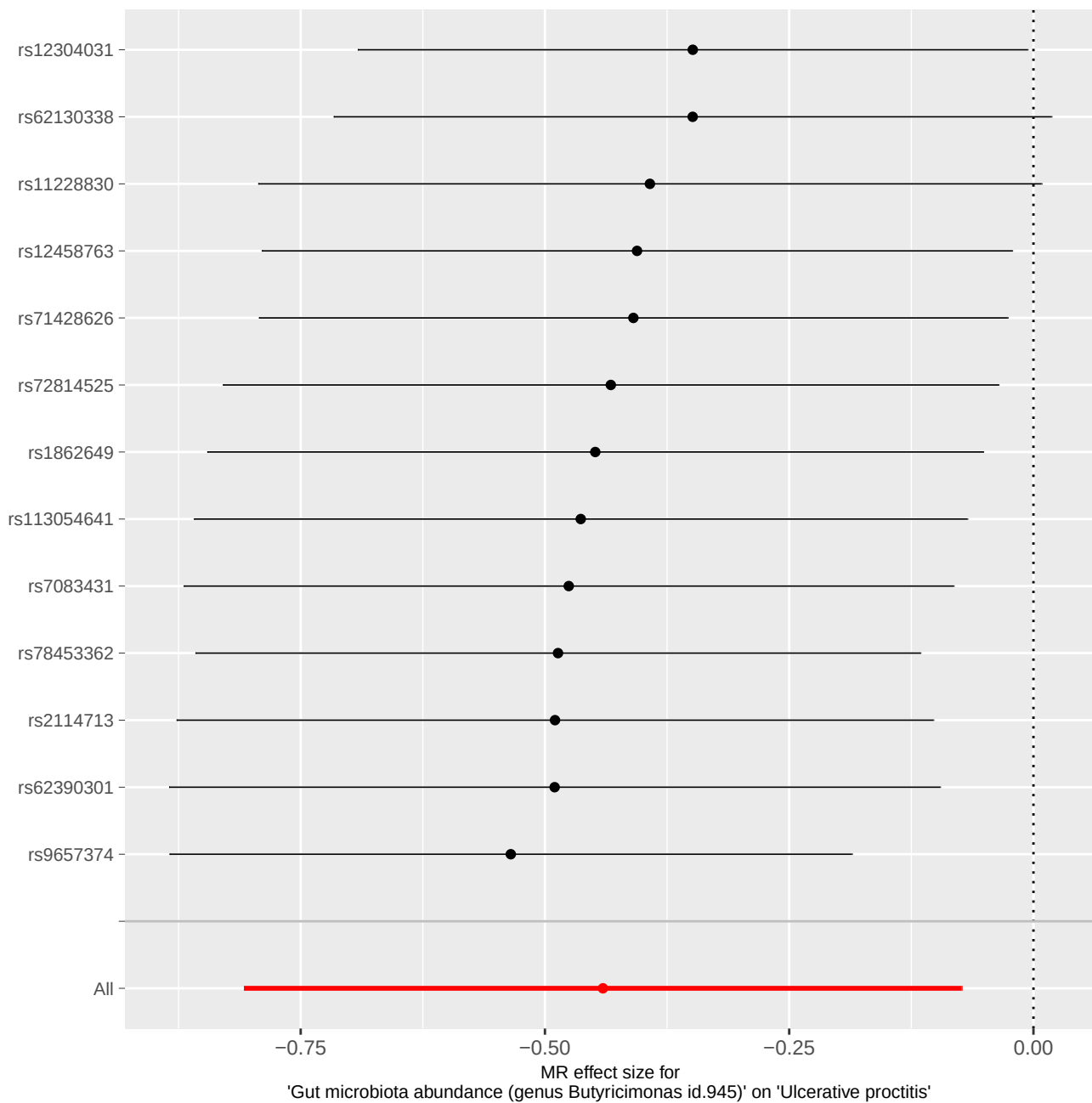
Batch 1393 : Gut microbiota abundance (genus *Barnesiella* id.944) on Ulcerative proctitis

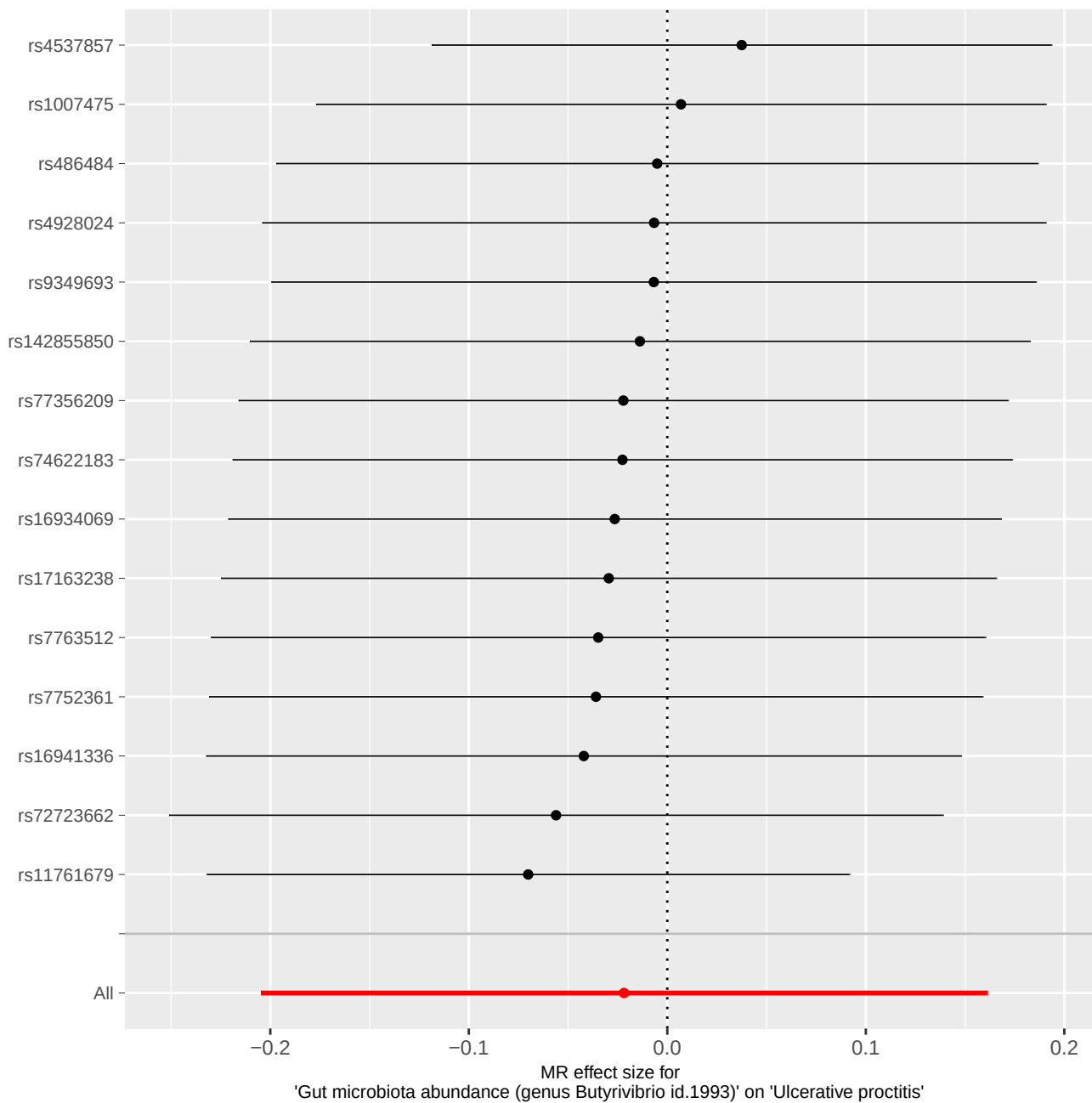


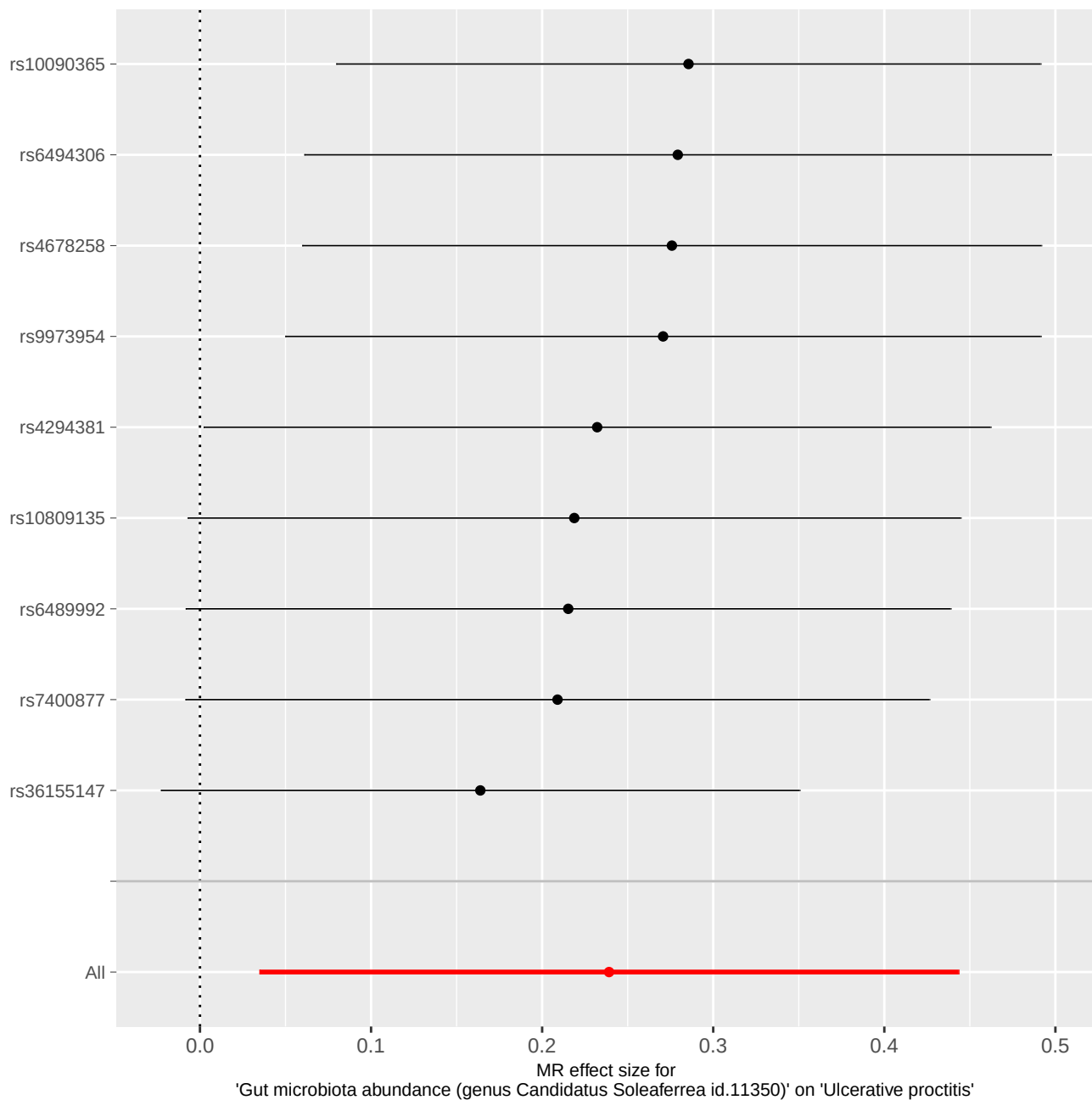


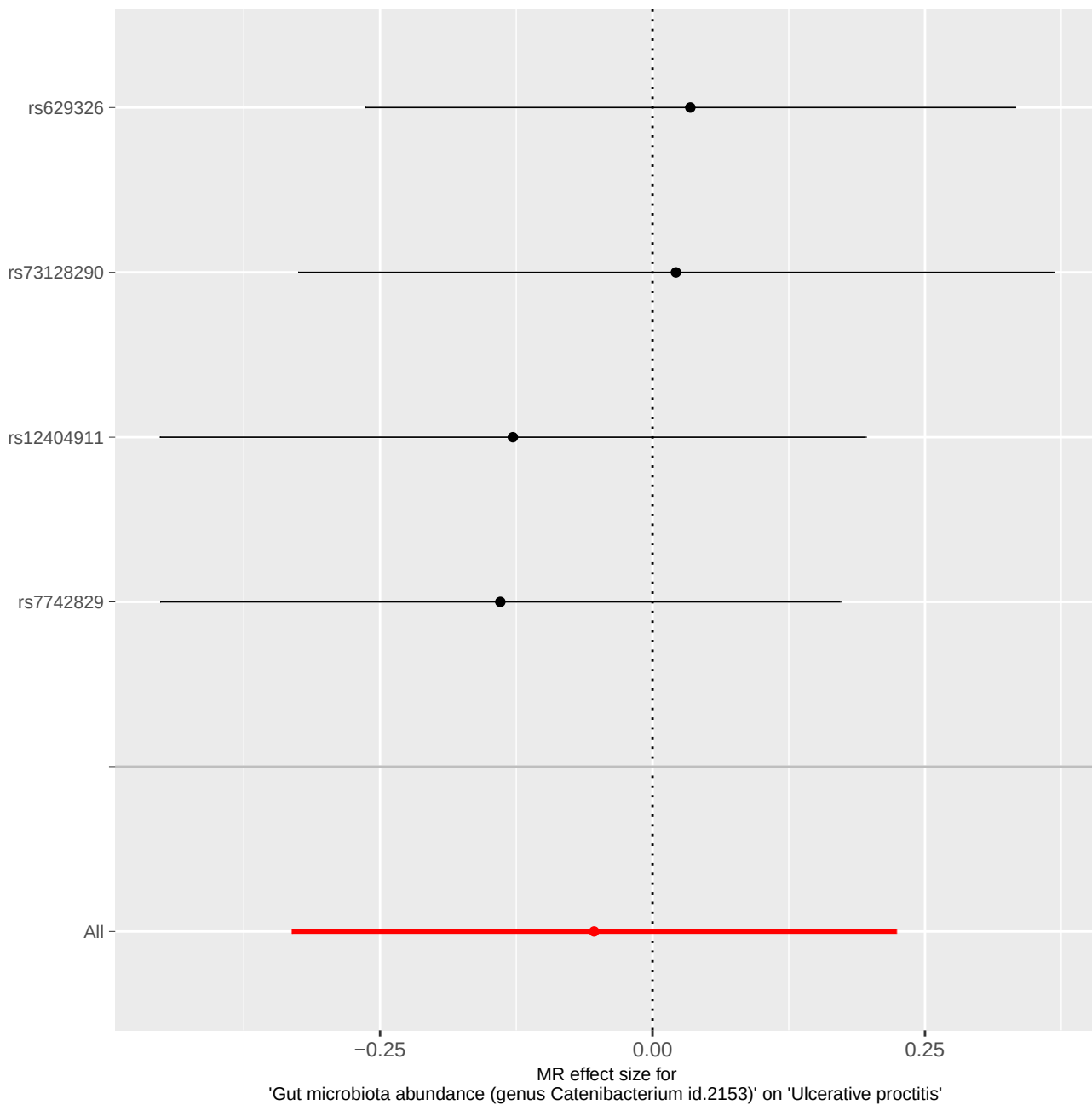


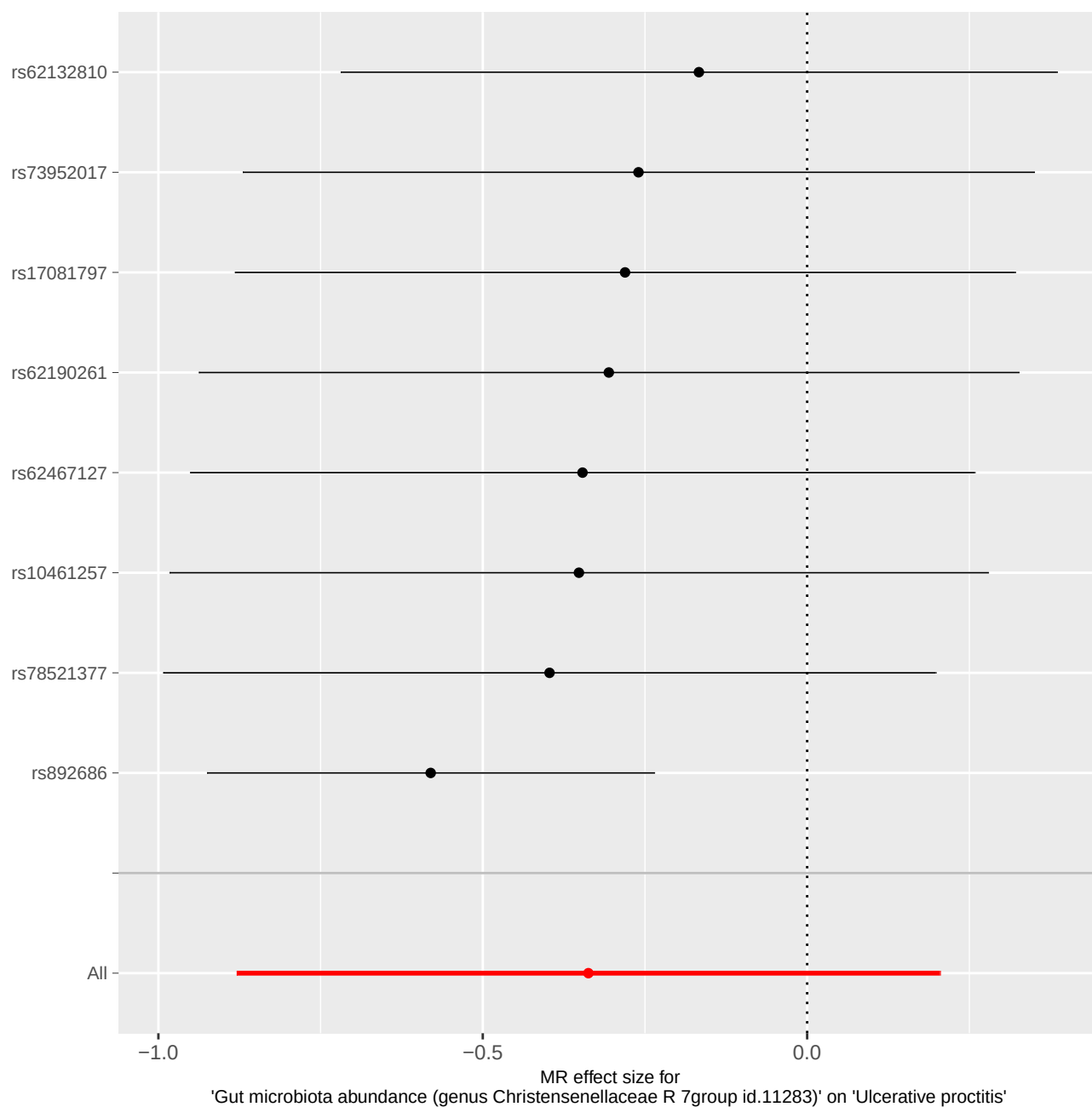




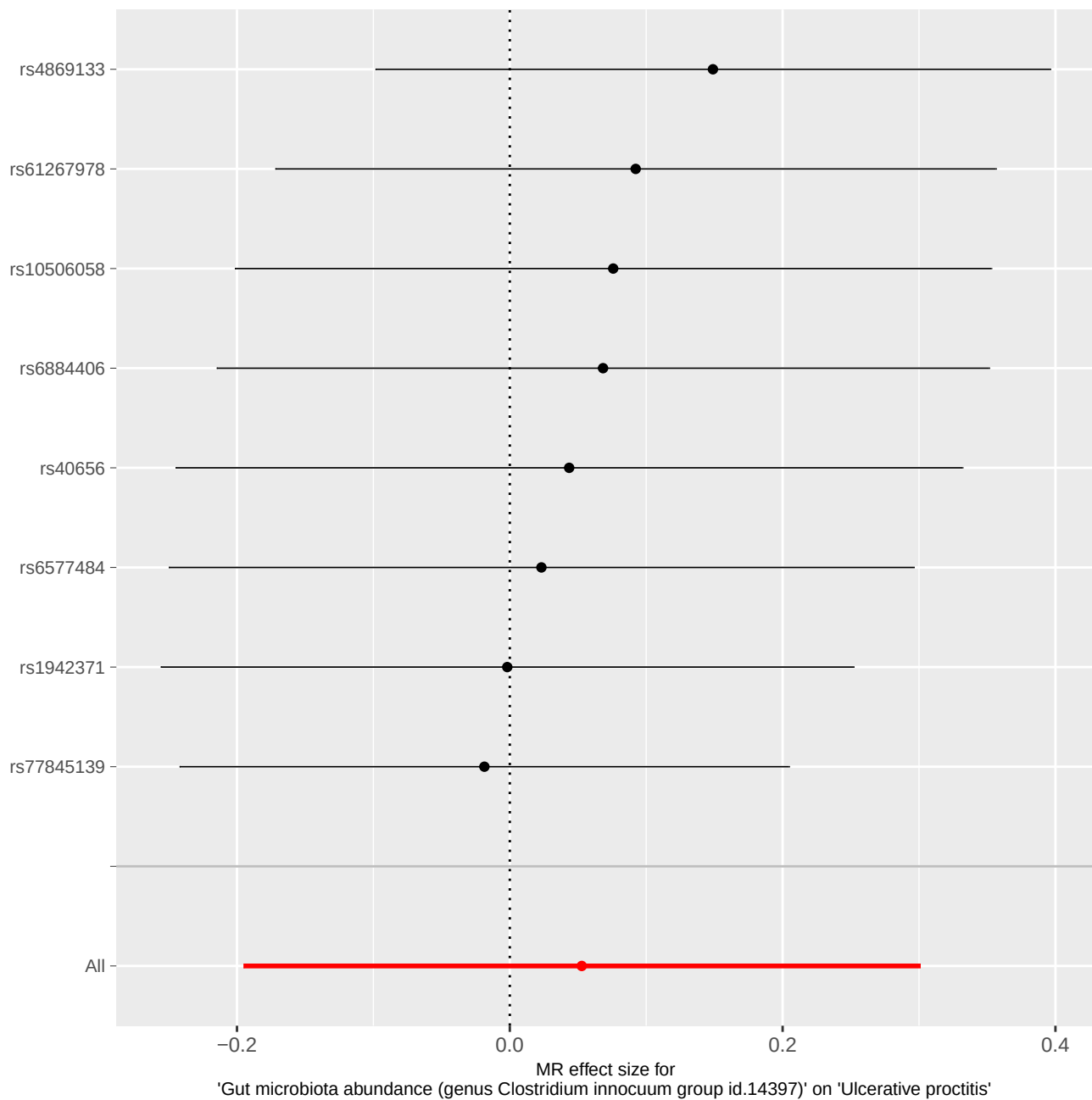


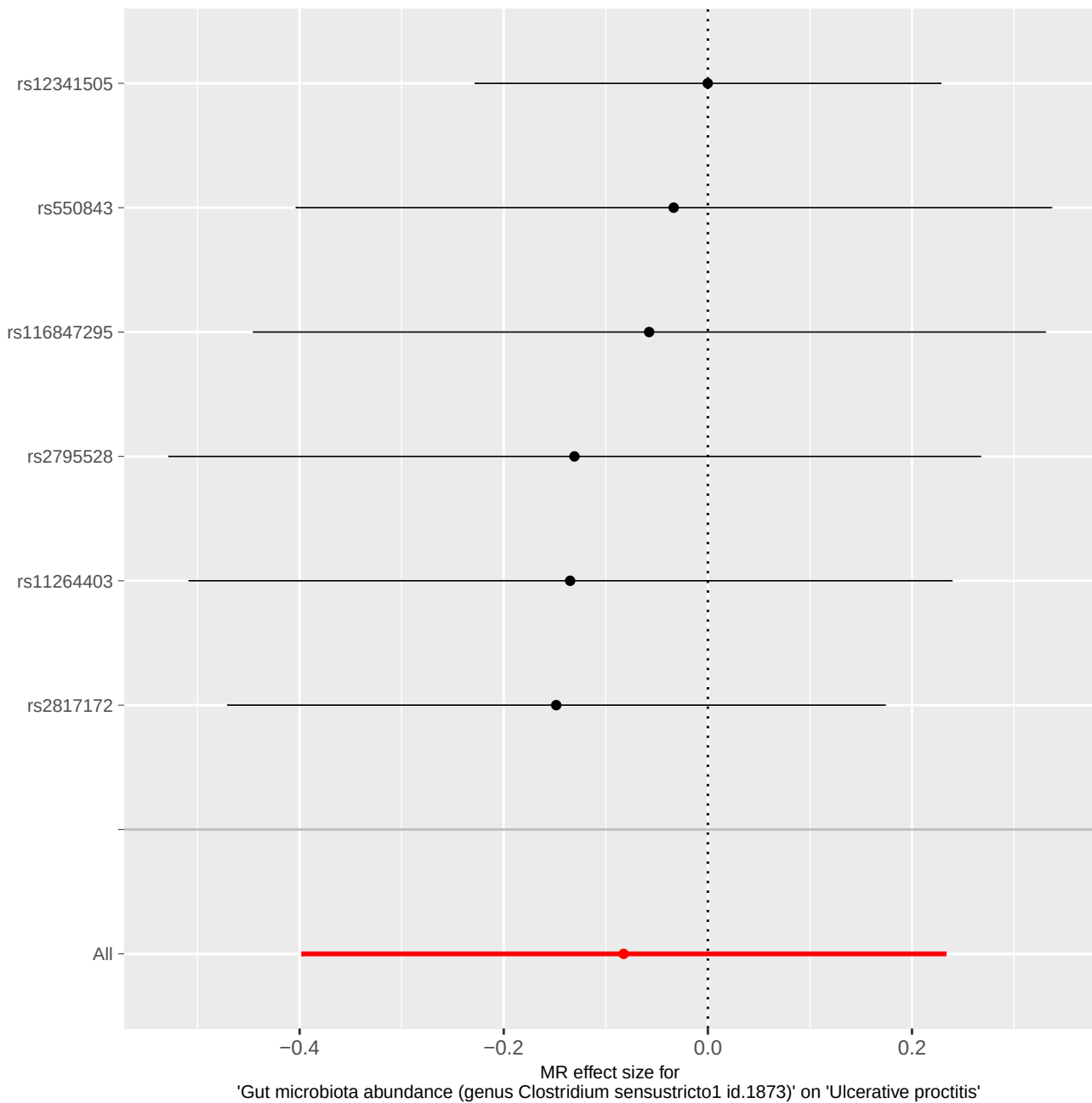


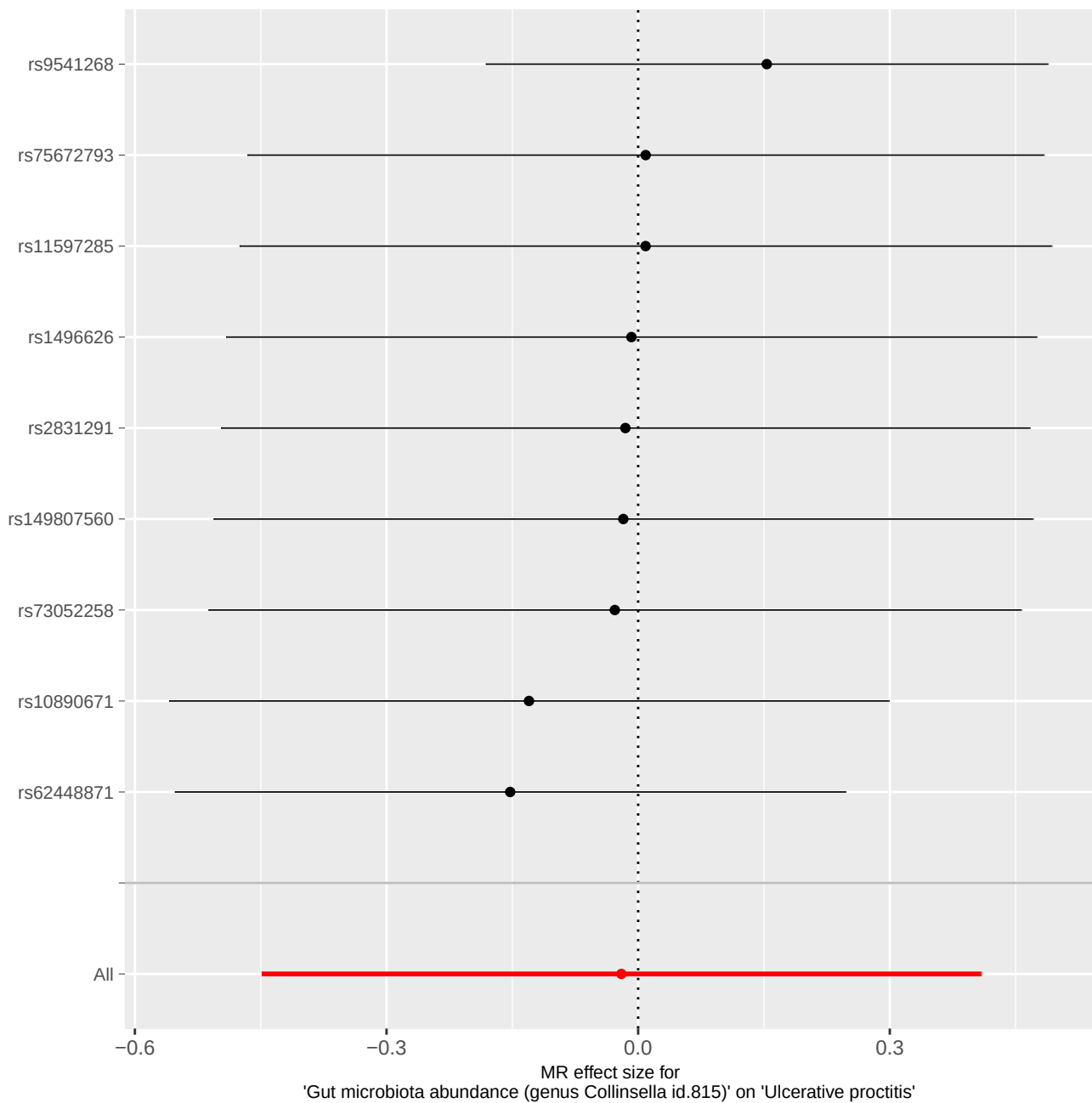


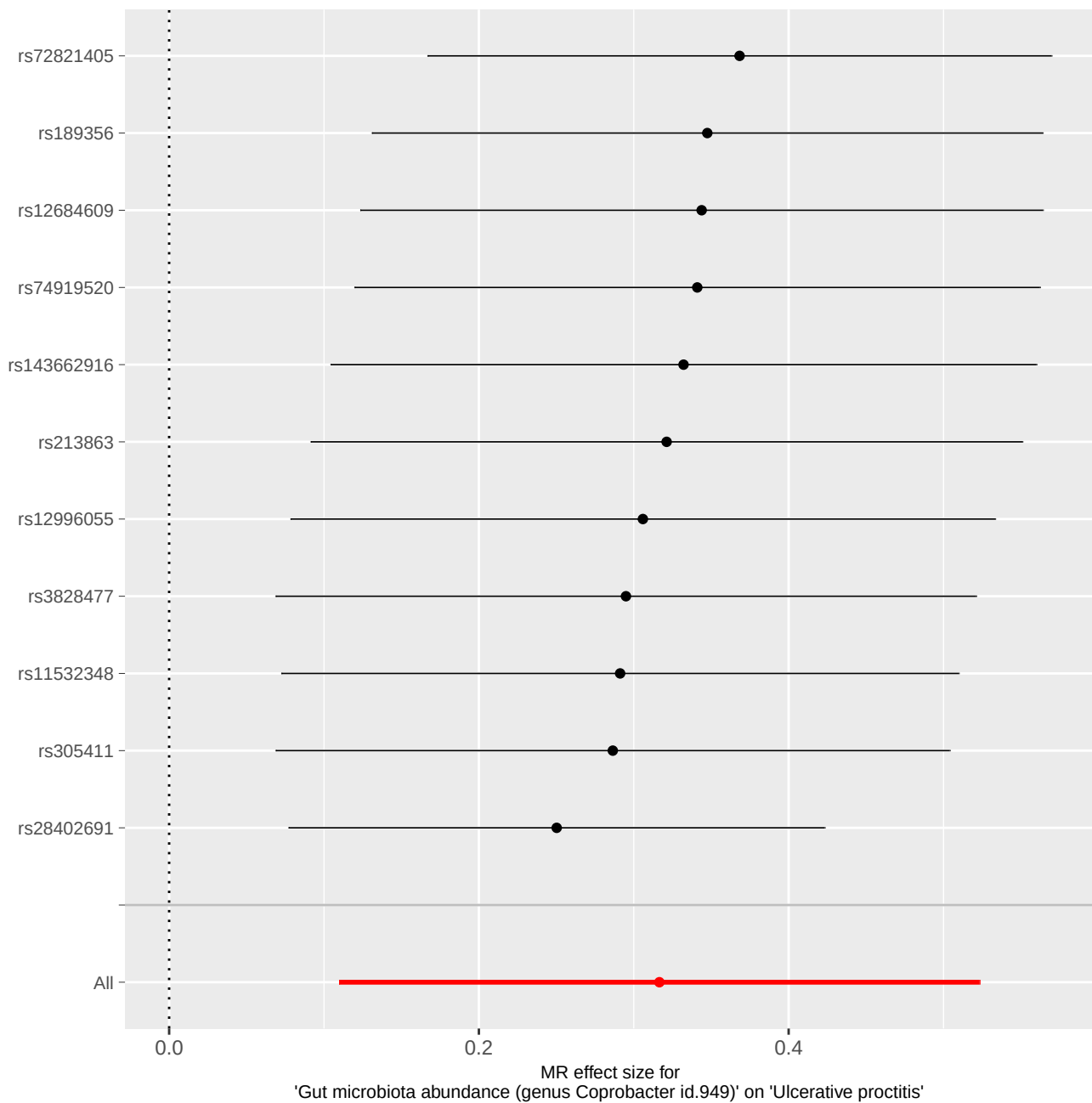


Batch 1403 : Gut microbiota abundance (genus Clostridium innocuum group id.14397) on Ulcerative proctitis

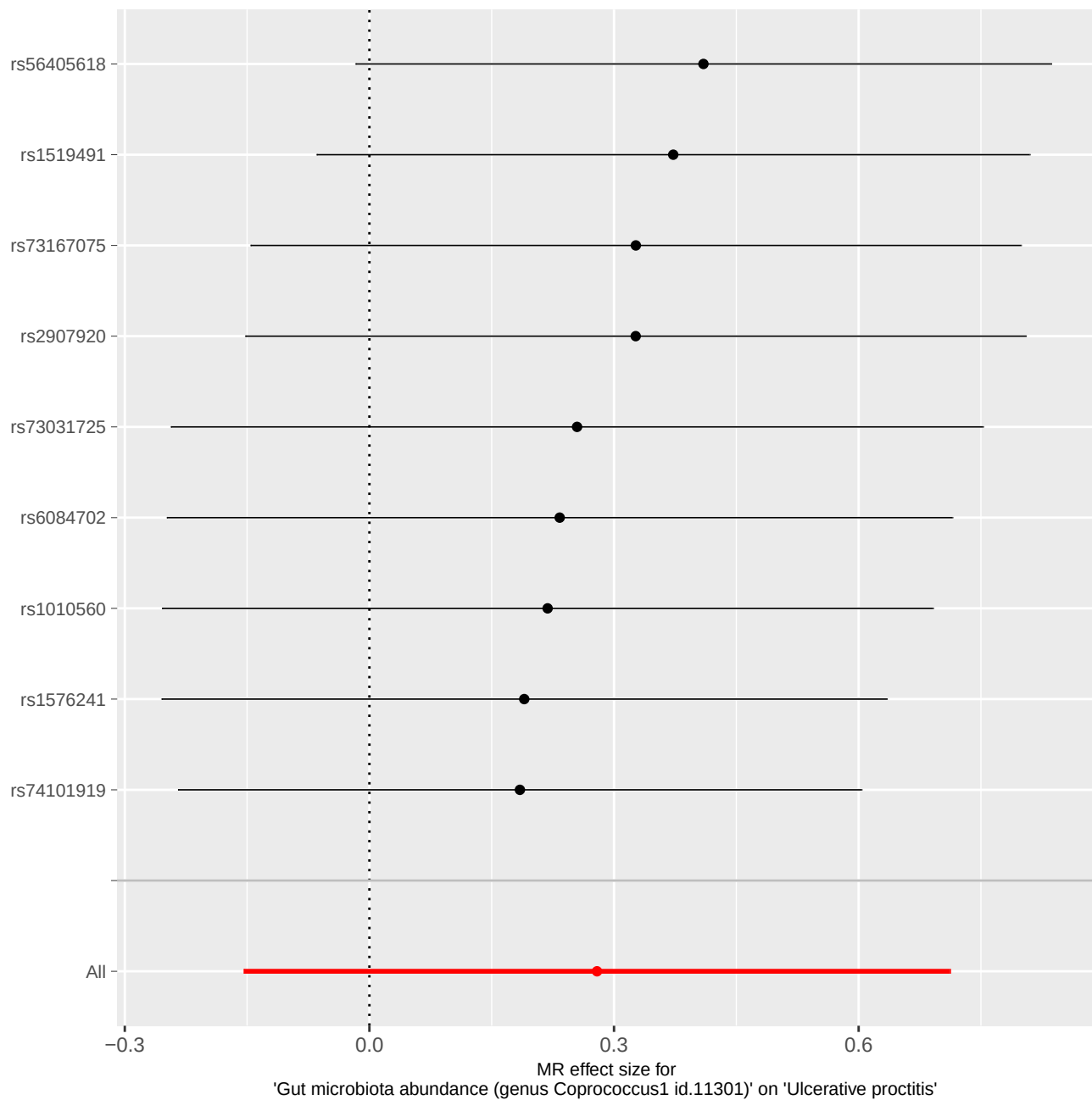


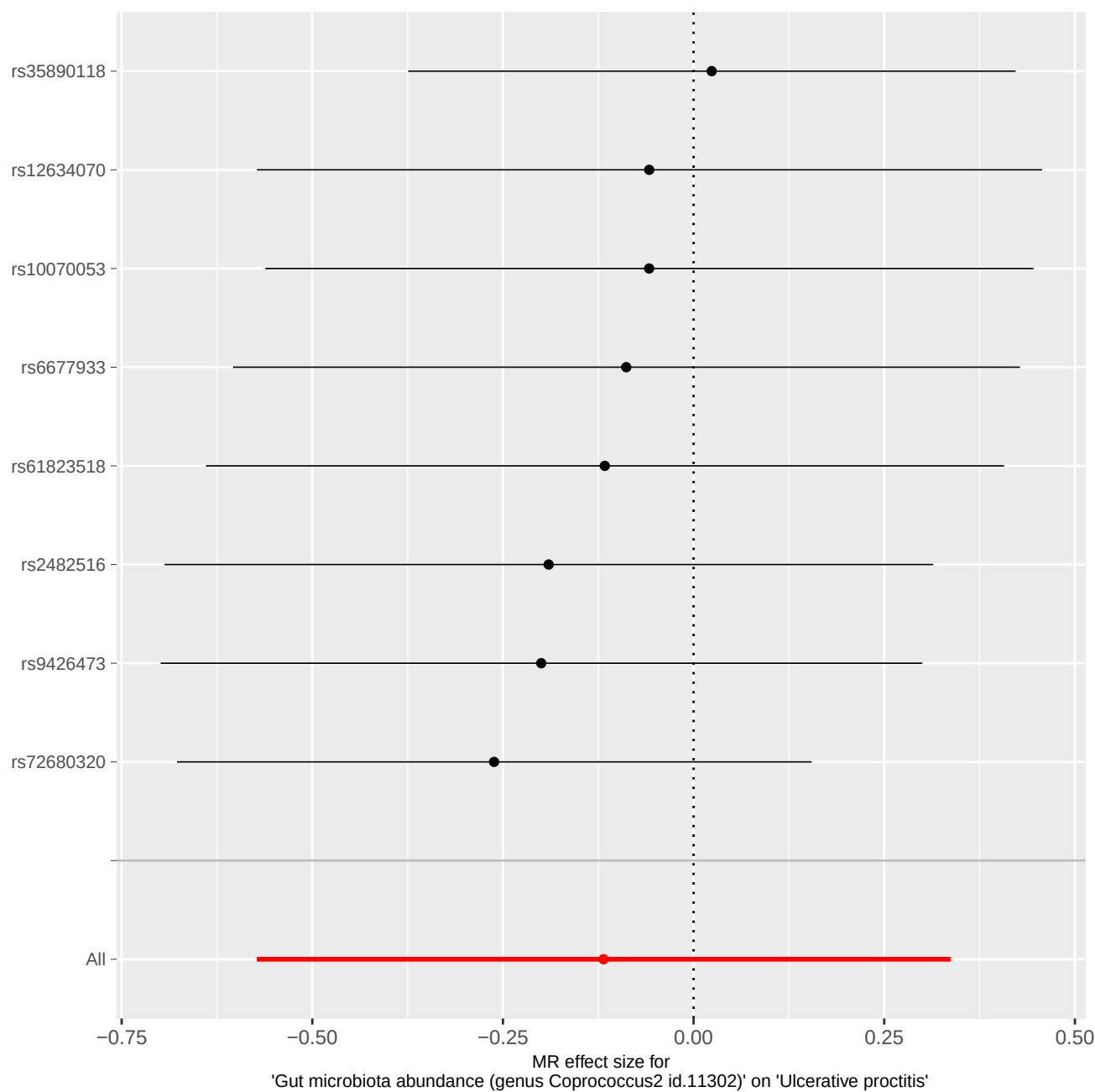




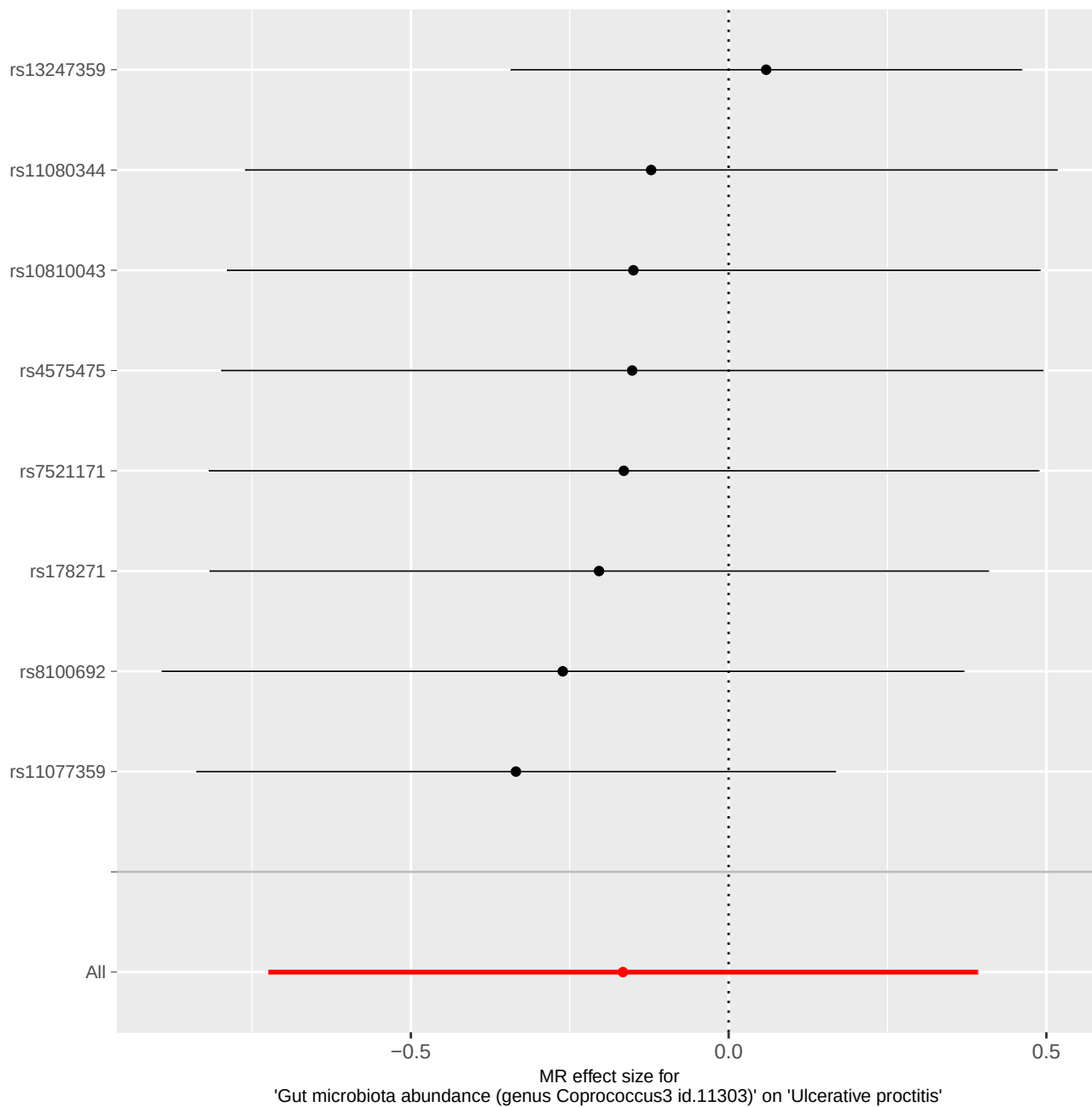


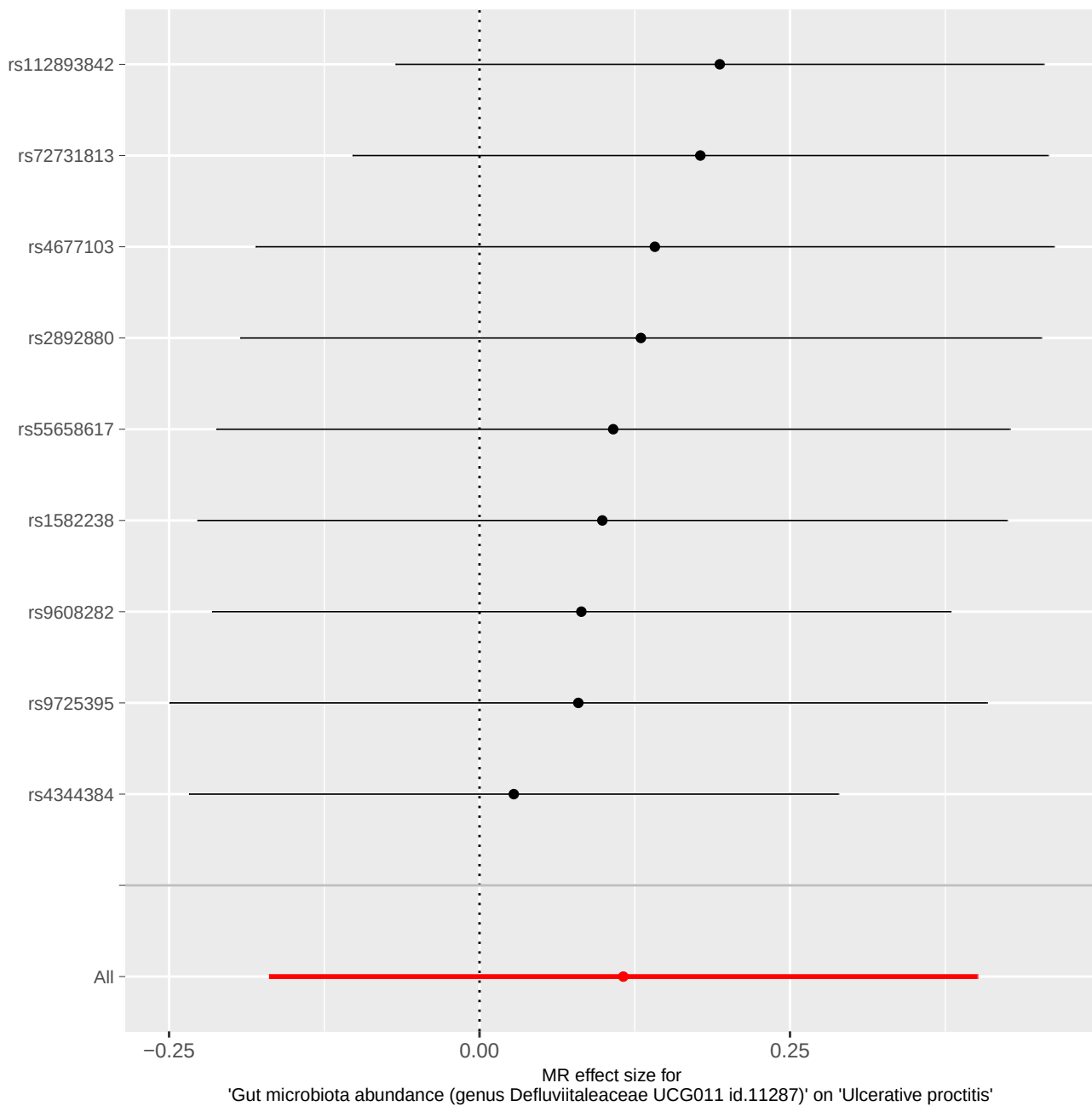
Batch 1407 : Gut microbiota abundance (genus Coprococcus1 id.11301) on Ulcerative proctitis

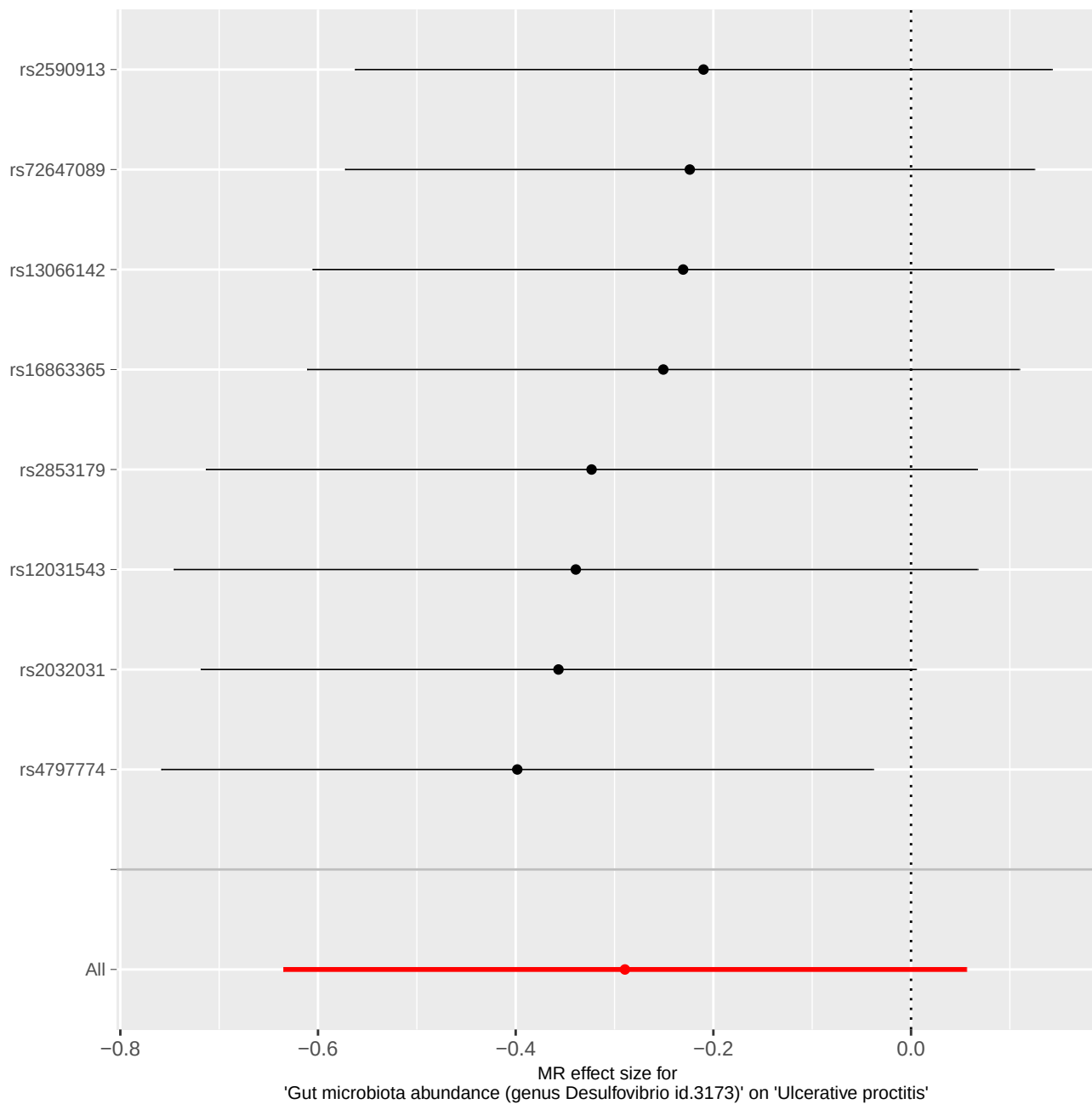


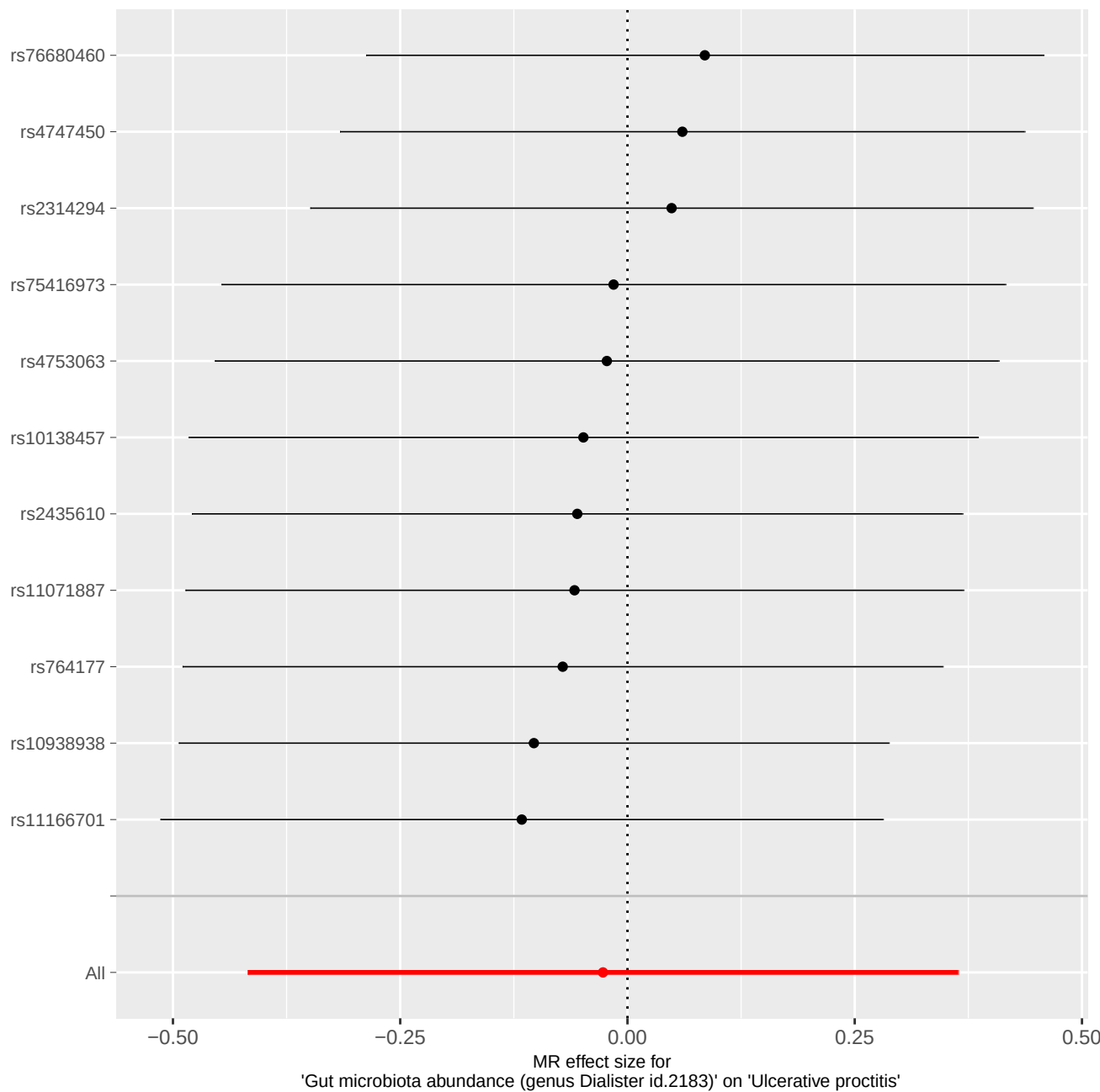


MR effect size for
'Gut microbiota abundance (genus Coprococcus2 id.11302)' on 'Ulcerative proctitis'

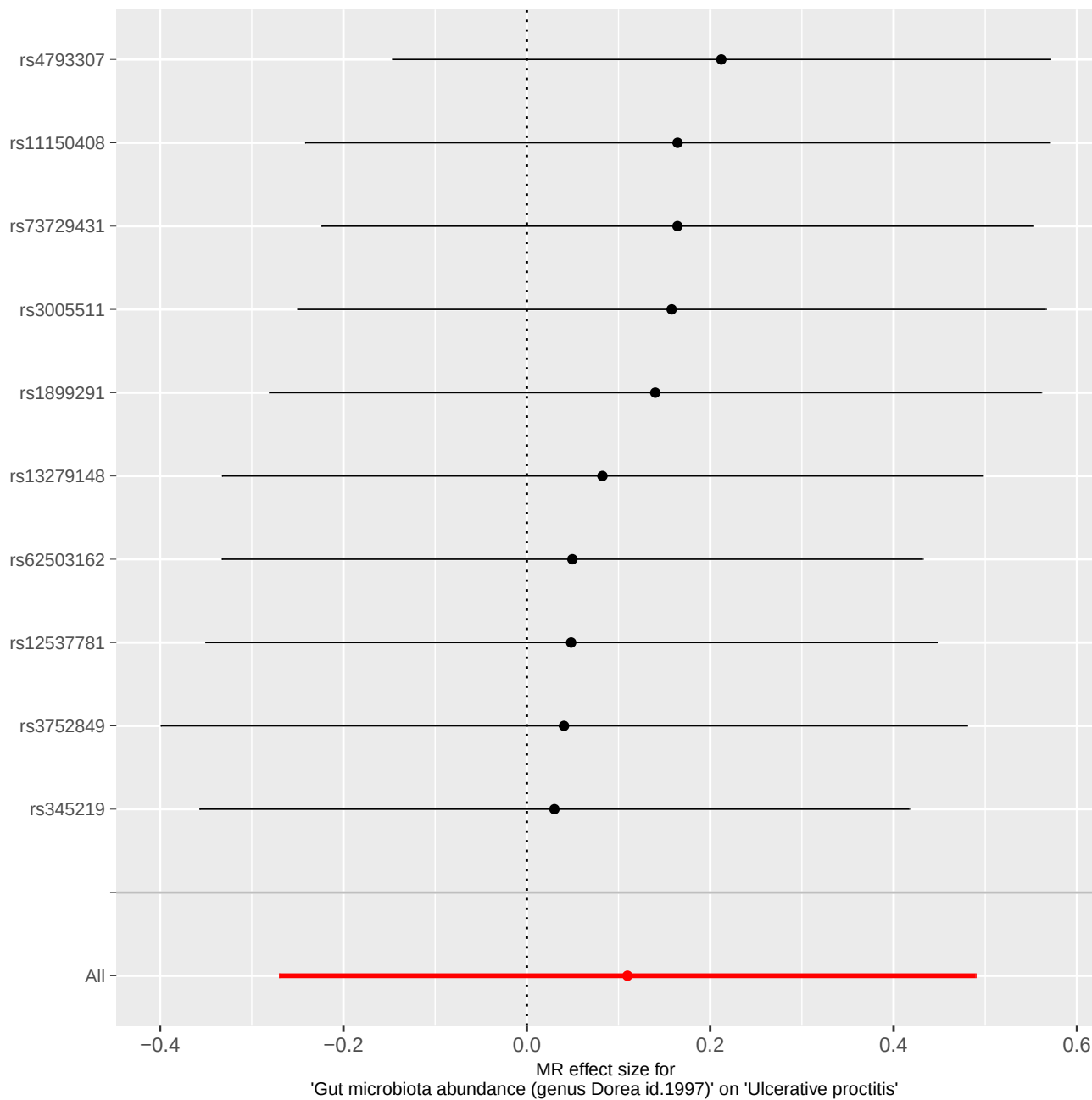




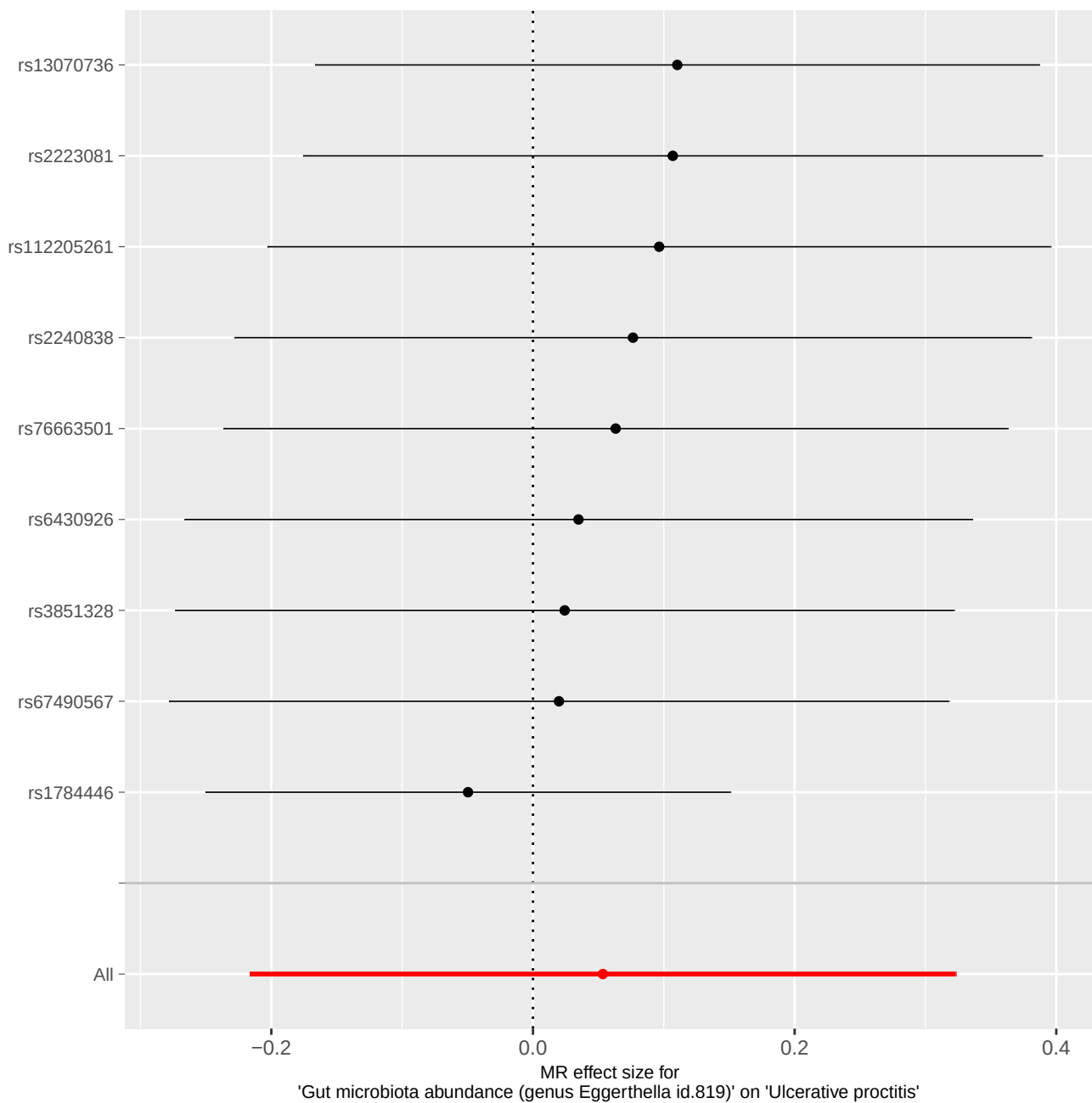




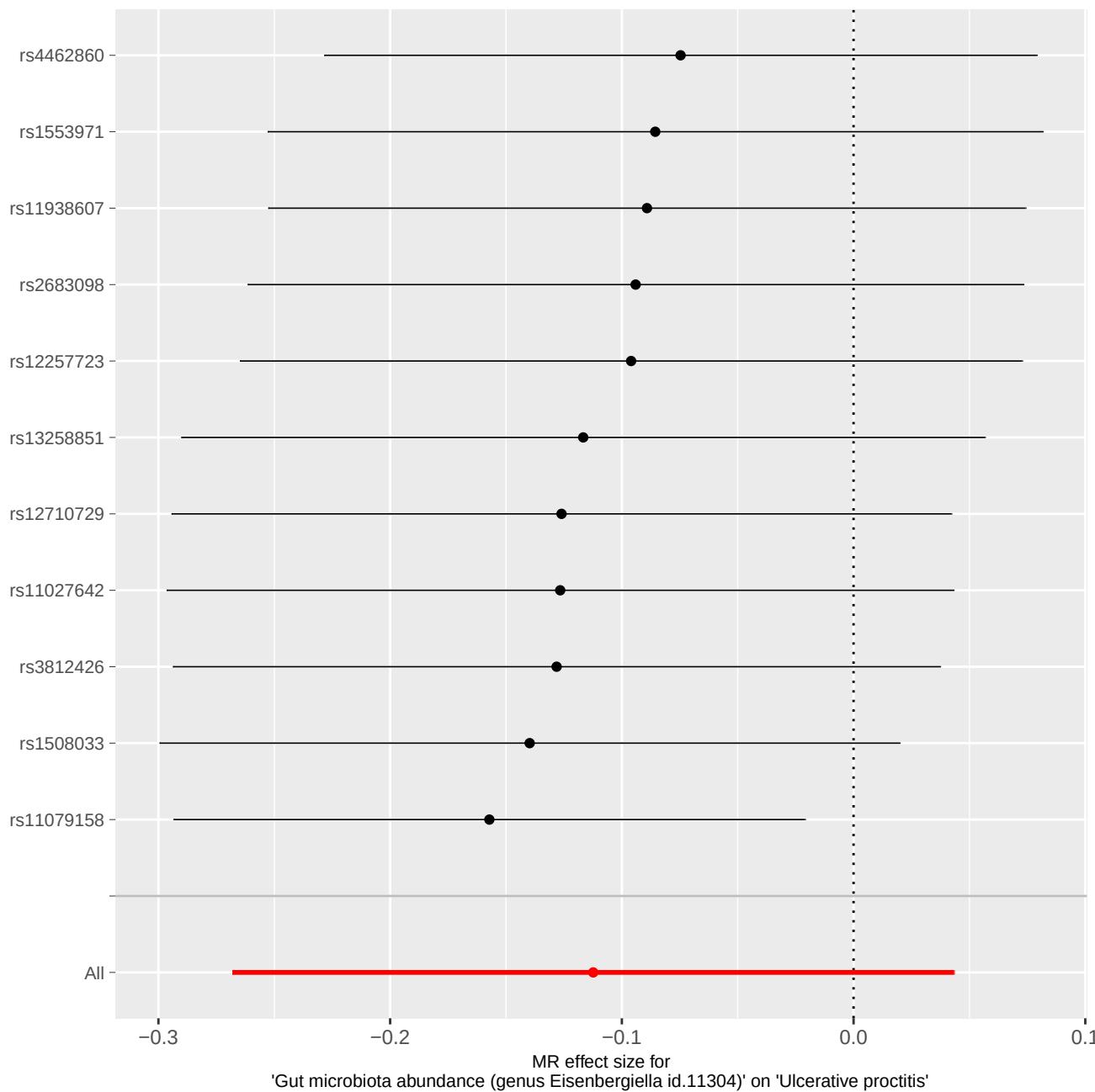
Batch 1413 : Gut microbiota abundance (genus Dorea id.1997) on Ulcerative proctitis

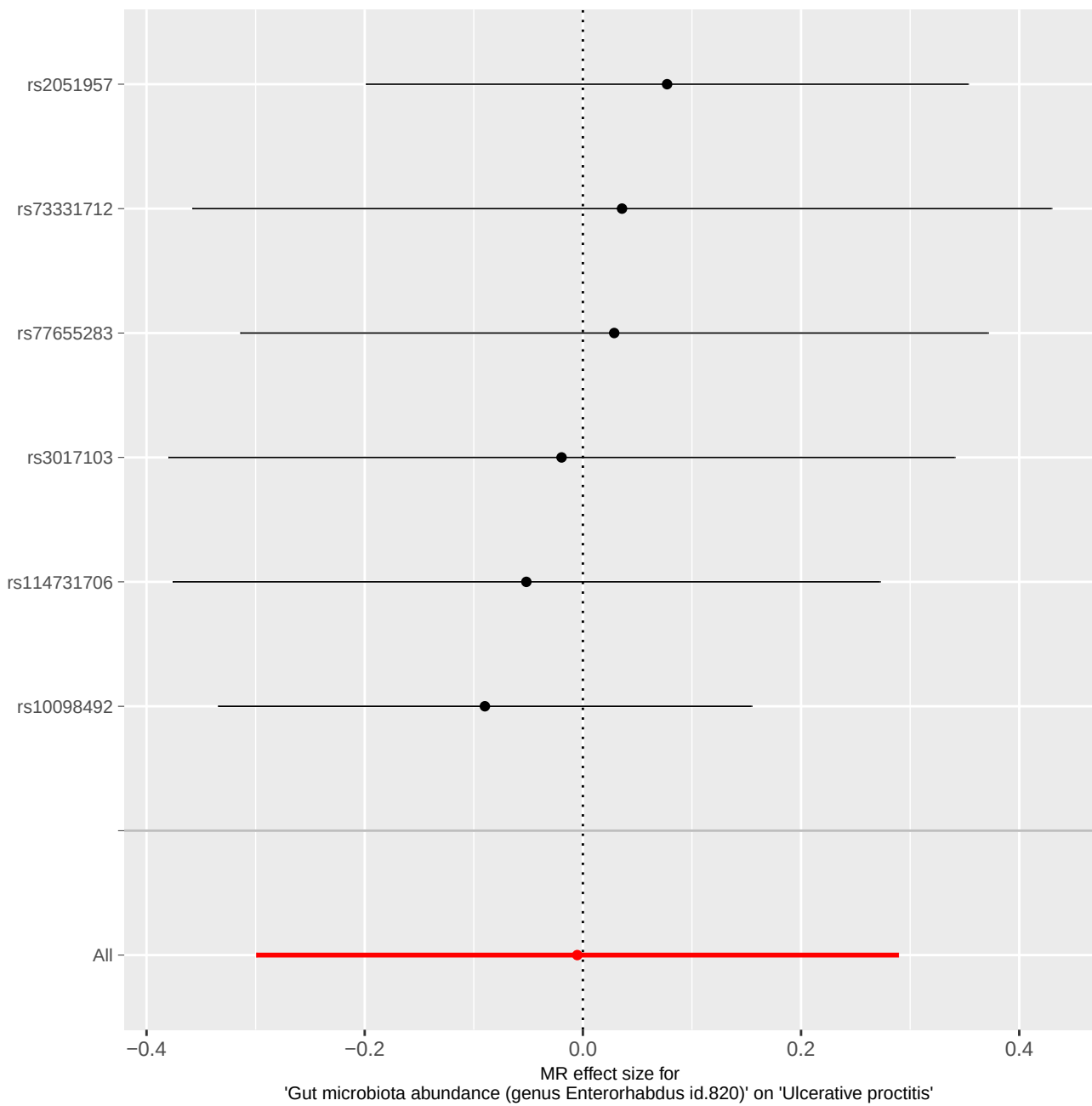


Batch 1414 : Gut microbiota abundance (genus Eggerthella id.819) on Ulcerative proctitis

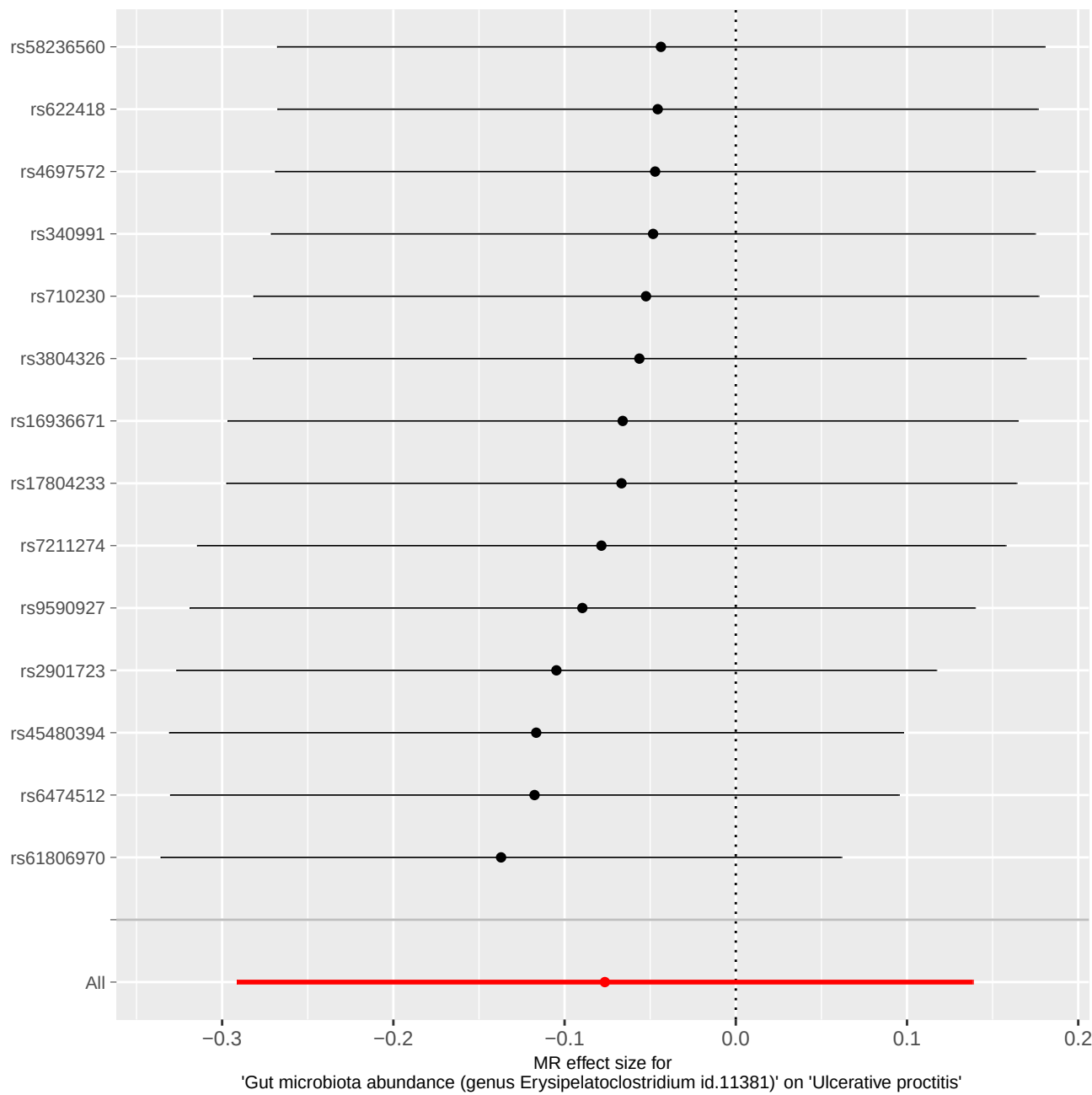


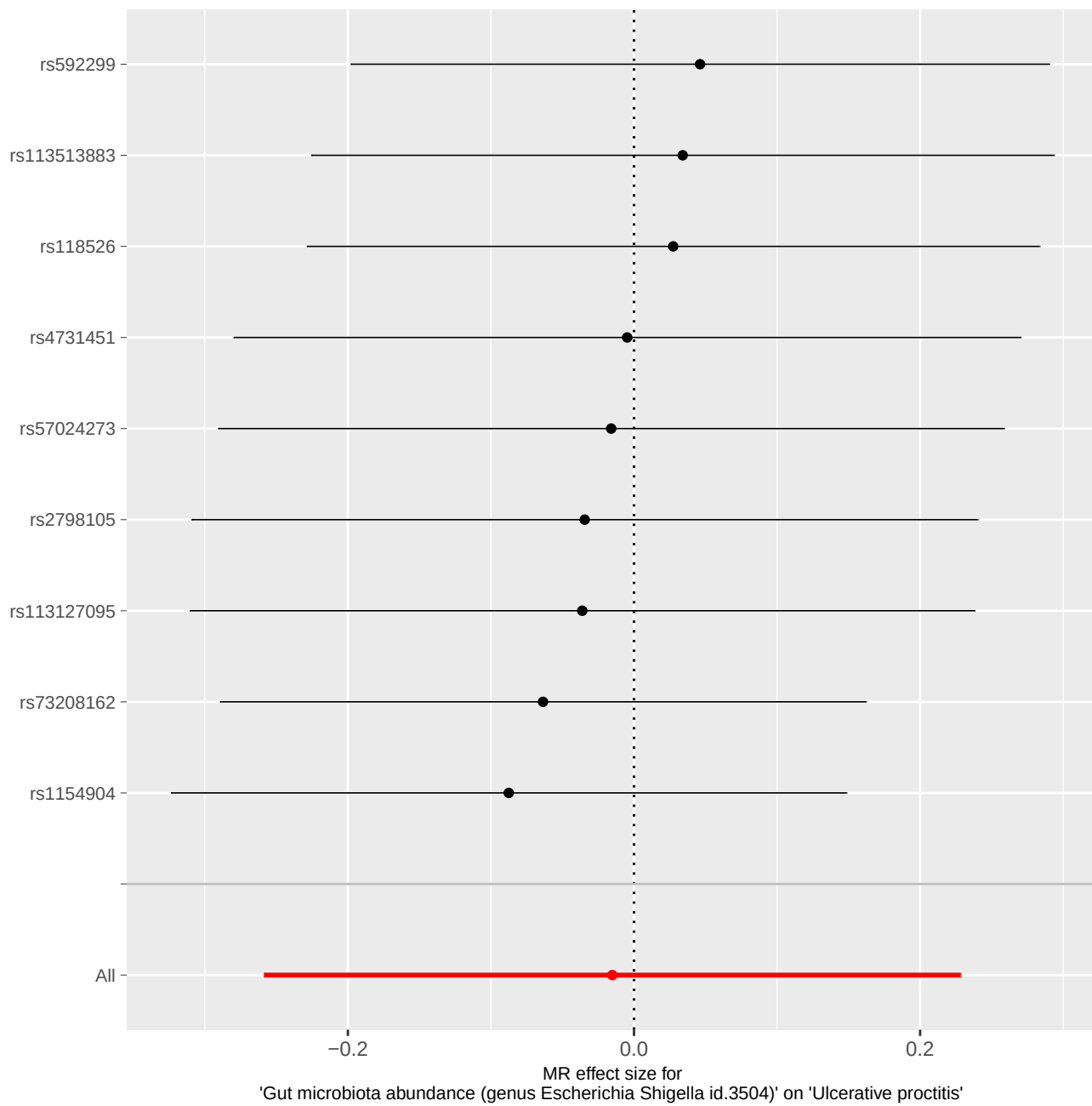
Batch 1415 : Gut microbiota abundance (genus Eisenbergiella id.11304) on Ulcerative proctitis

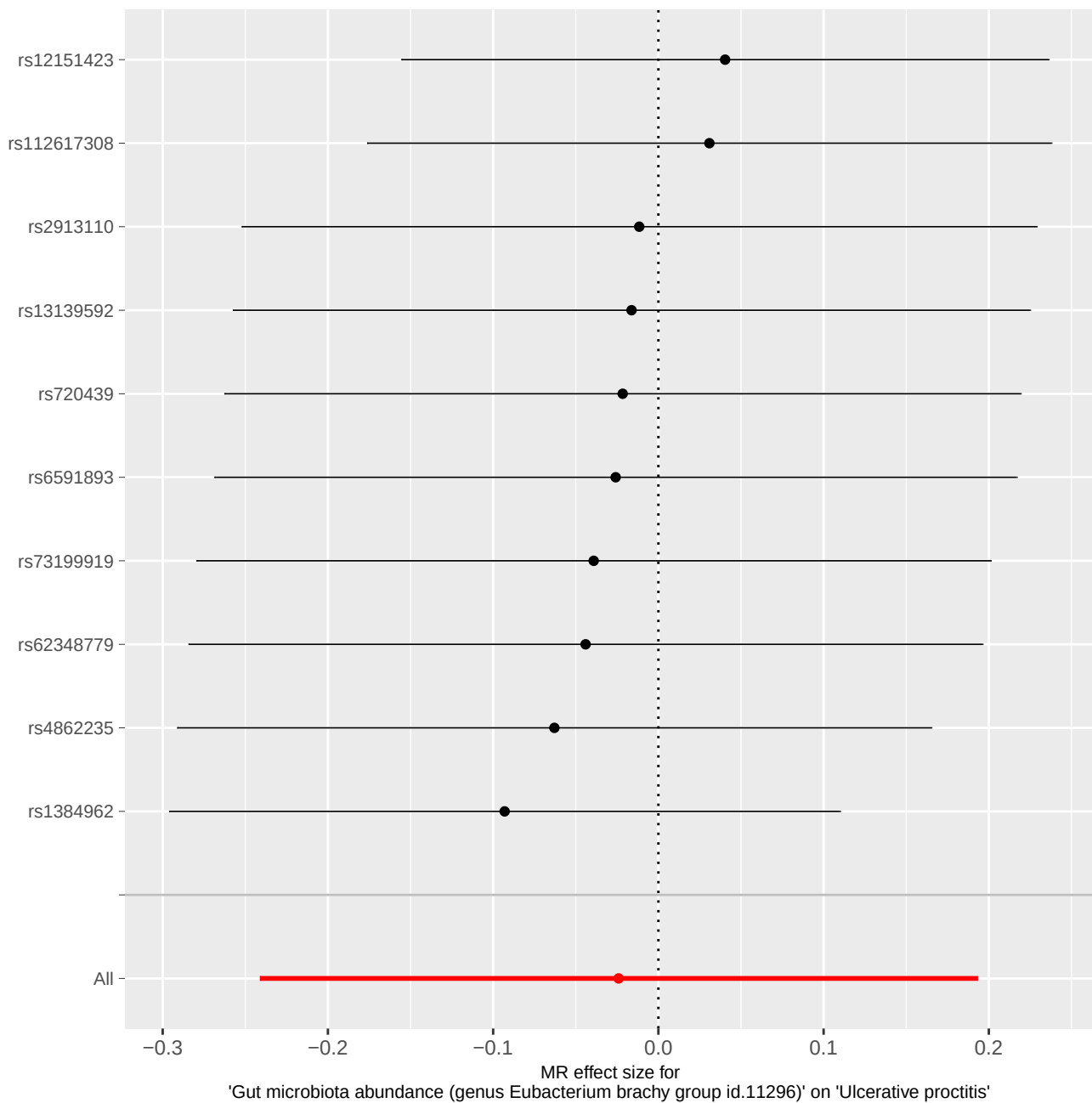


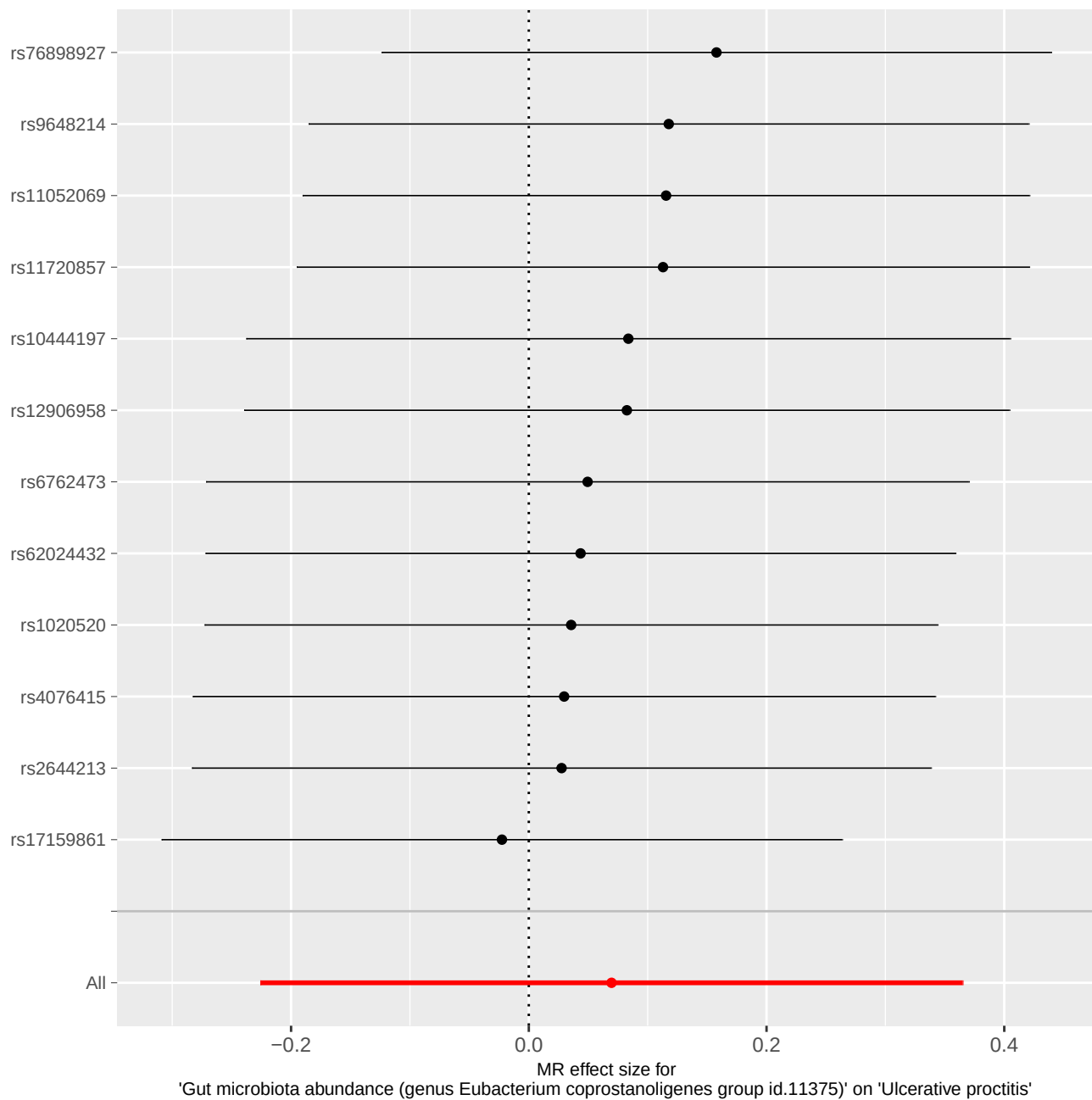


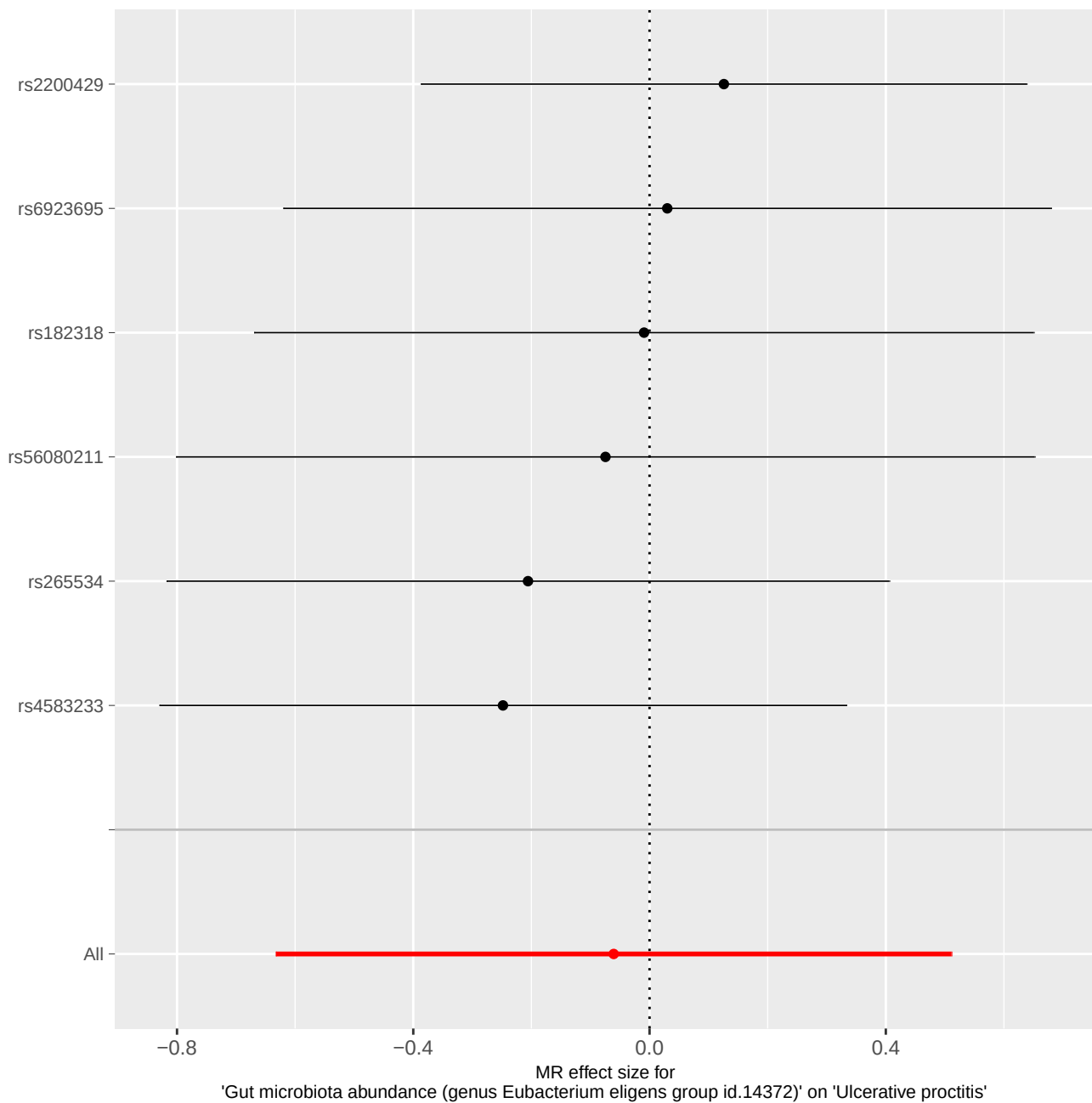
Batch 1417 : Gut microbiota abundance (genus Erysipelatoclostridium id.11381) on Ulcerative proctitis

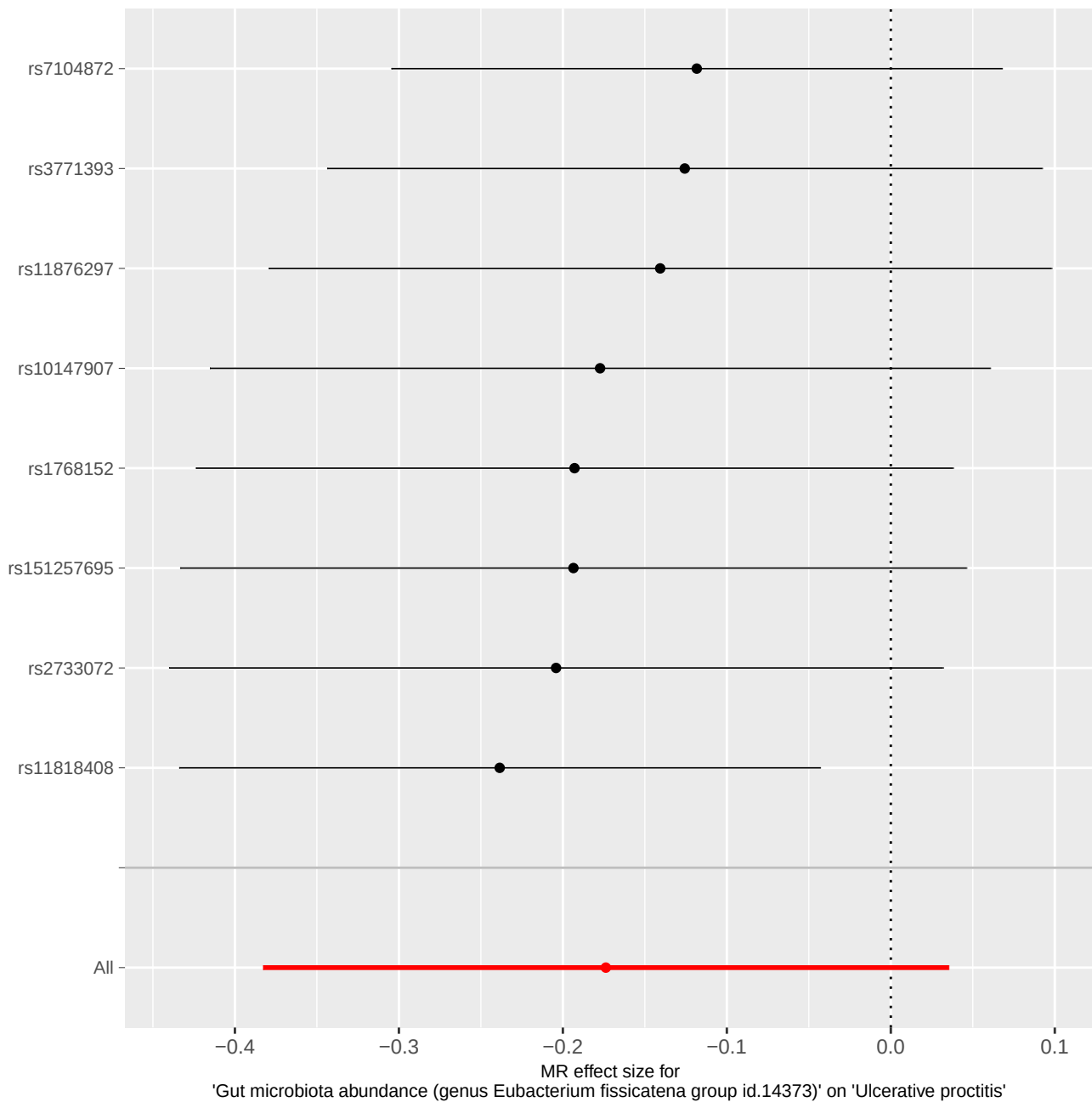


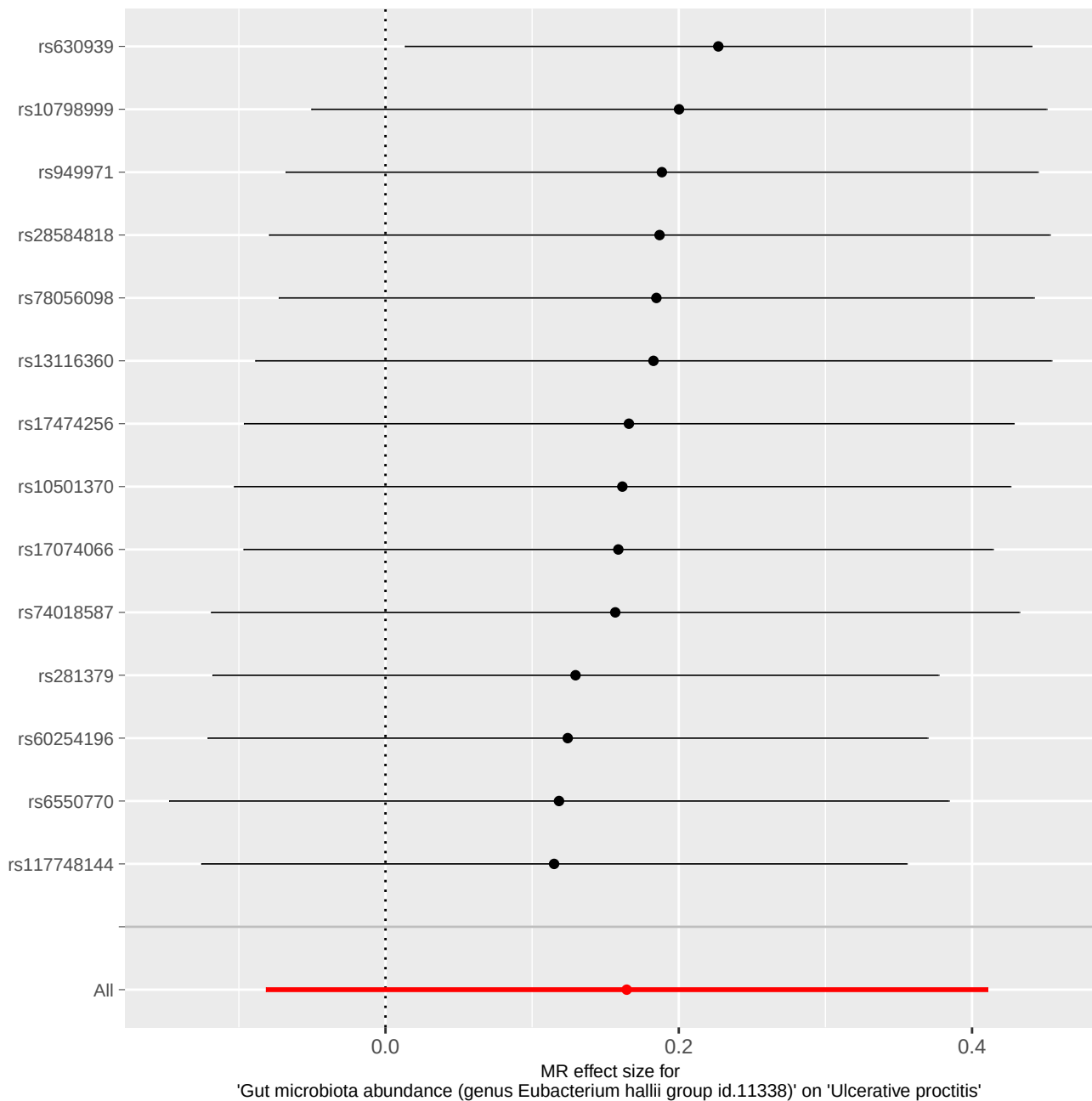


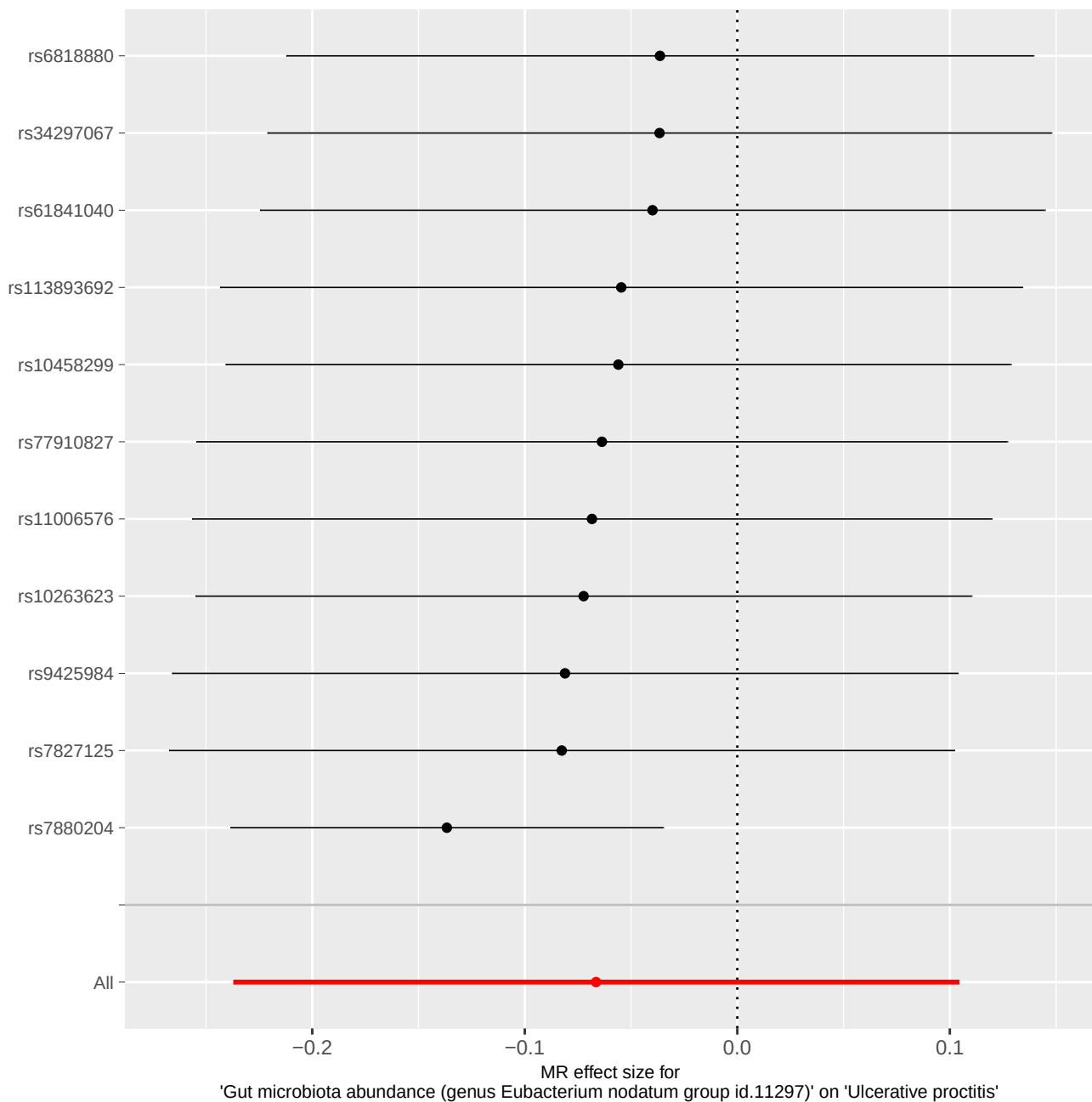


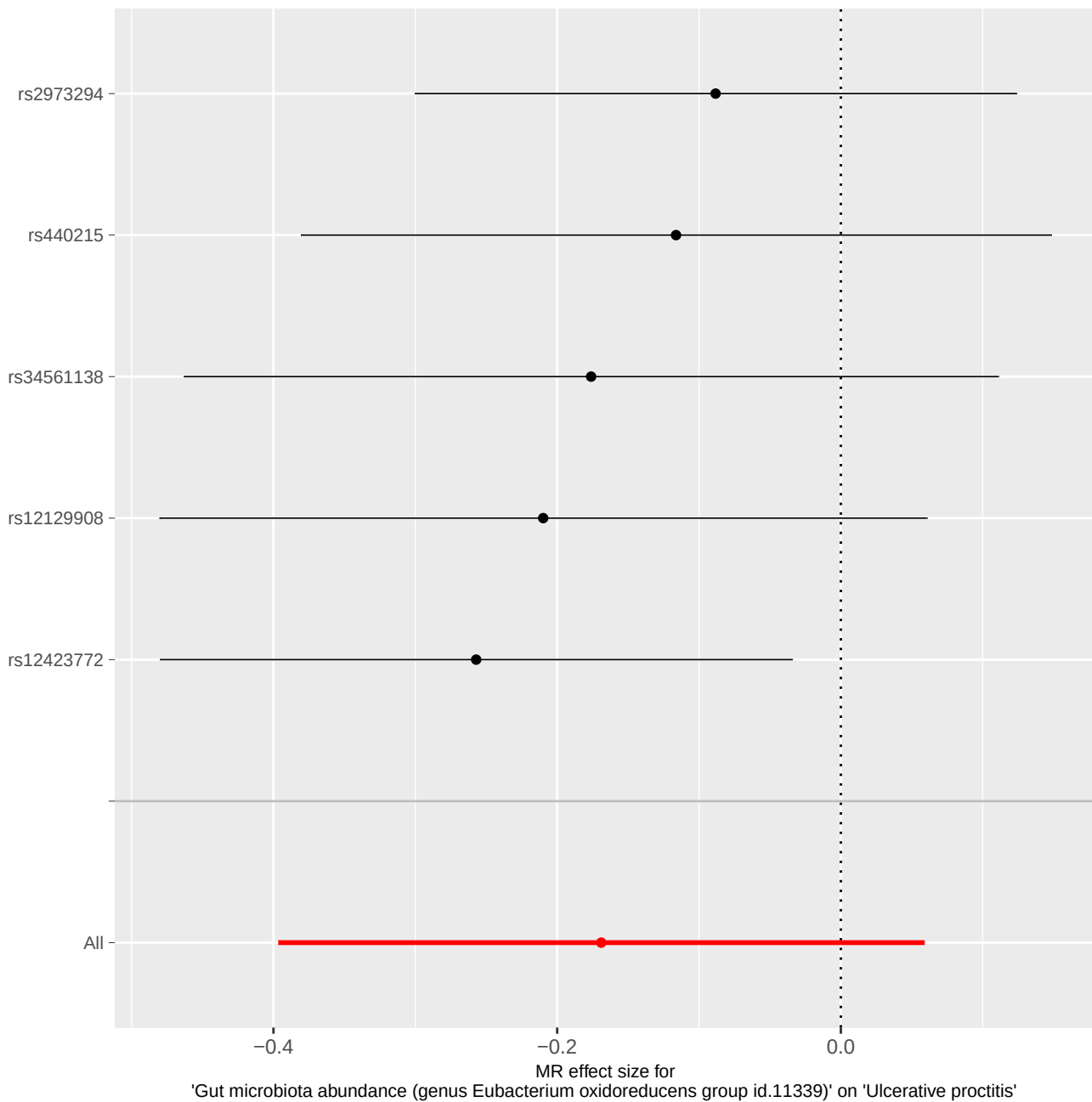


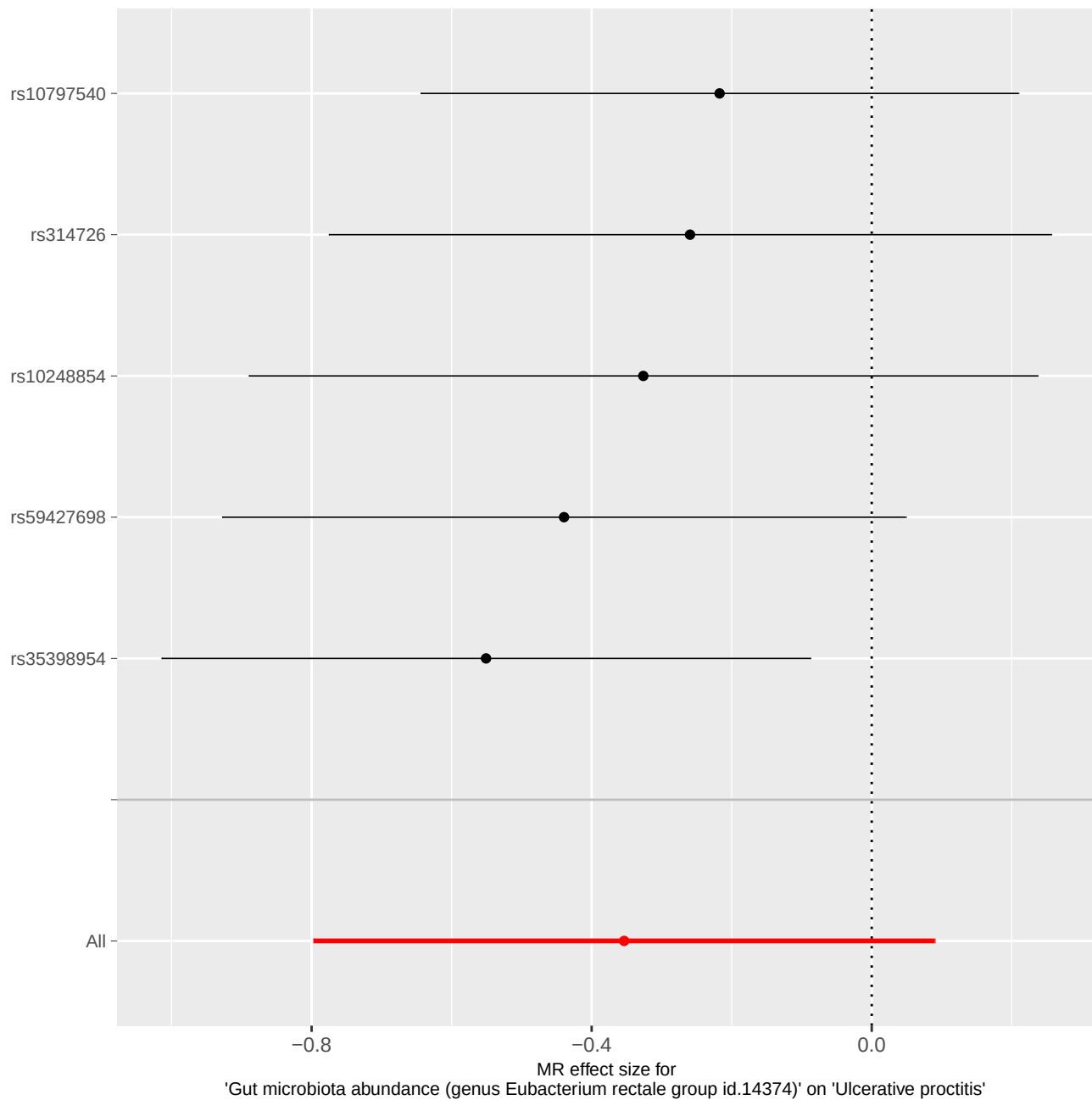


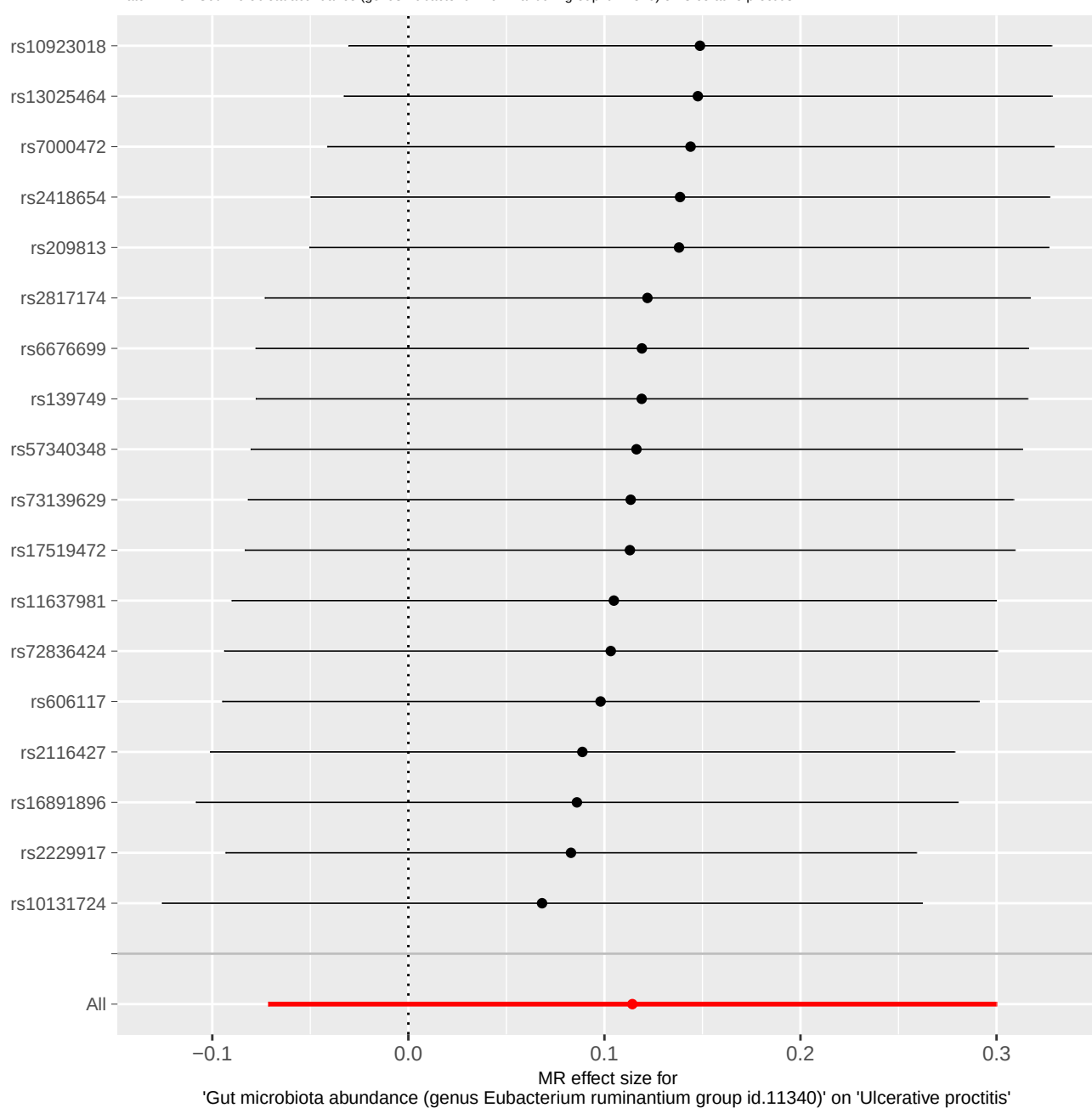


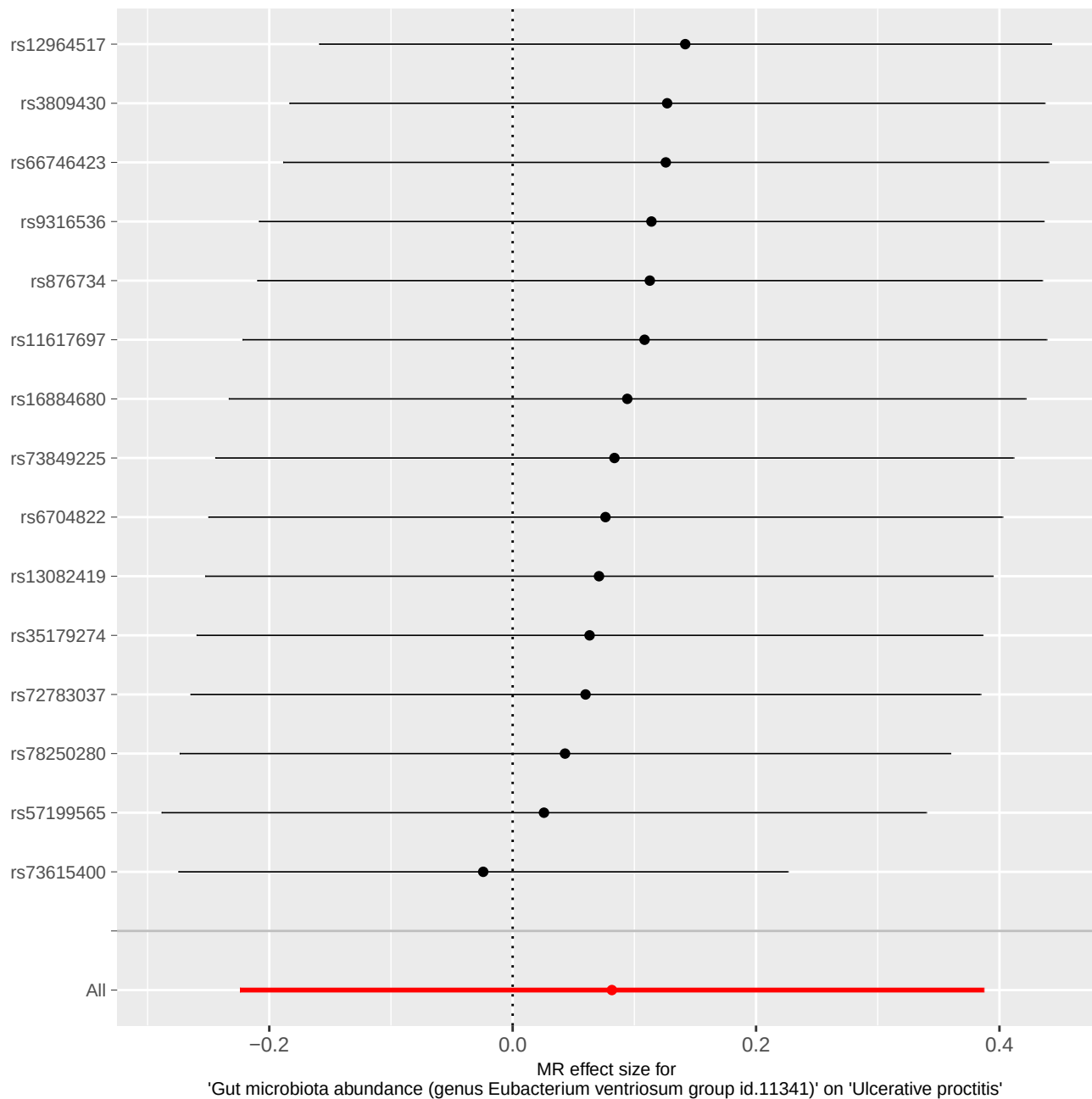


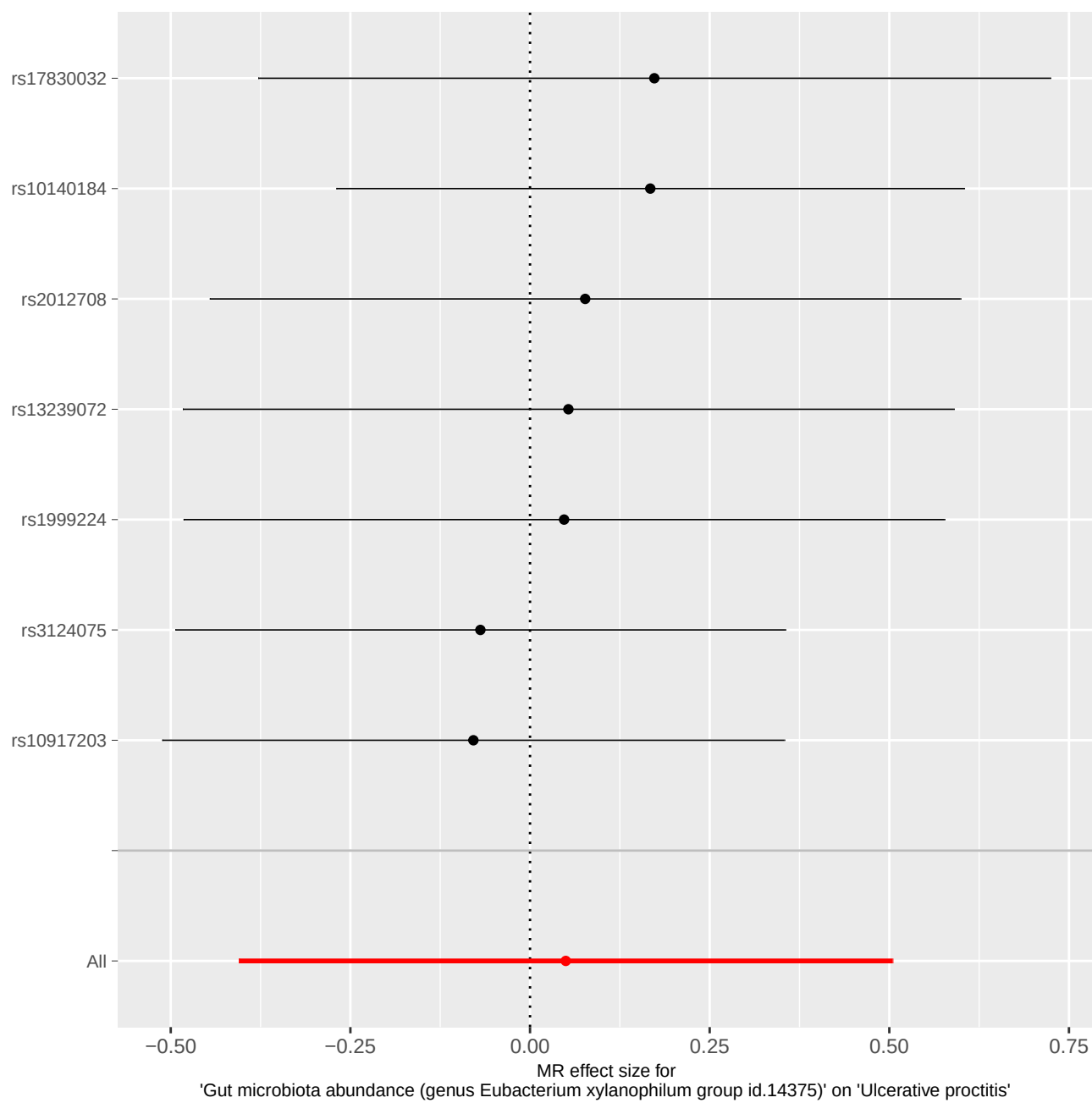


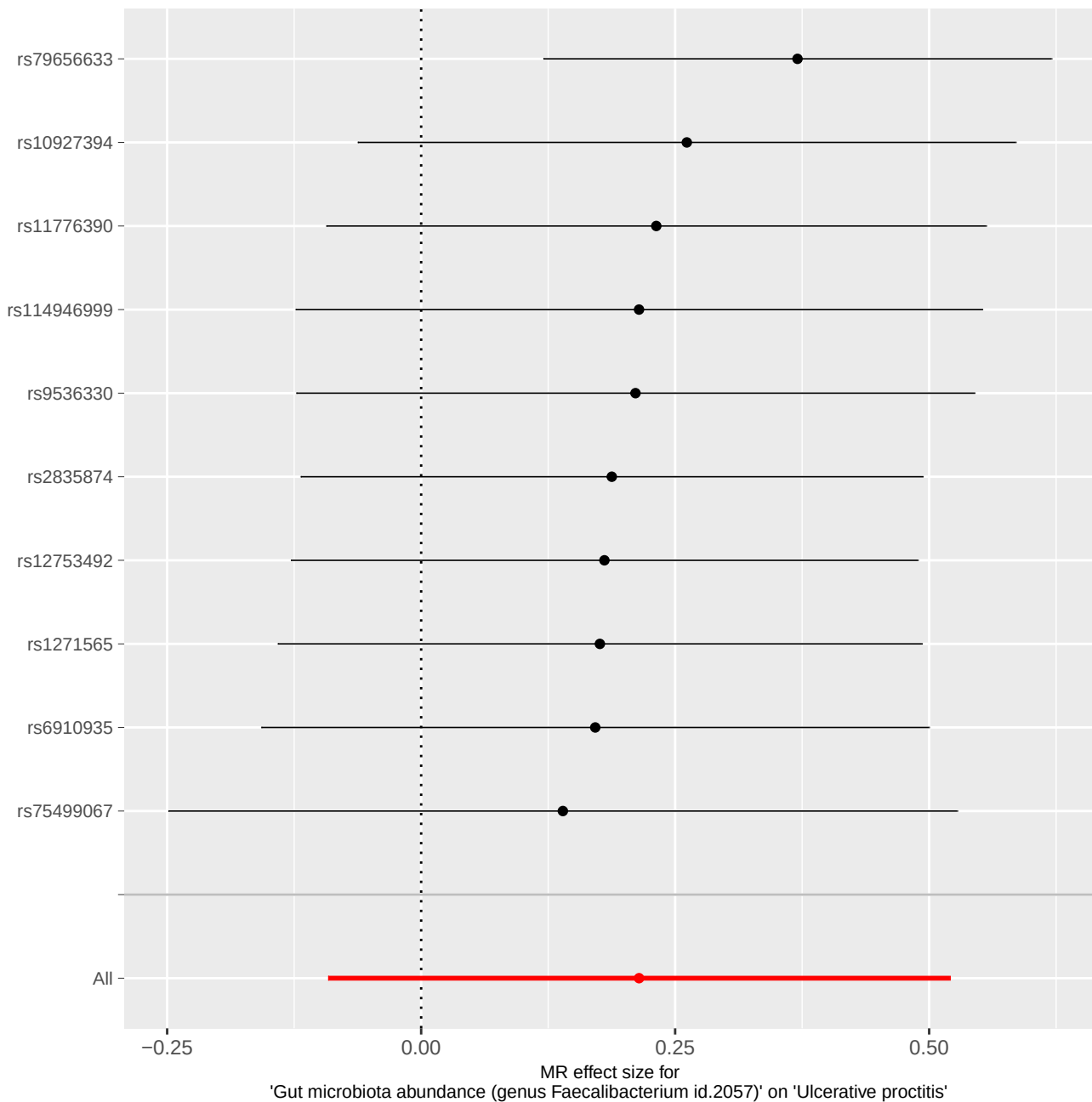


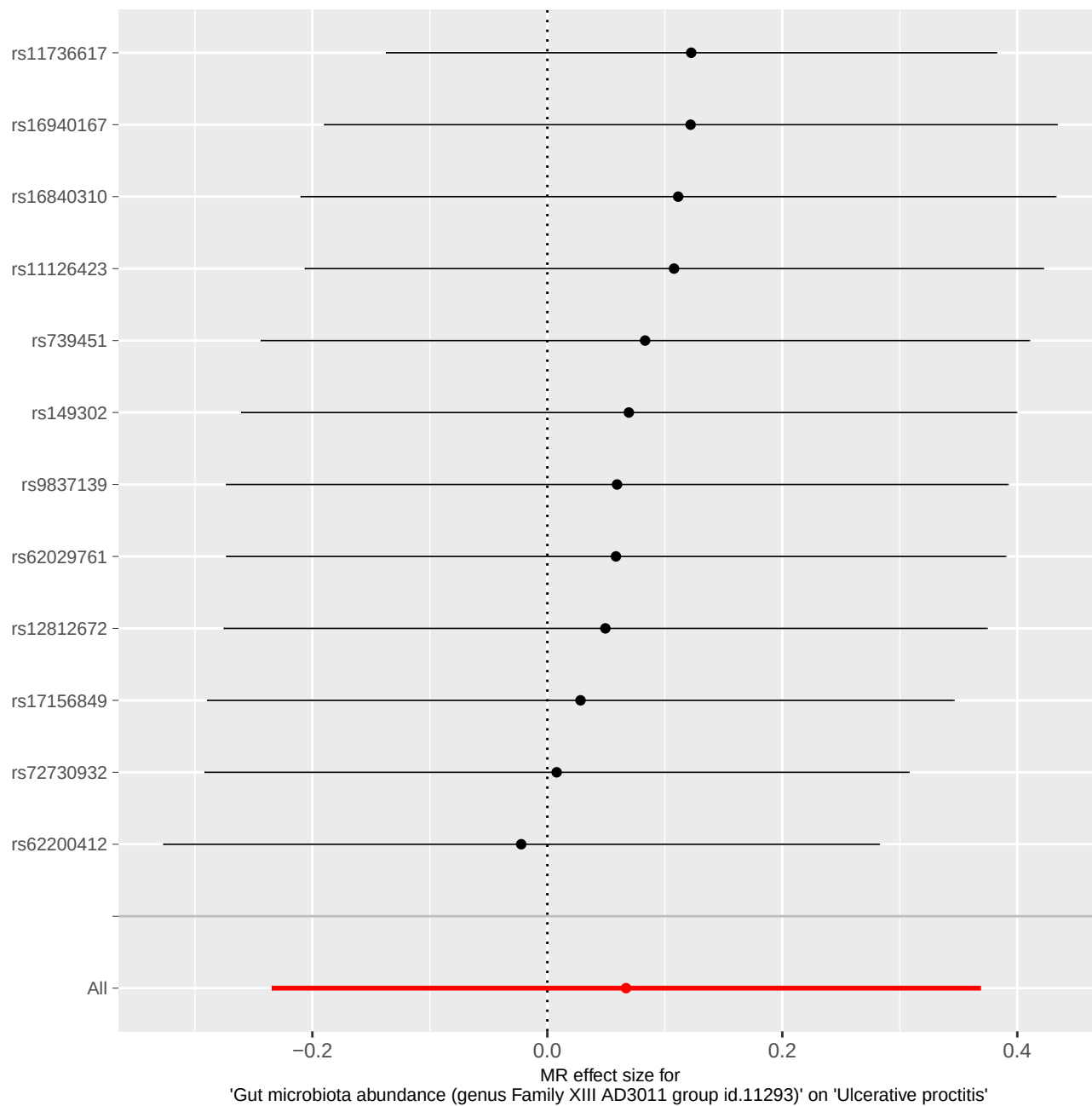


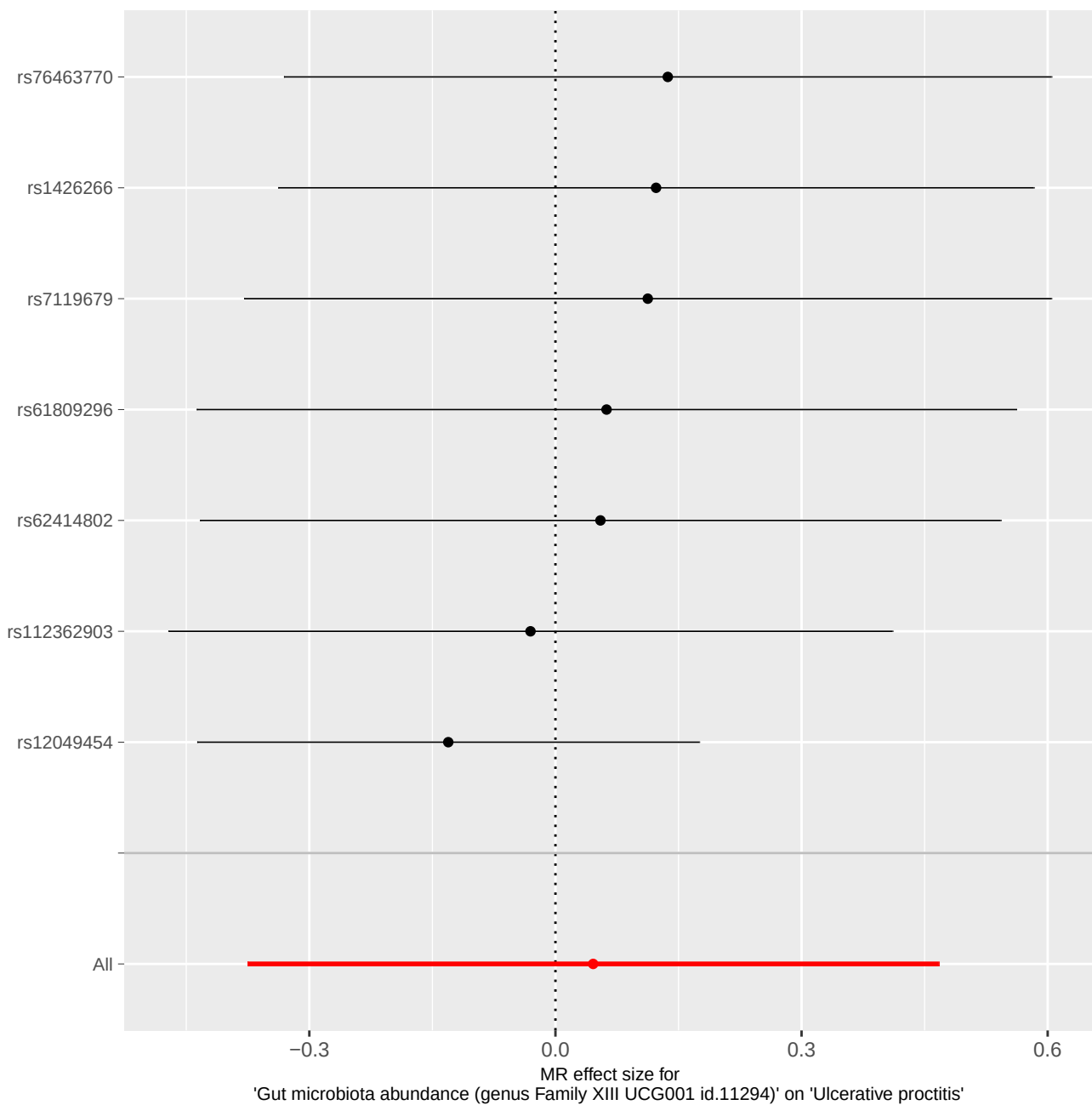


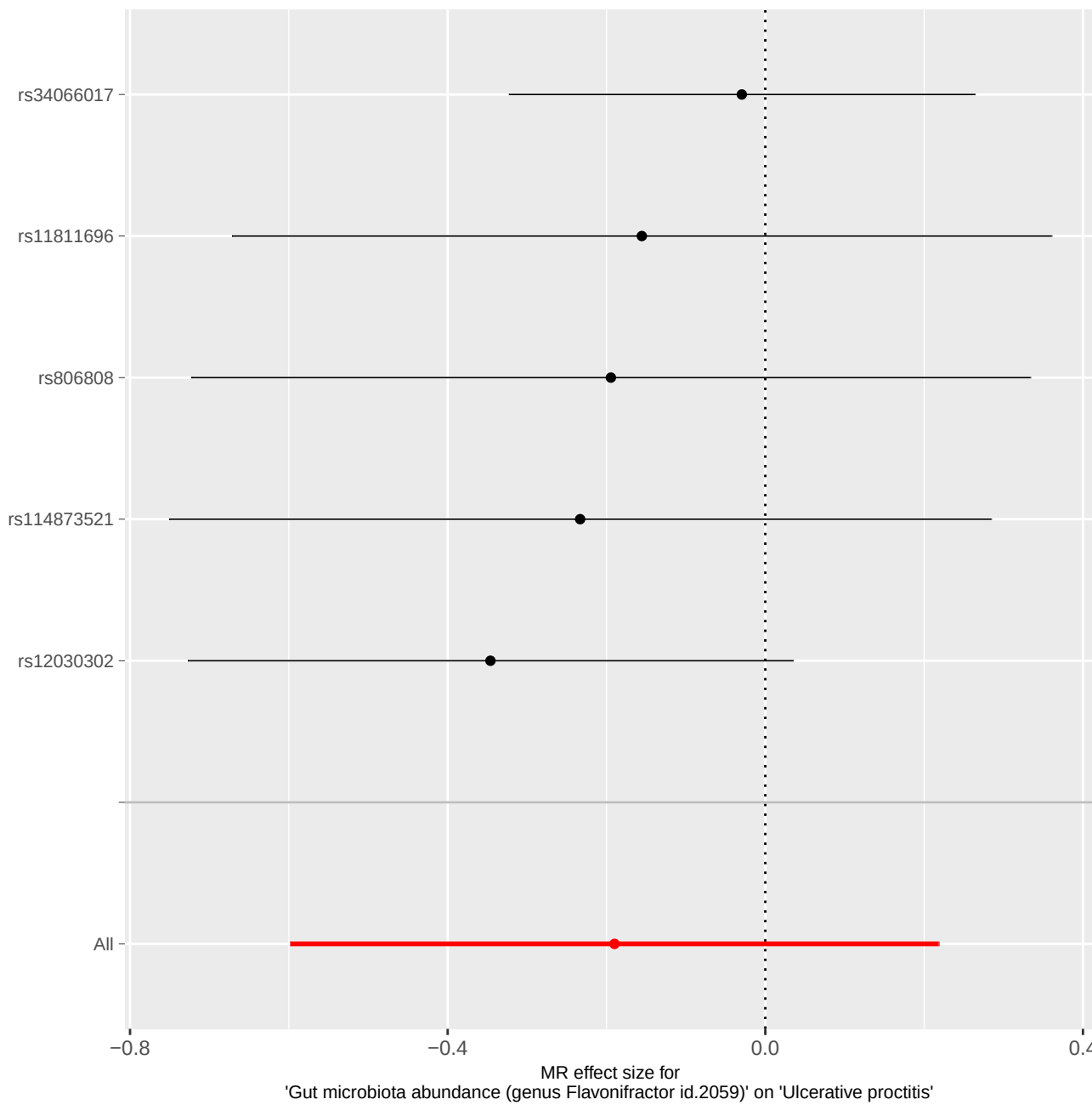


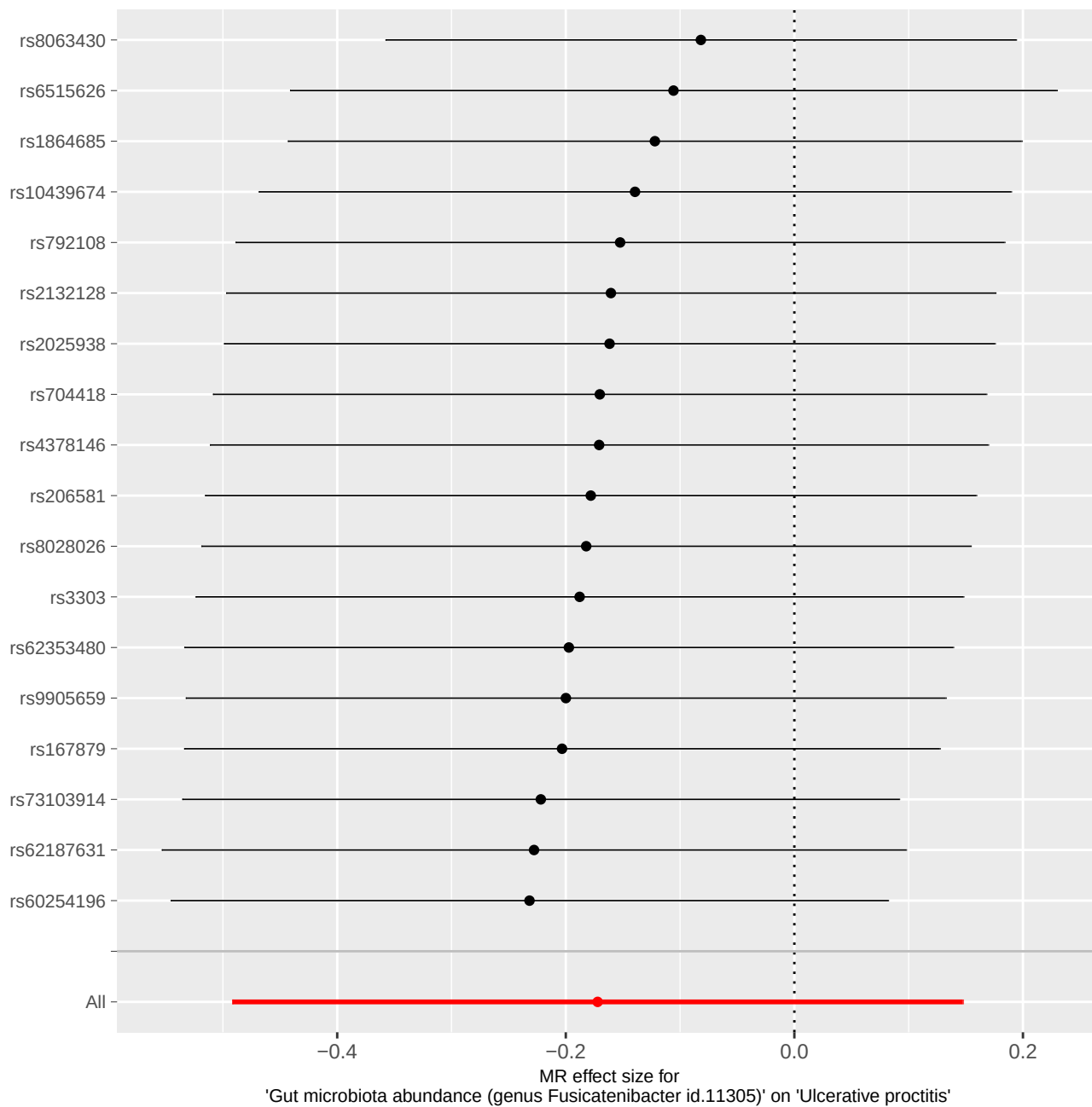




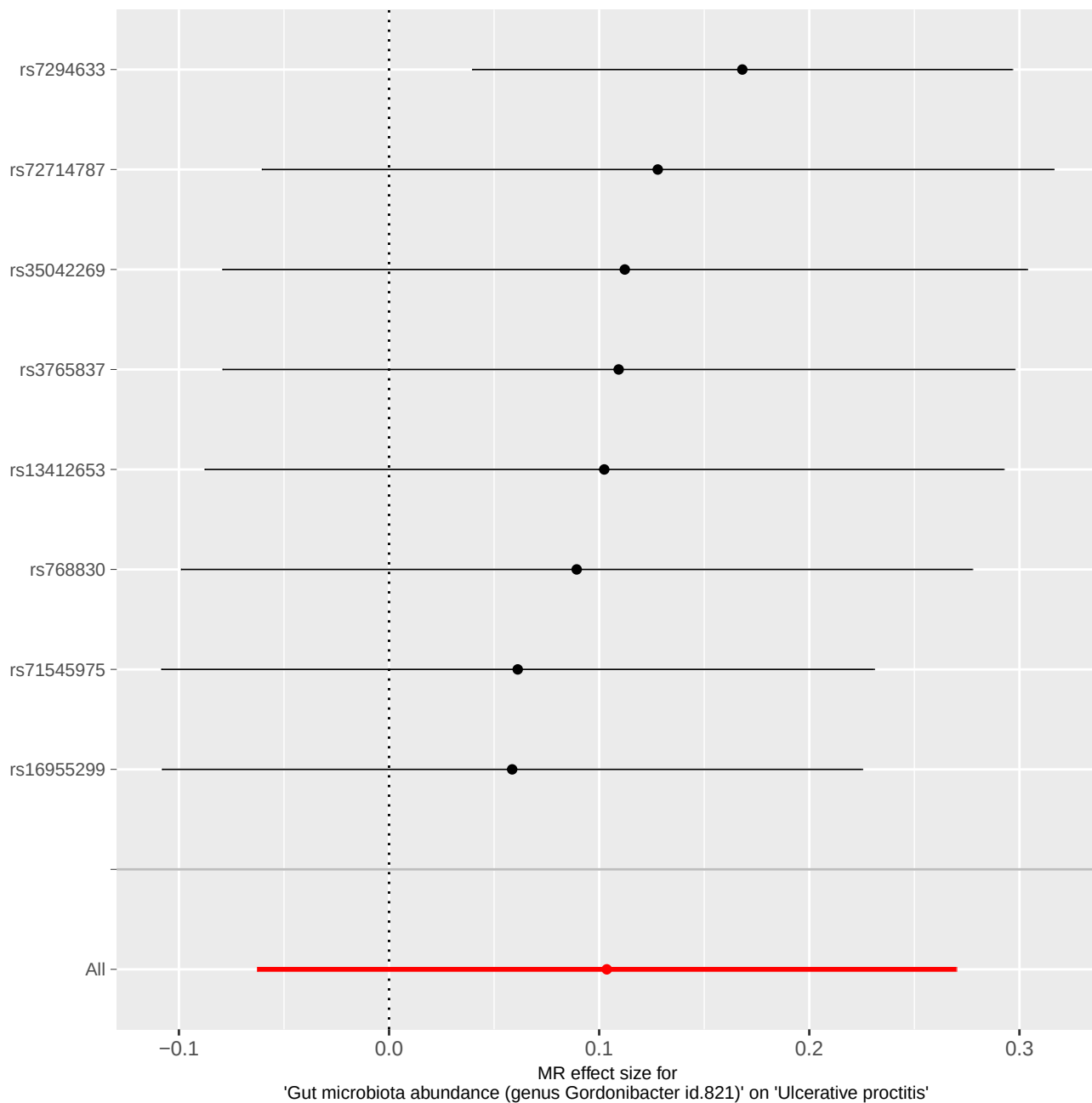


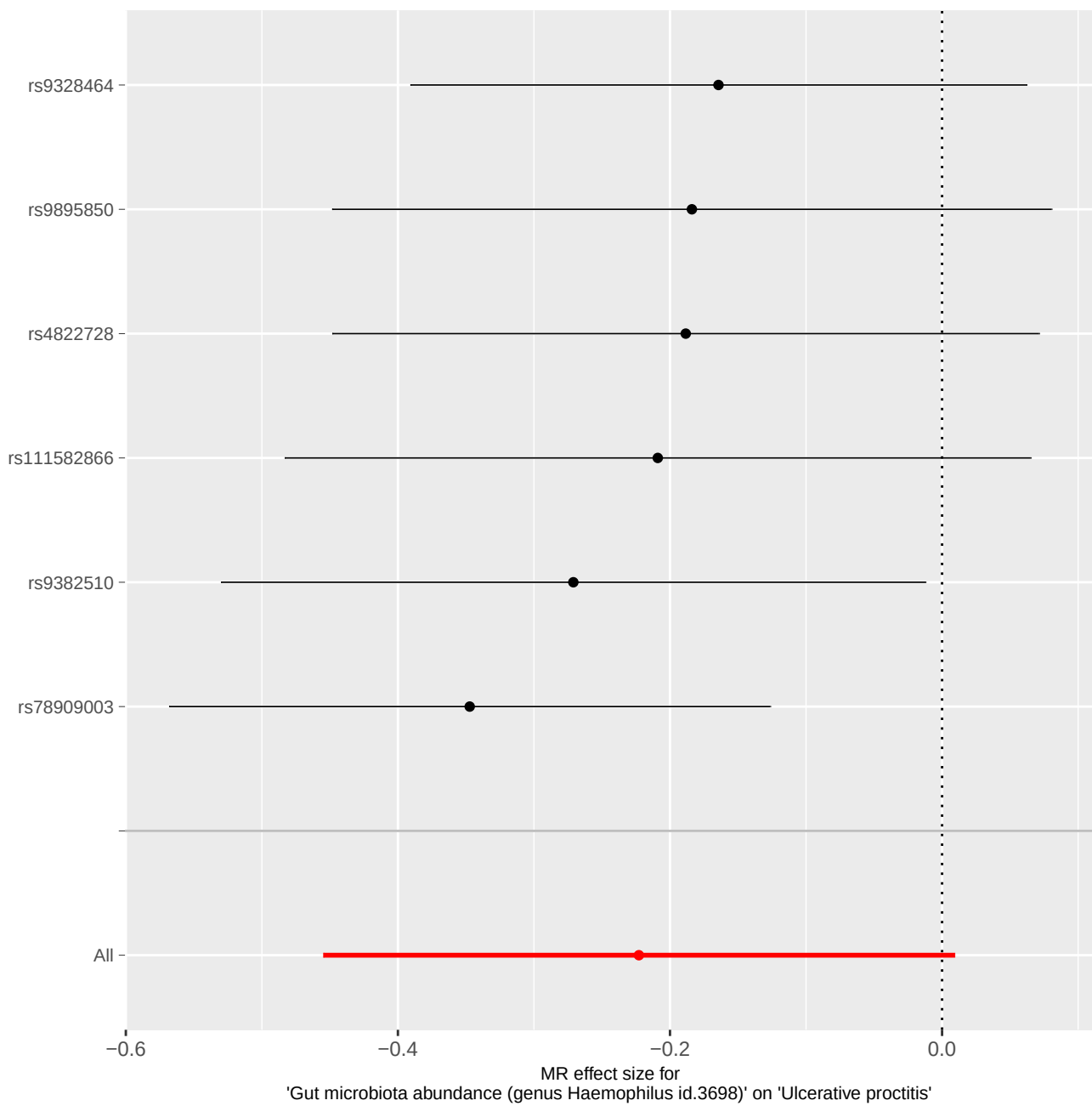


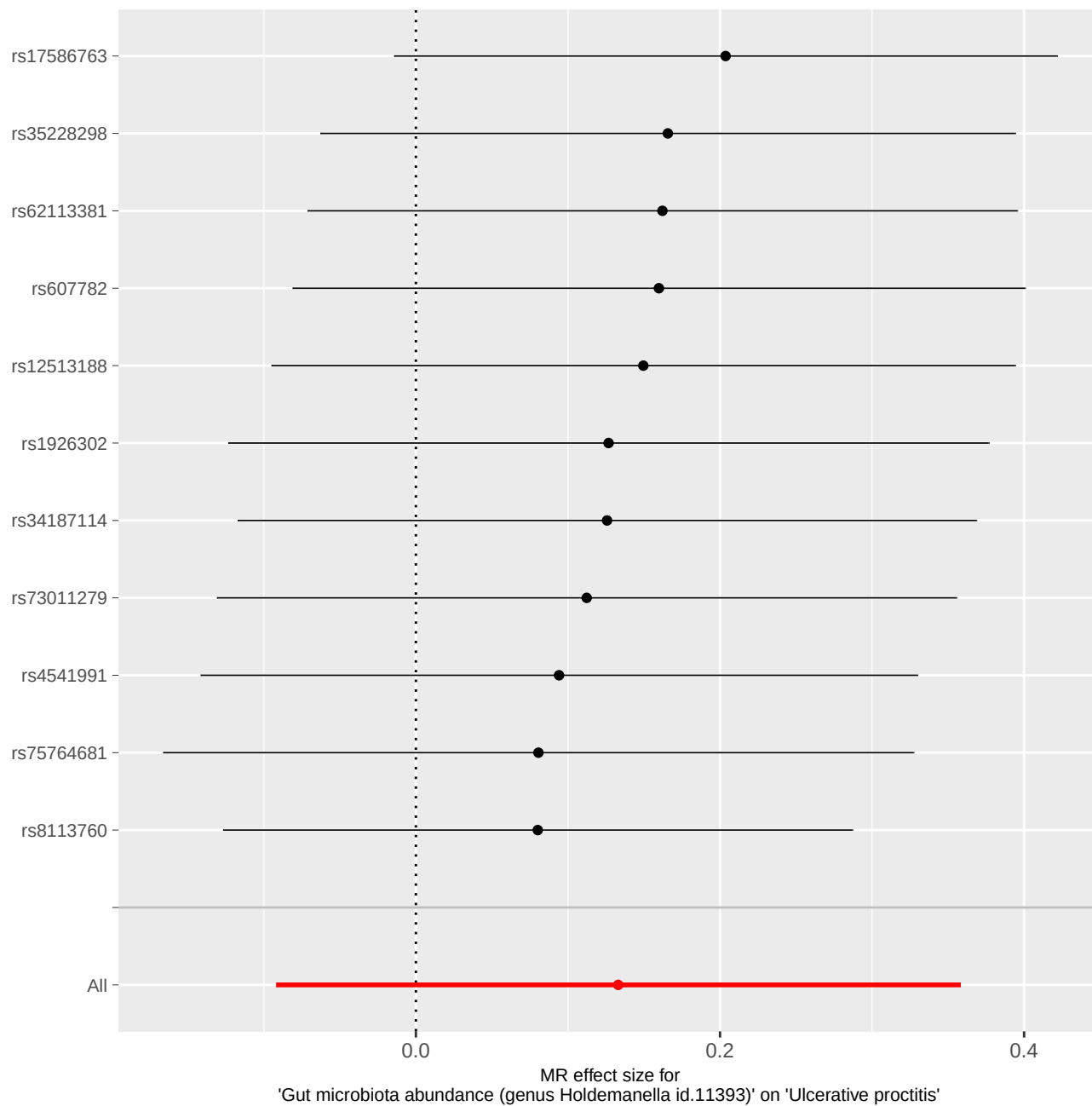


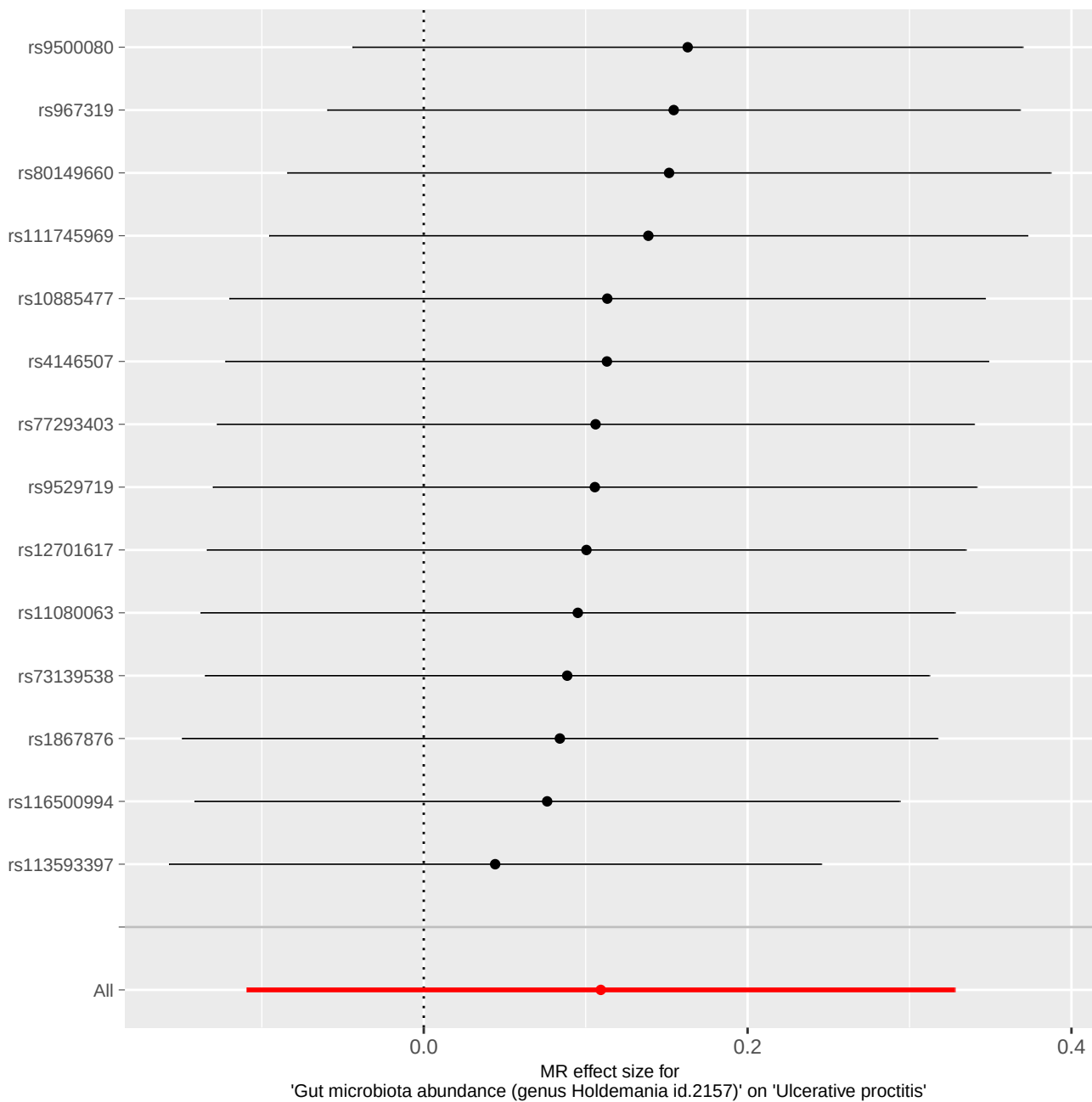


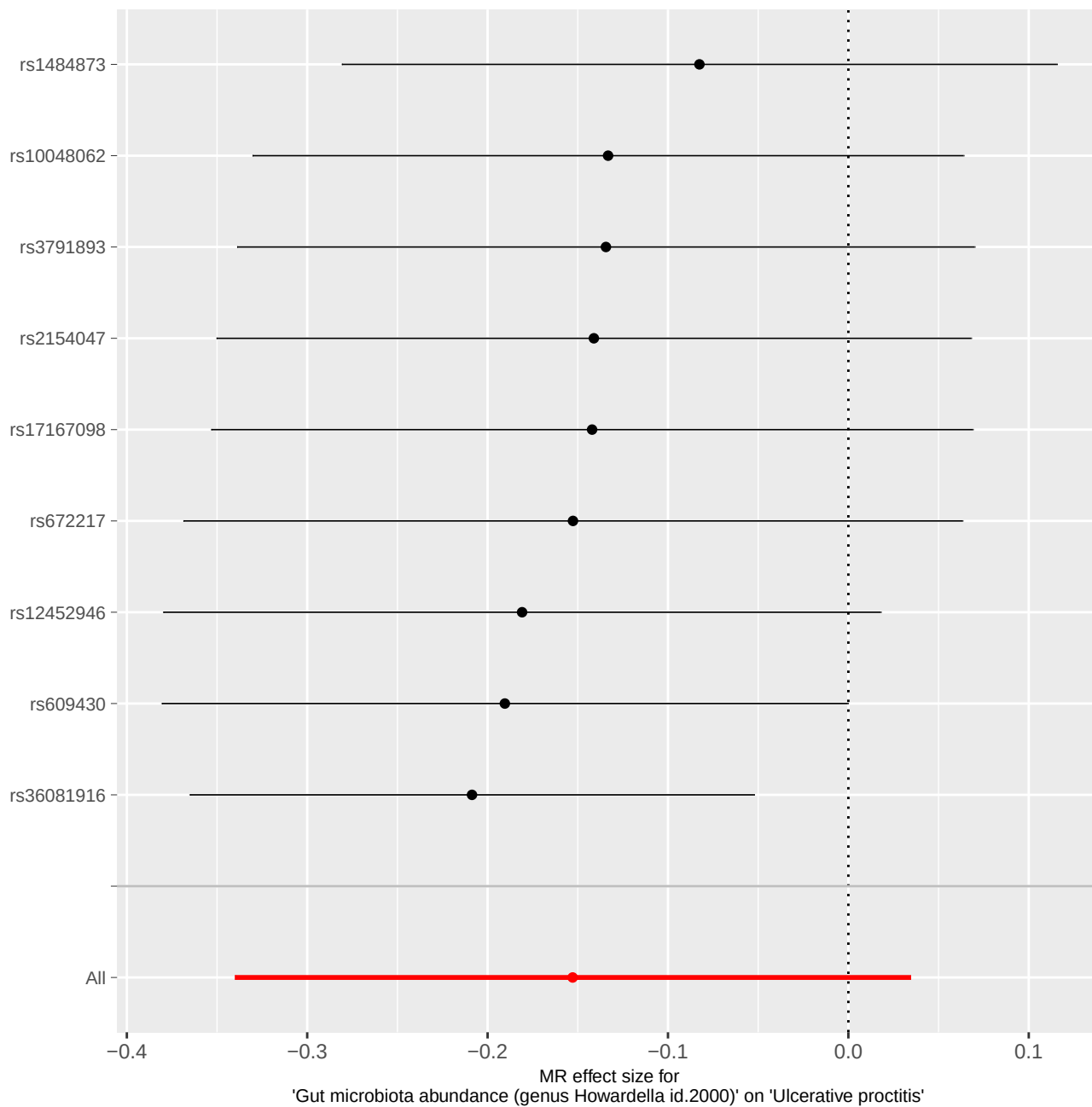
Batch 1436 : Gut microbiota abundance (genus *Gordonibacter* id.821) on Ulcerative proctitis



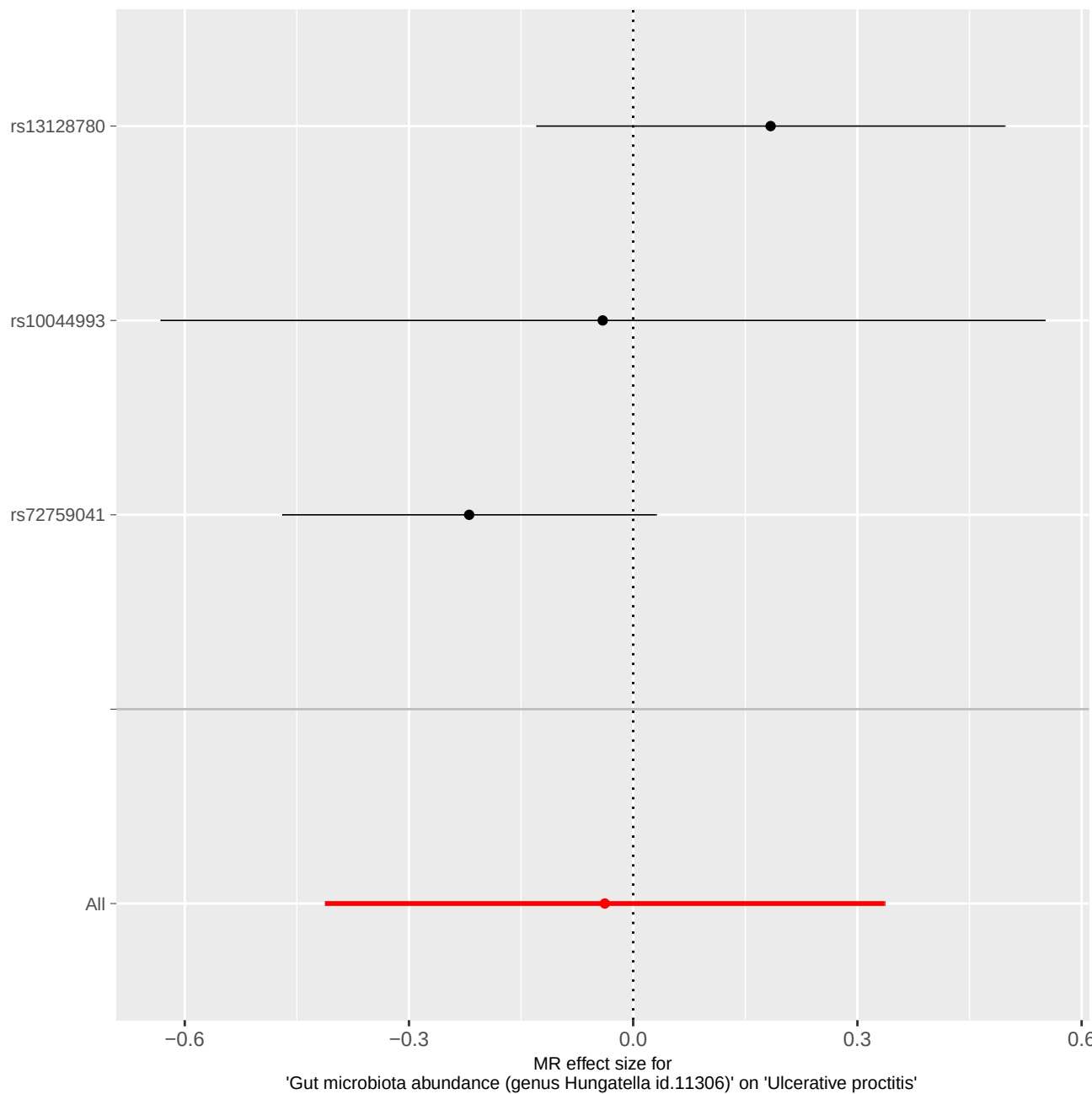


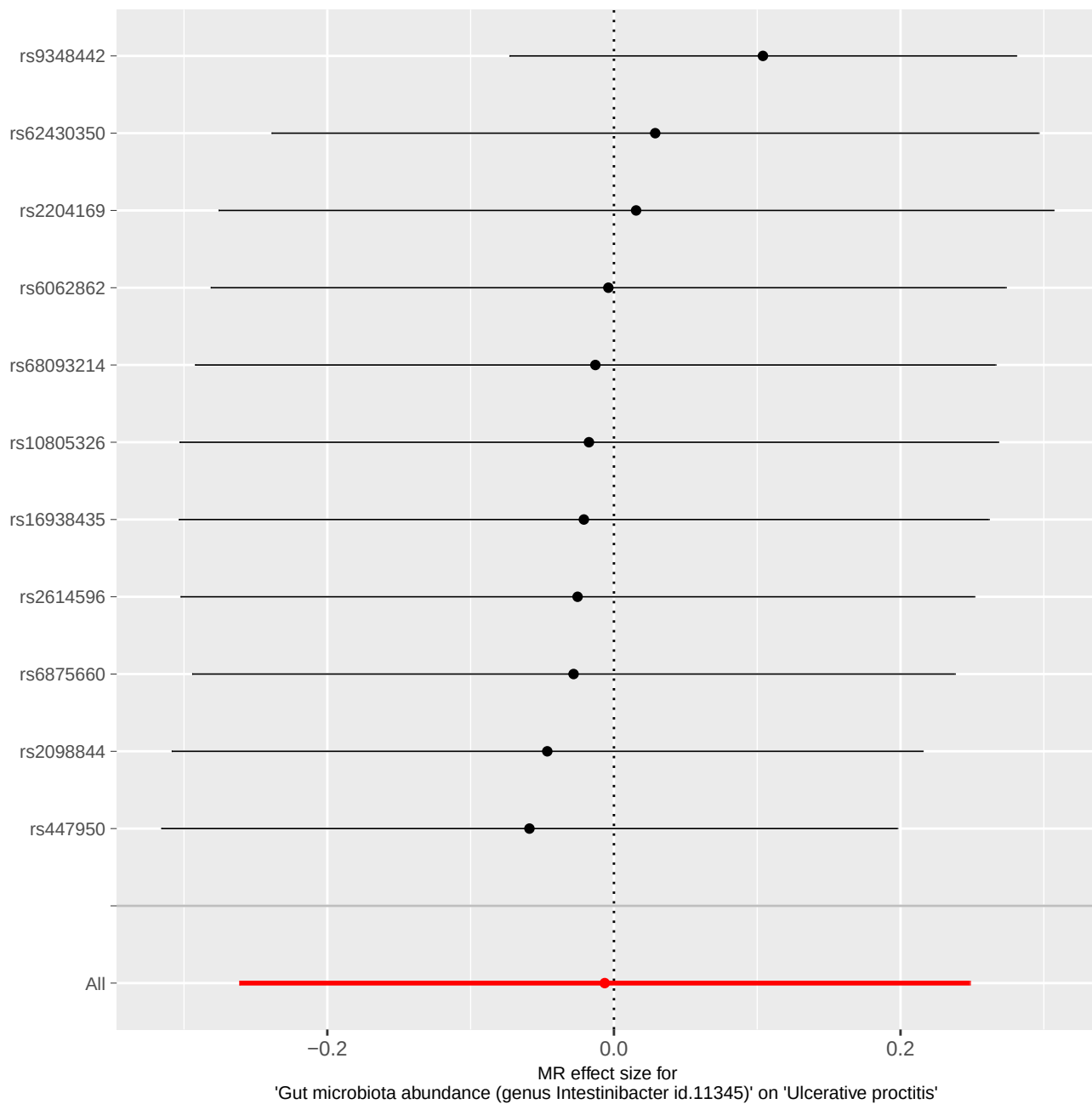


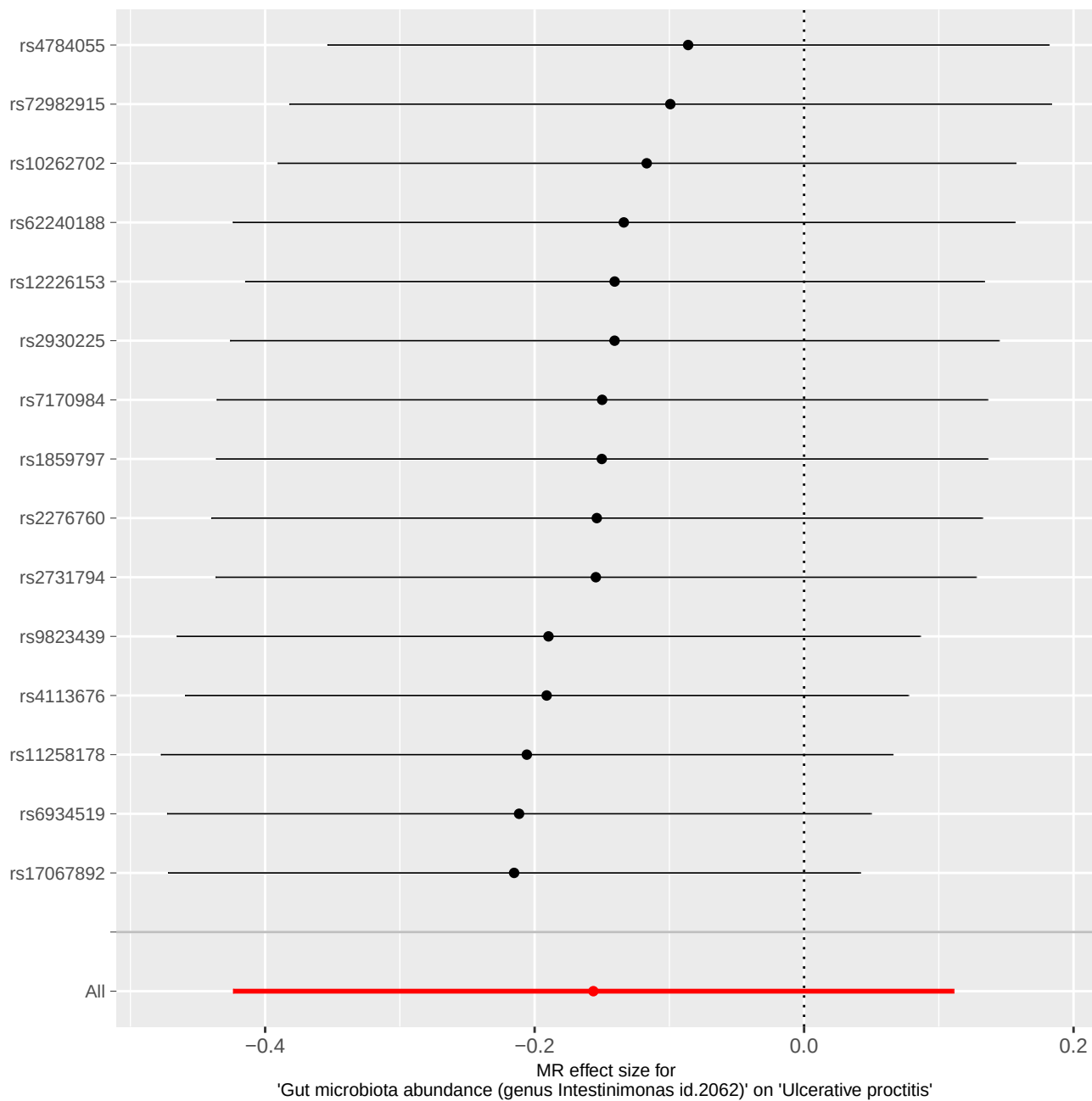


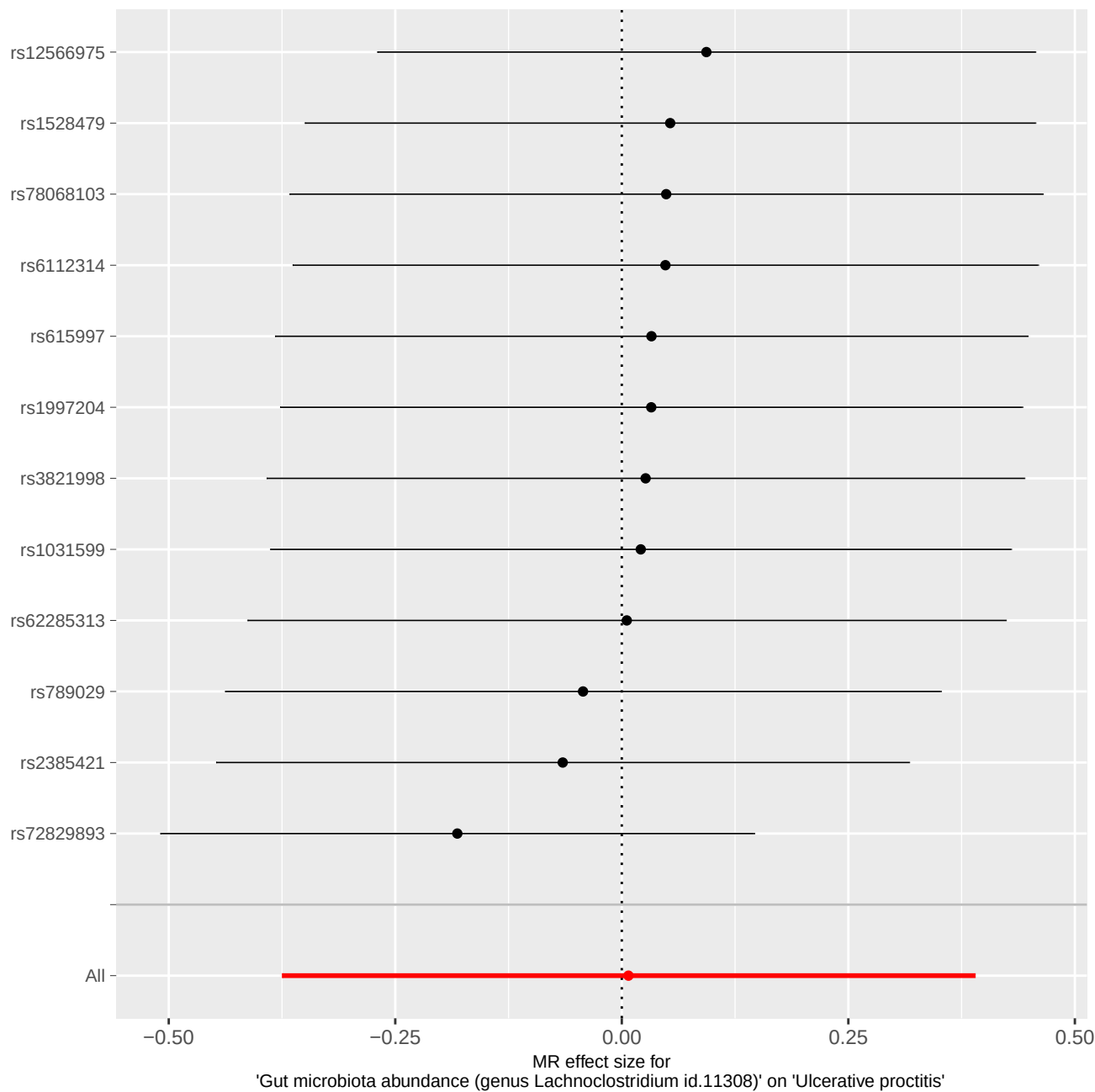


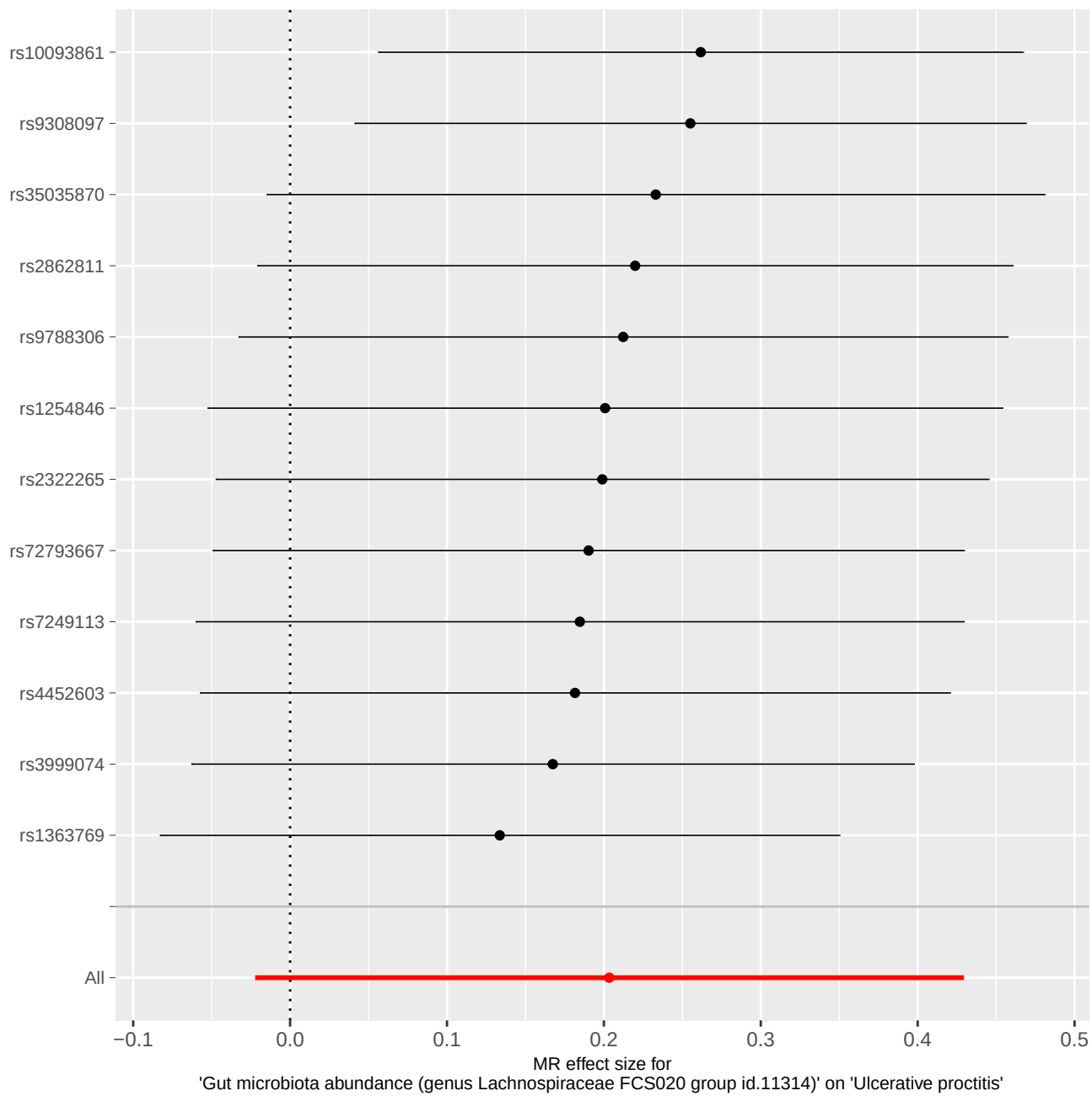
MR effect size for
'Gut microbiota abundance (genus Howardella id.2000) on 'Ulcerative proctitis'

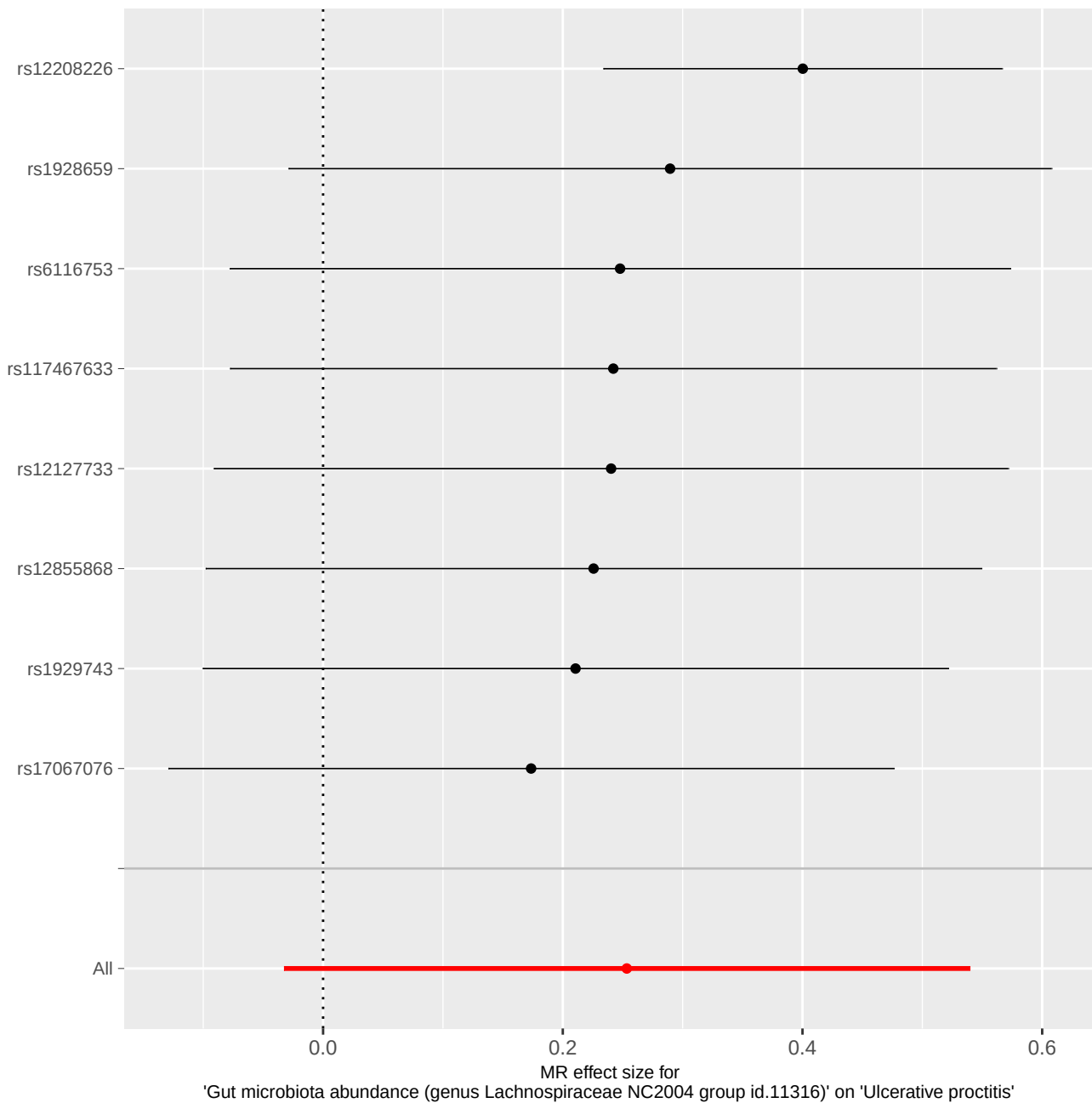


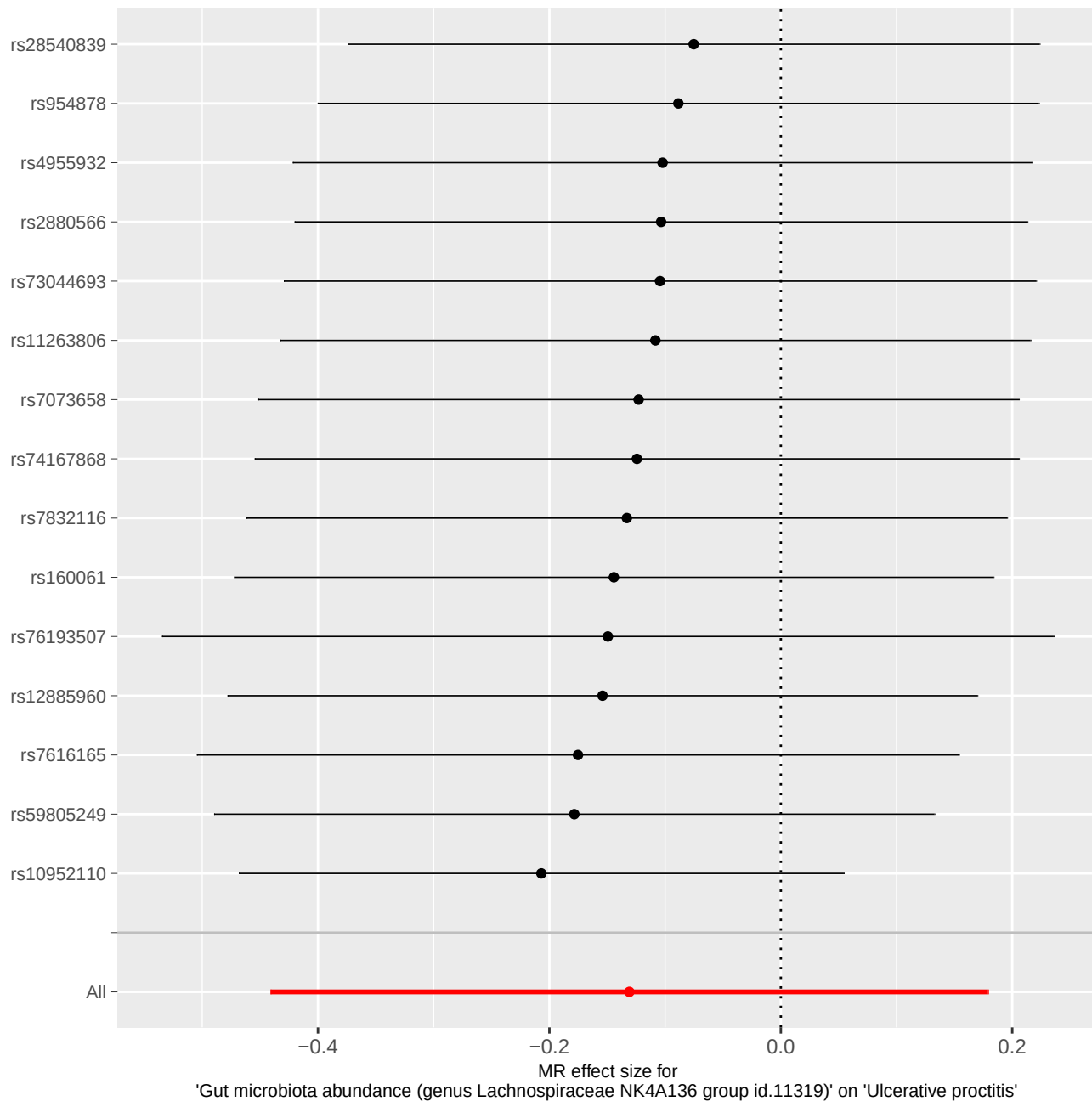


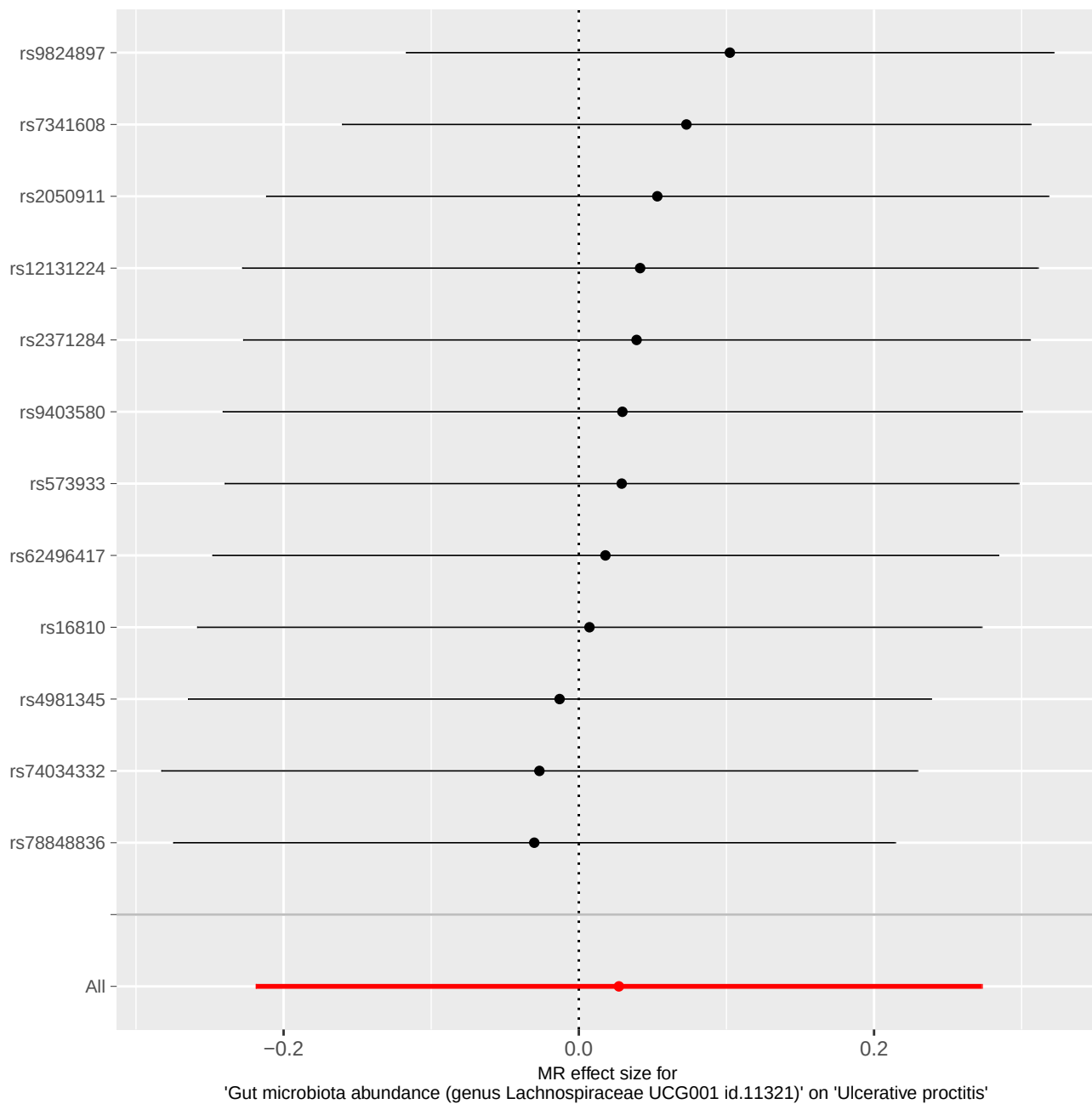


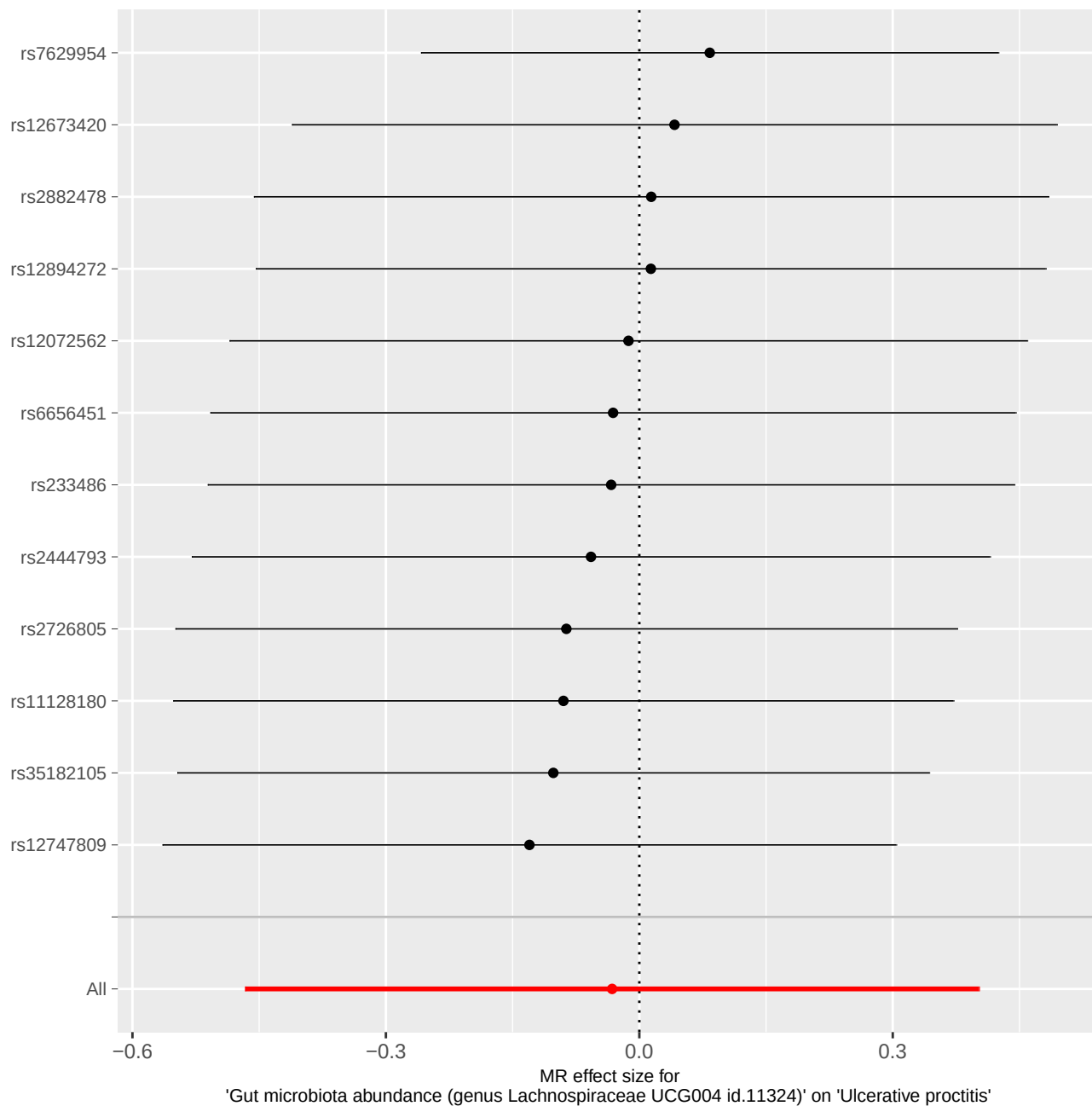


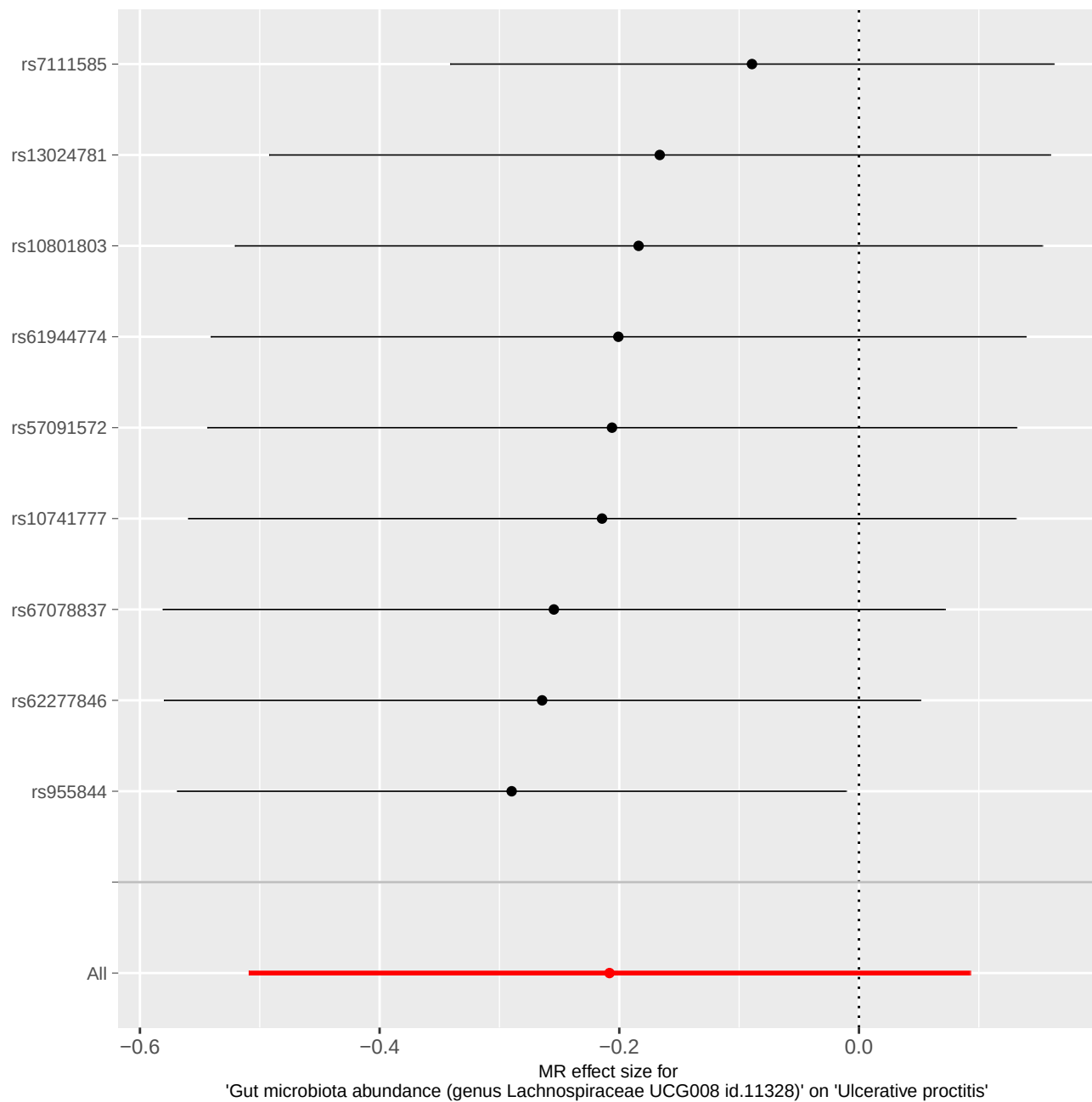




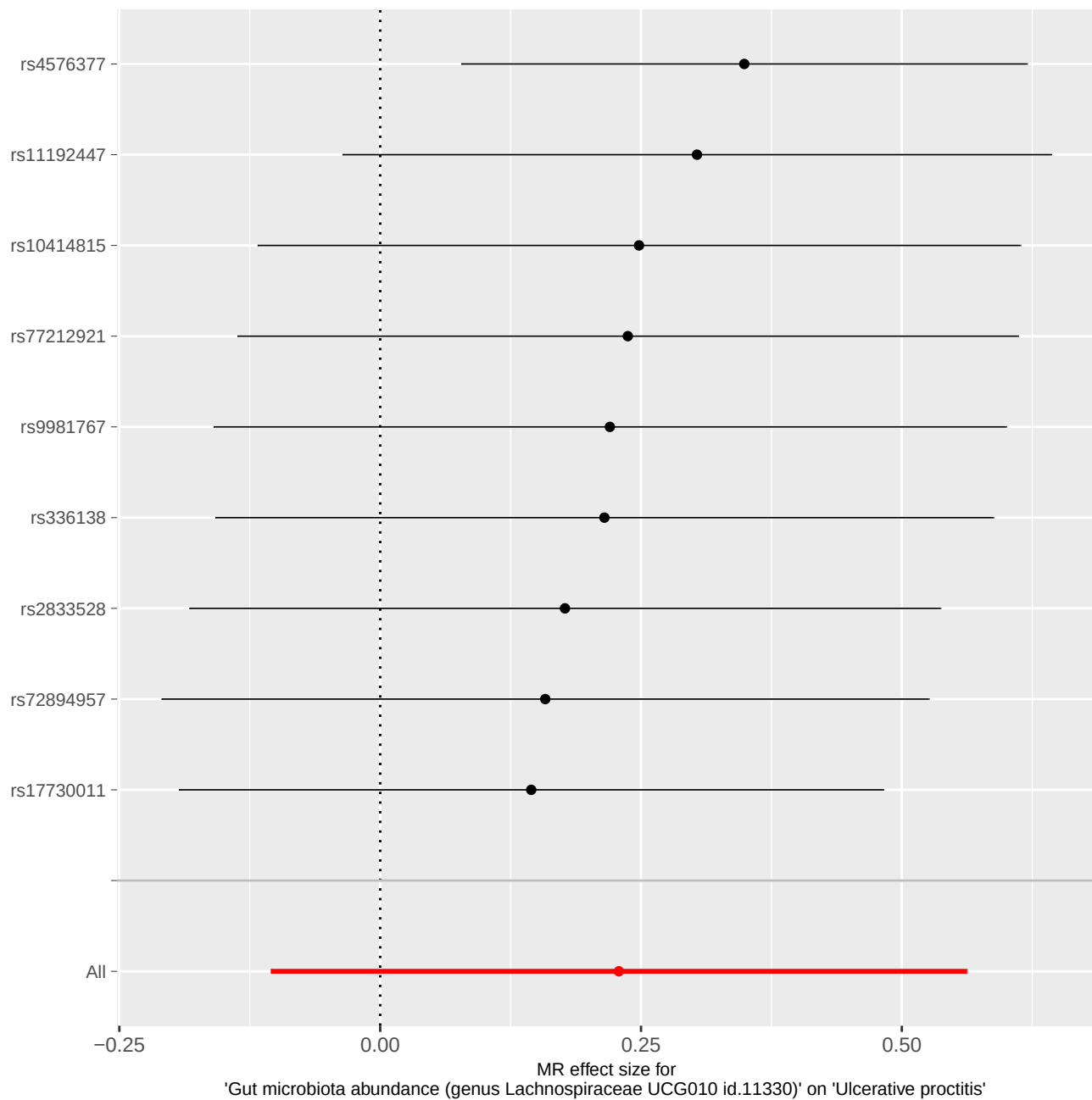


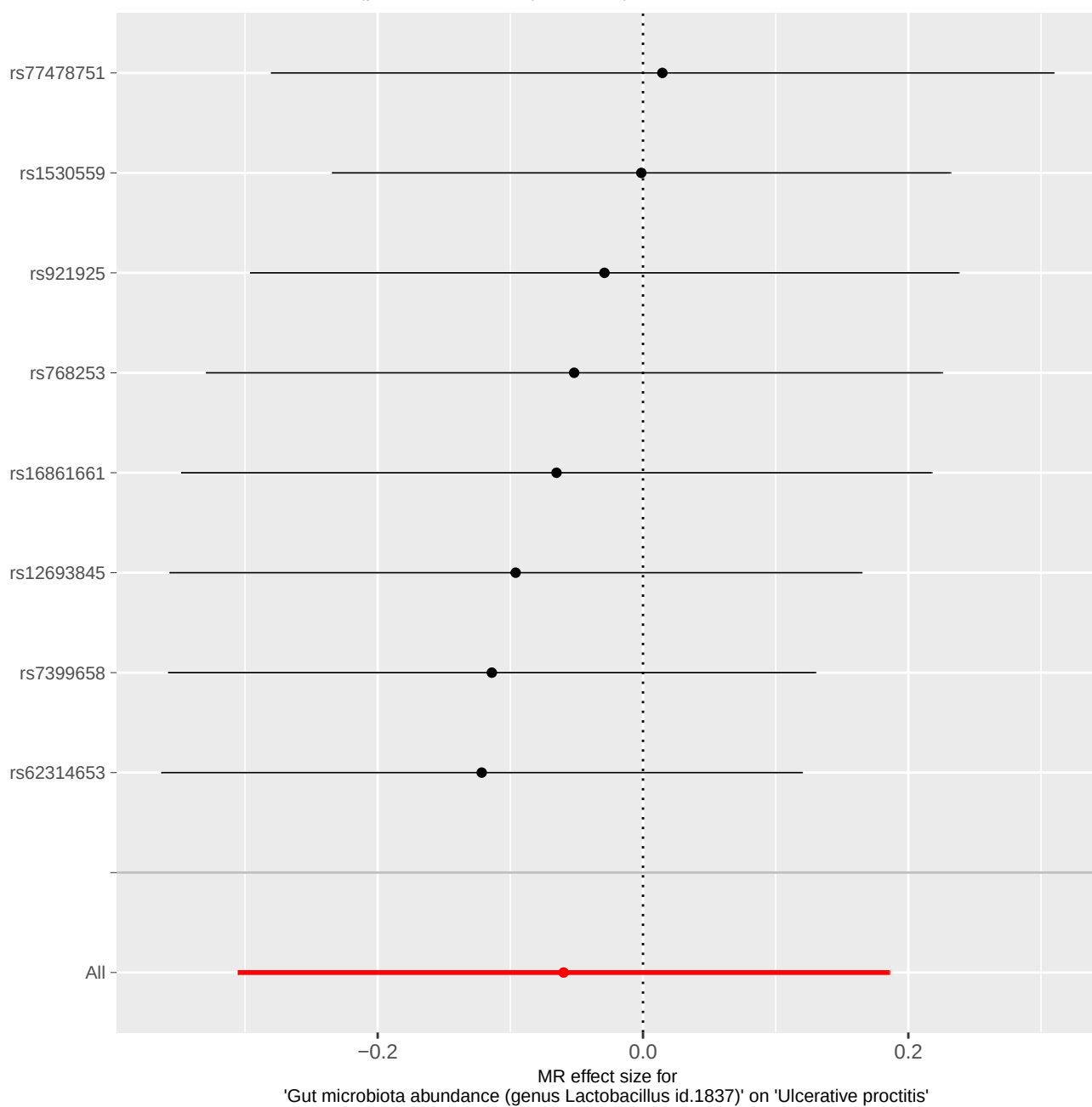




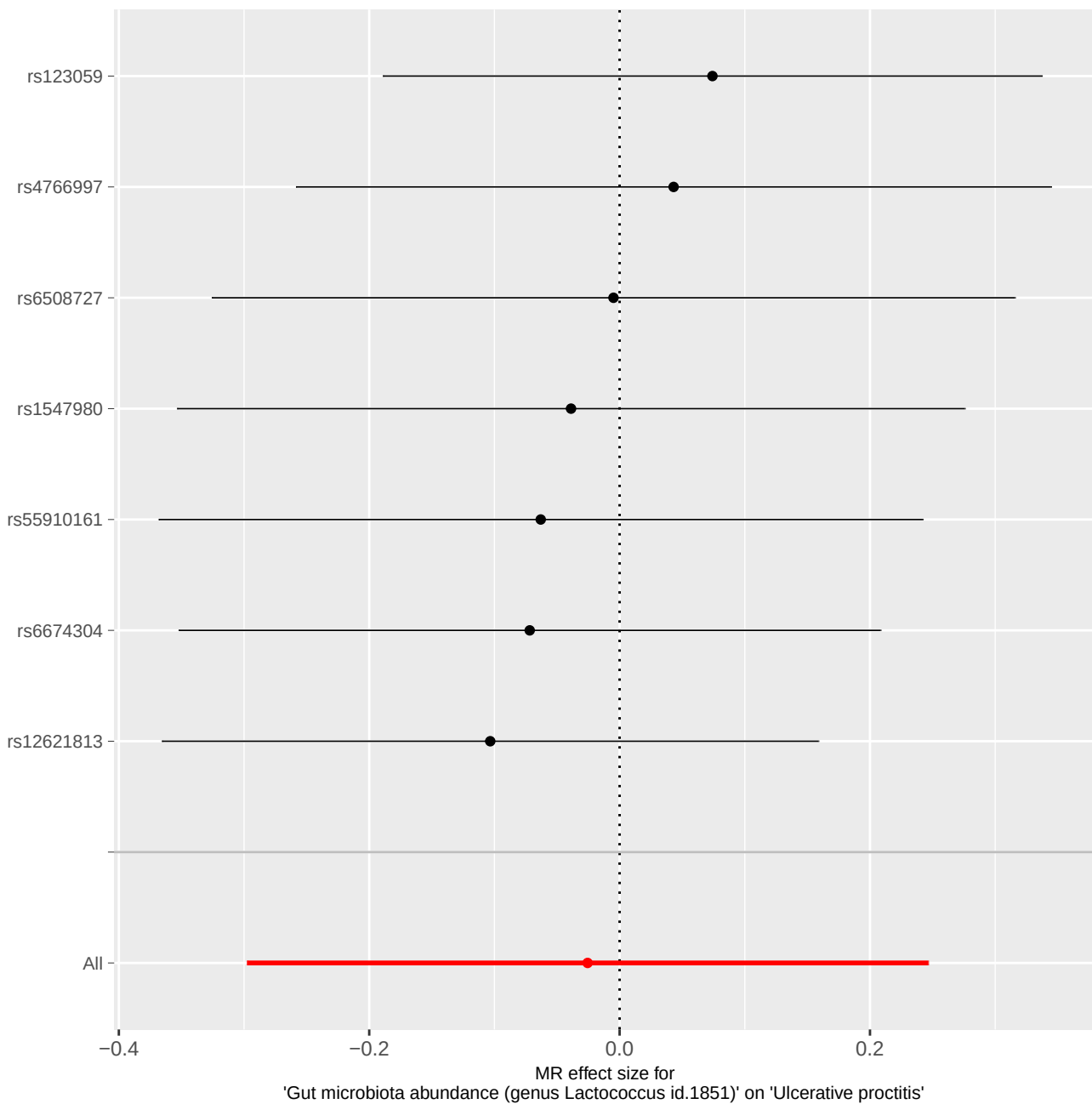


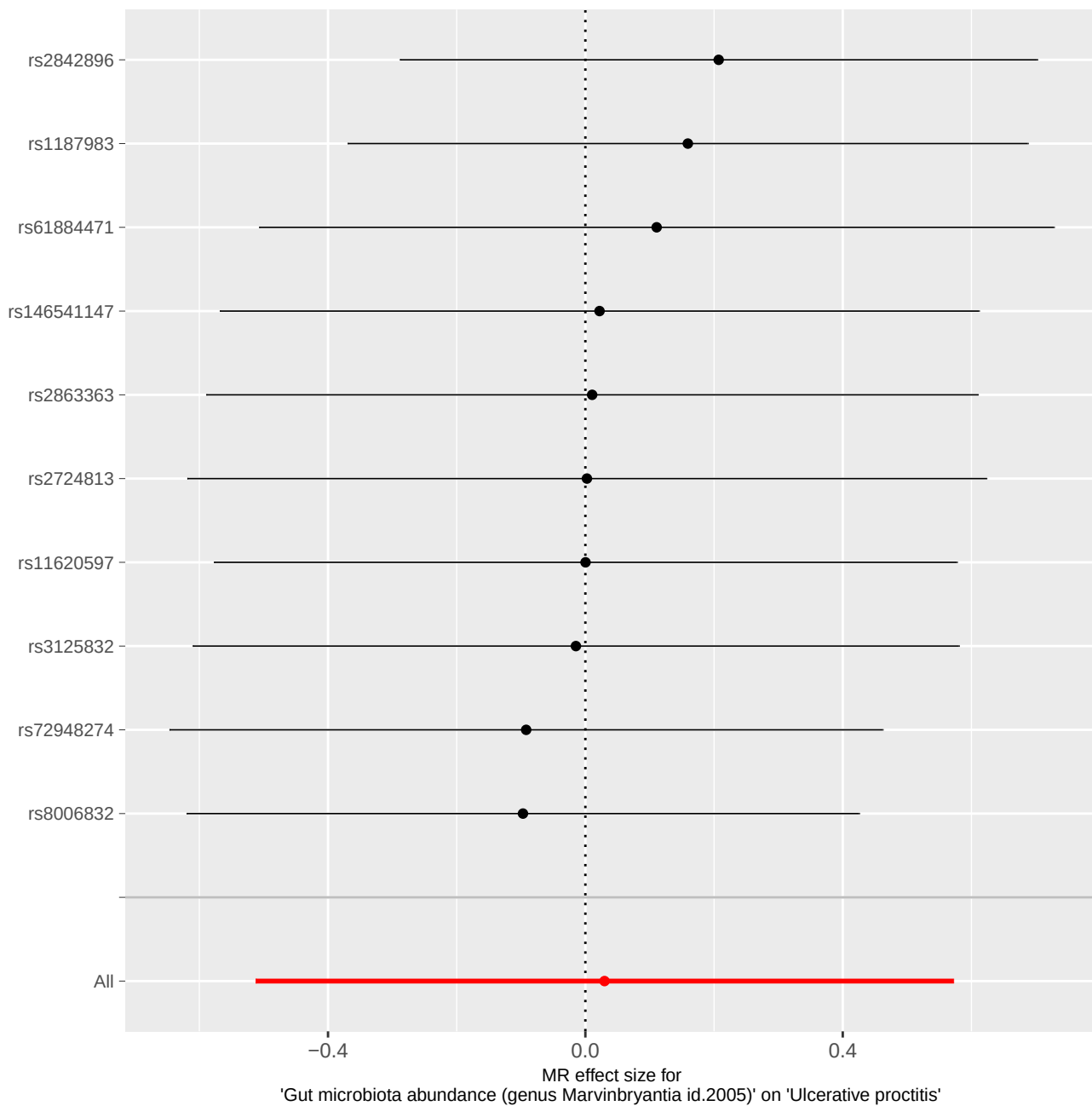
MR effect size for
'Gut microbiota abundance (genus Lachnospiraceae UCG008 id.11328)' on 'Ulcerative proctitis'

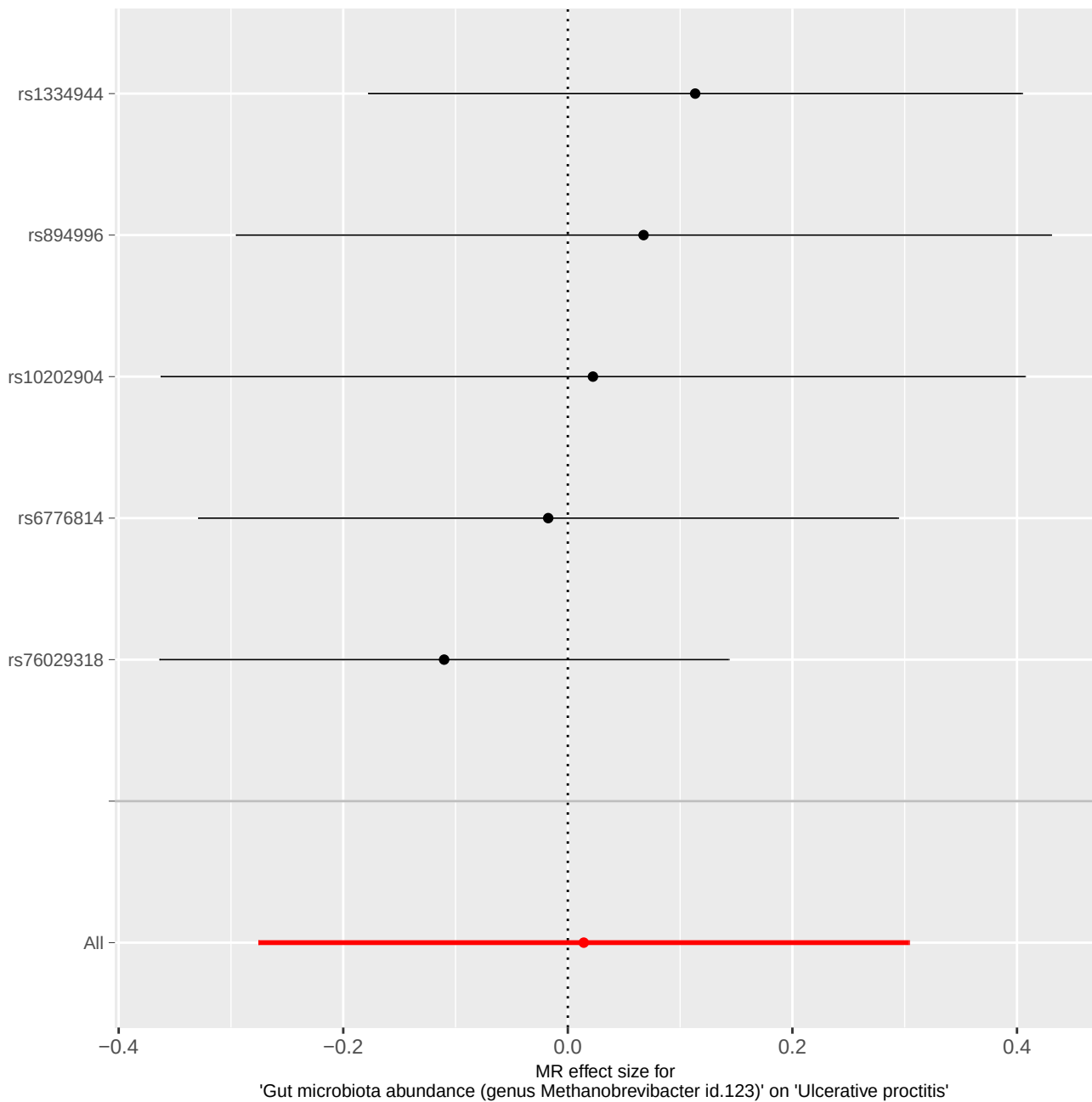




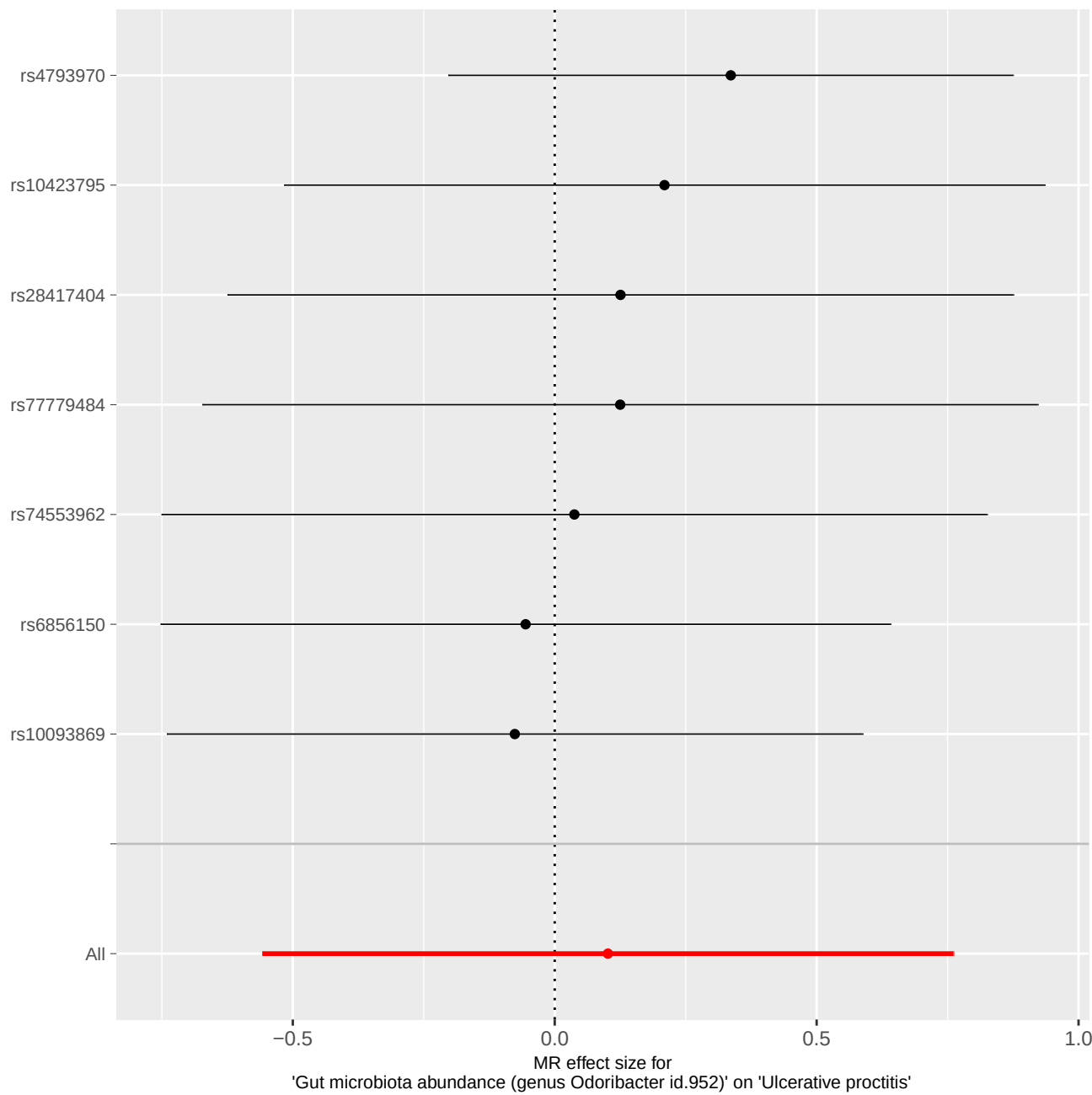
Batch 1455 : Gut microbiota abundance (genus Lactococcus id.1851) on Ulcerative proctitis

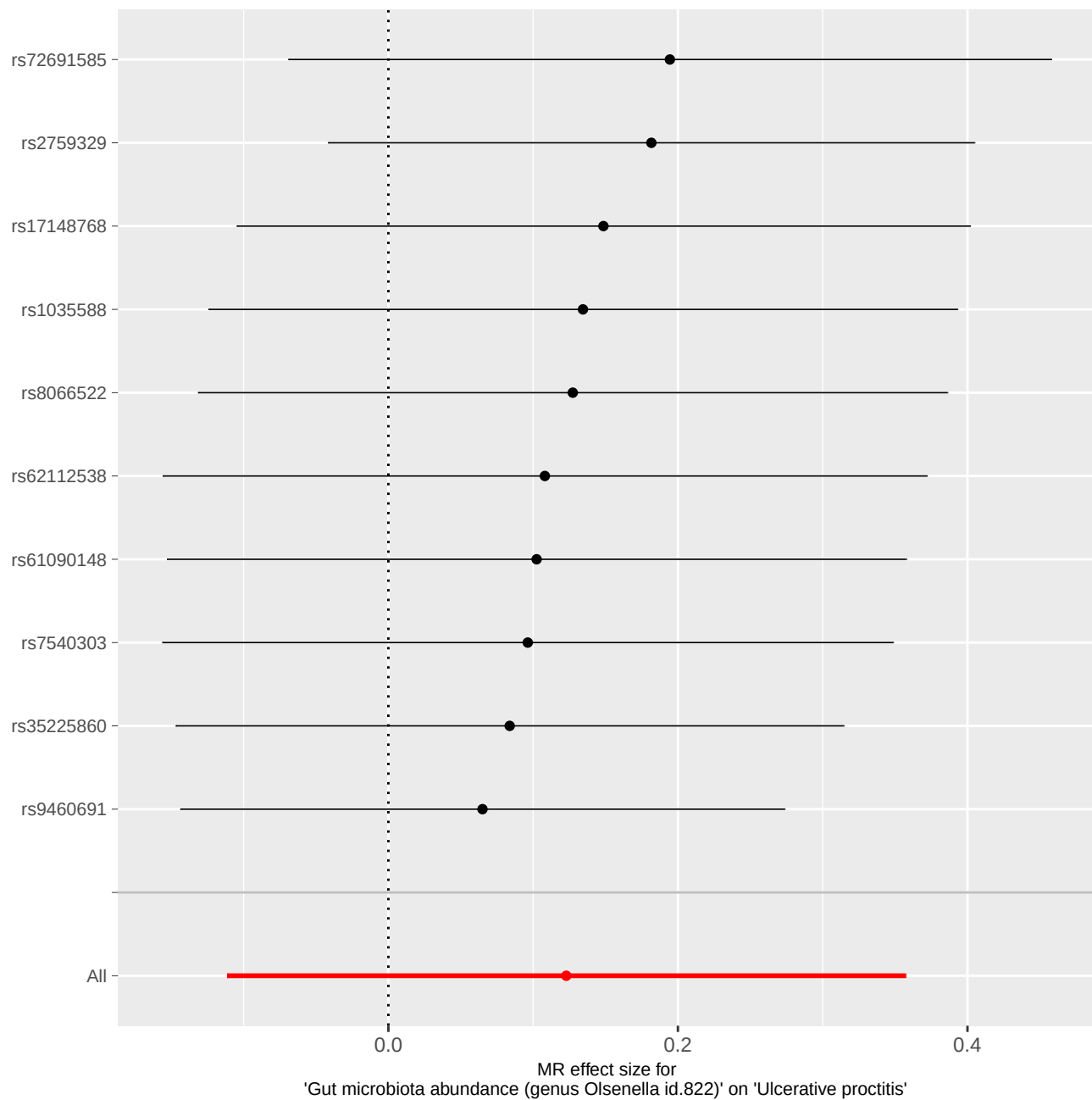


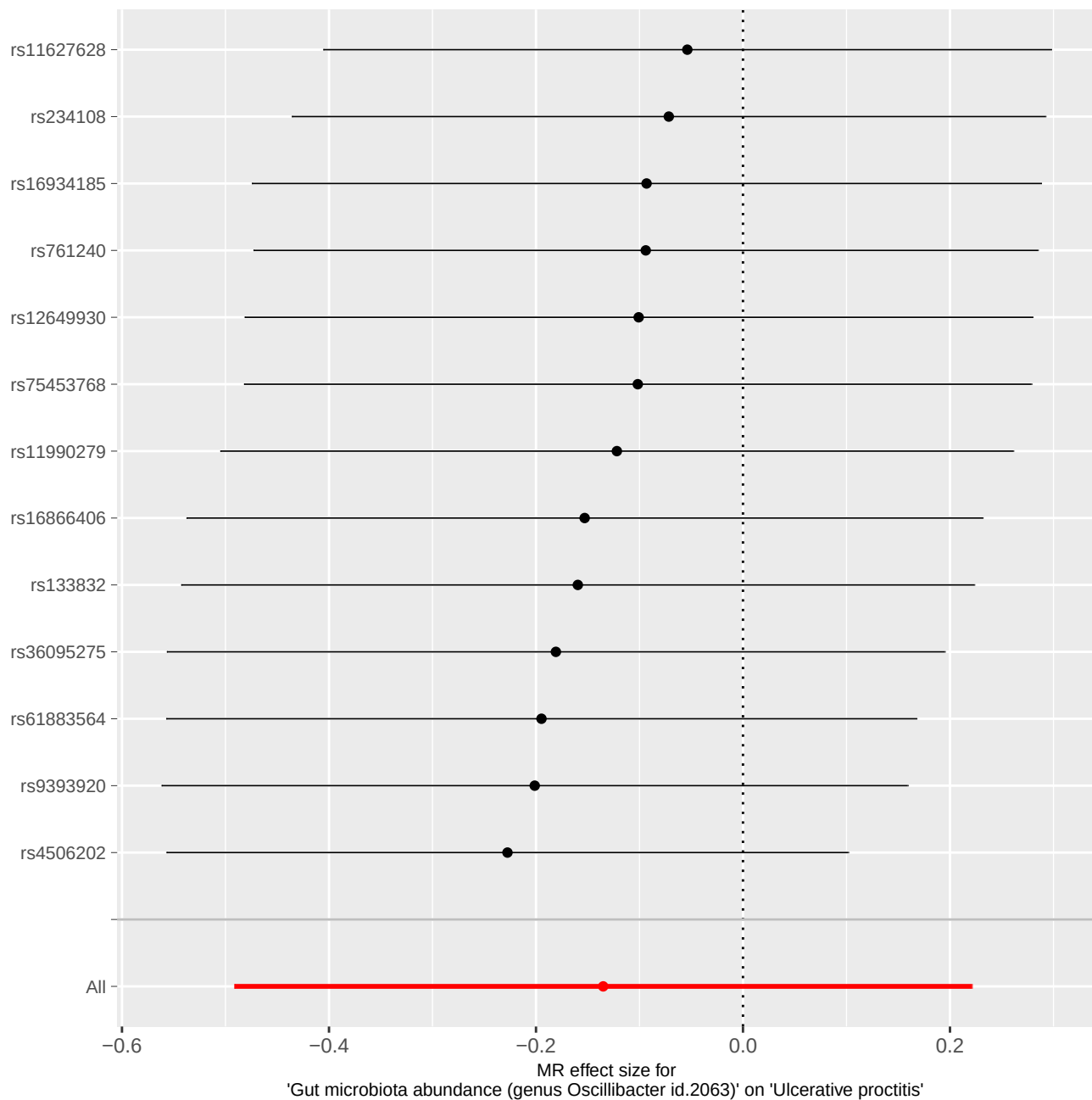


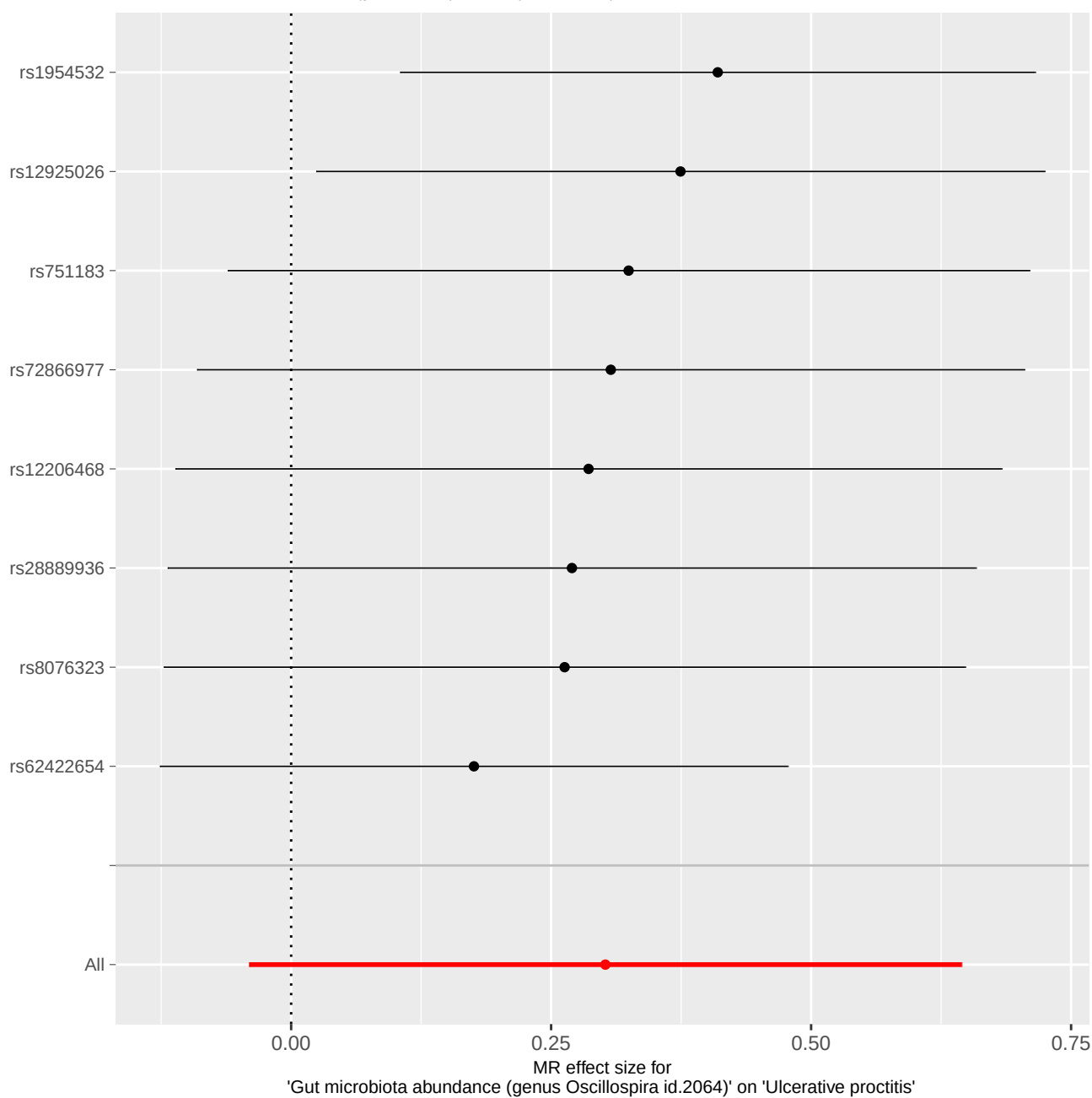


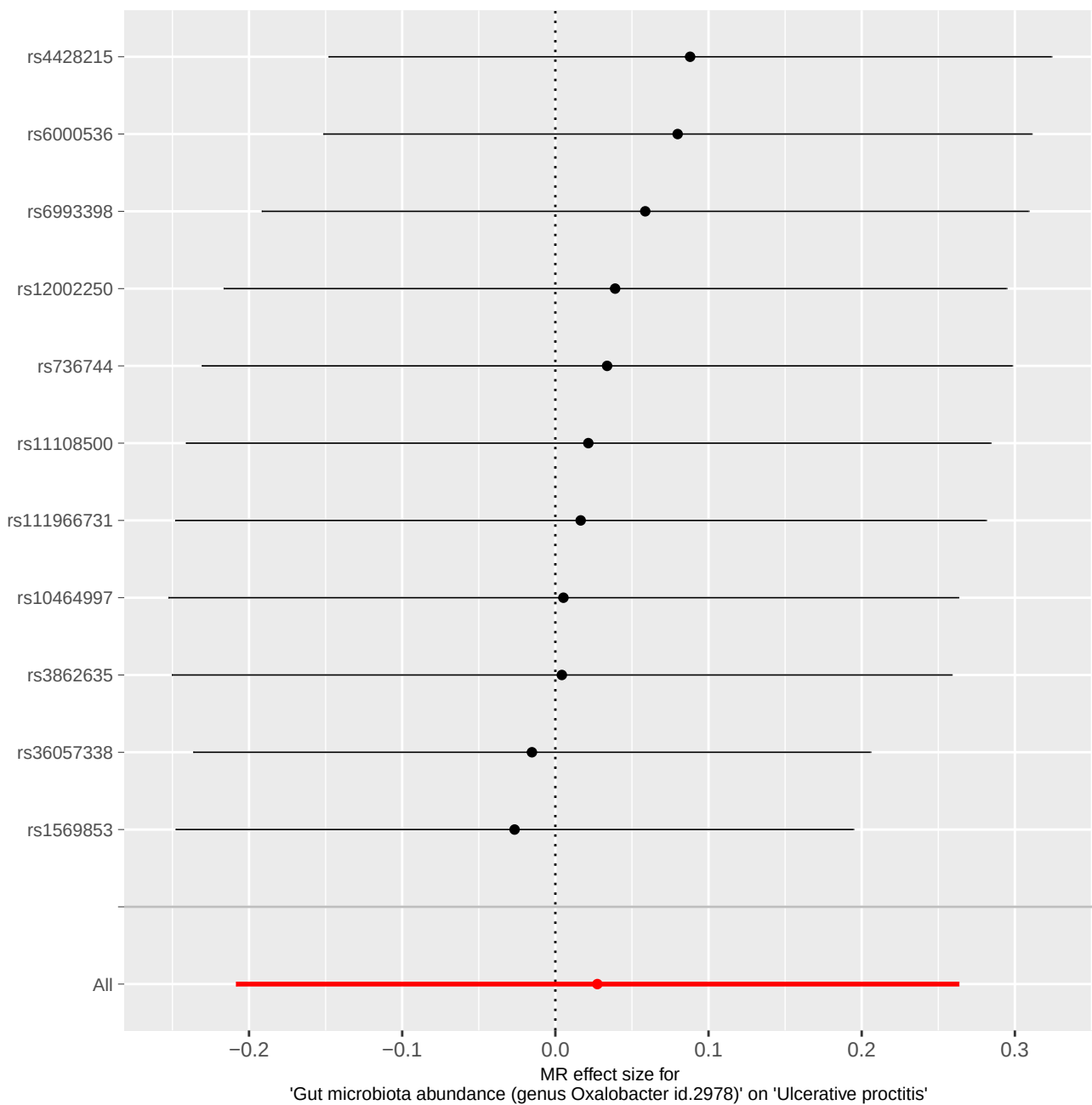
Batch 1458 : Gut microbiota abundance (genus Odoribacter id.952) on Ulcerative proctitis

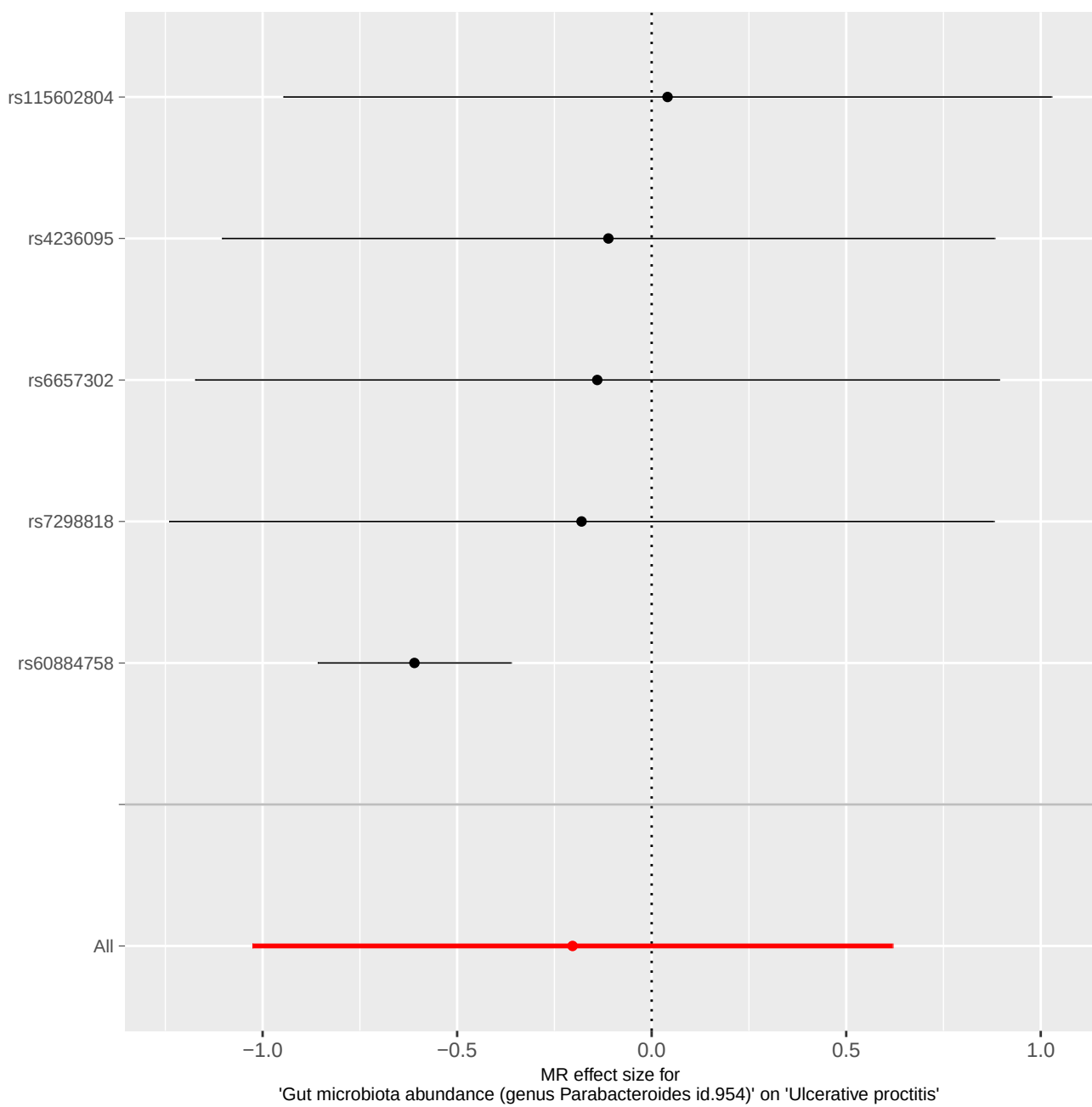


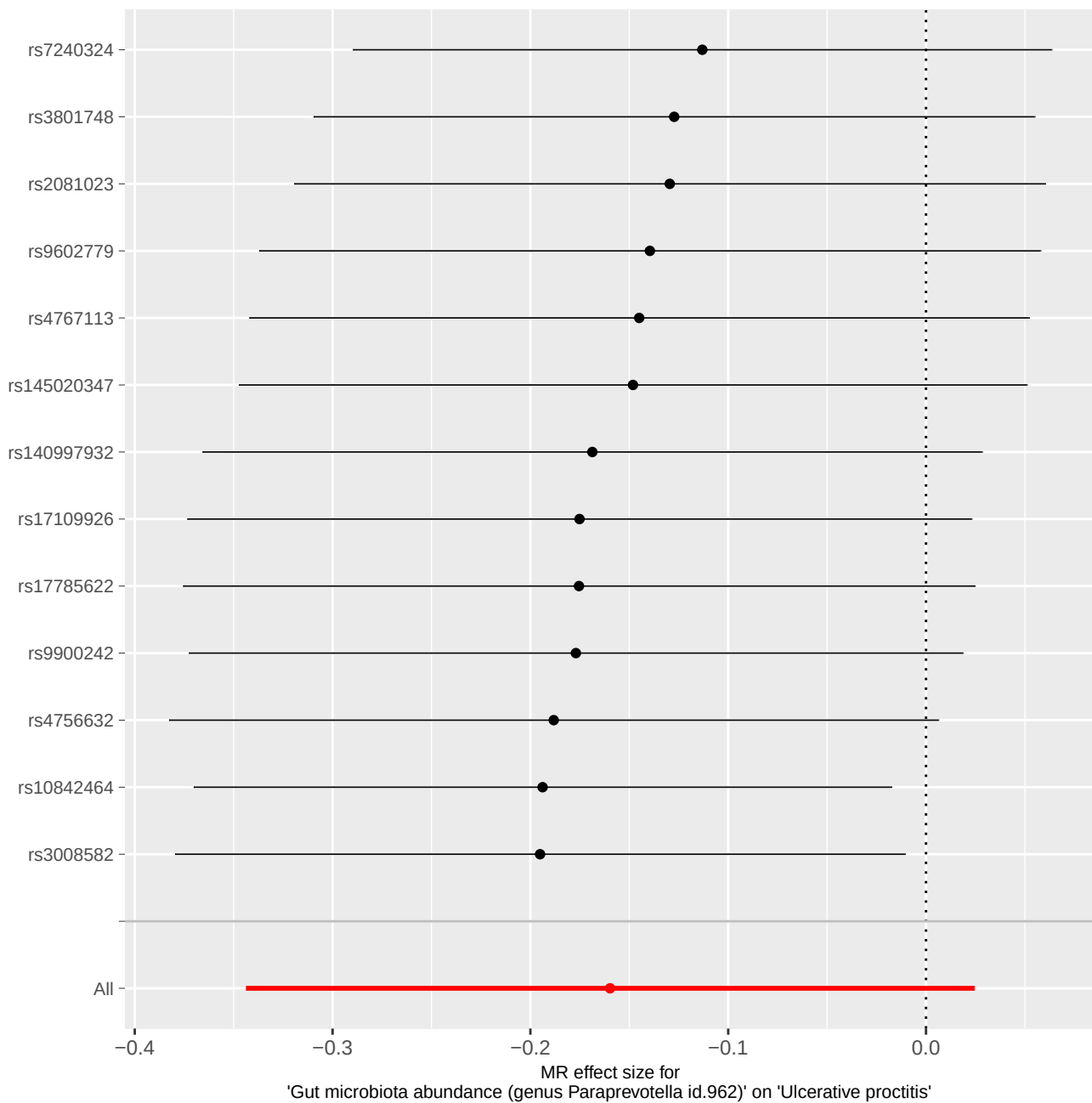


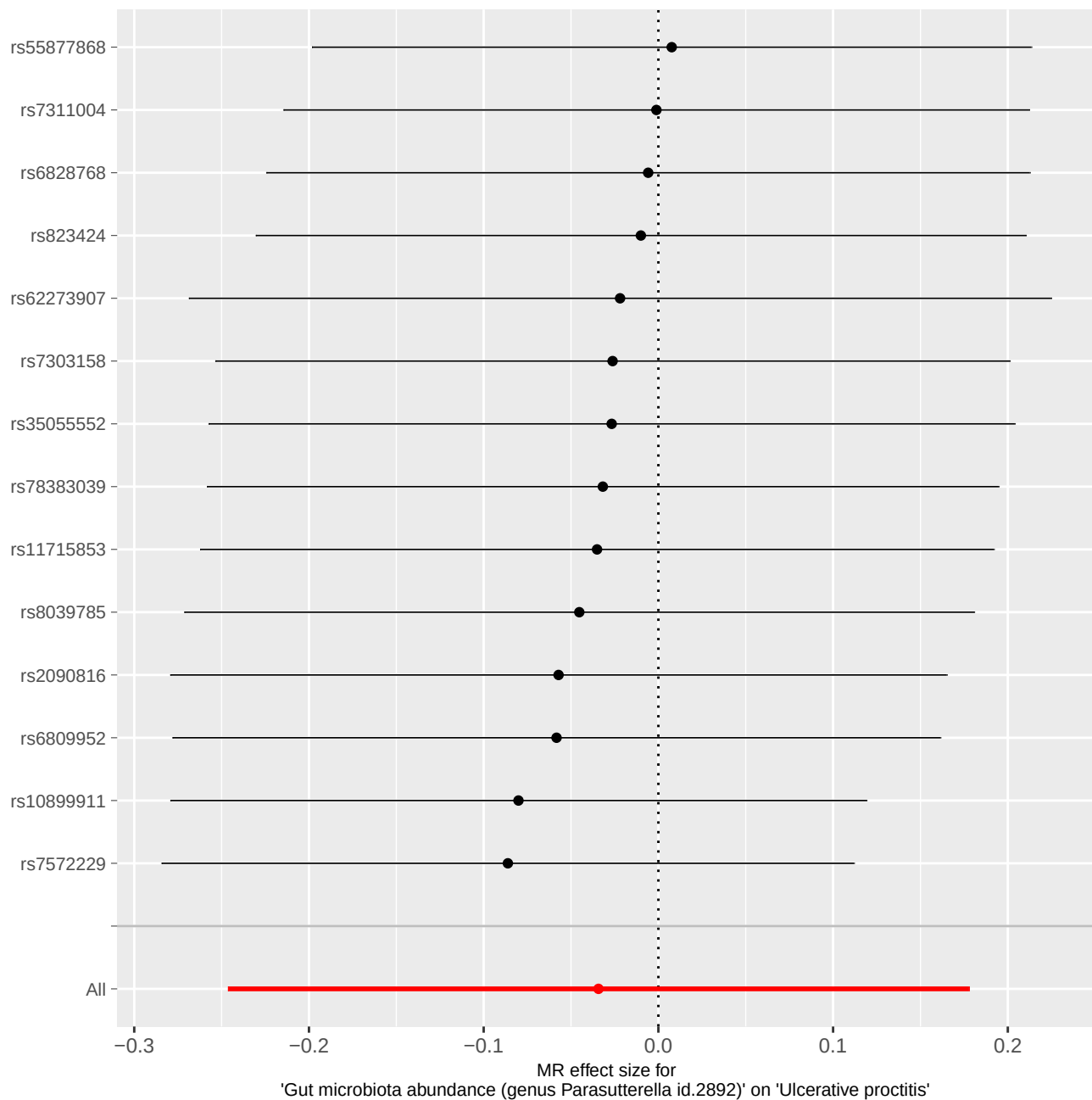


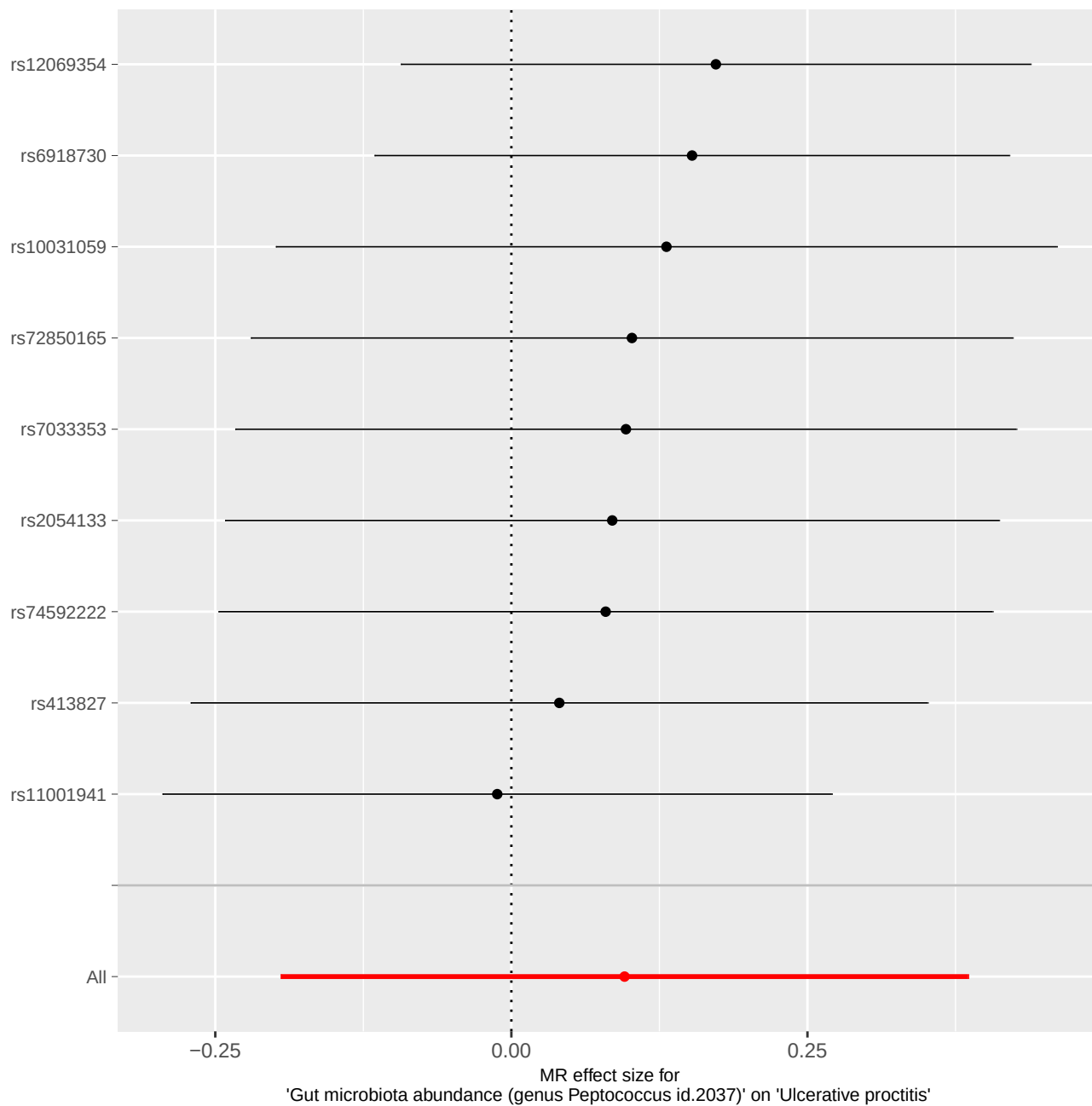


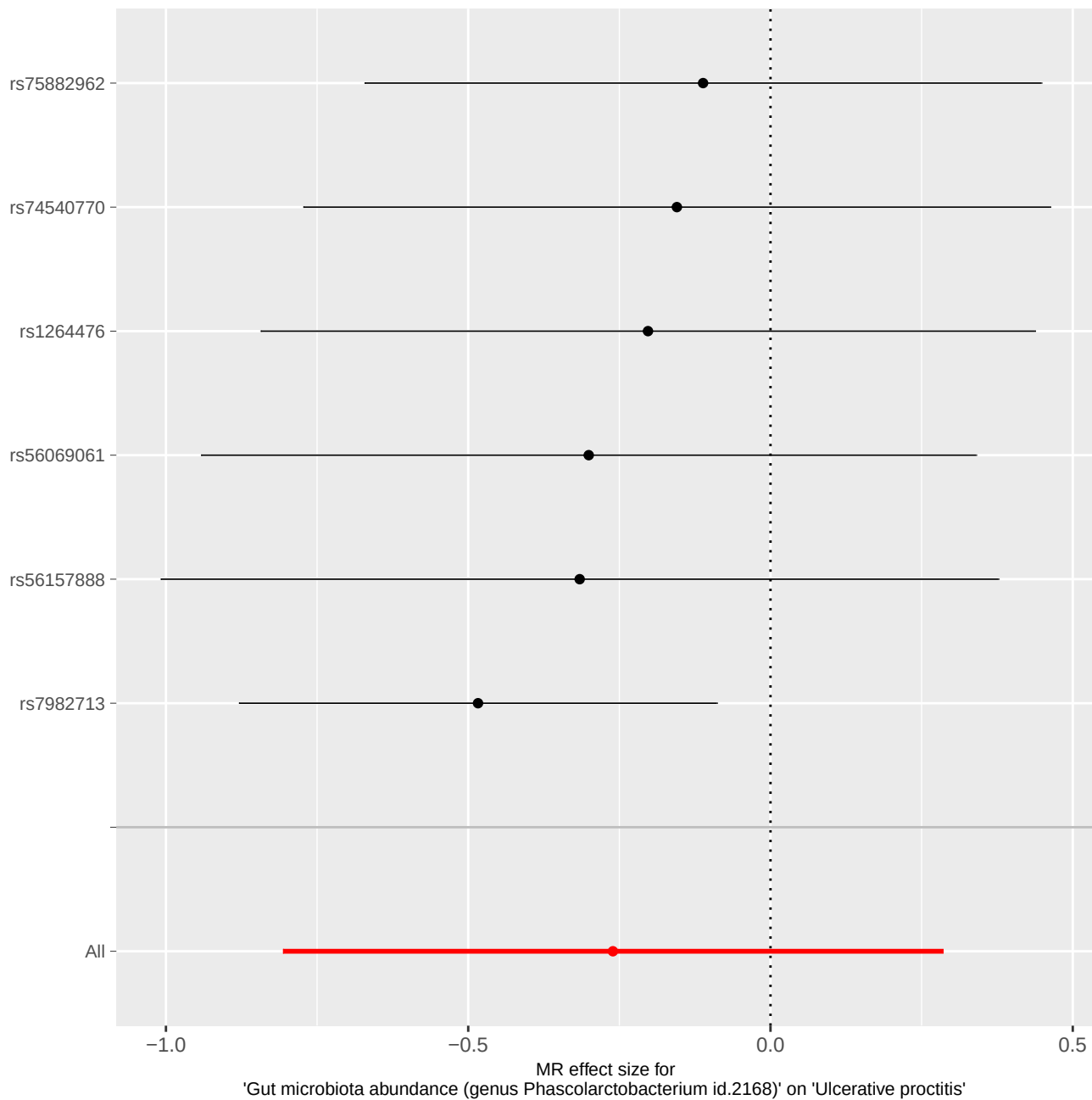


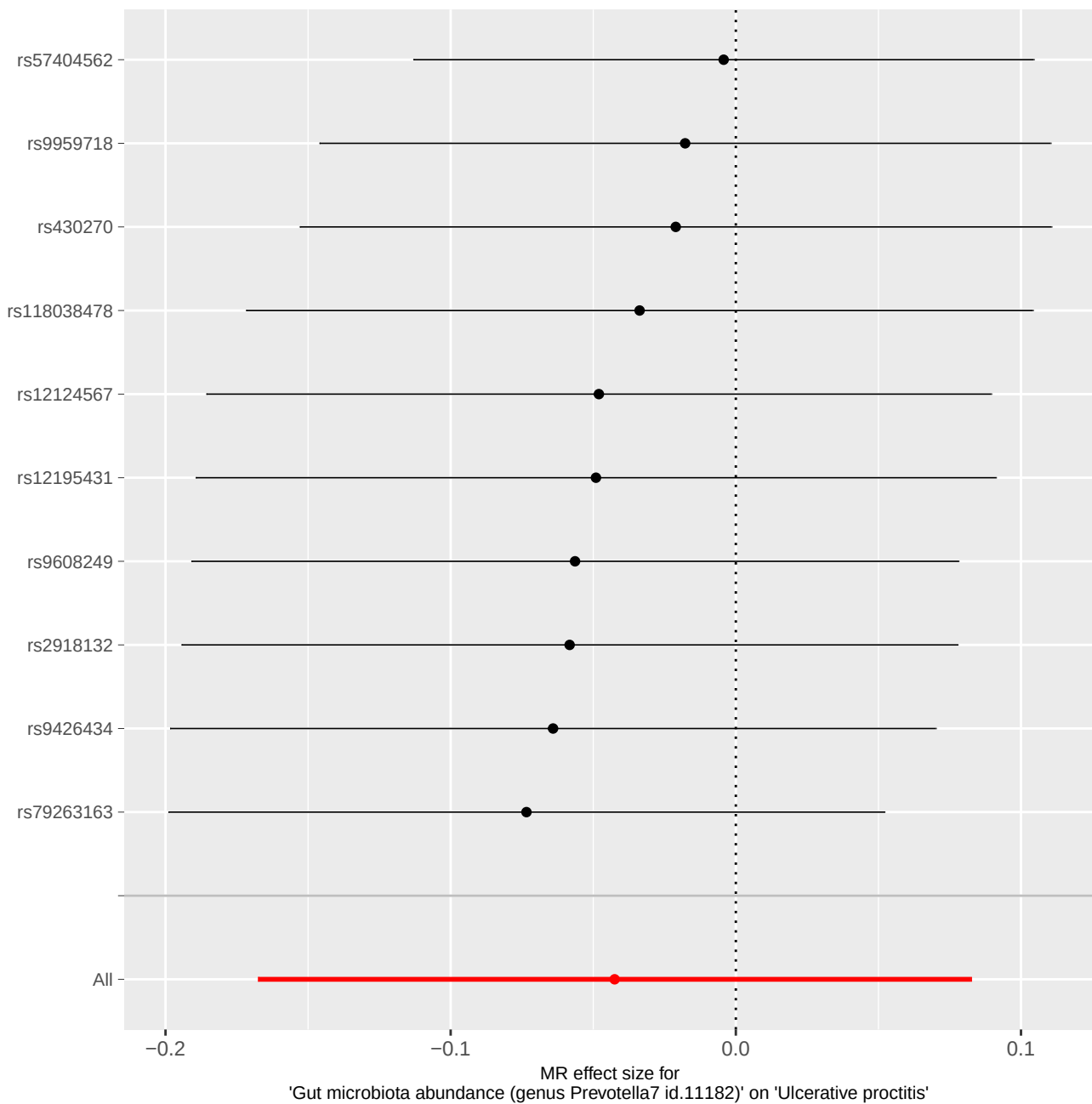


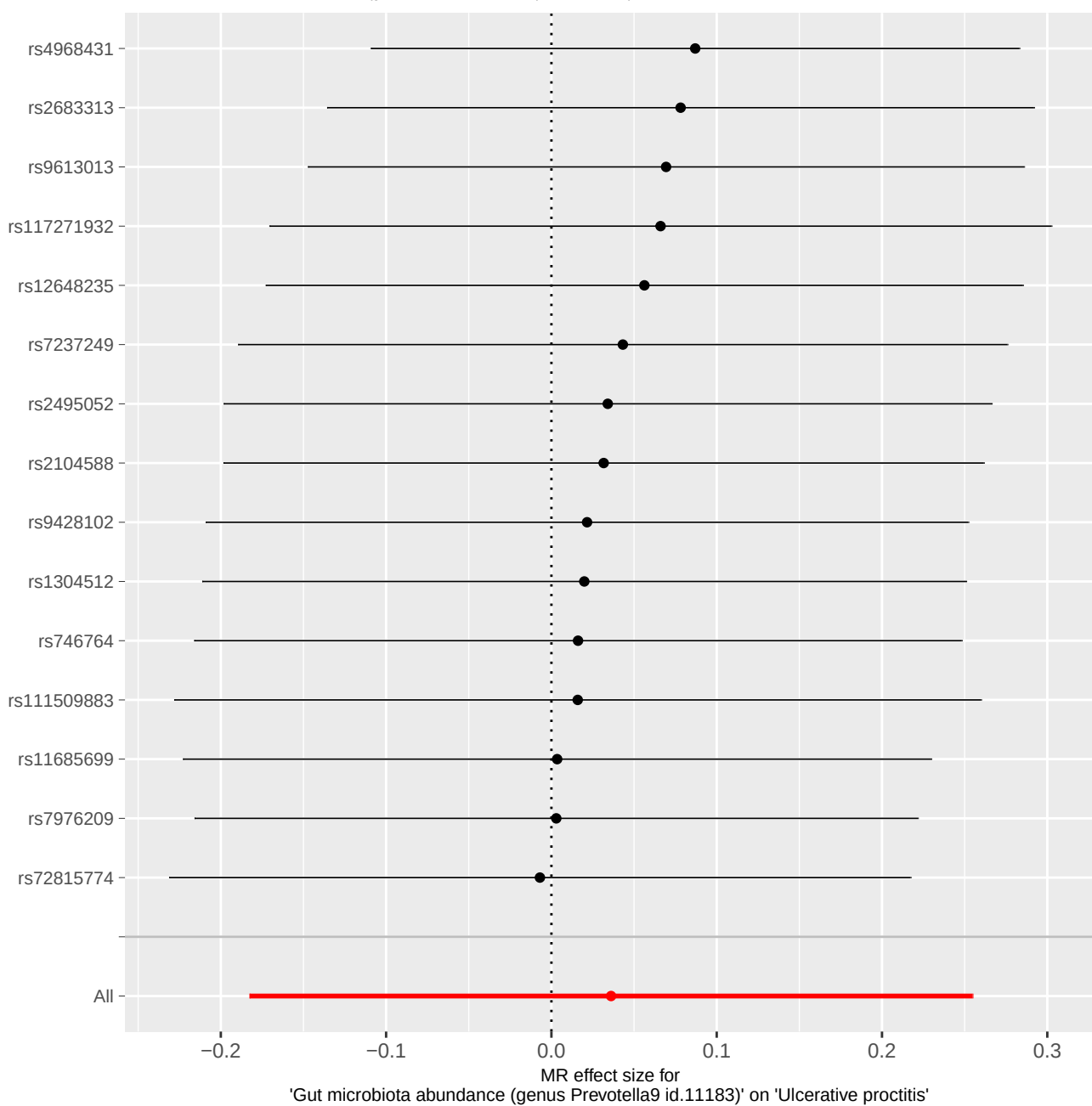


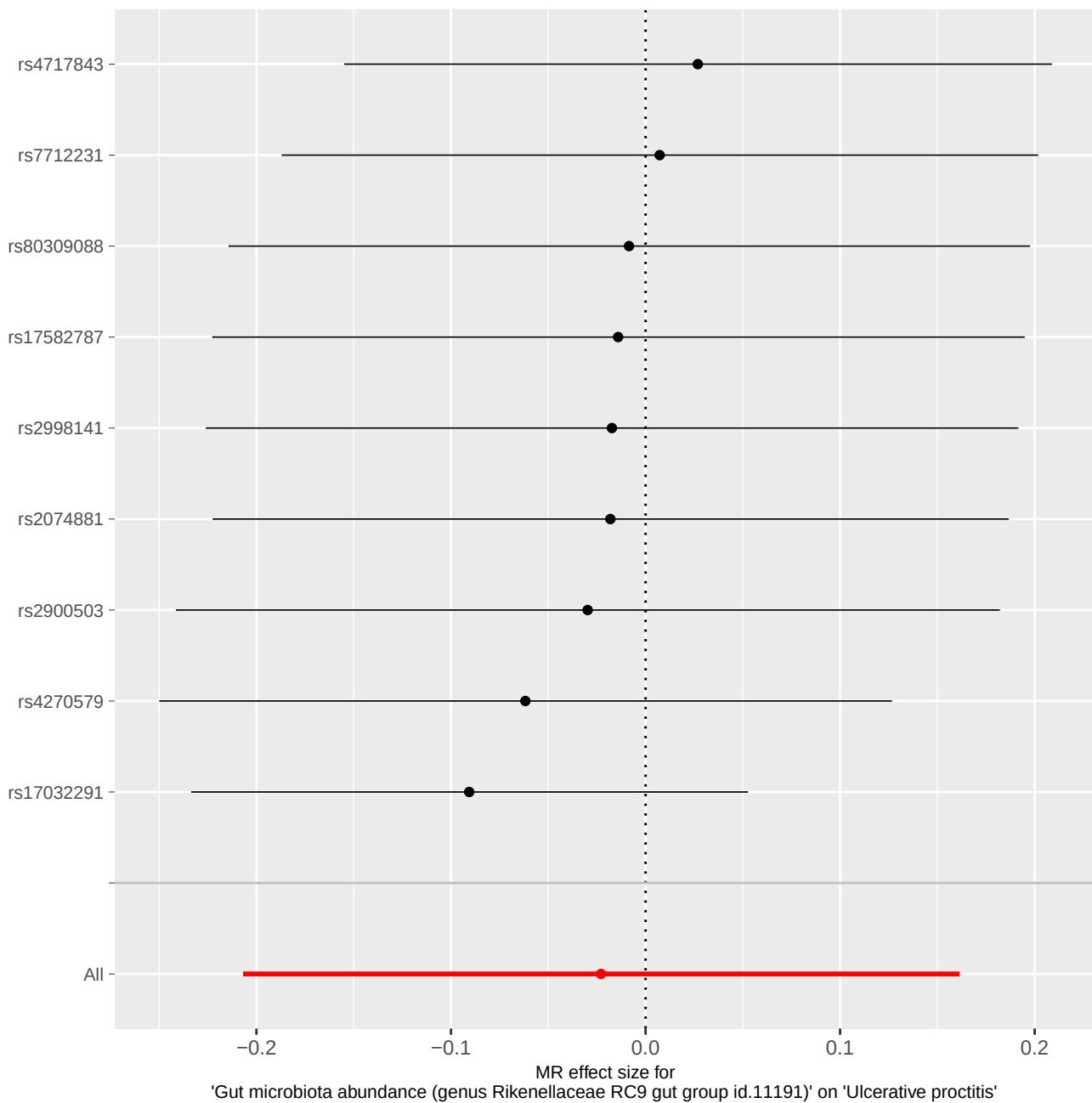


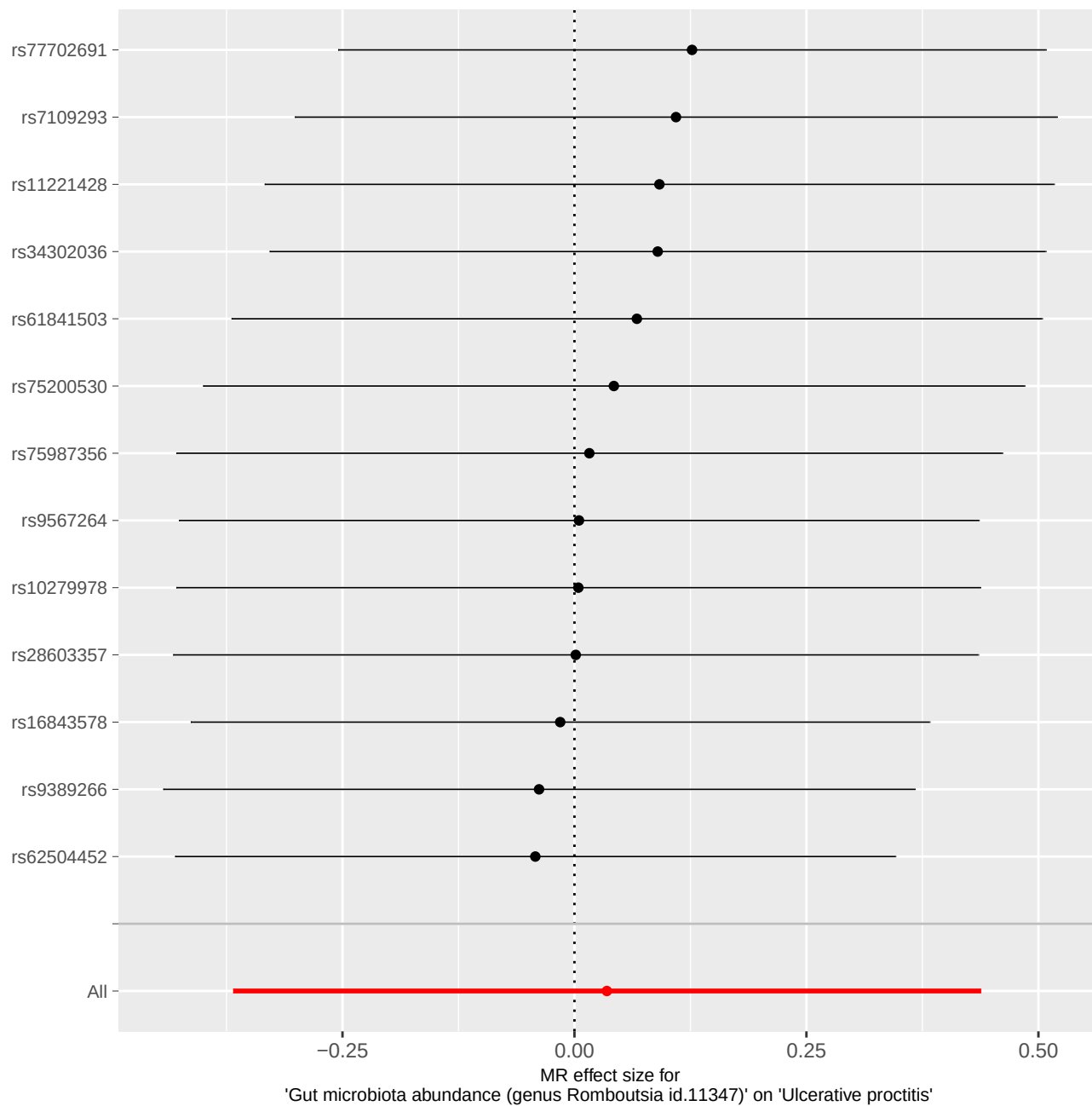


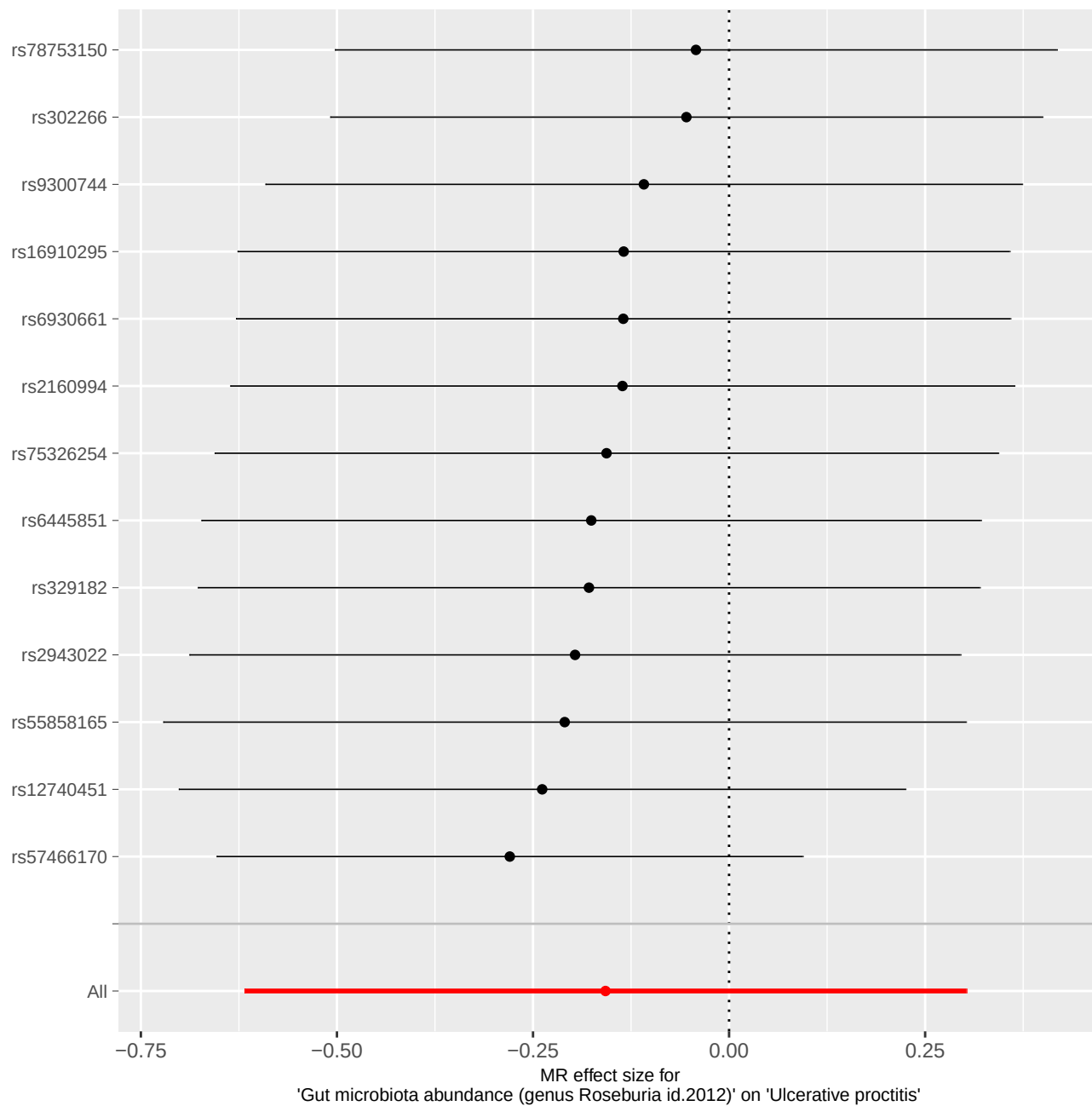


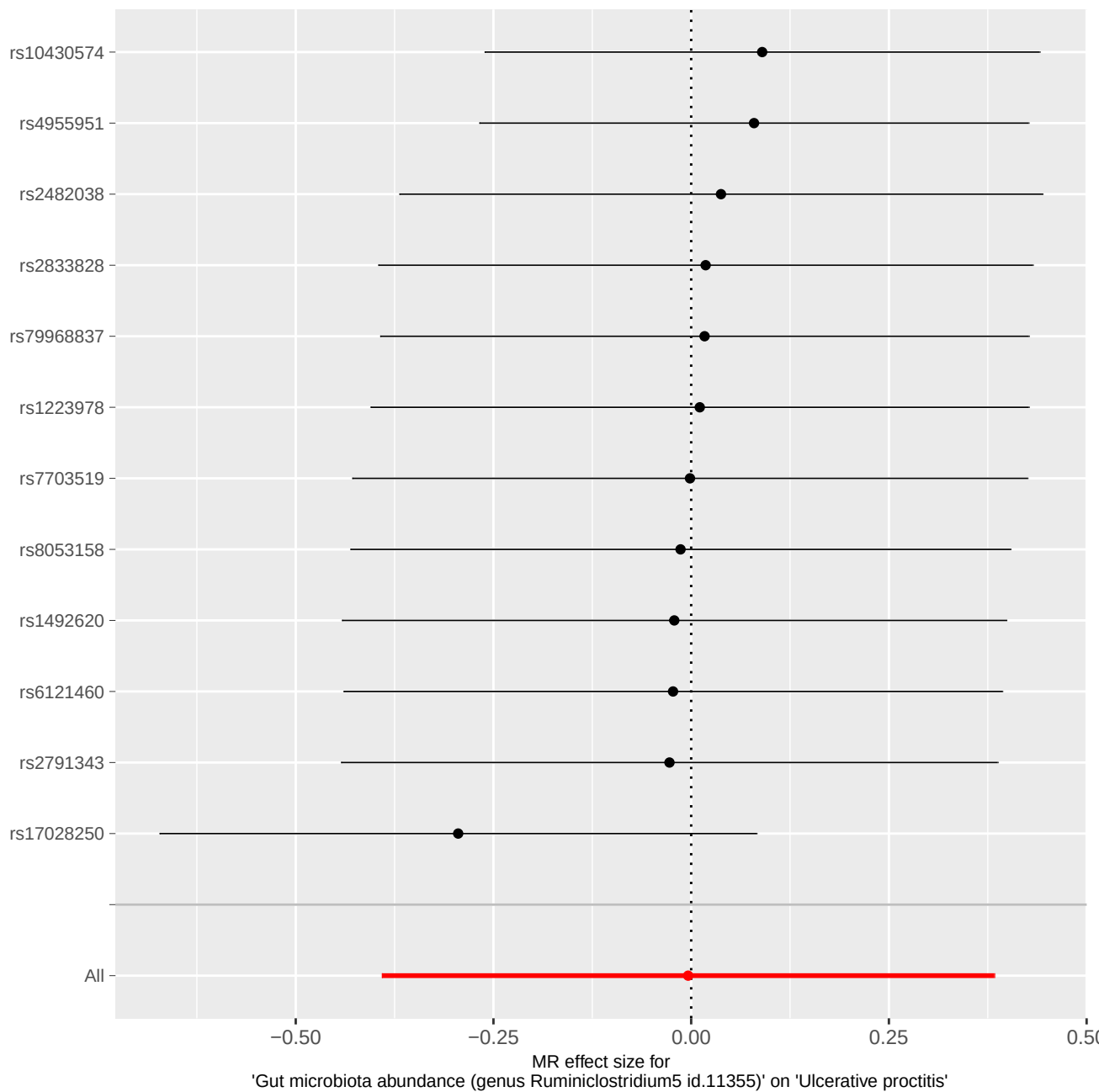


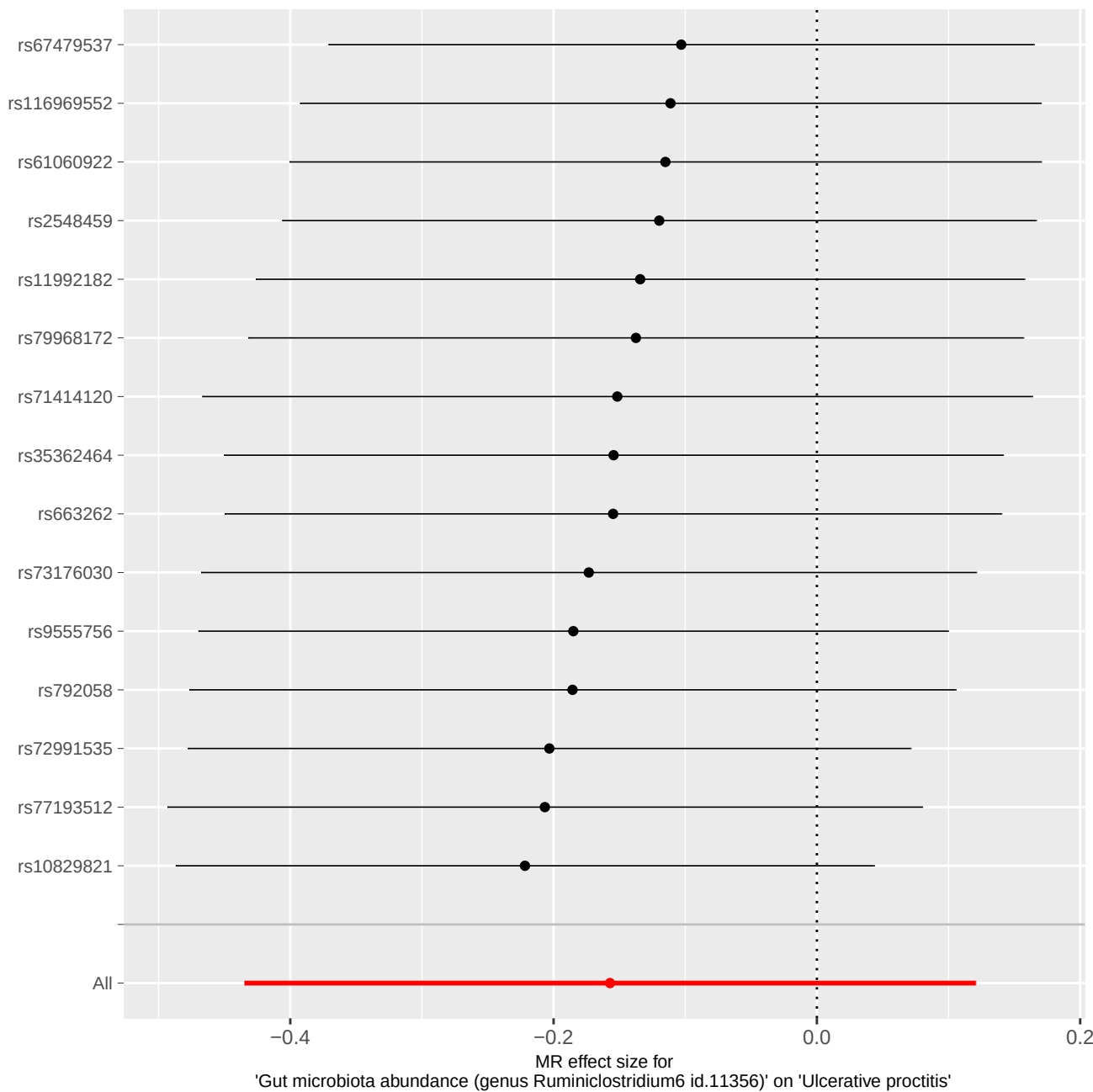


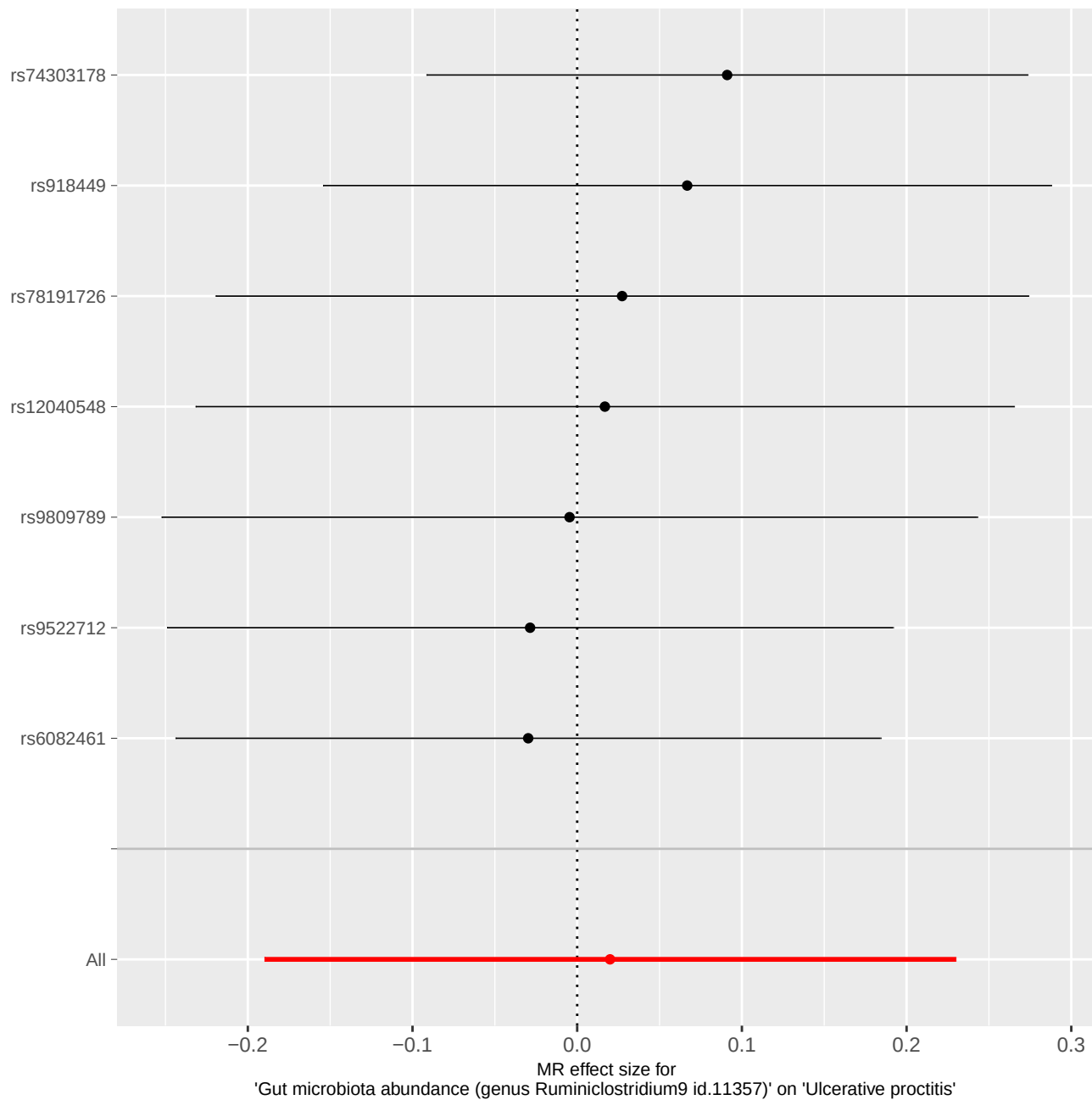


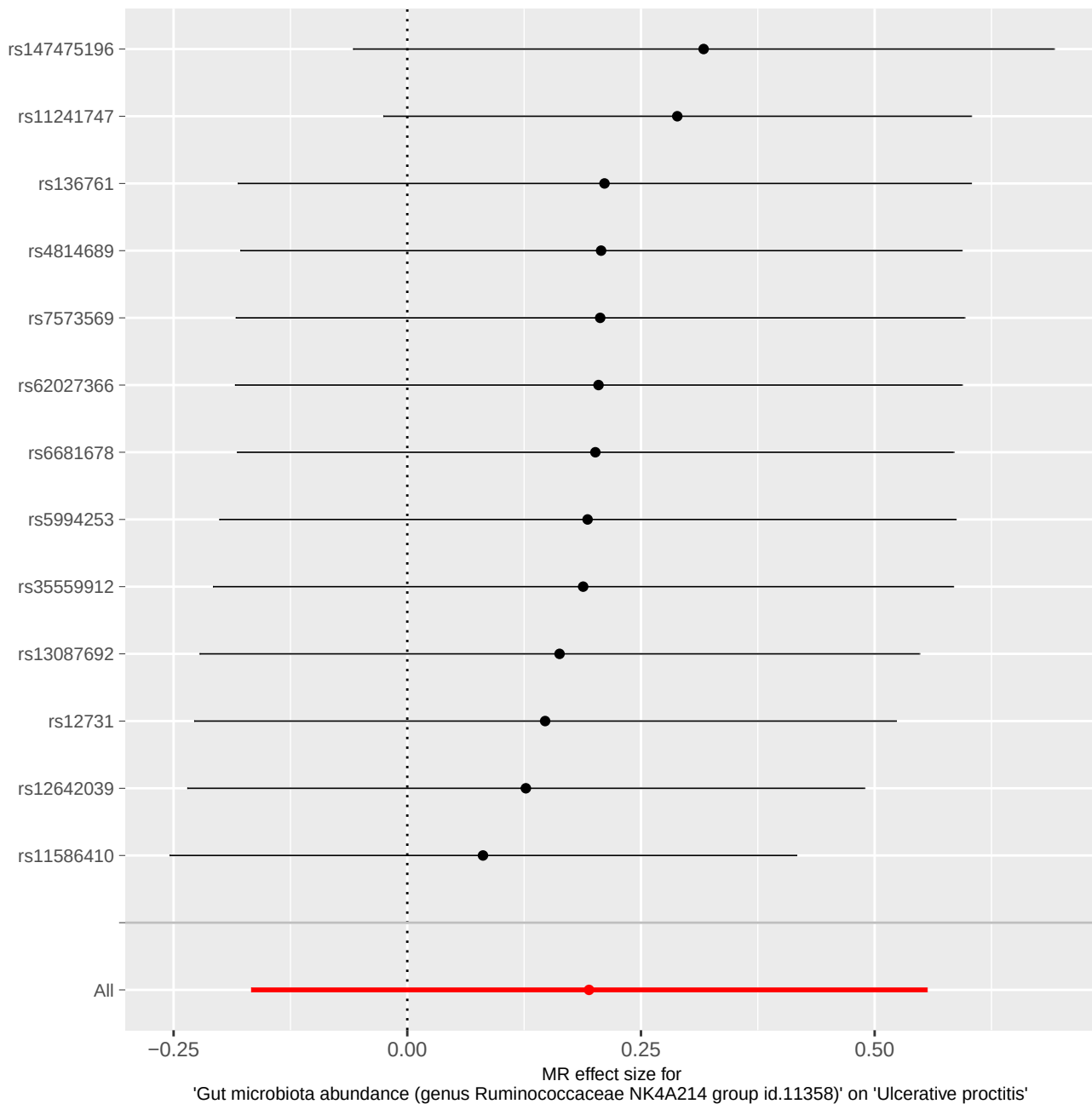


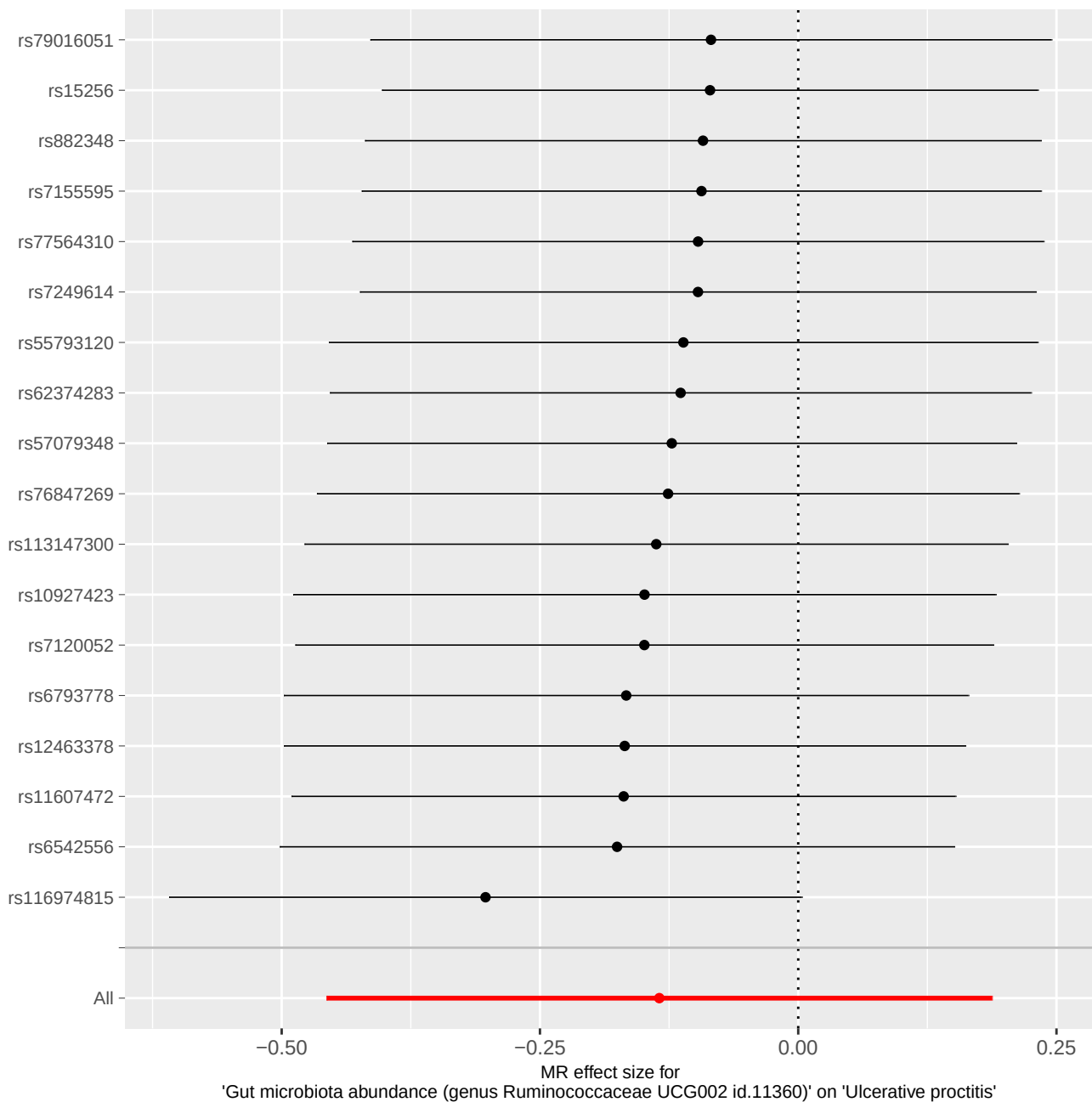


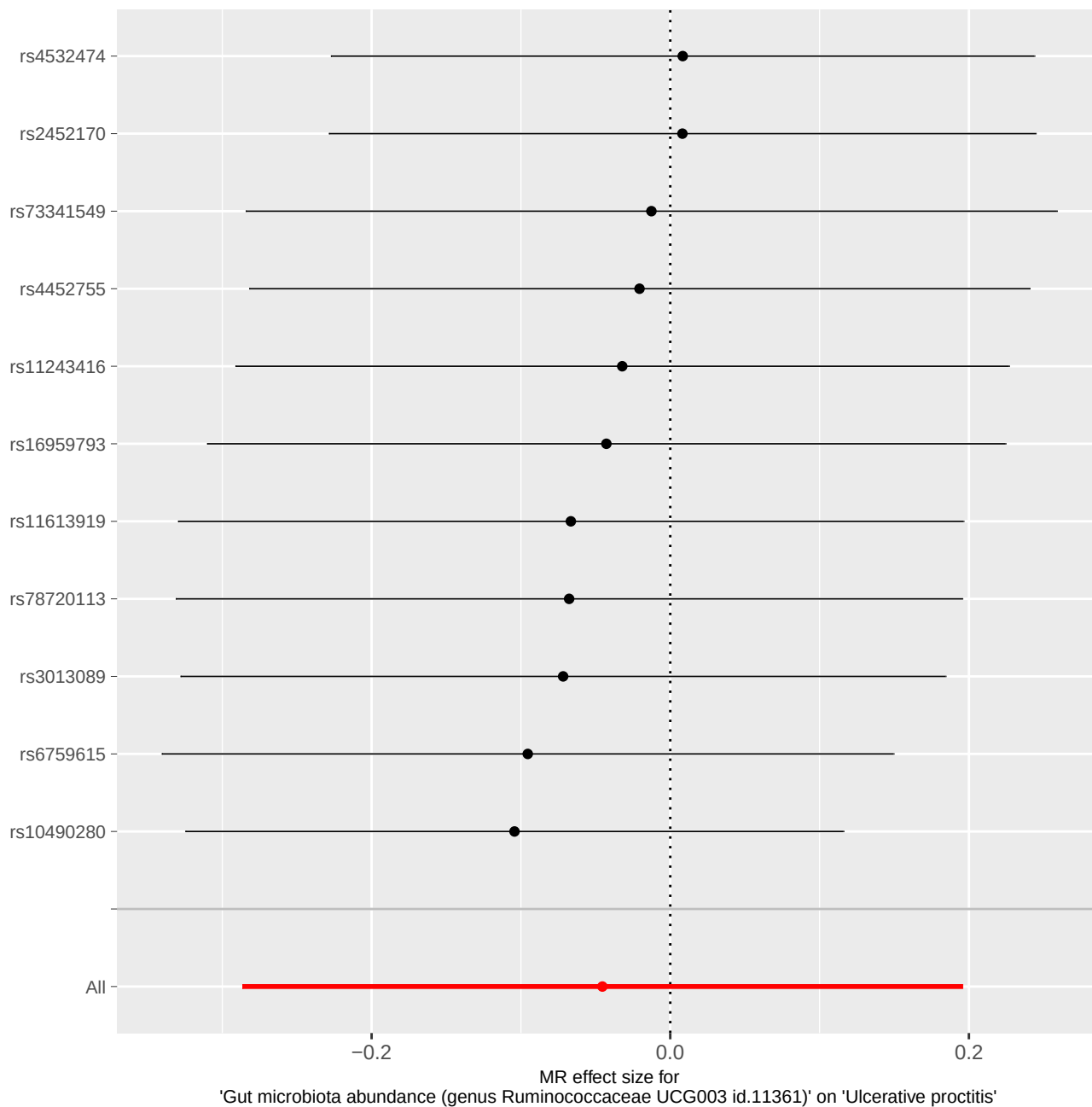


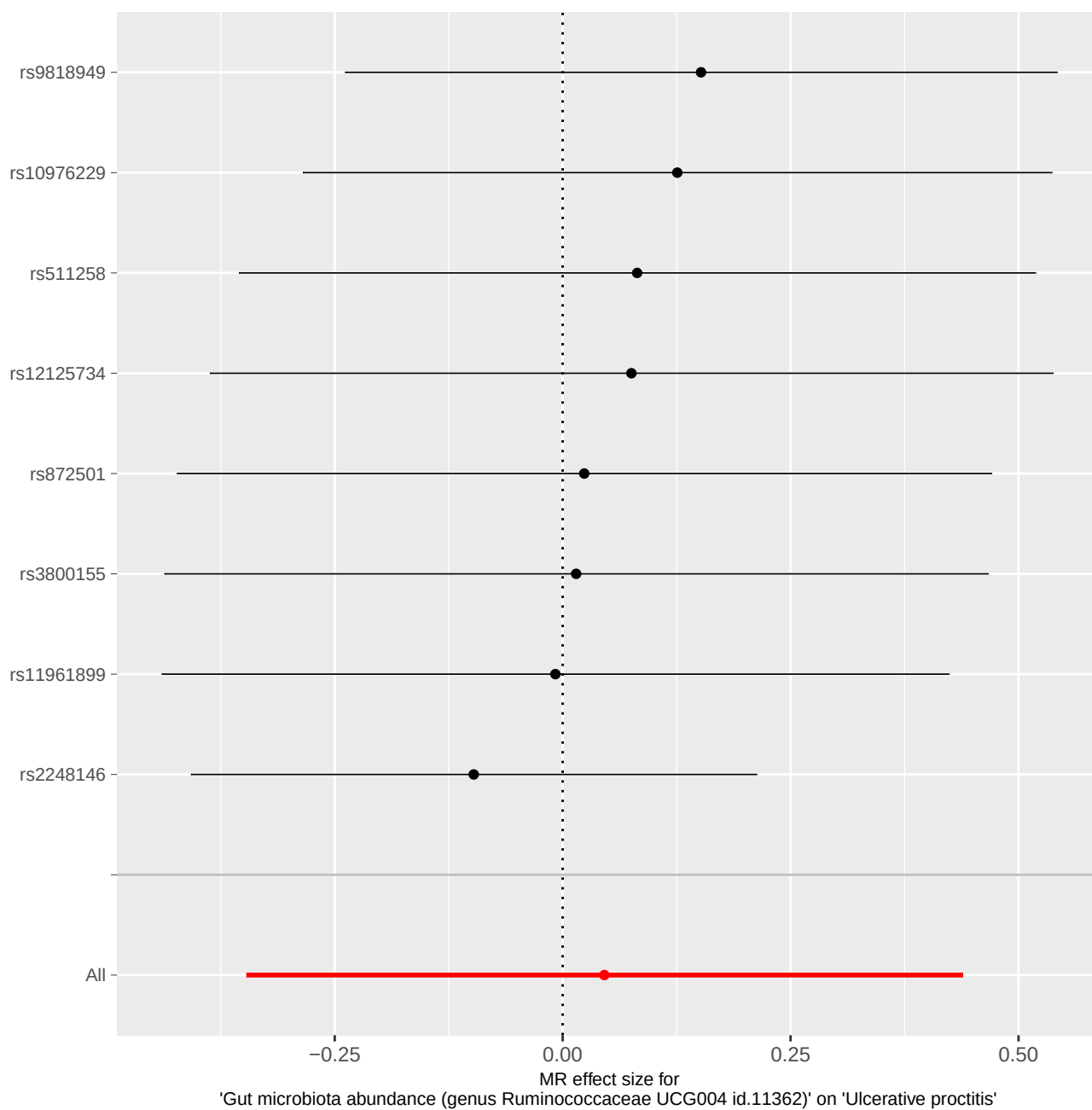


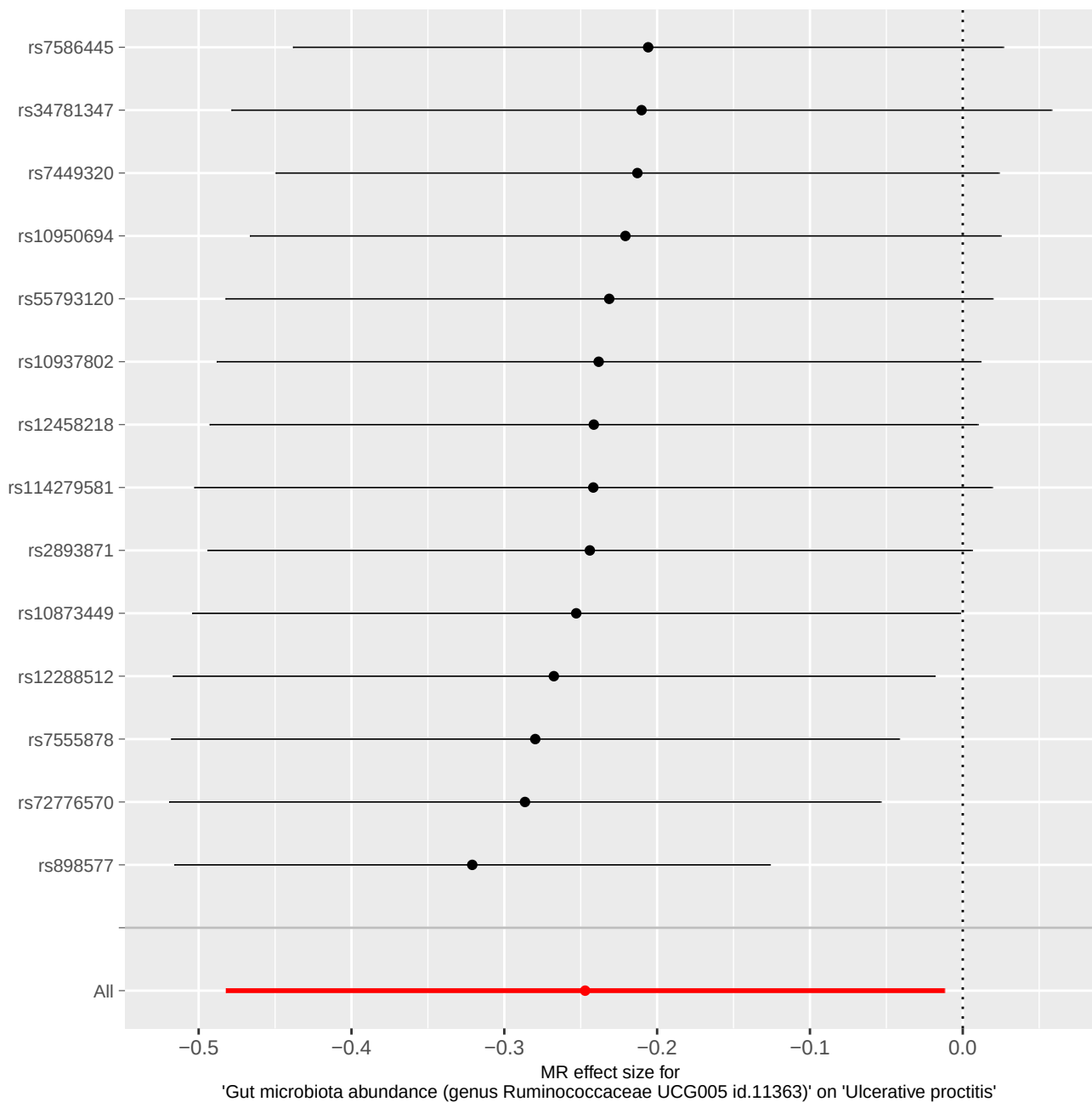


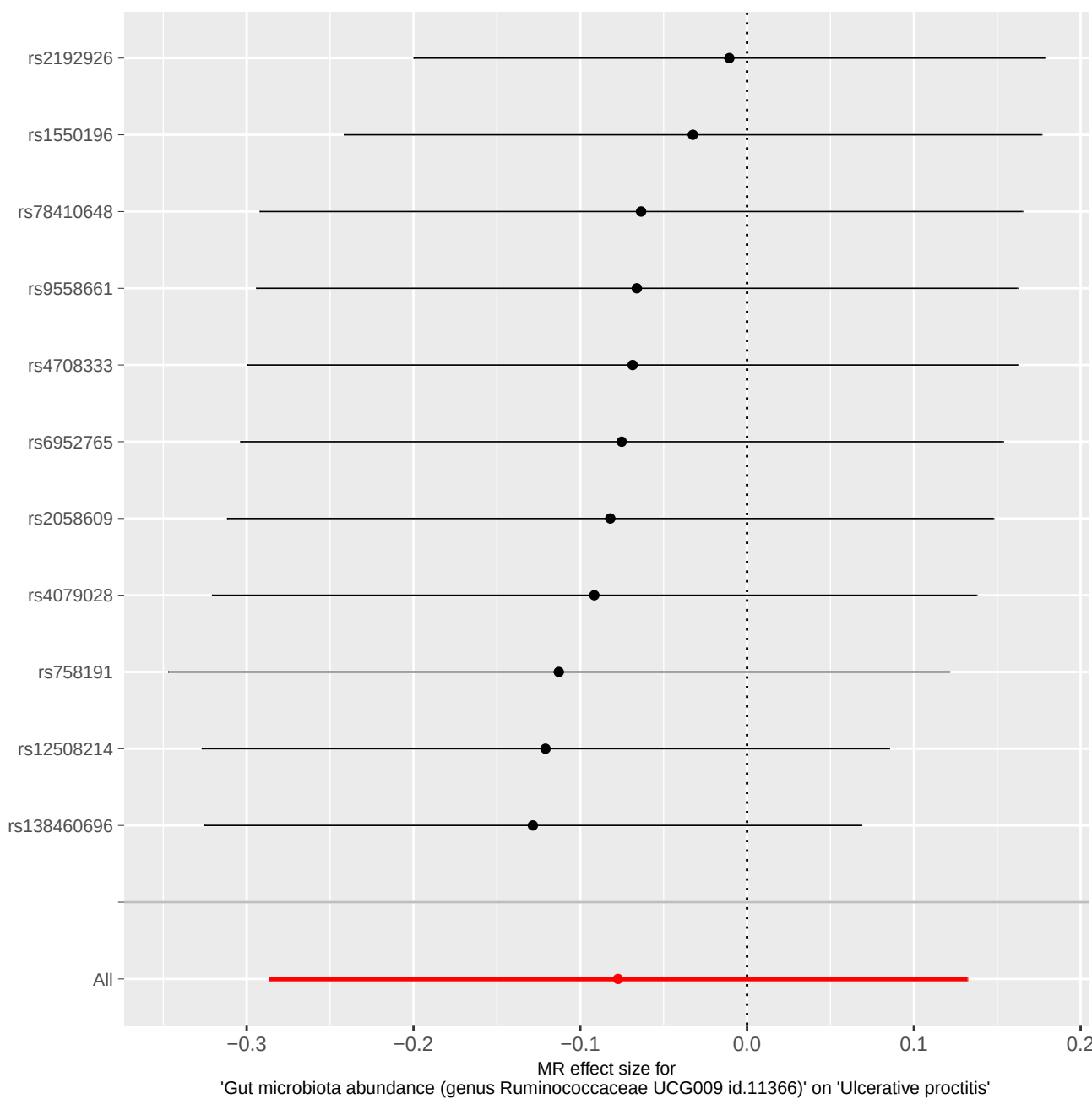


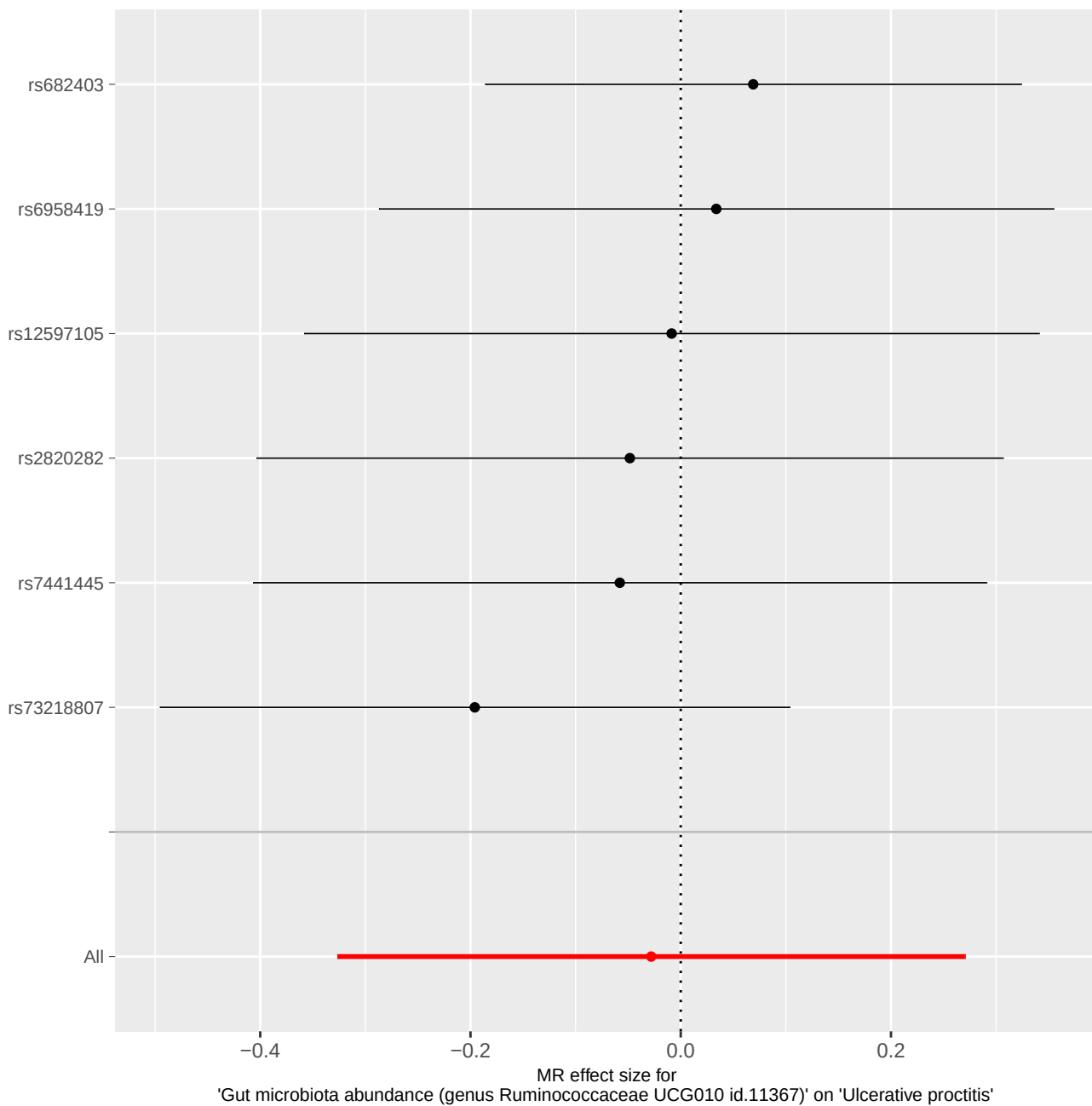


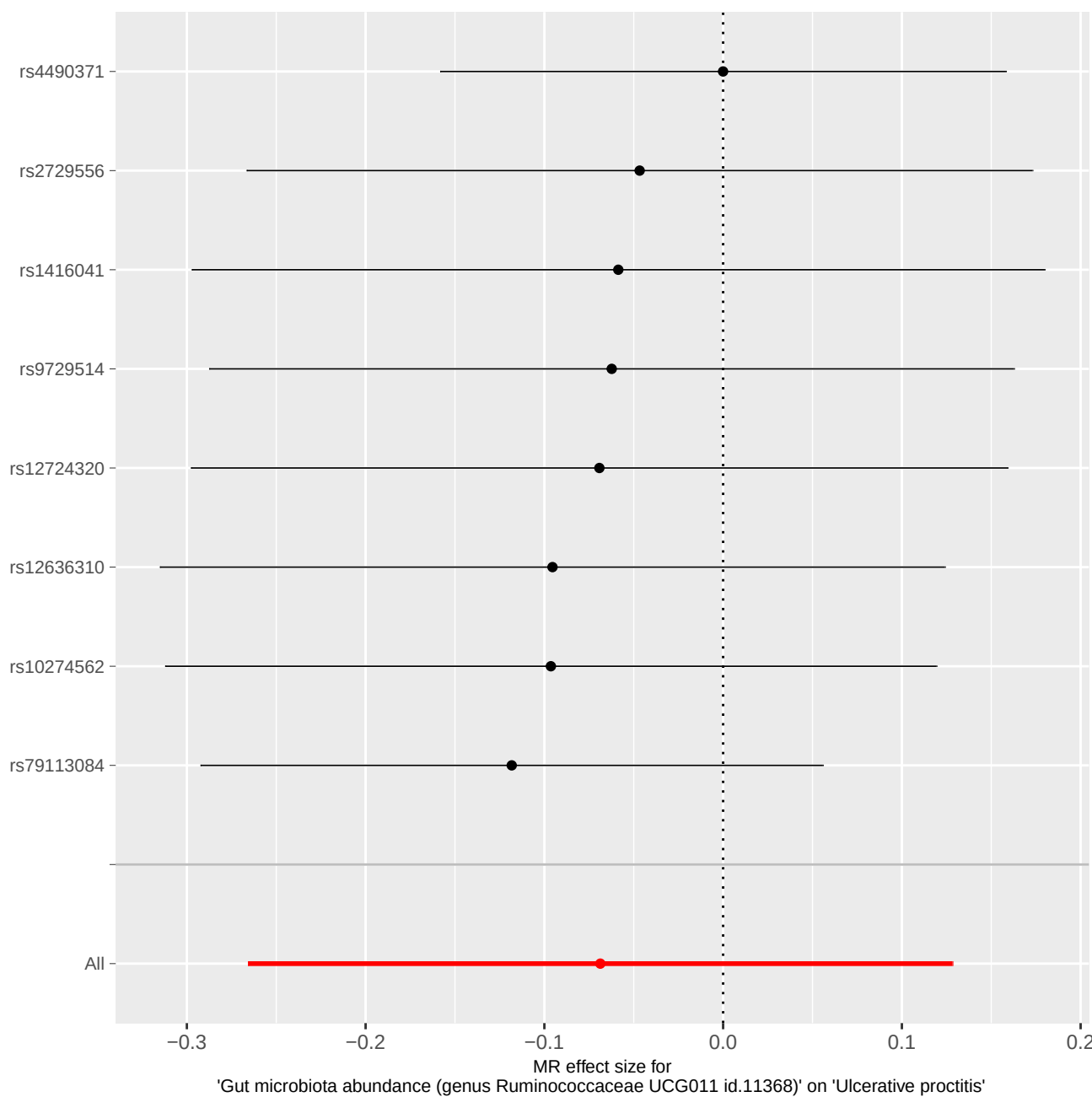


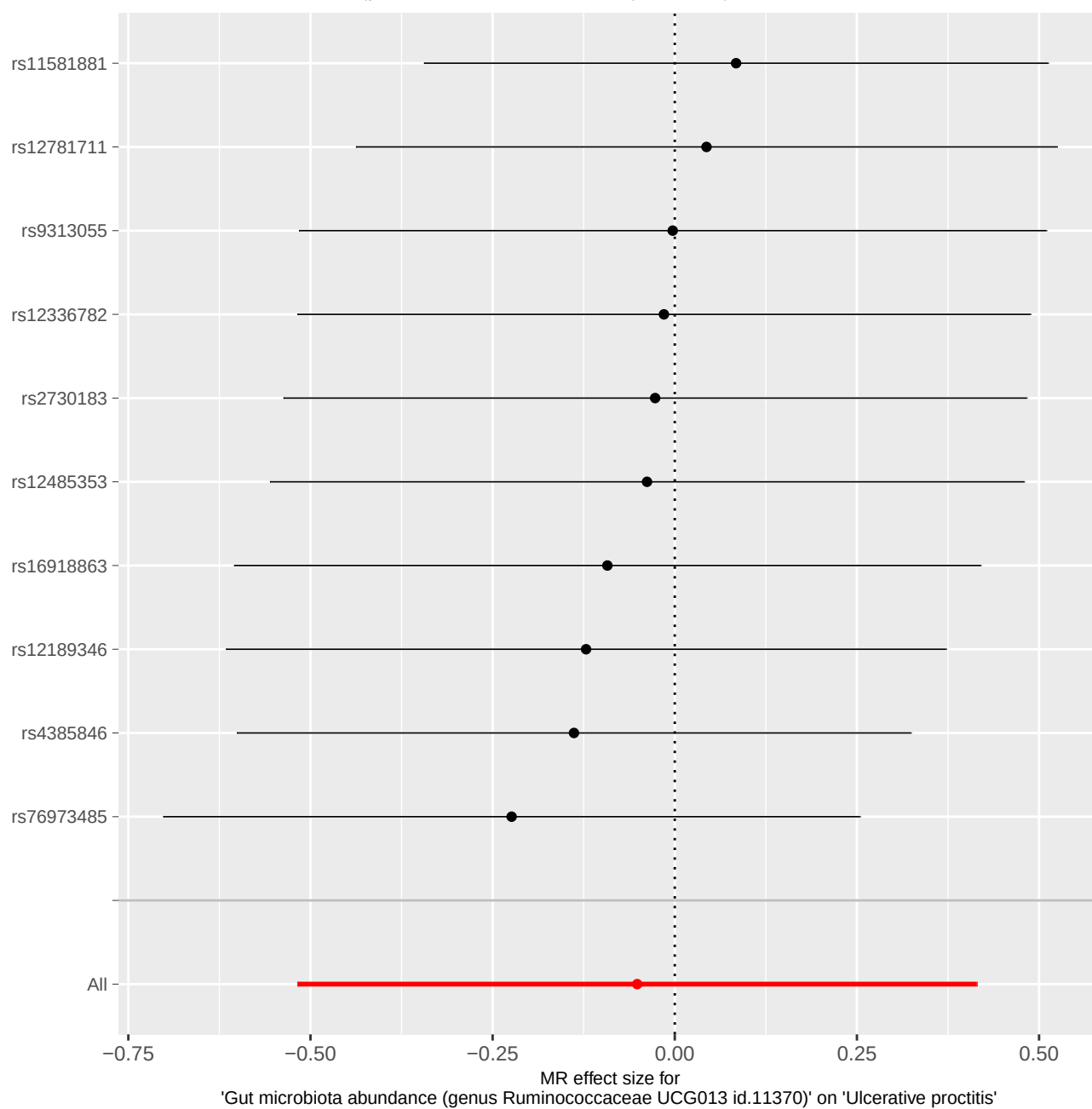


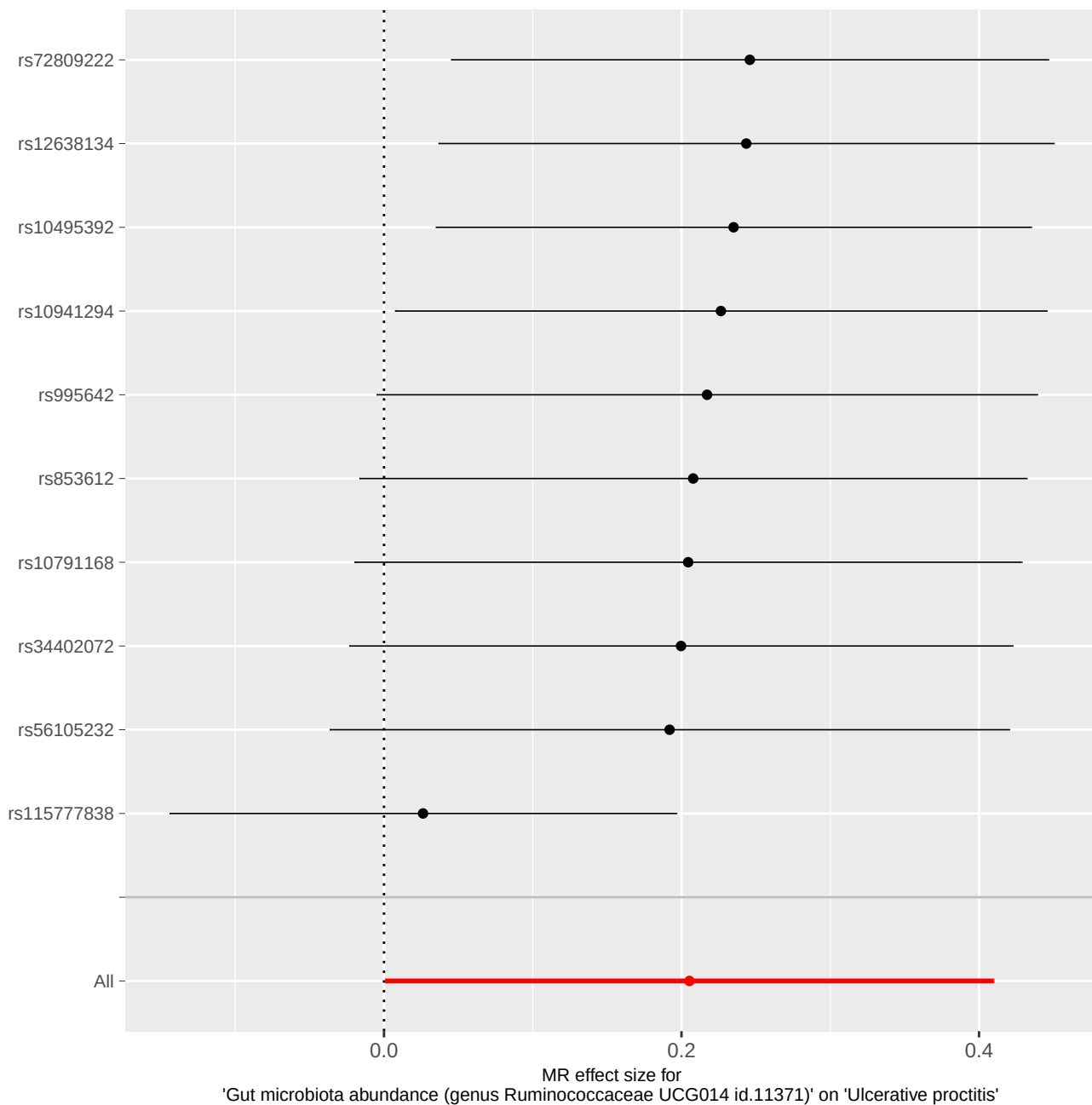


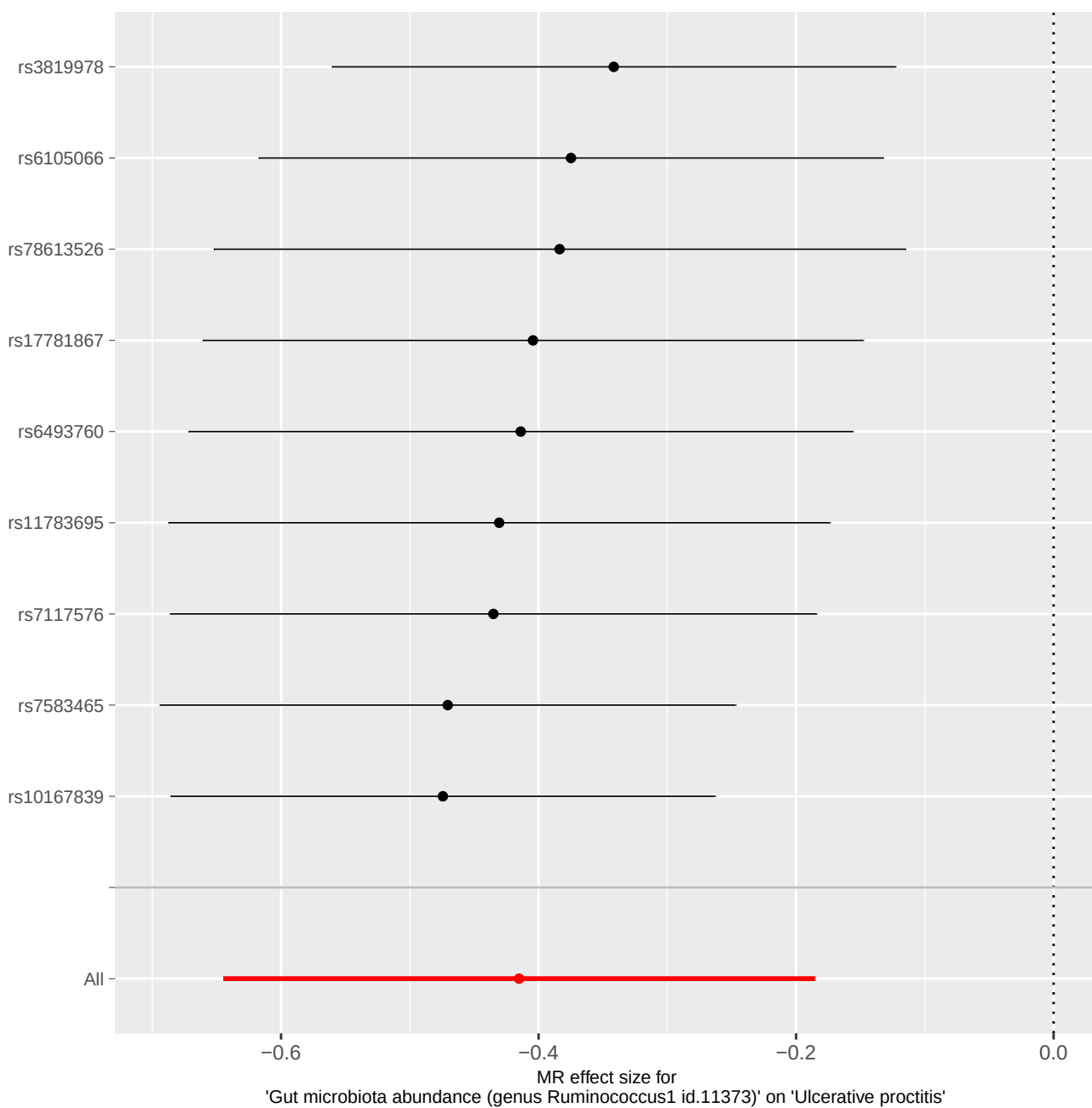


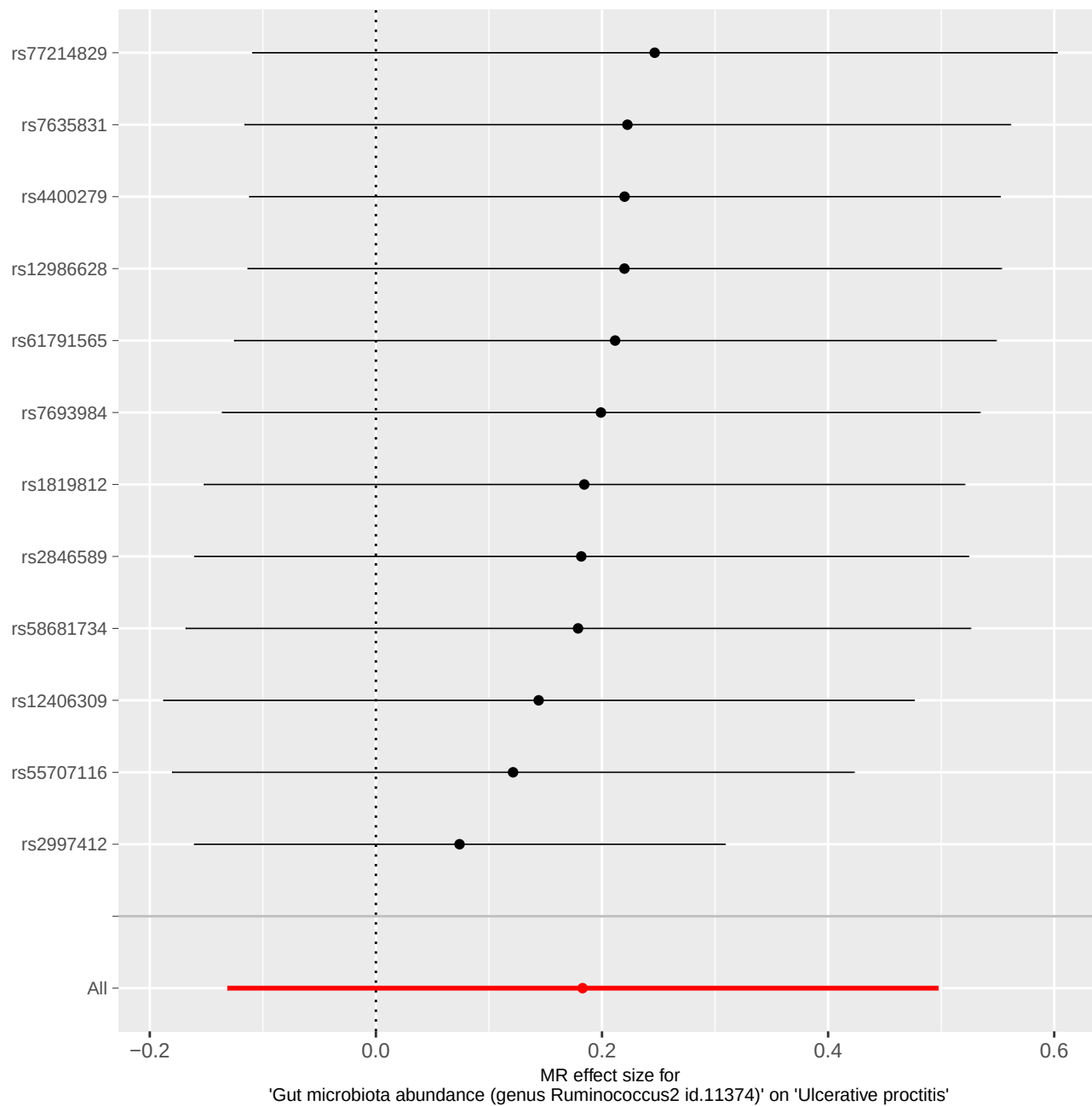


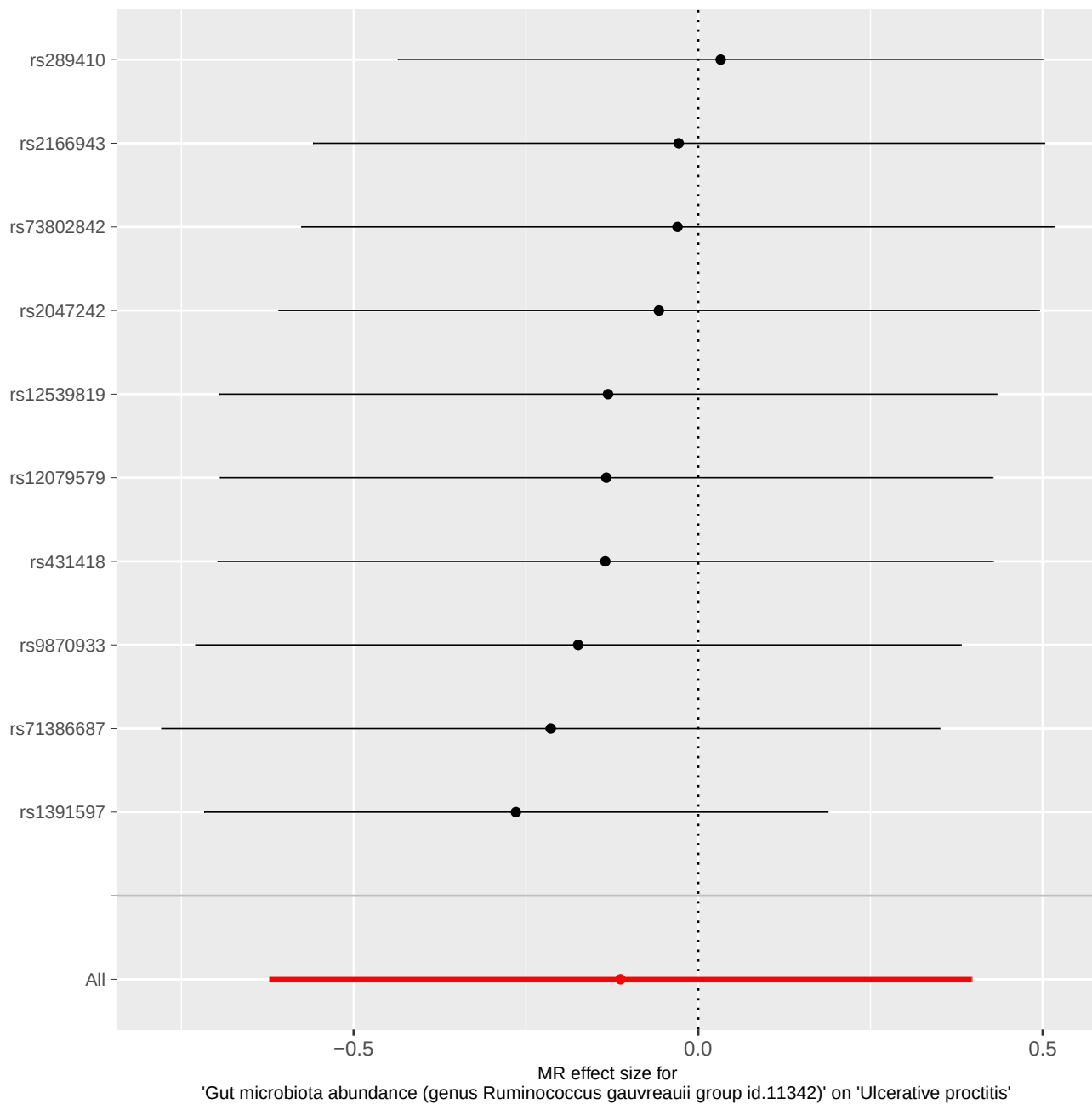


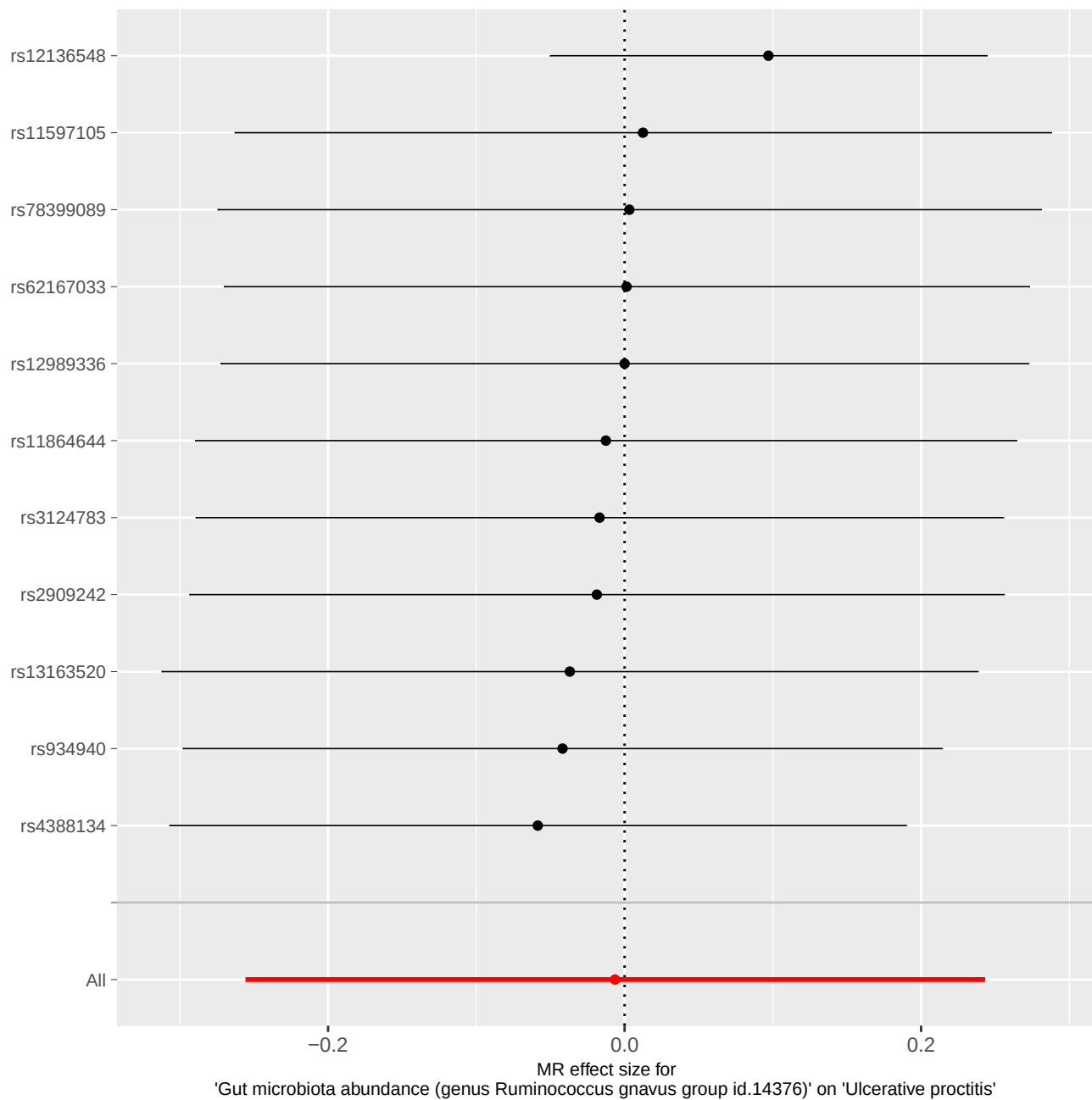


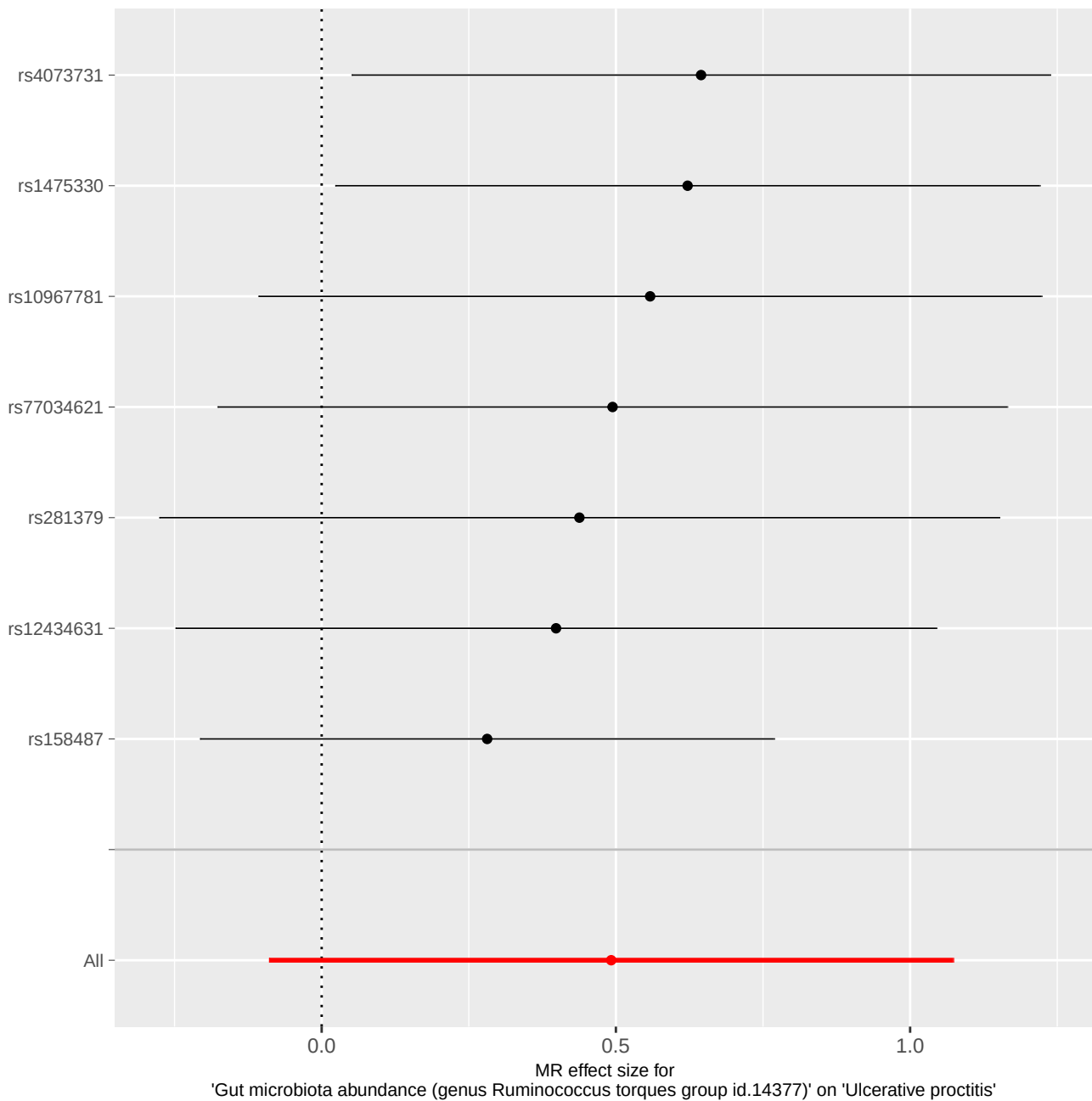


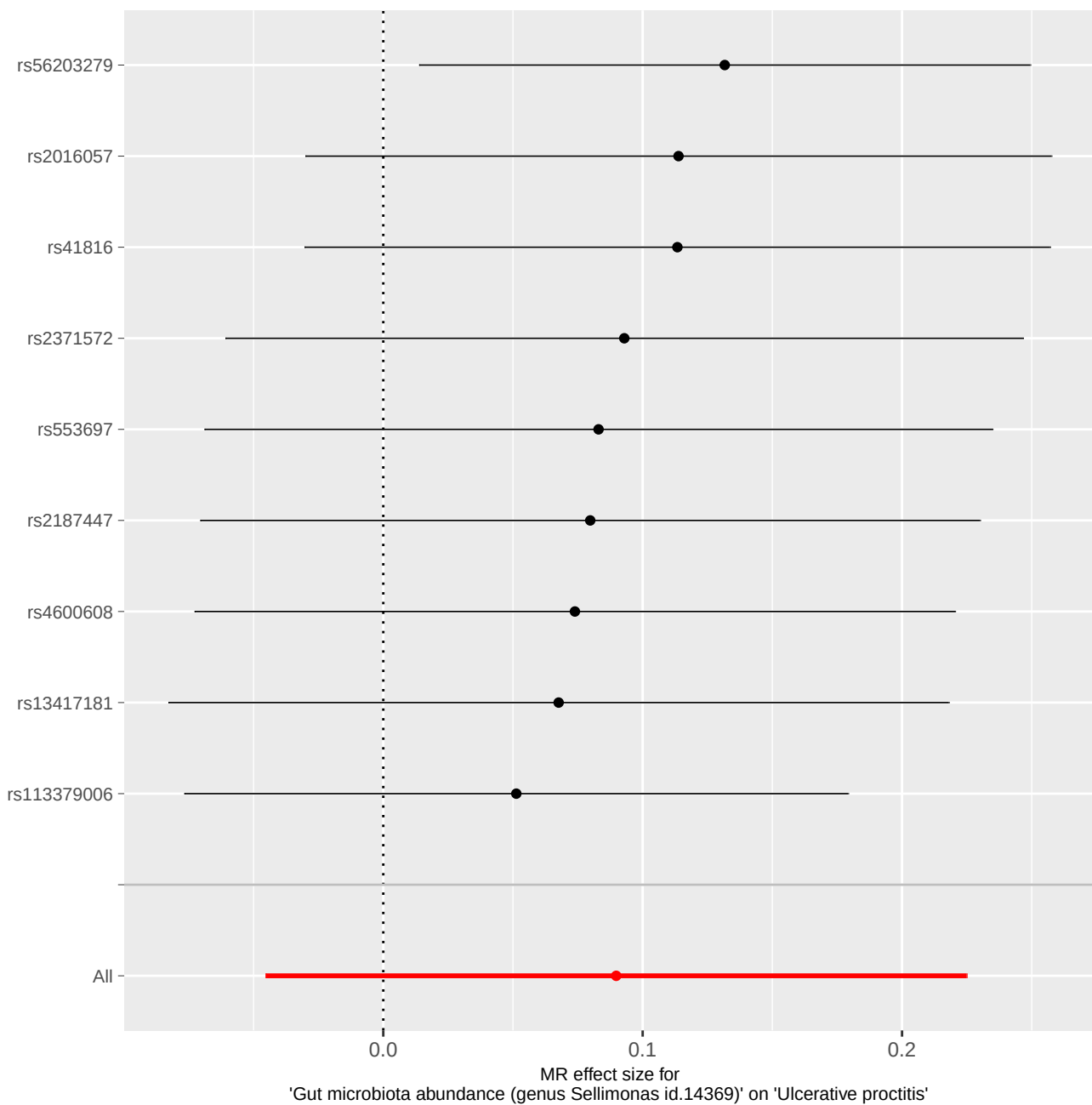


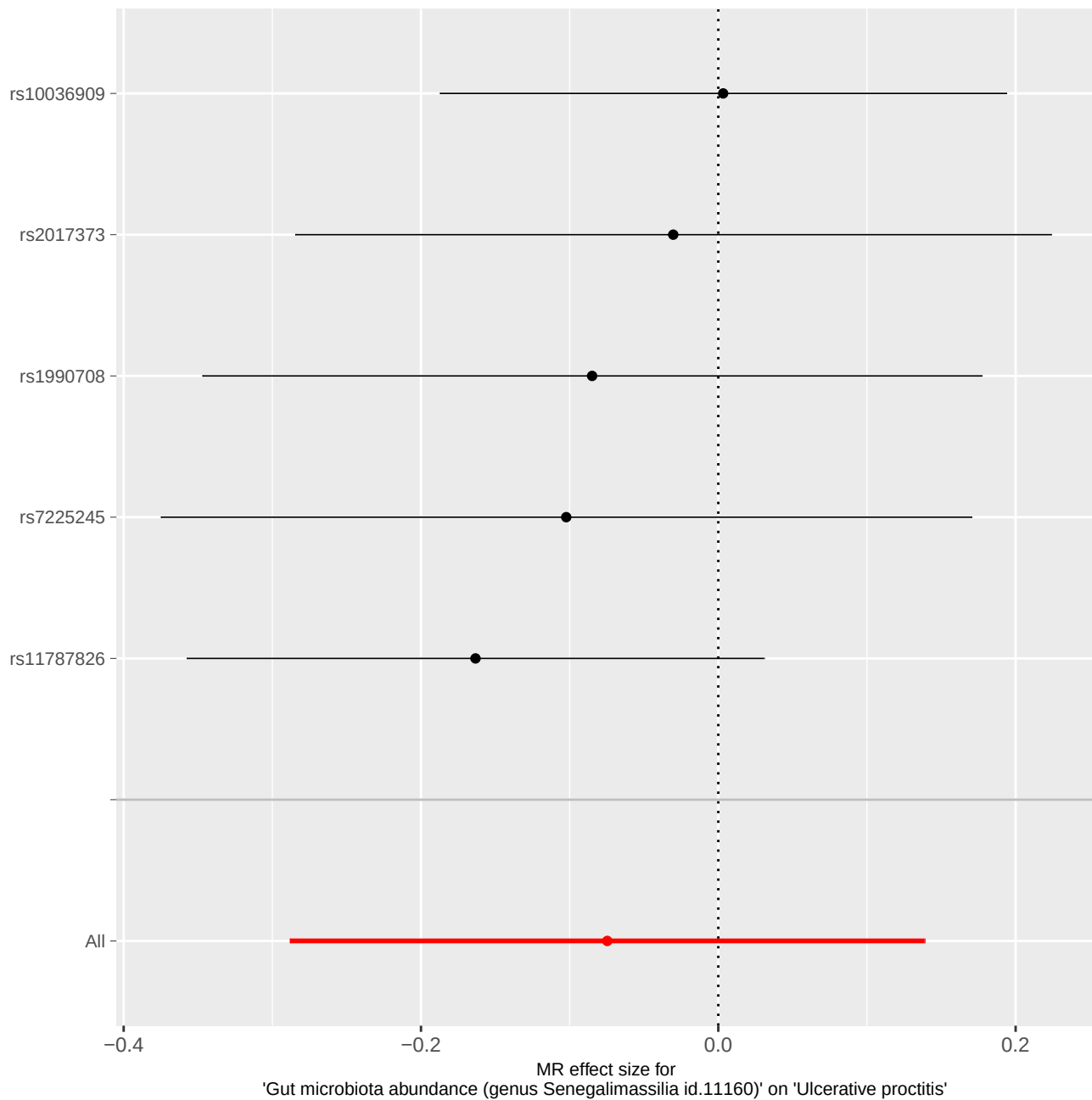


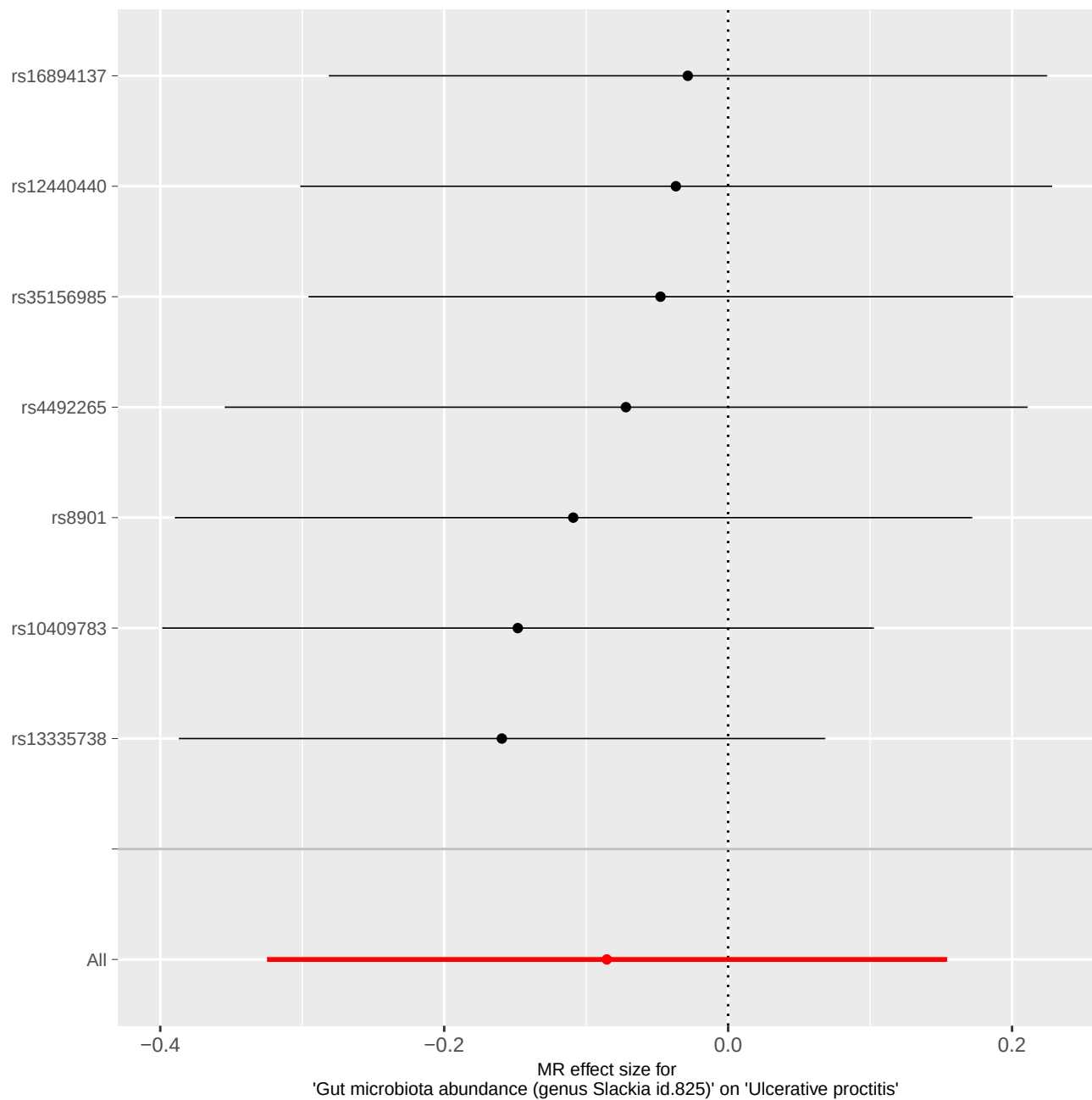


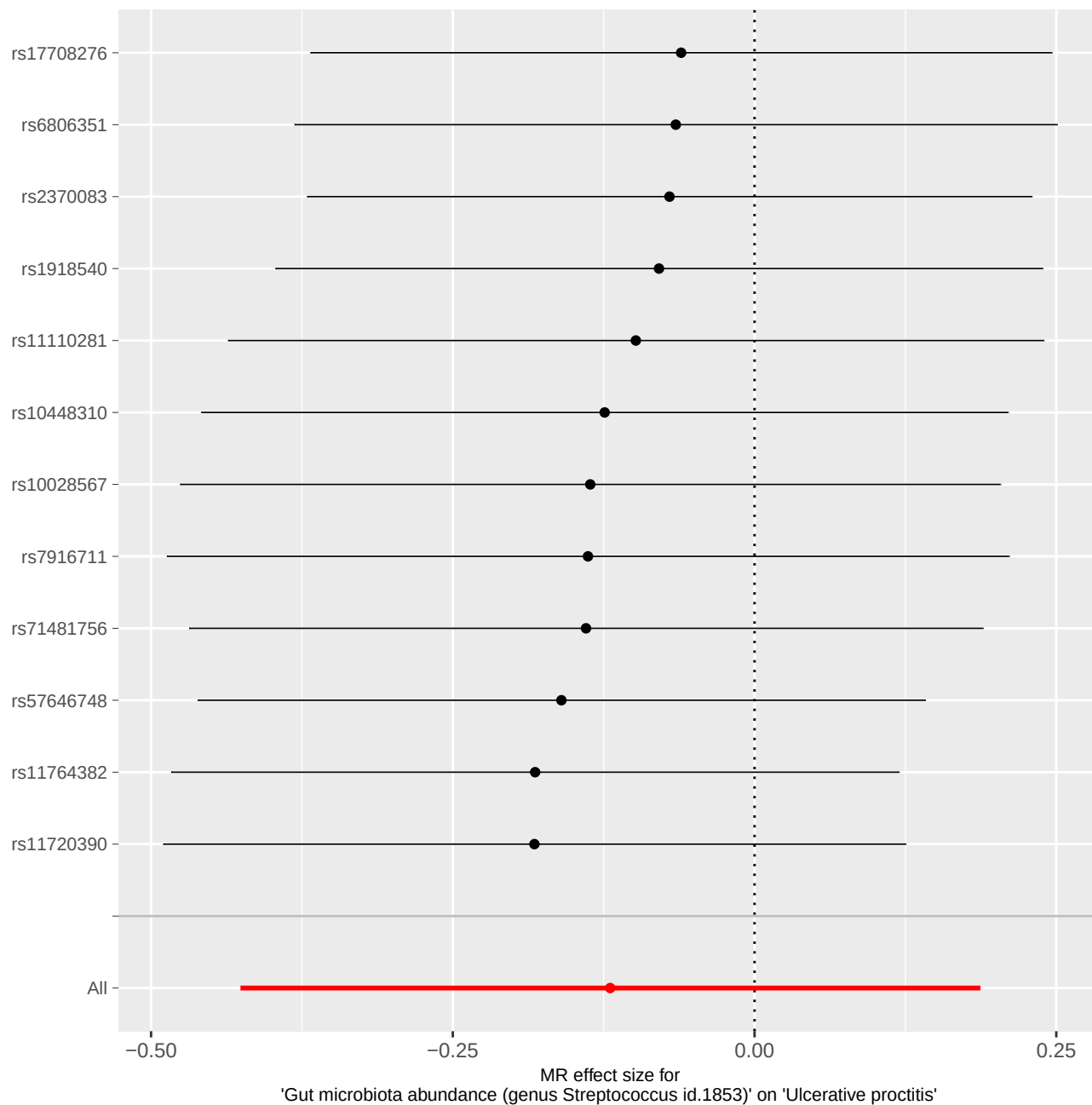


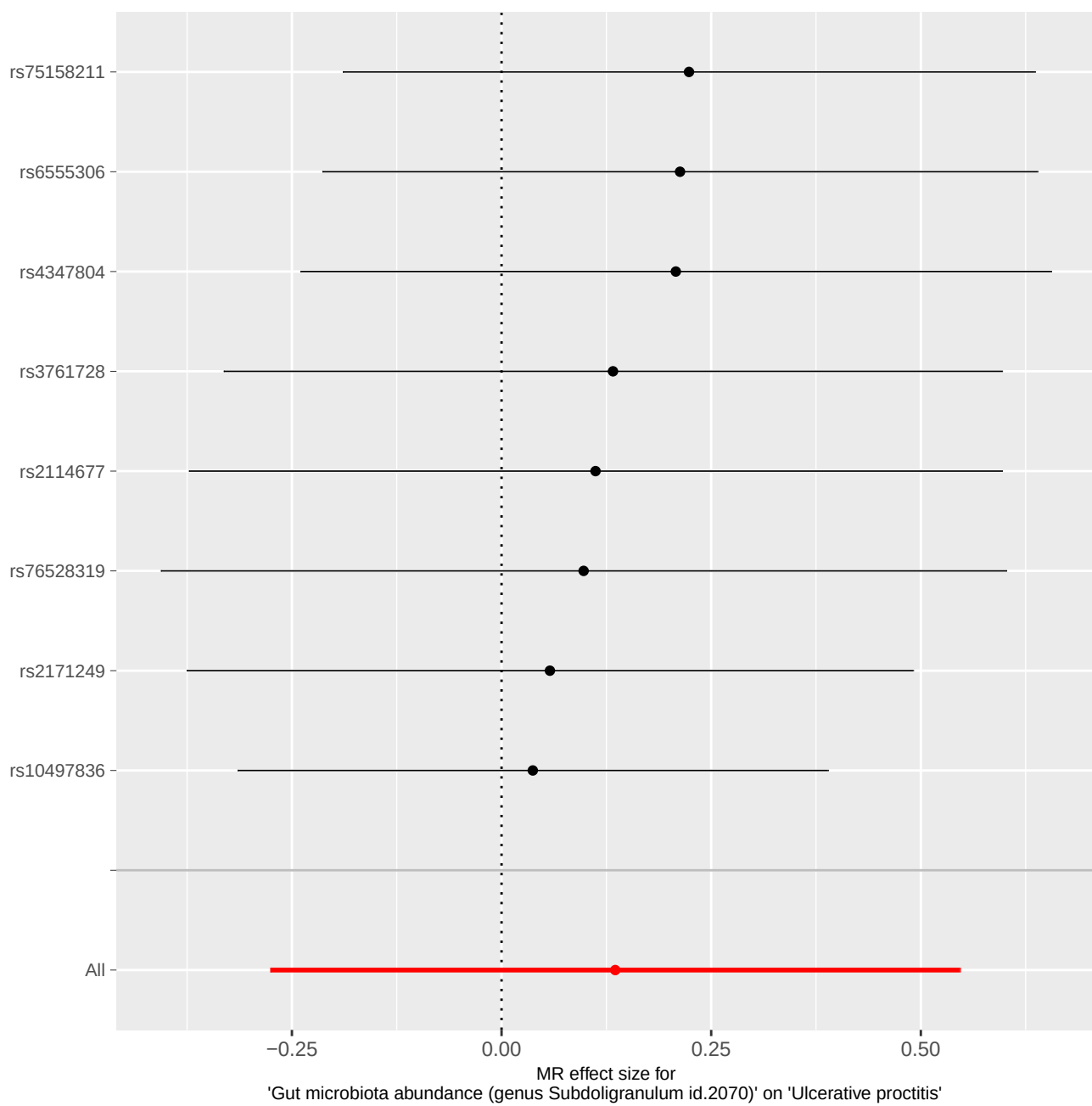


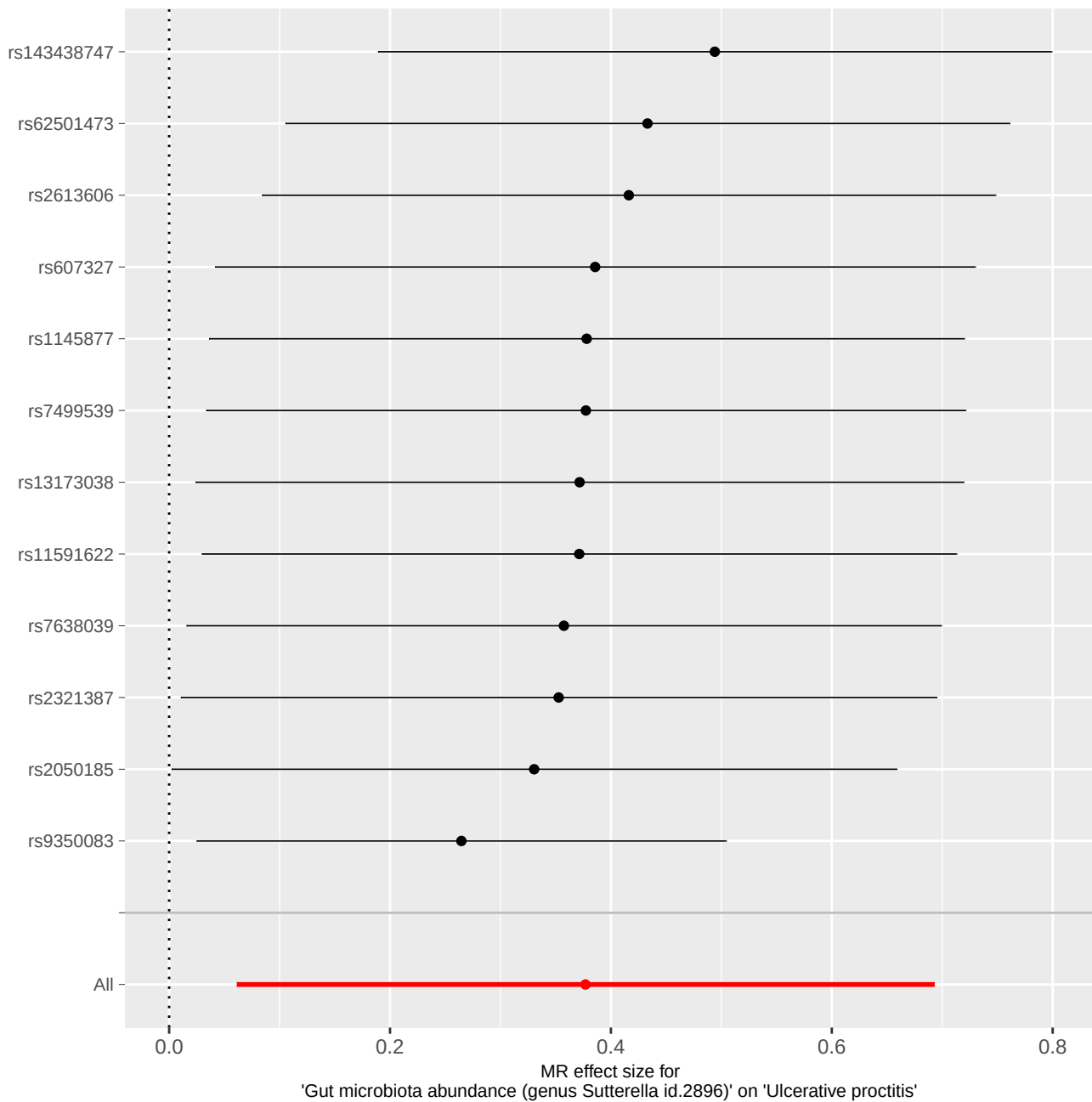


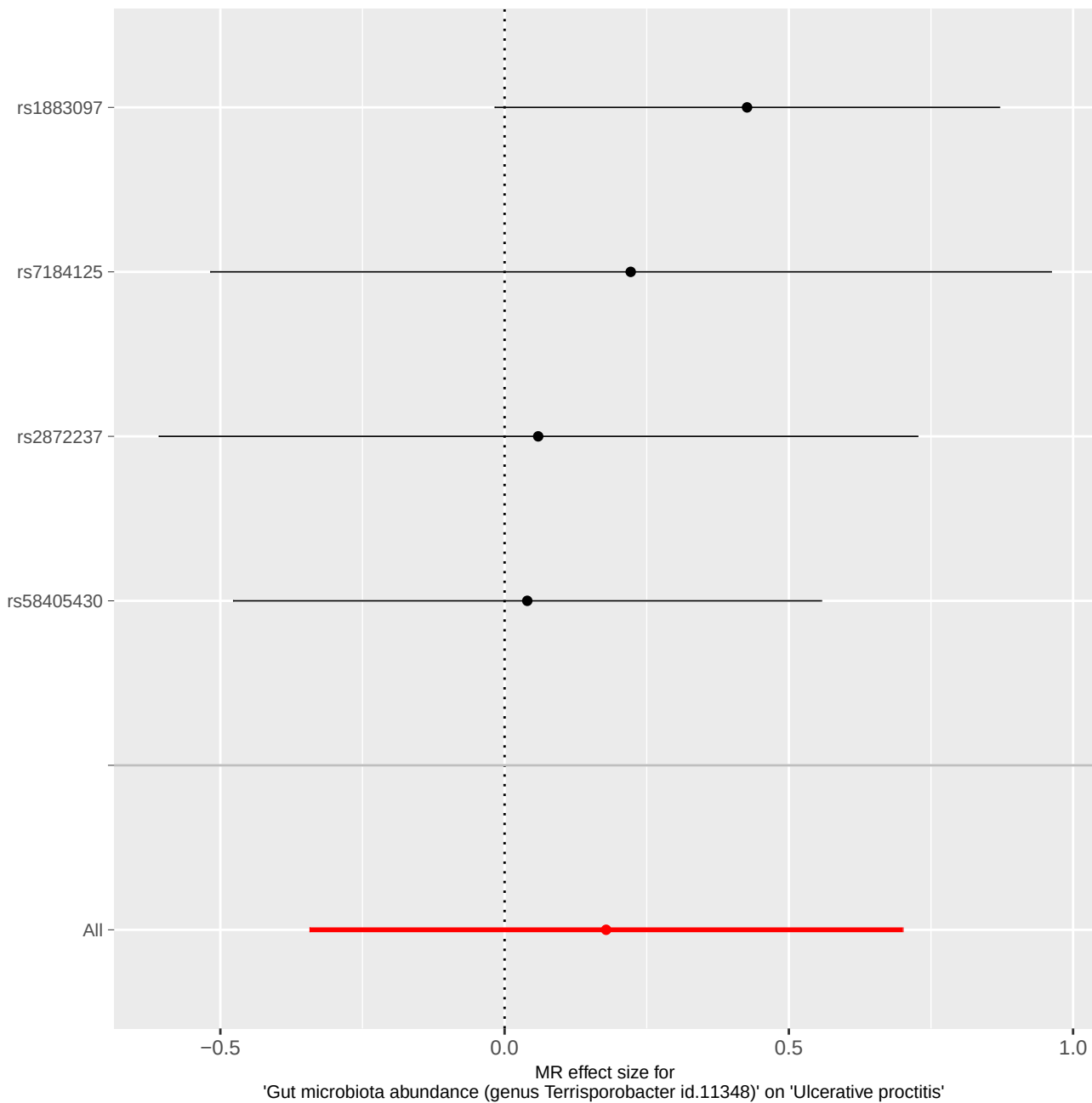


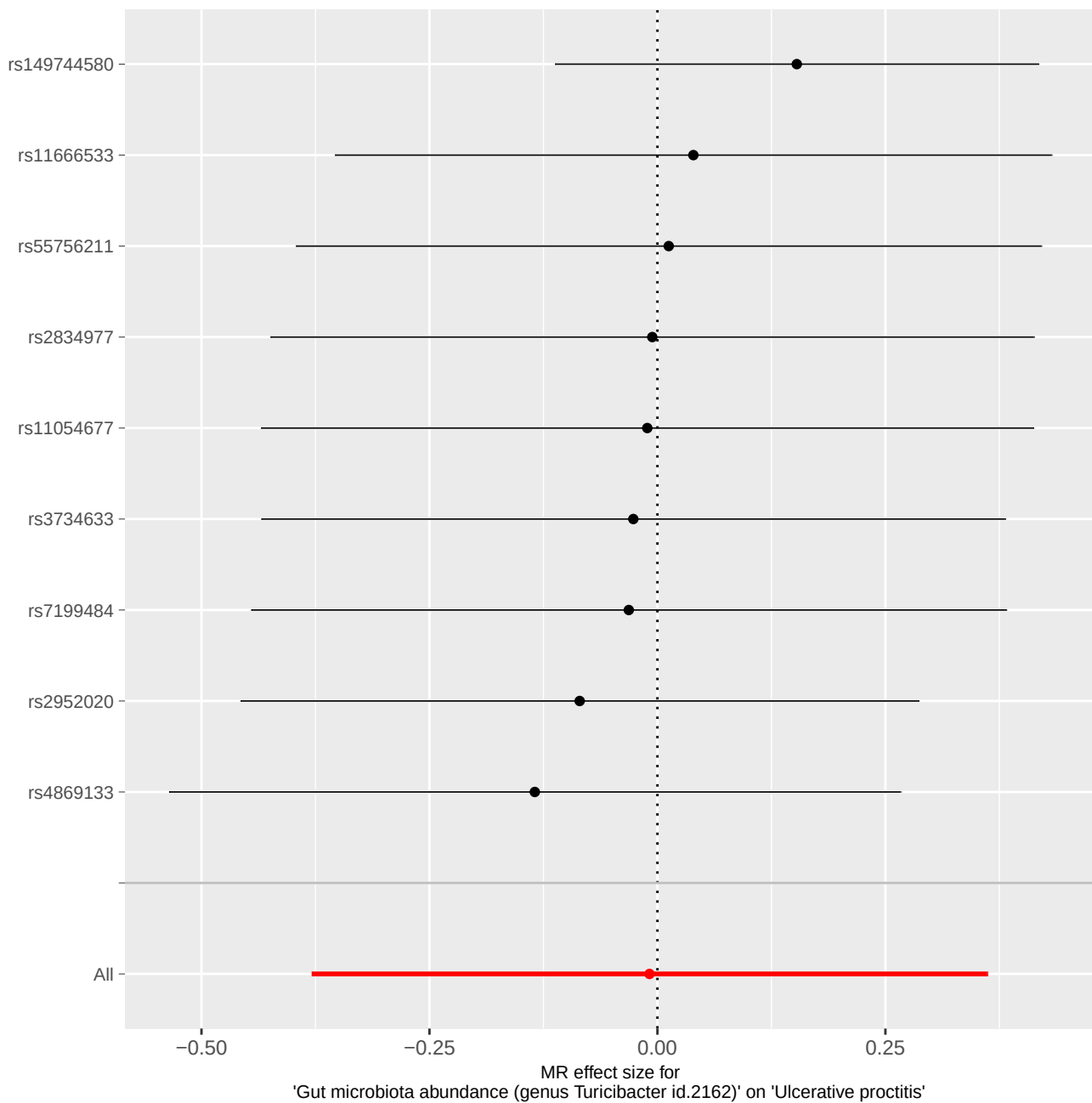


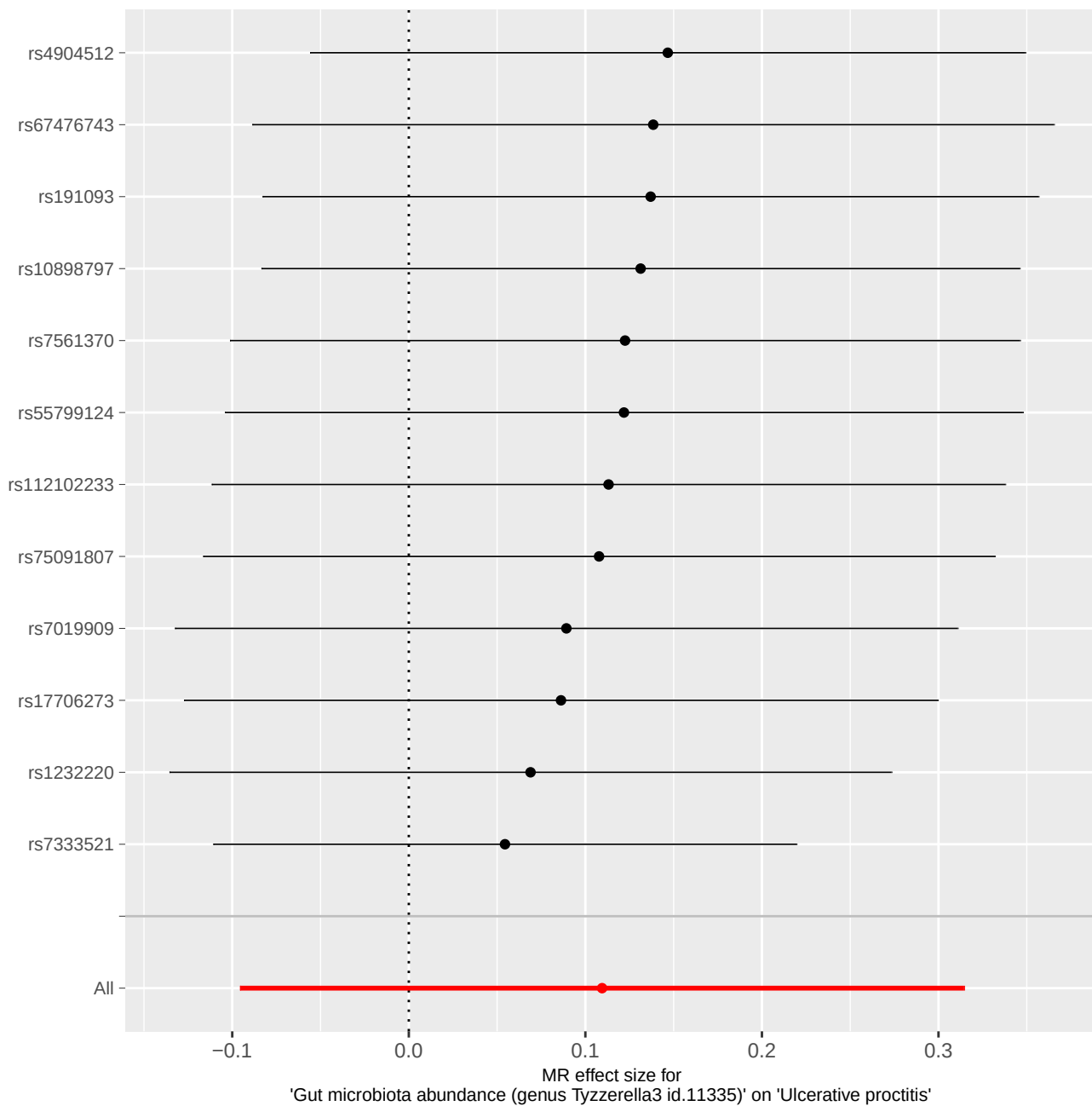


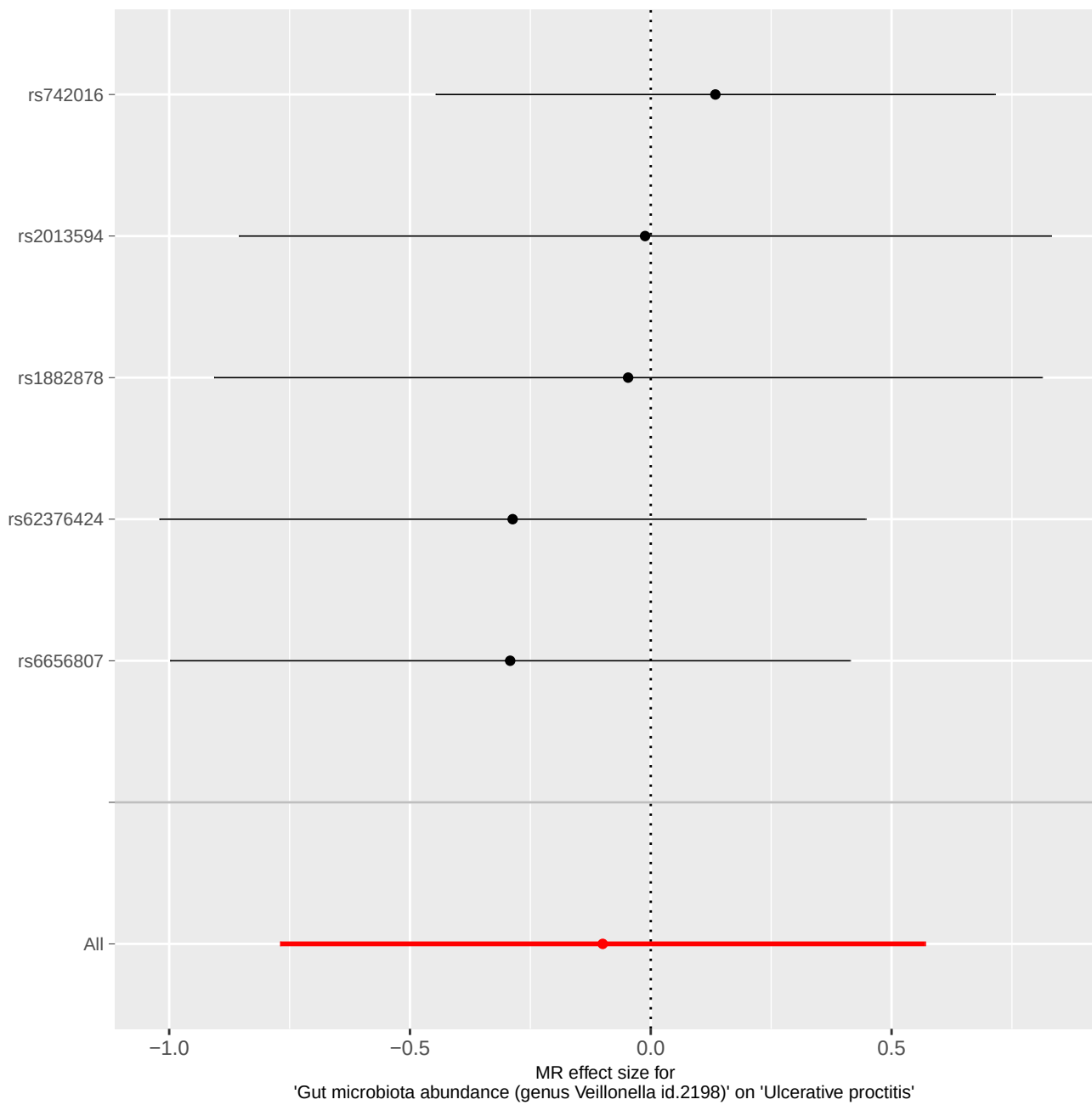


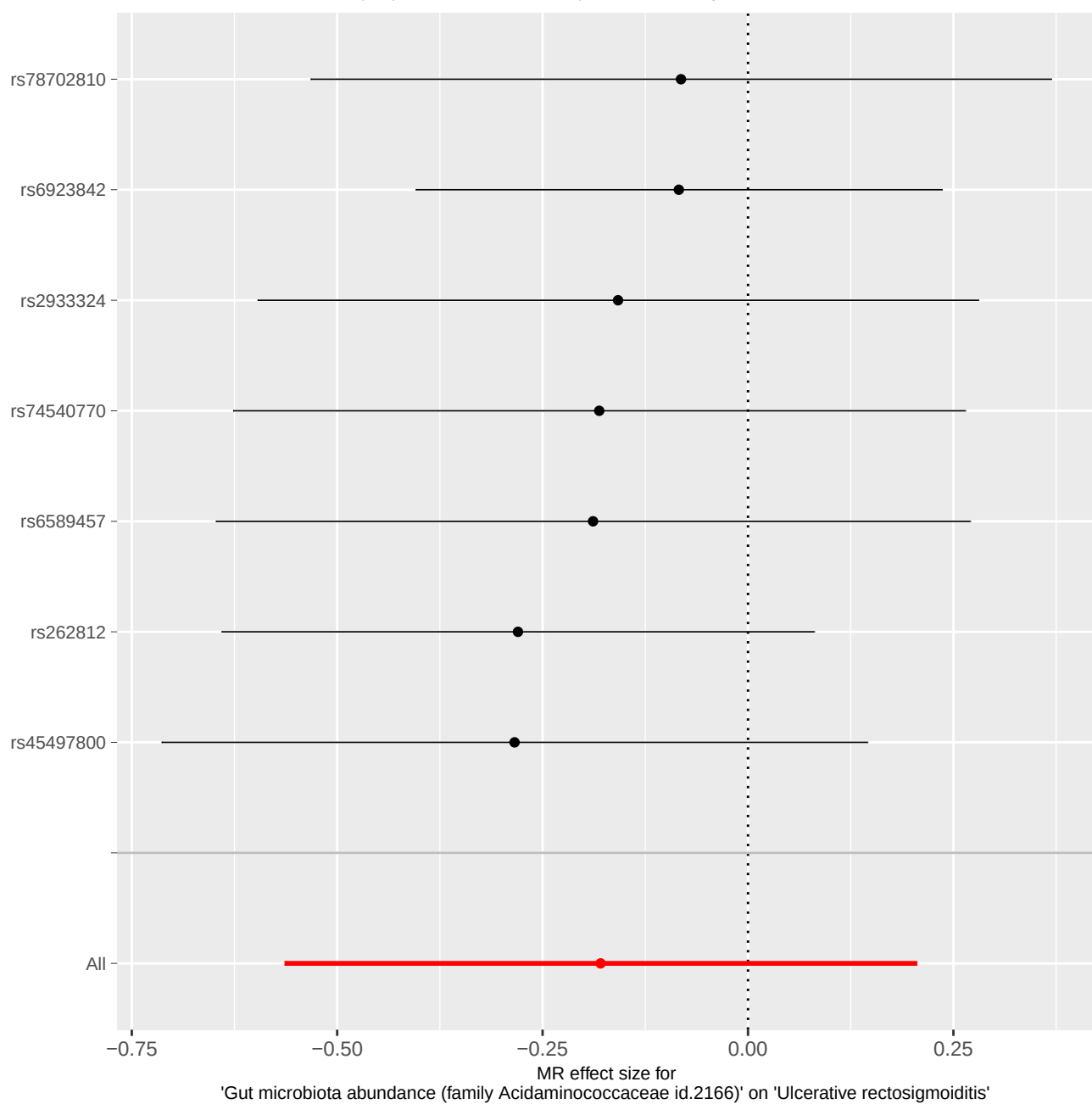


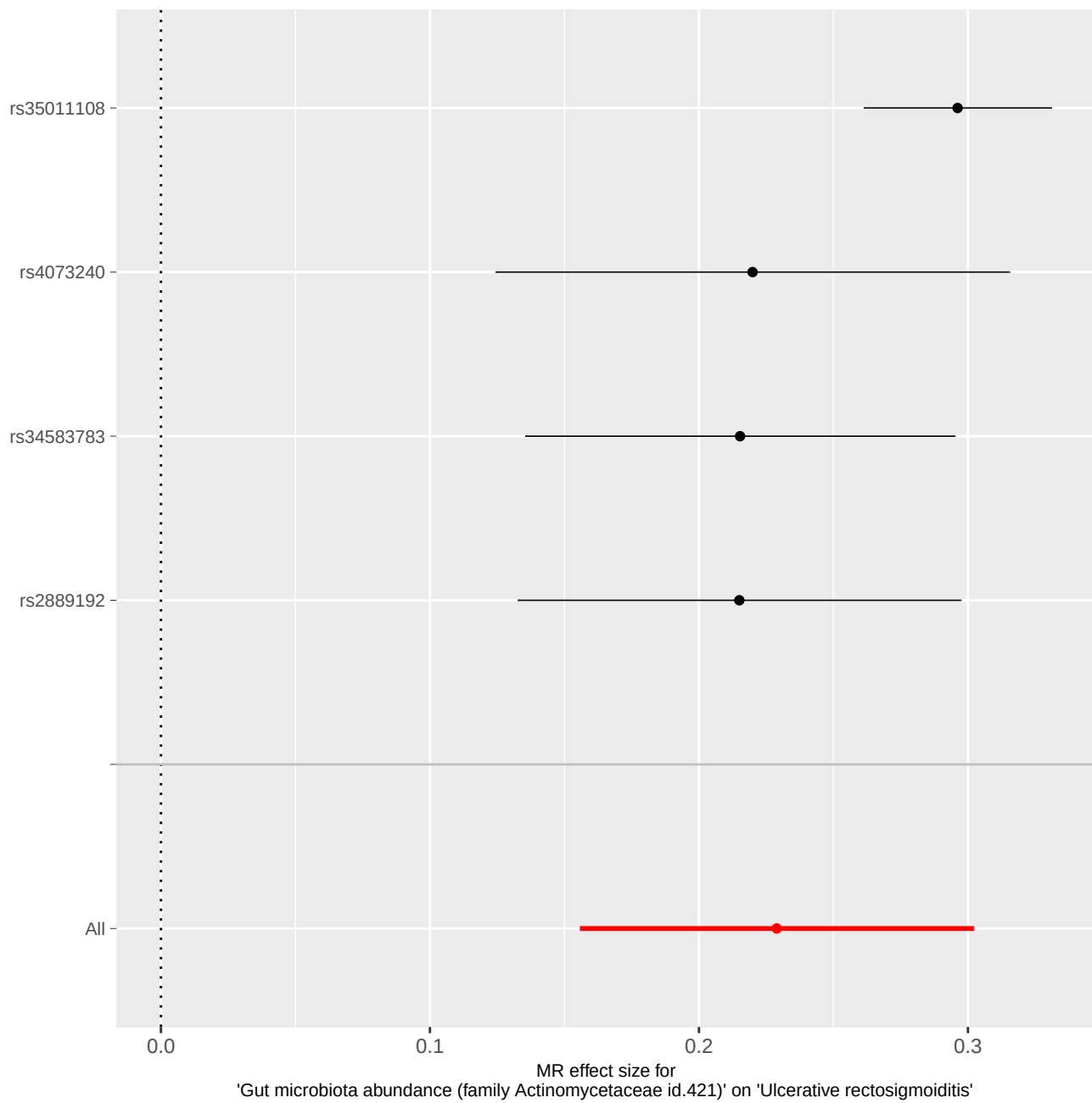


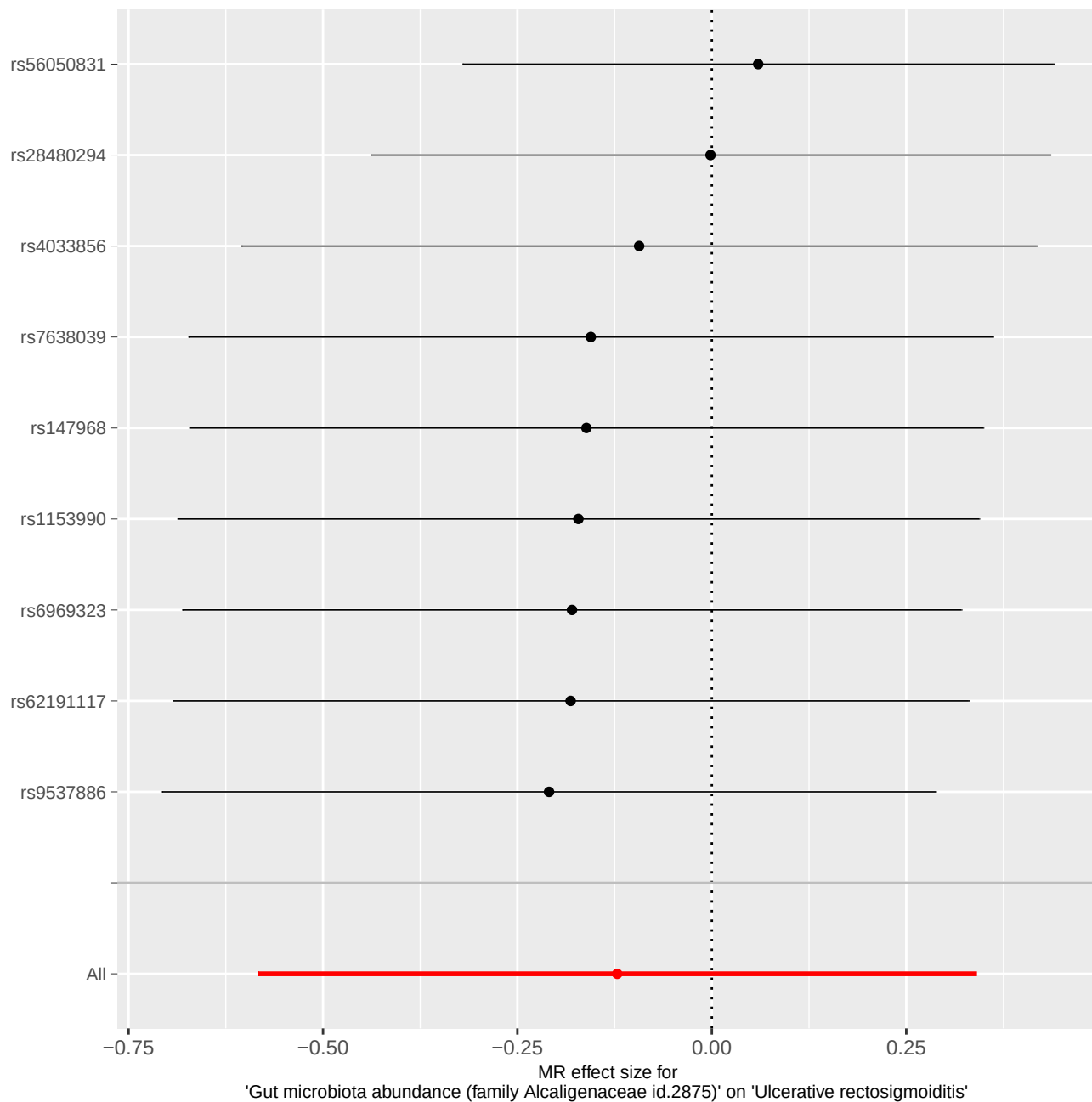


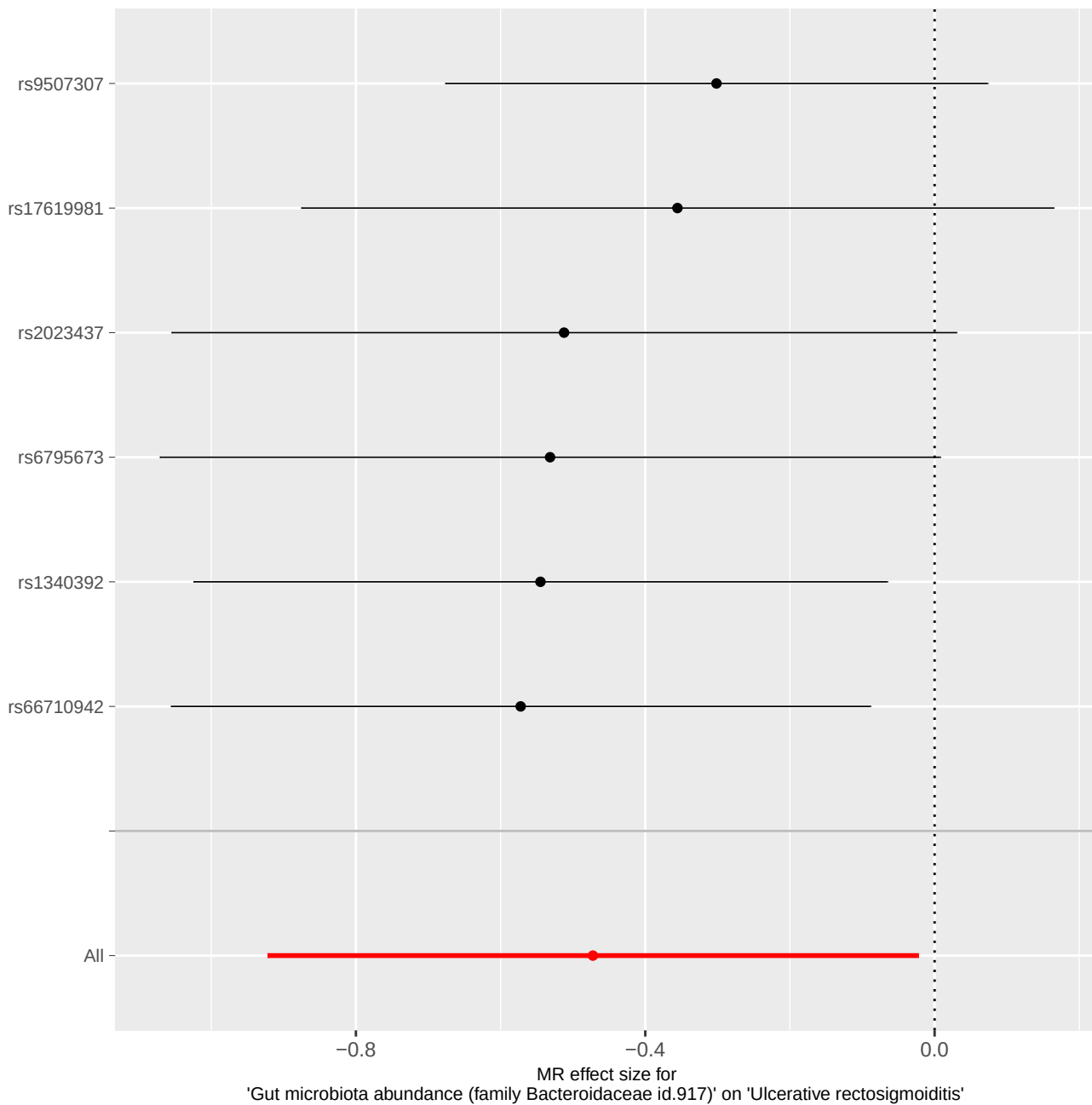


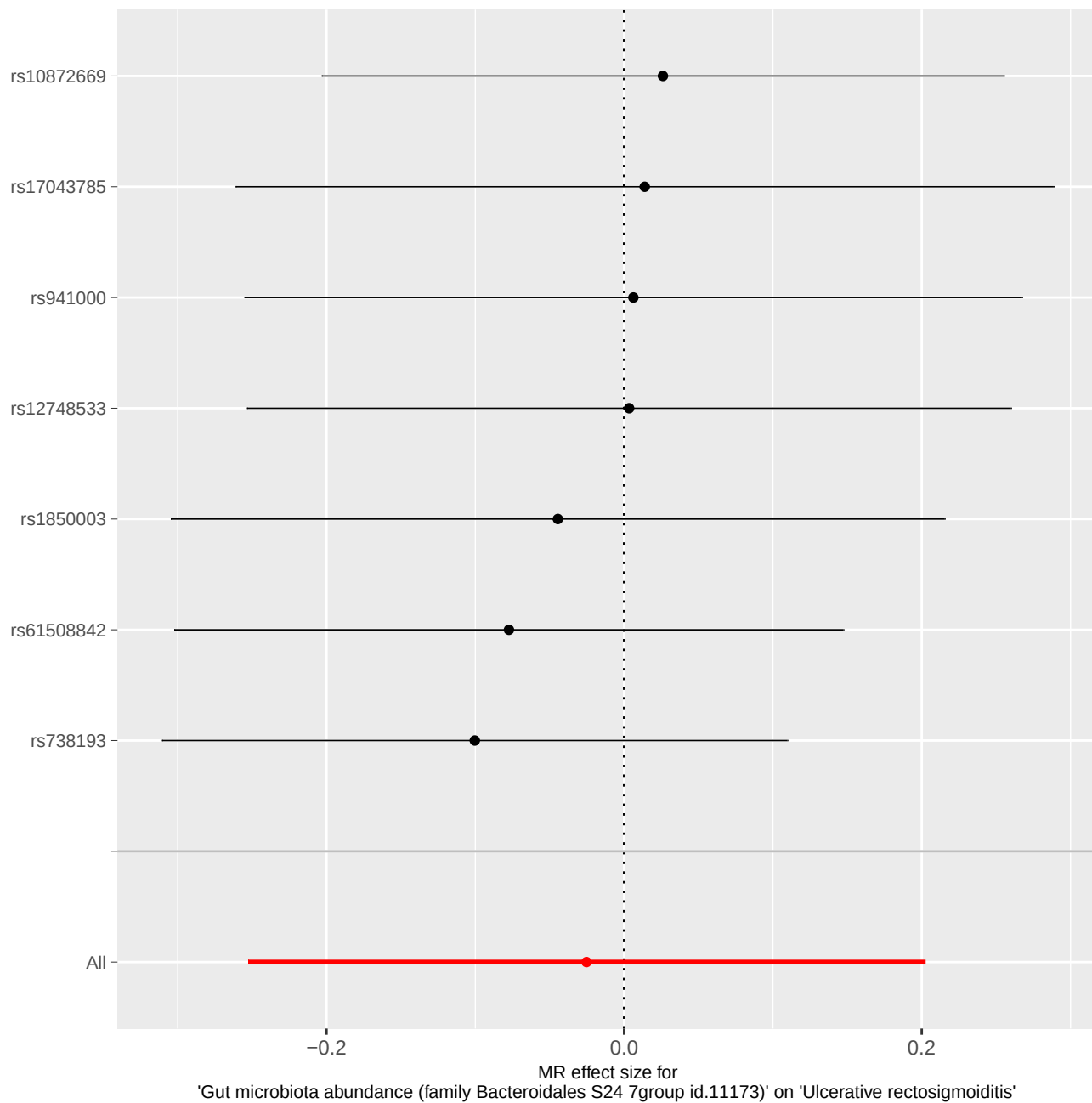


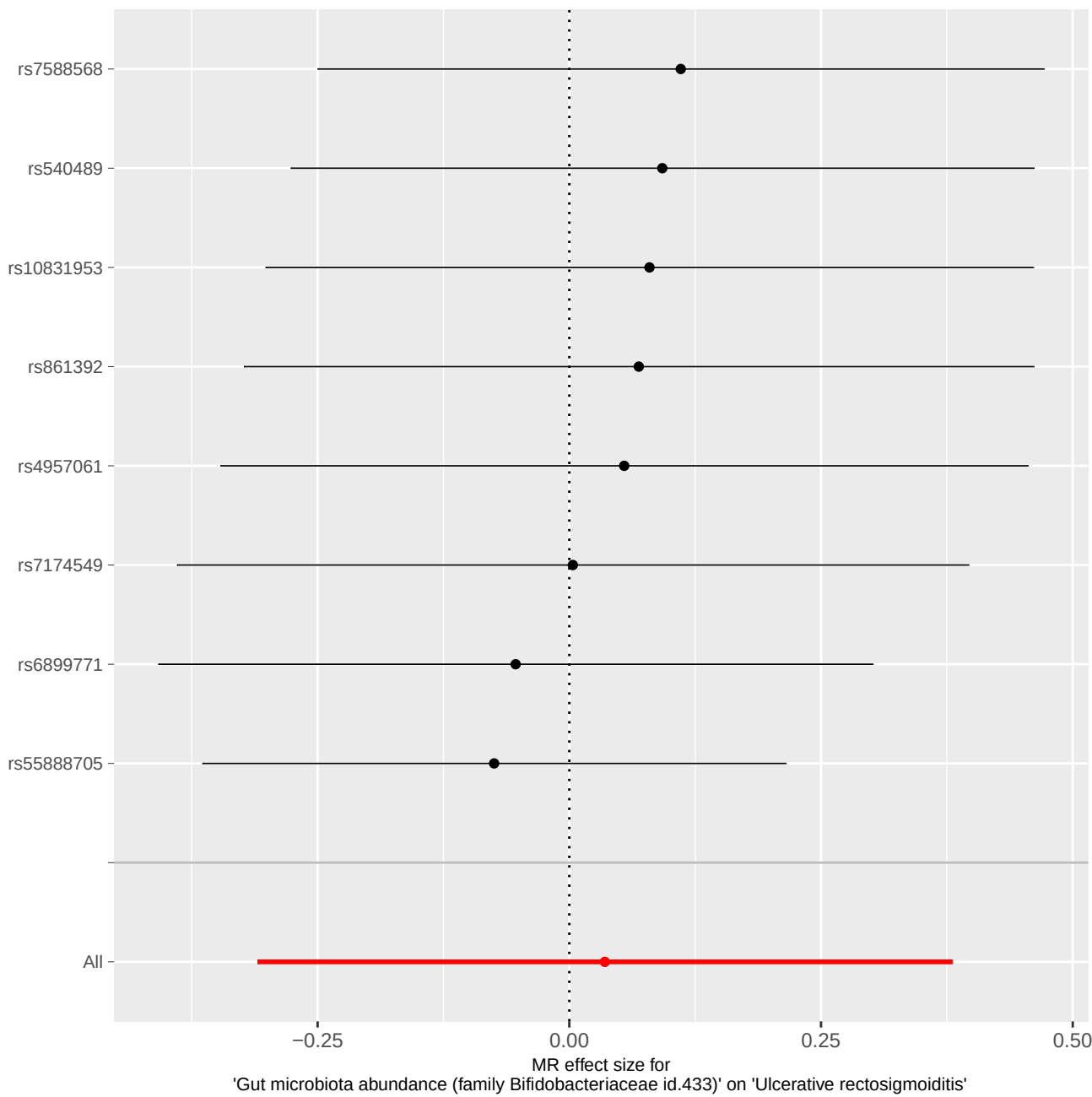


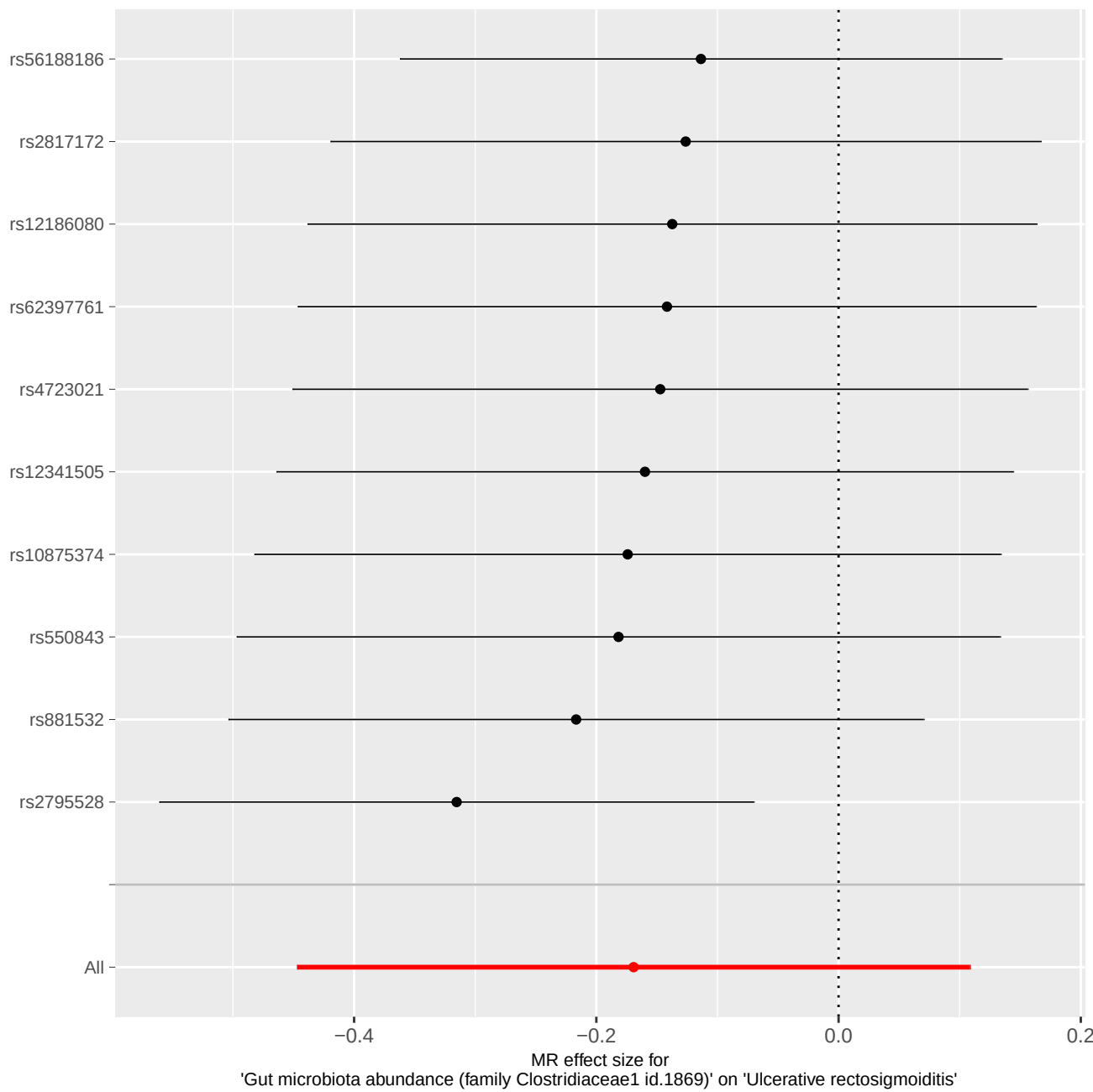


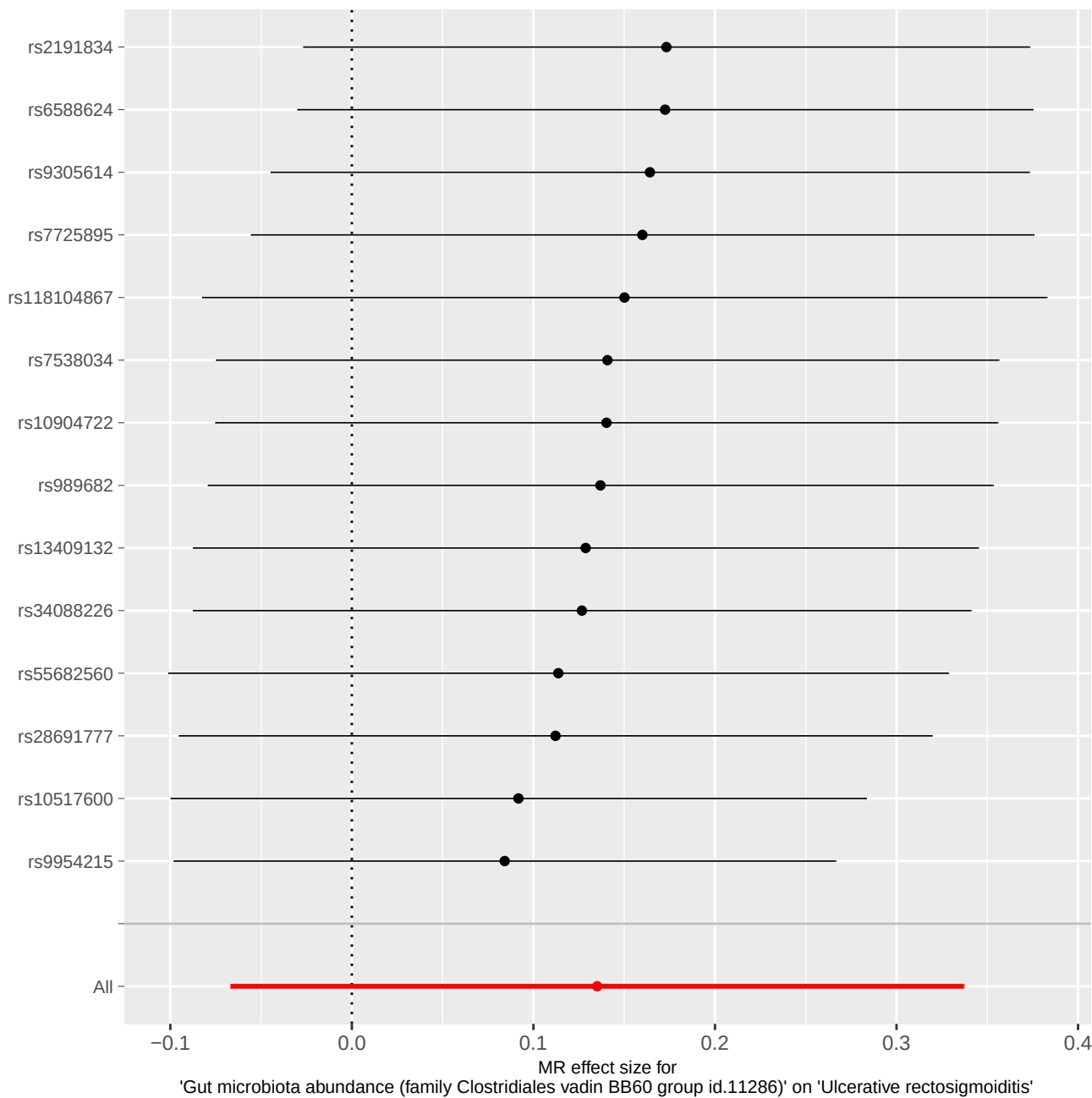


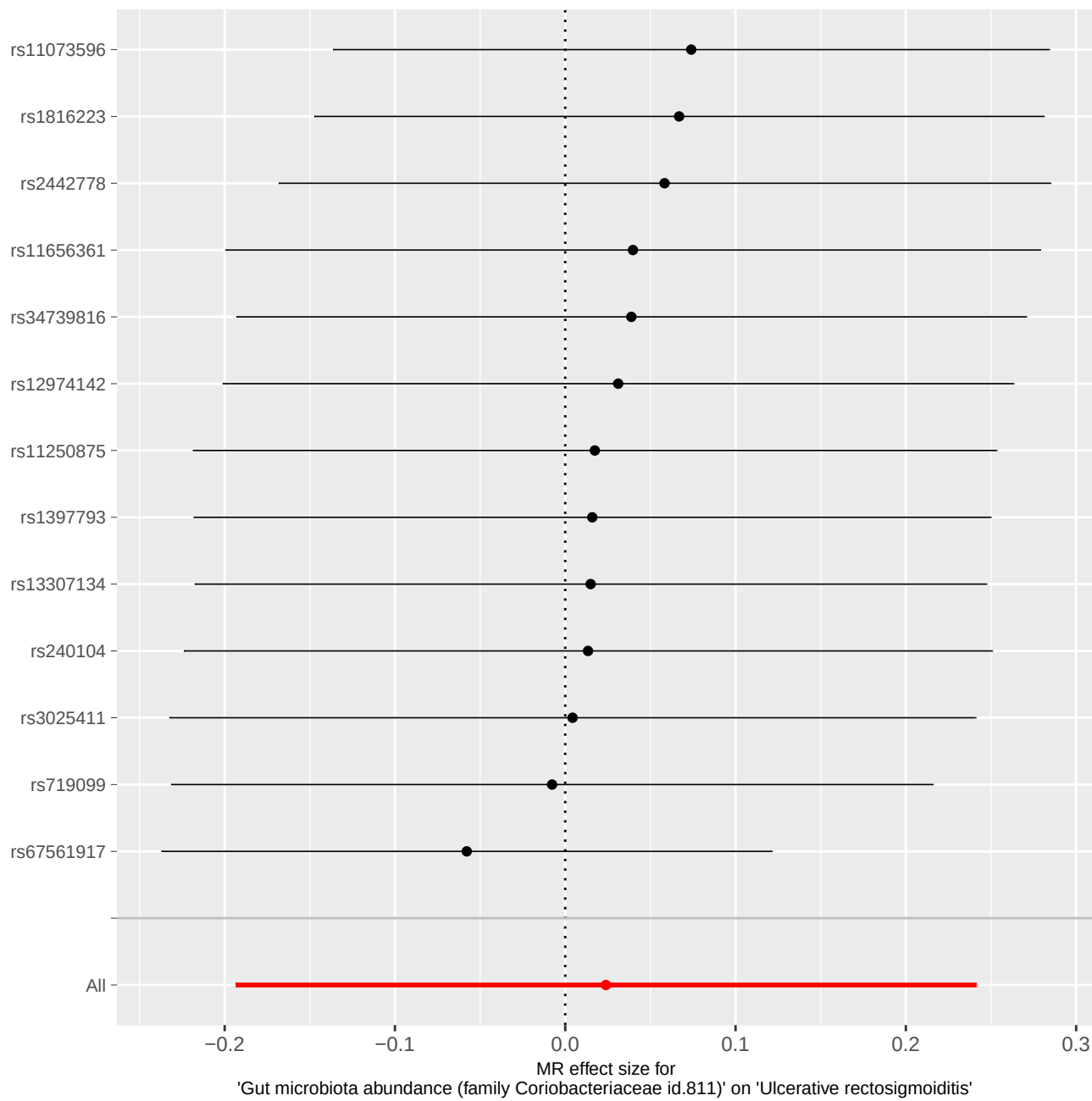


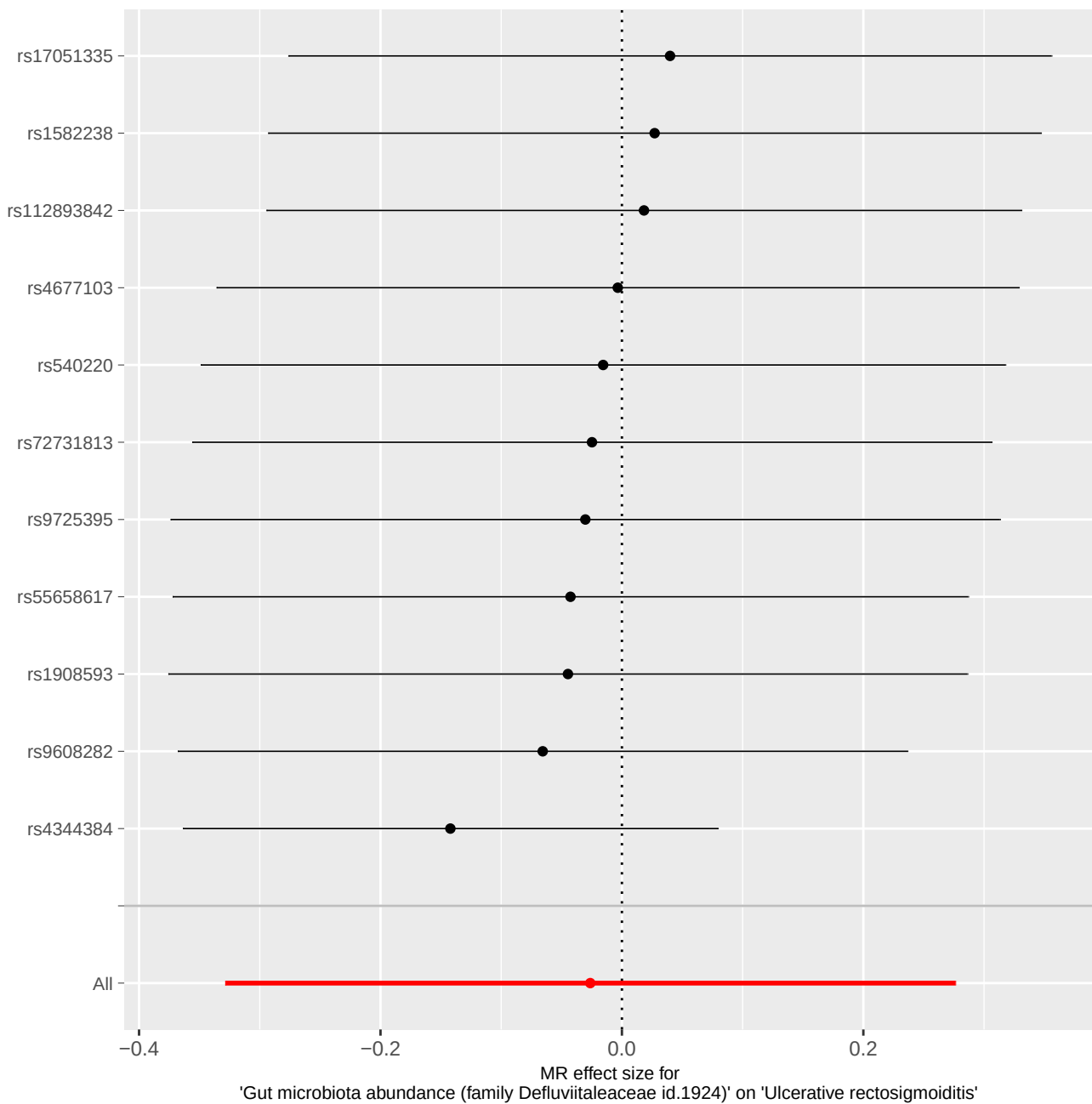


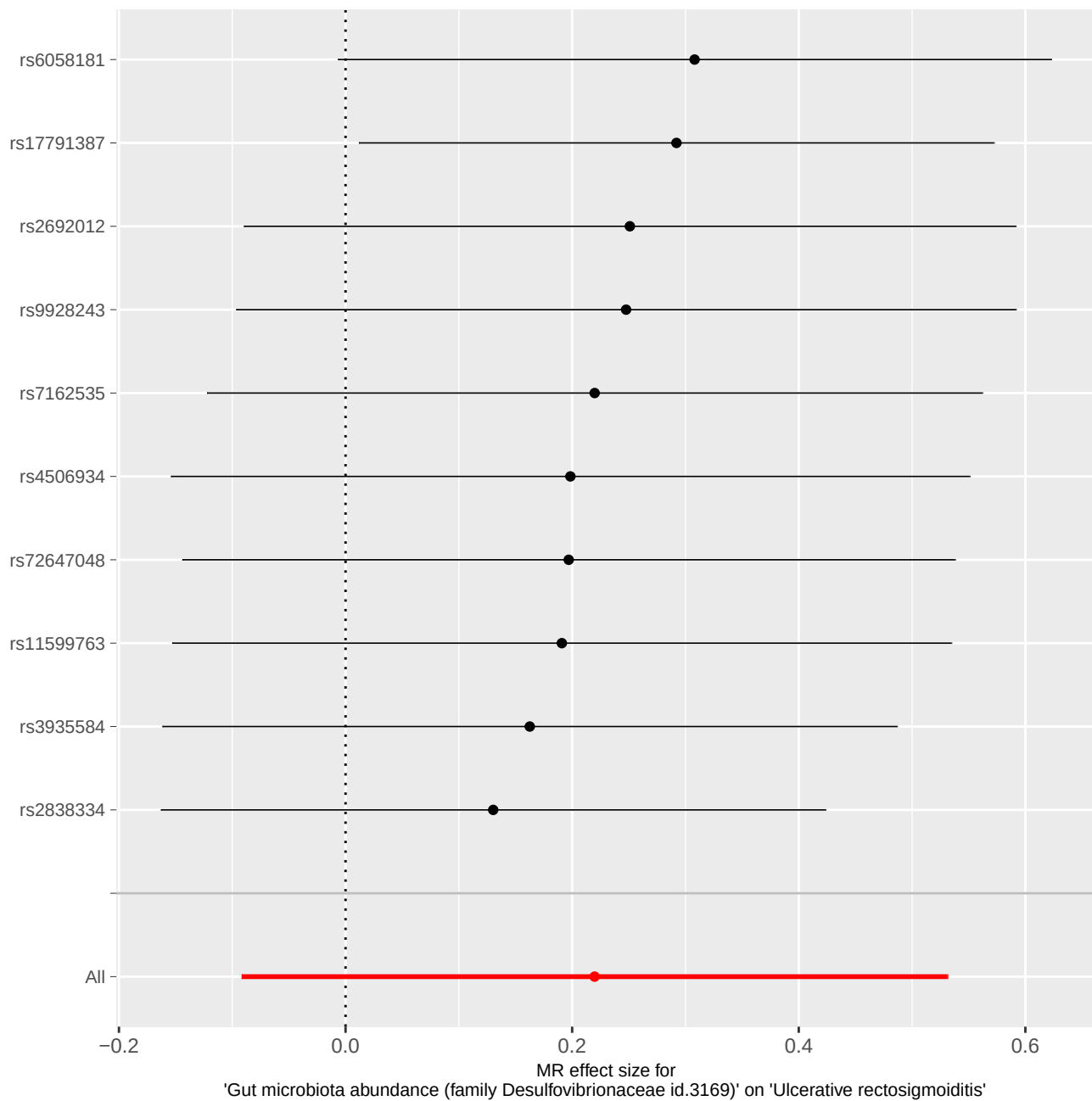


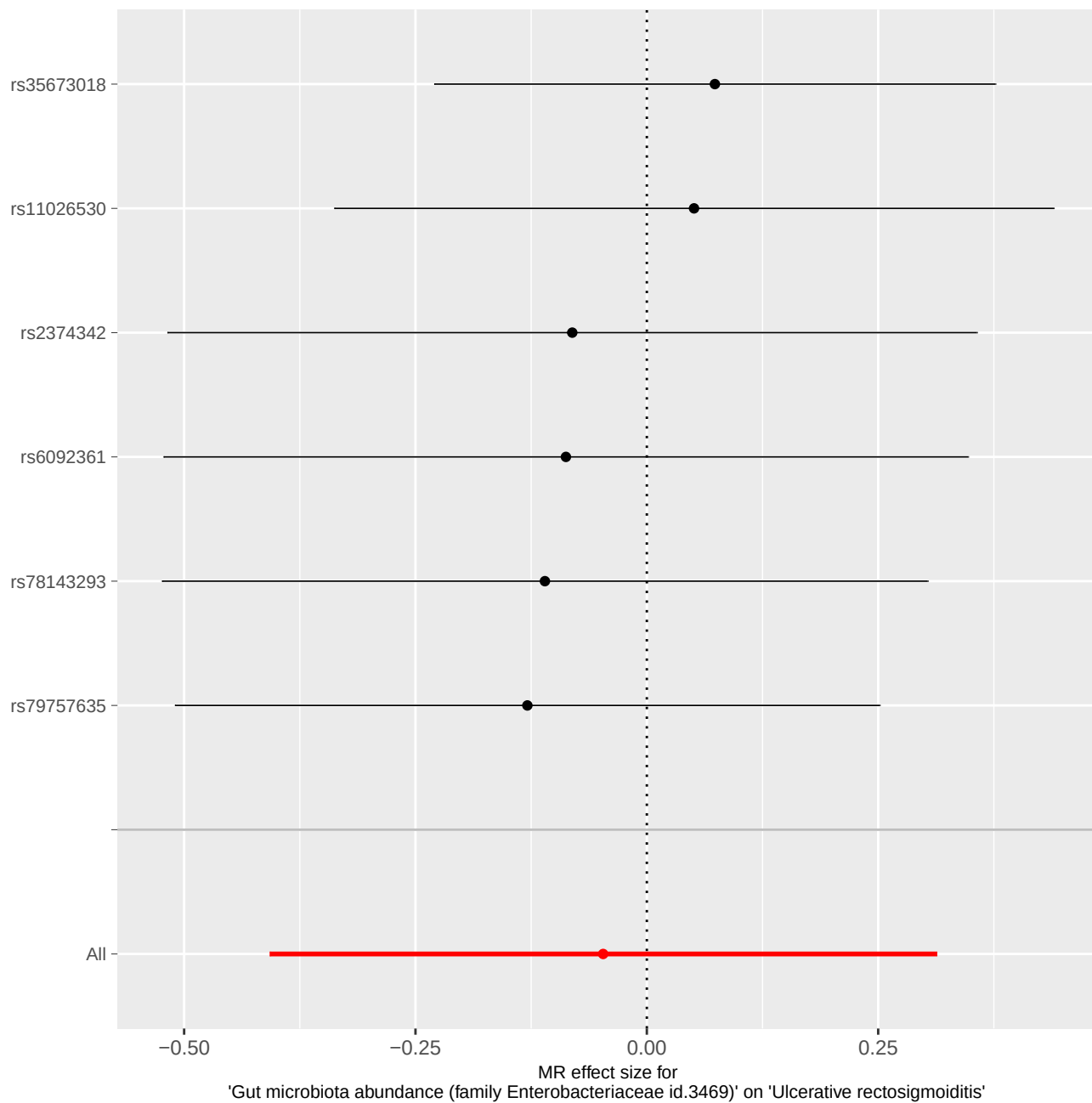


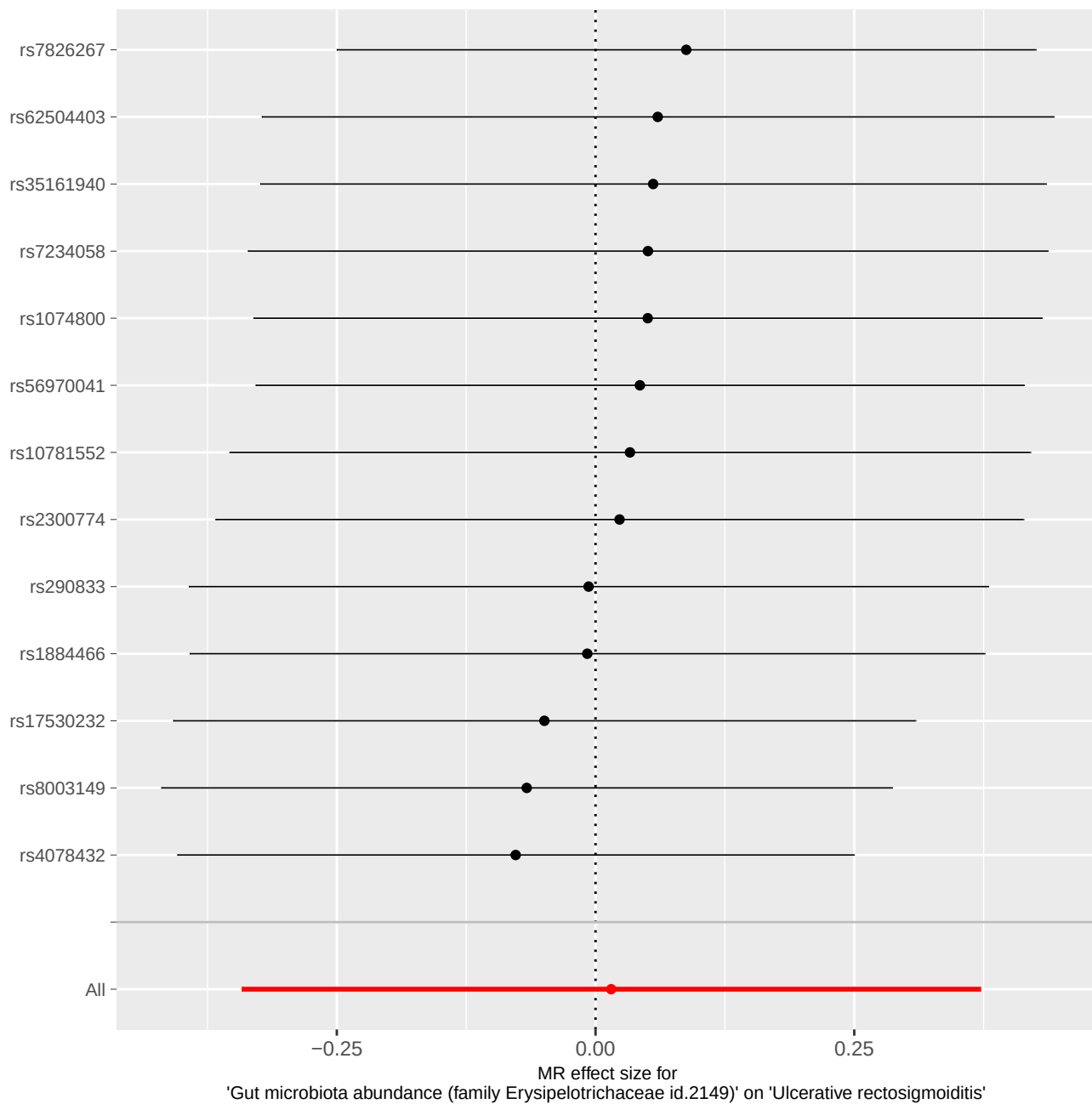


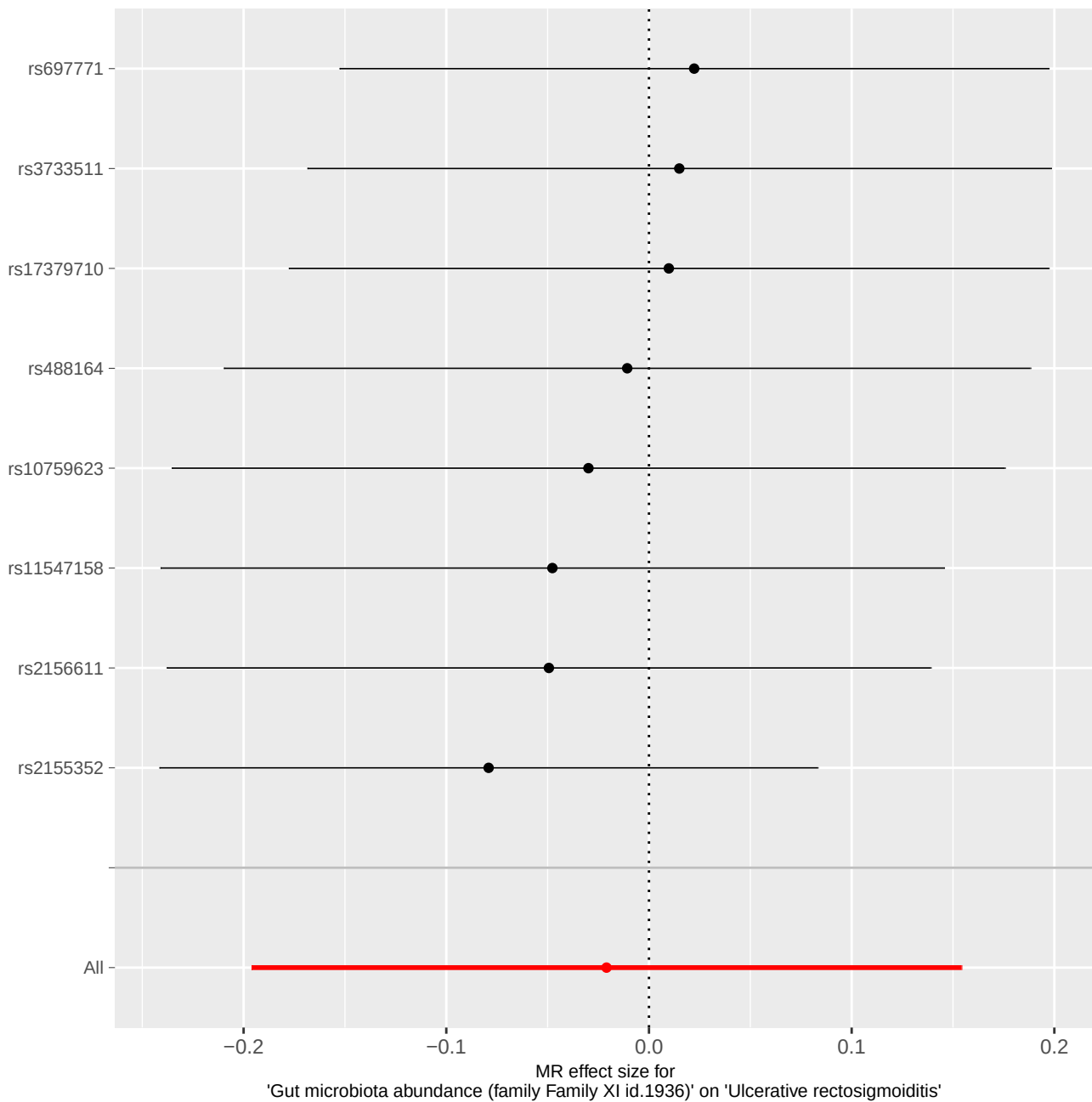


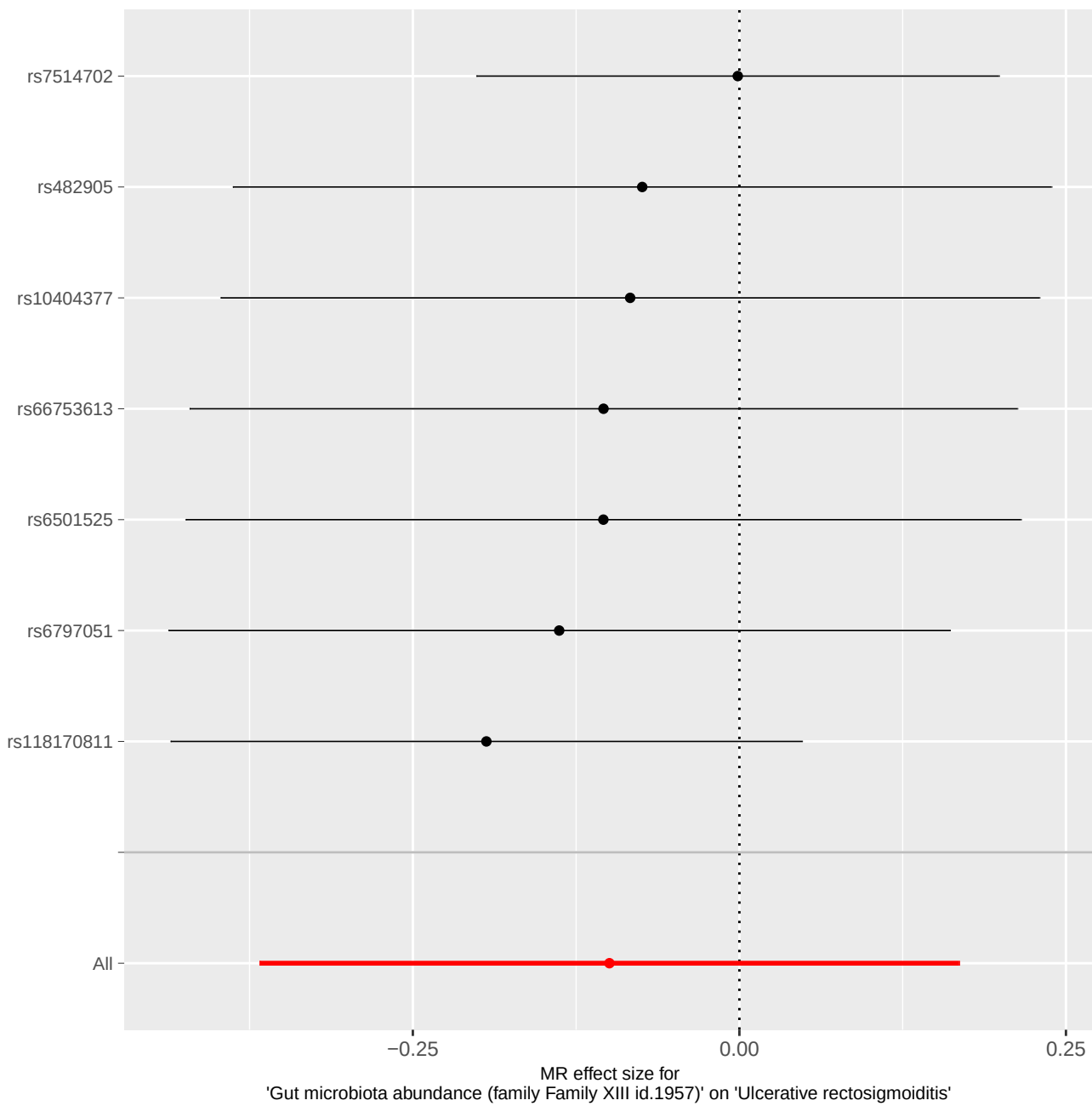




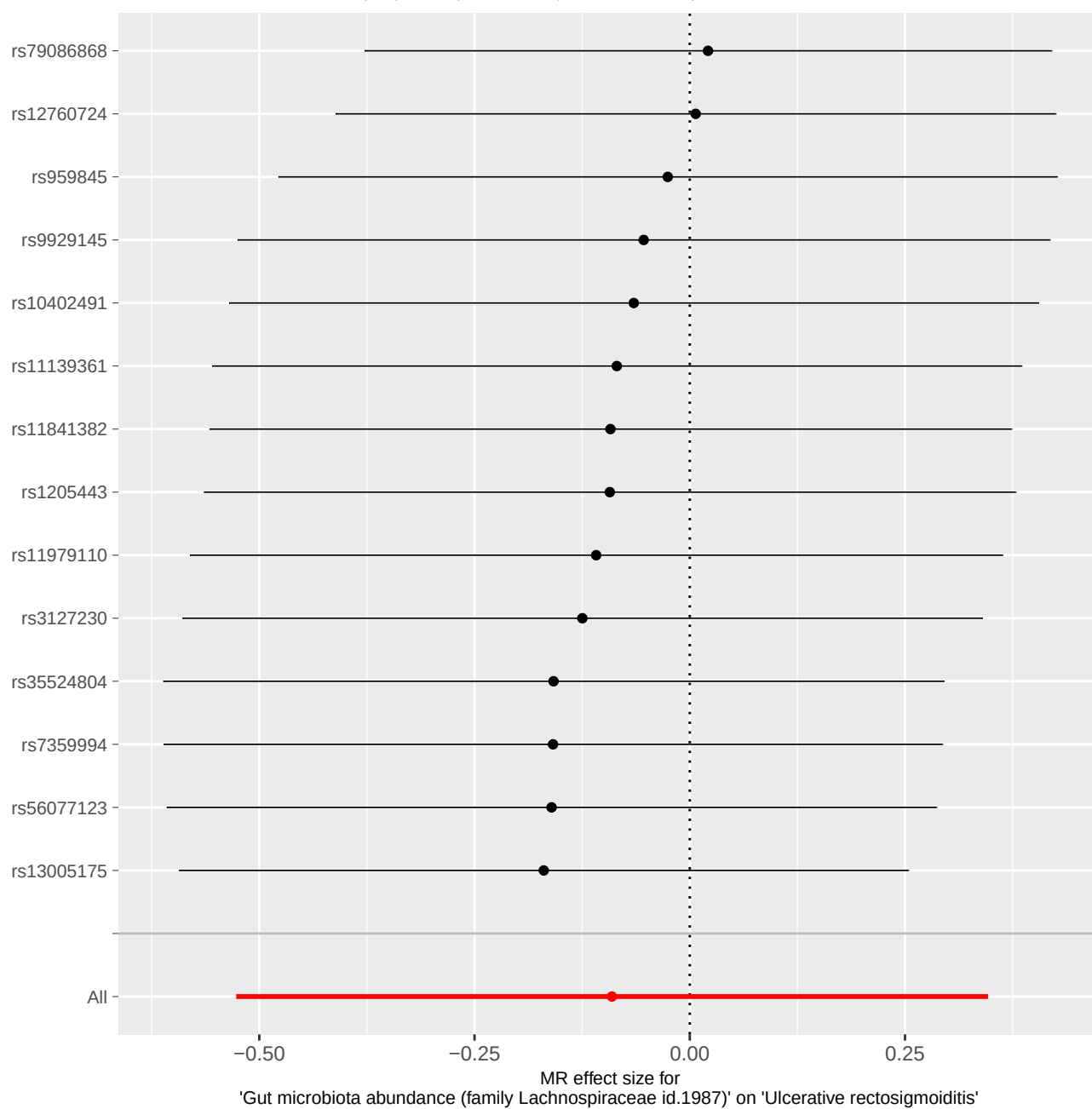


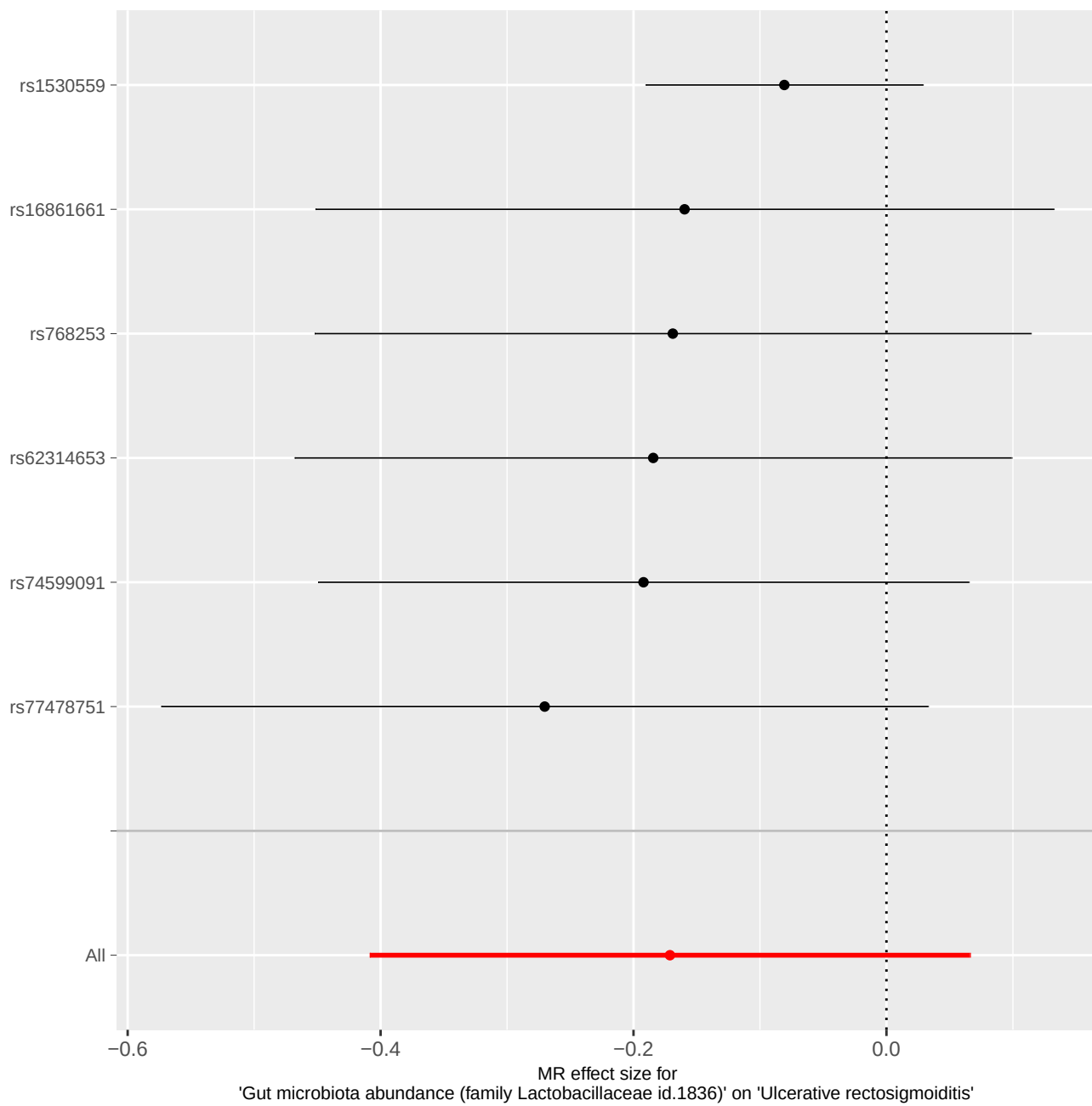


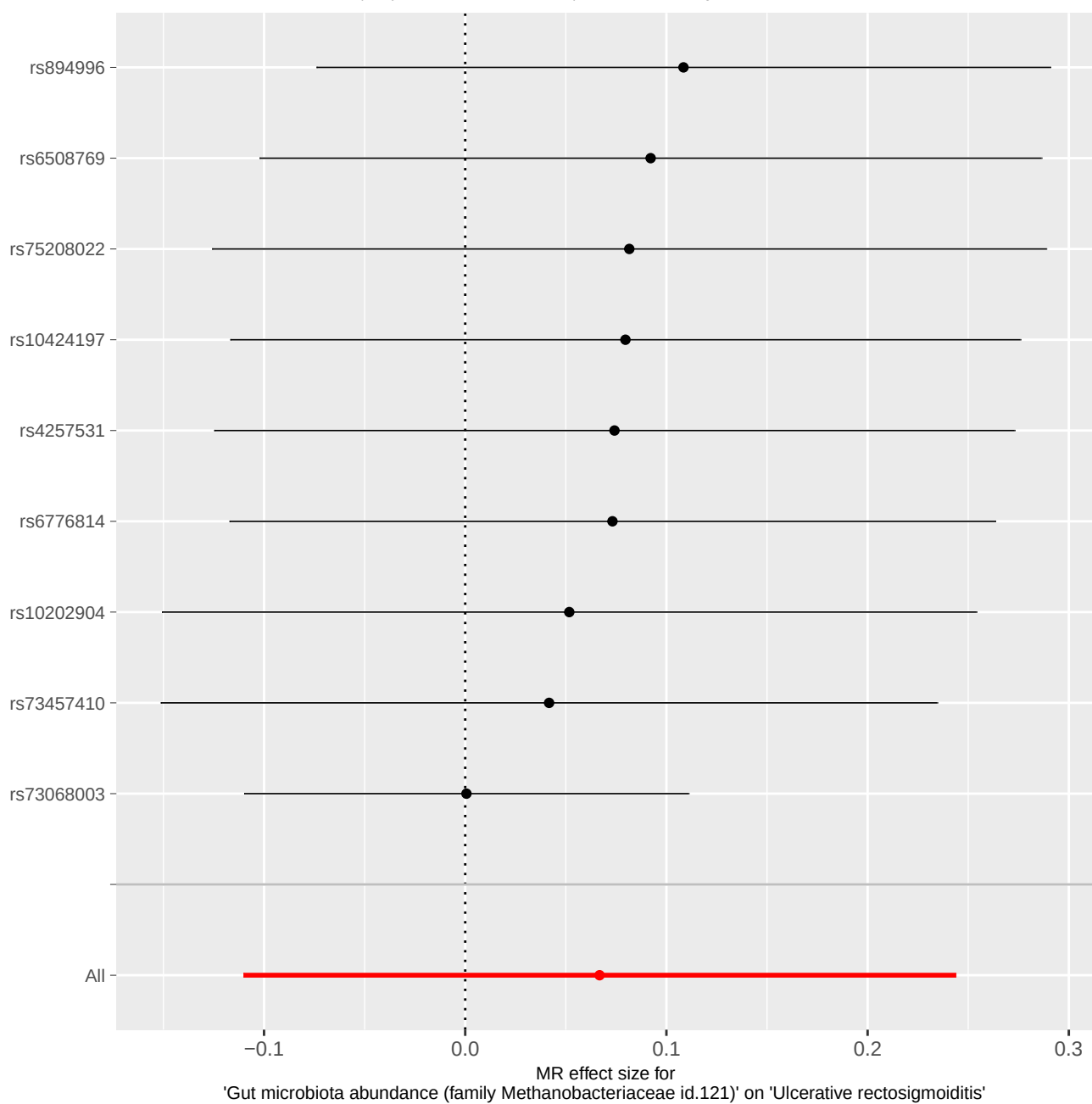


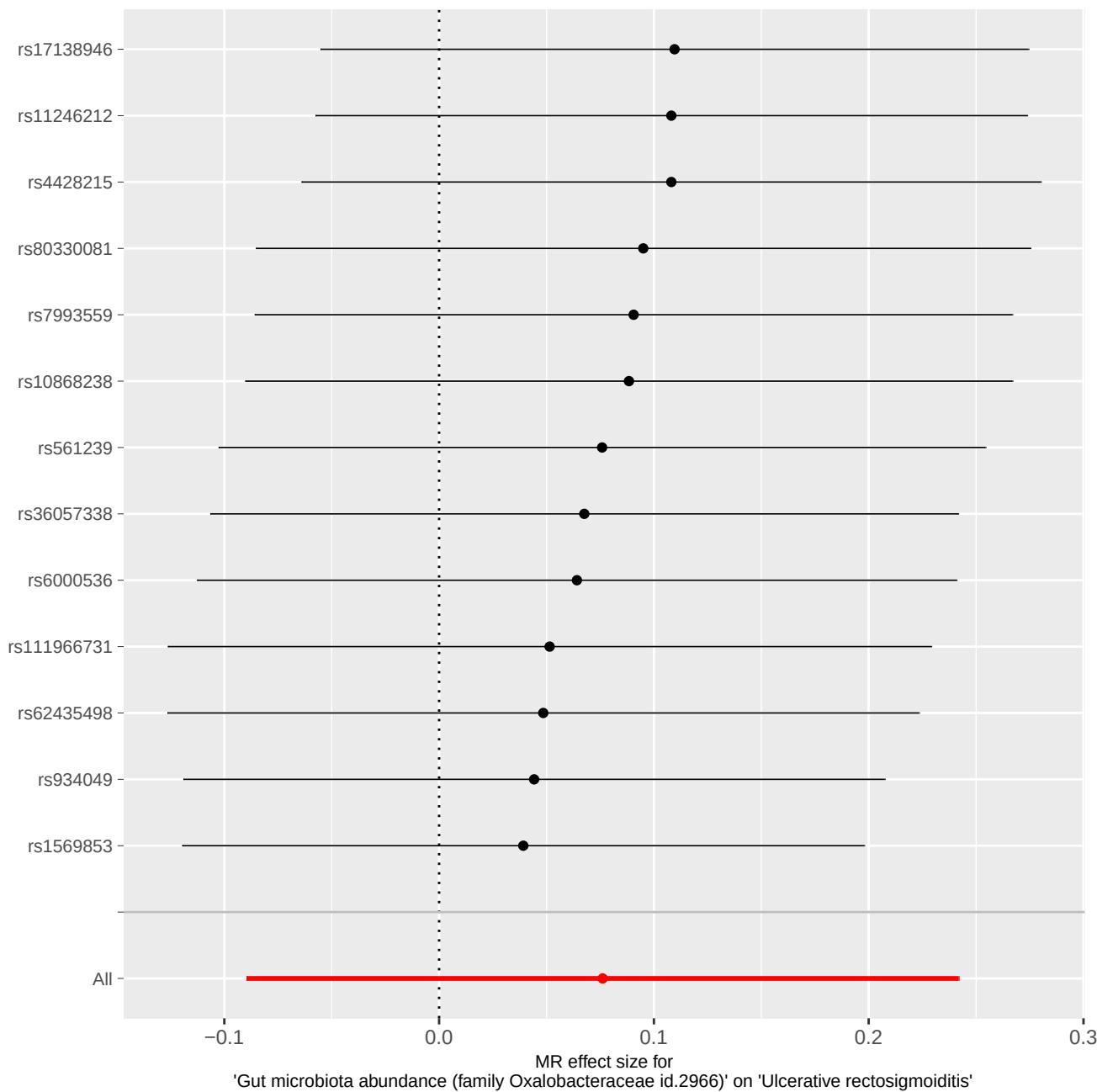


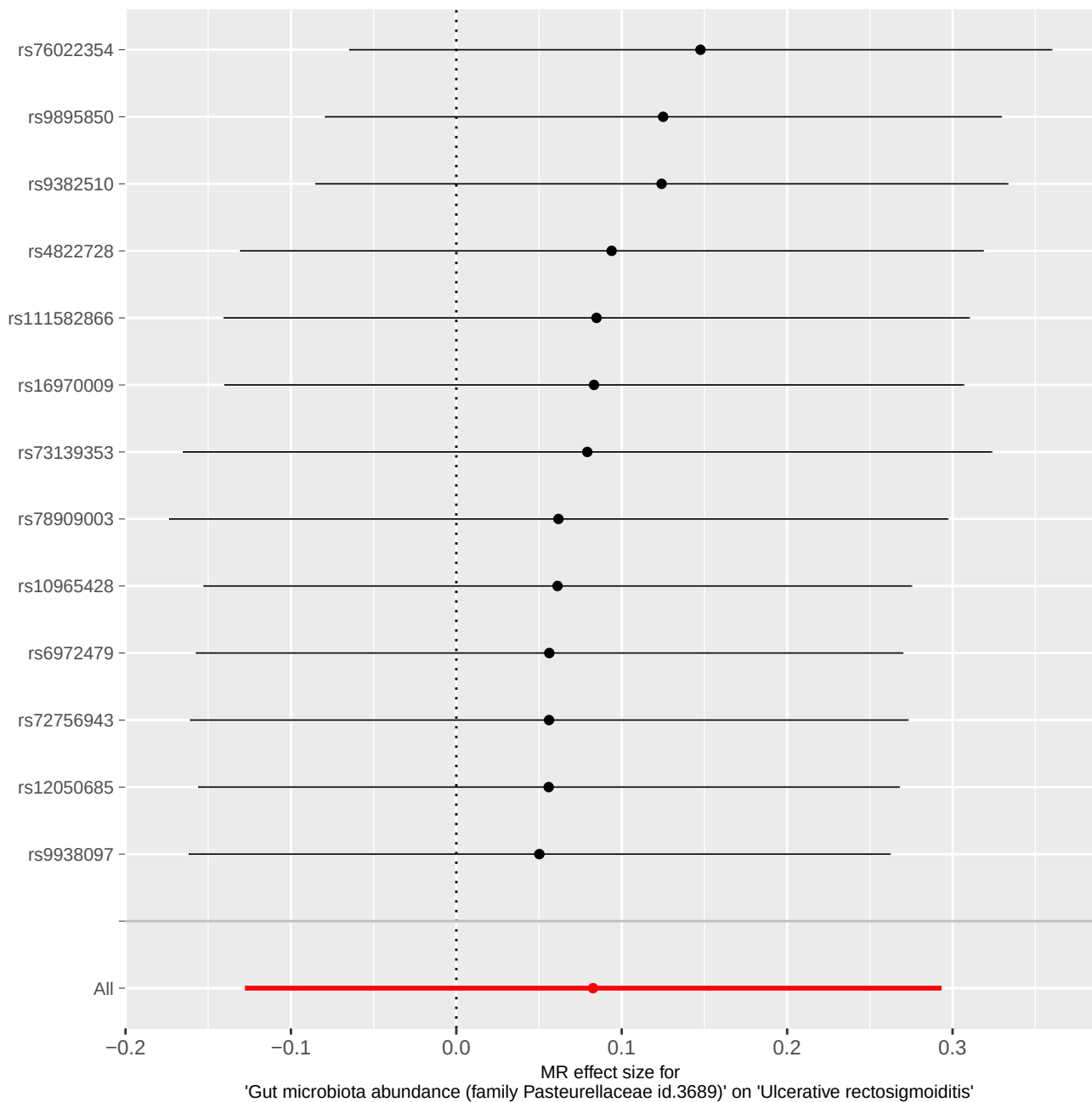
Batch 1517 : Gut microbiota abundance (family Lachnospiraceae id.1987) on Ulcerative rectosigmoiditis

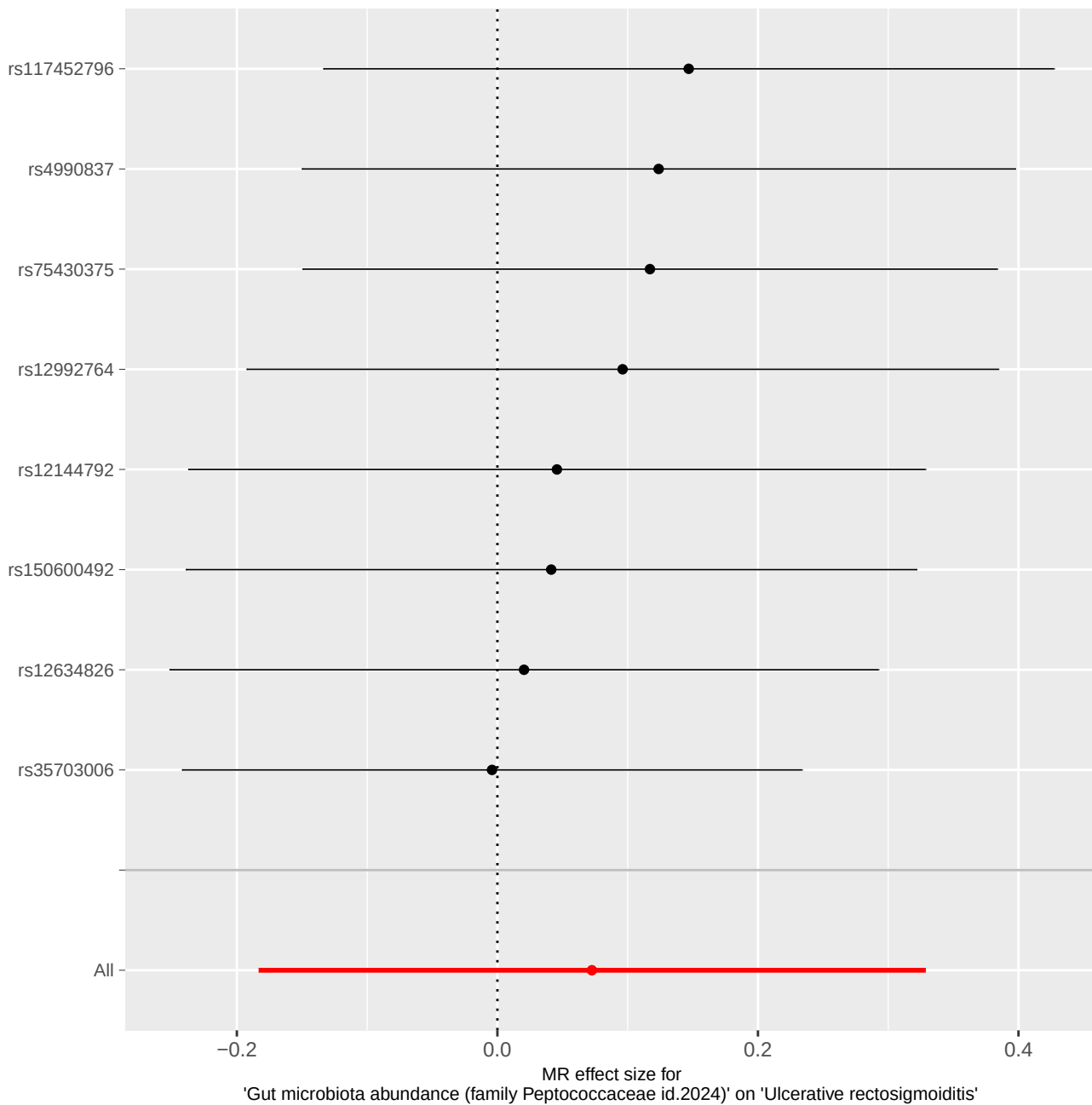


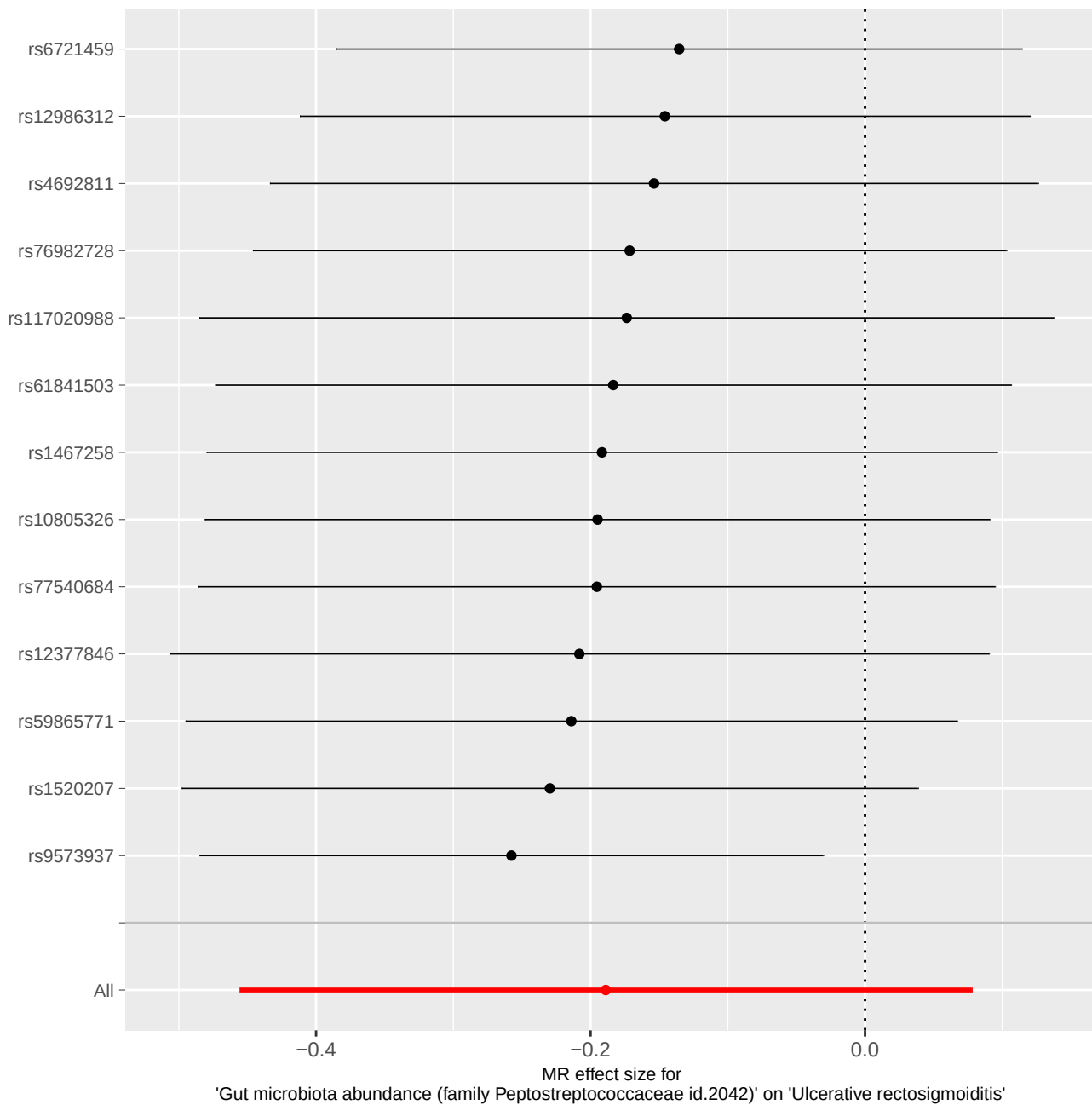


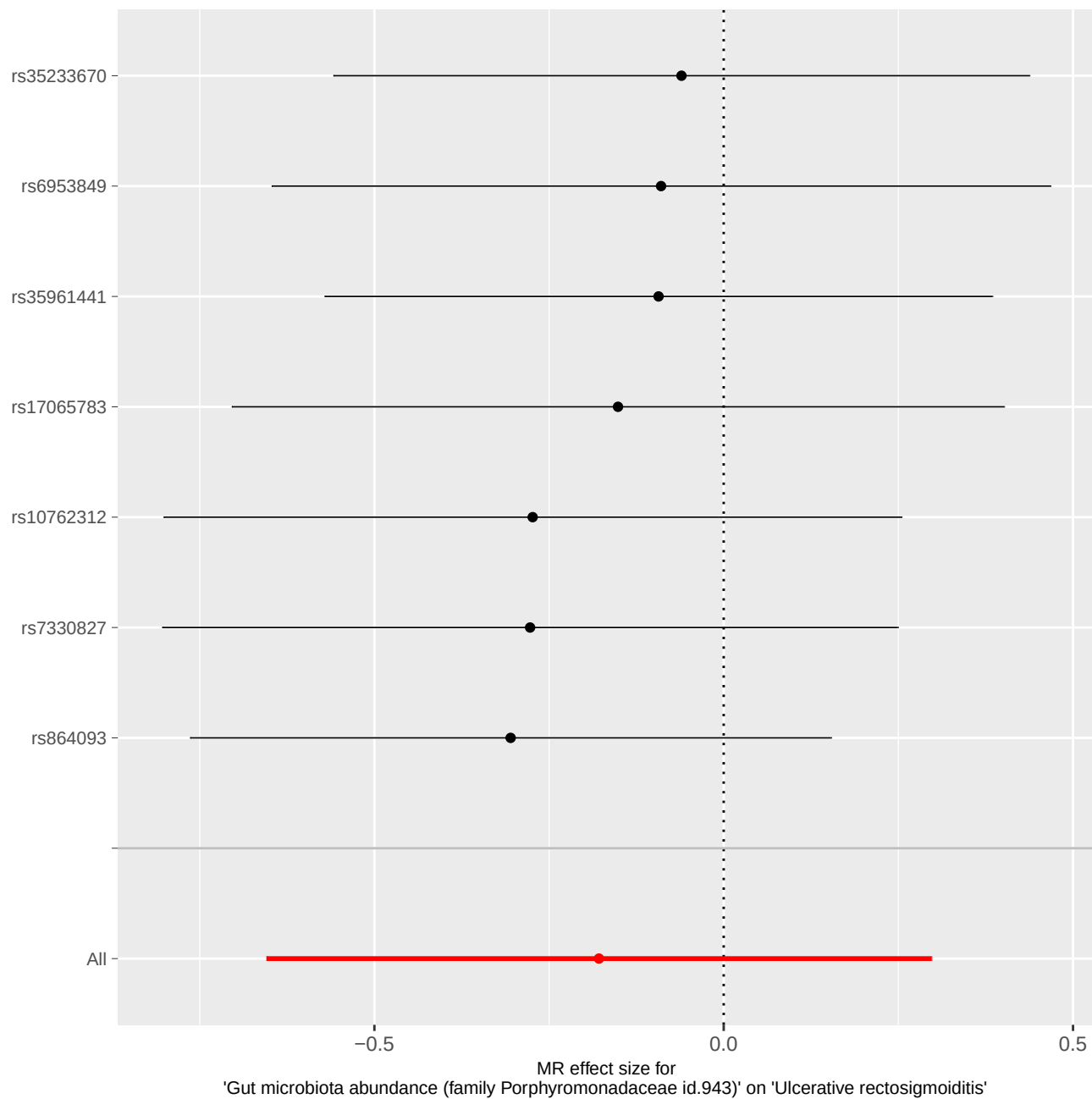


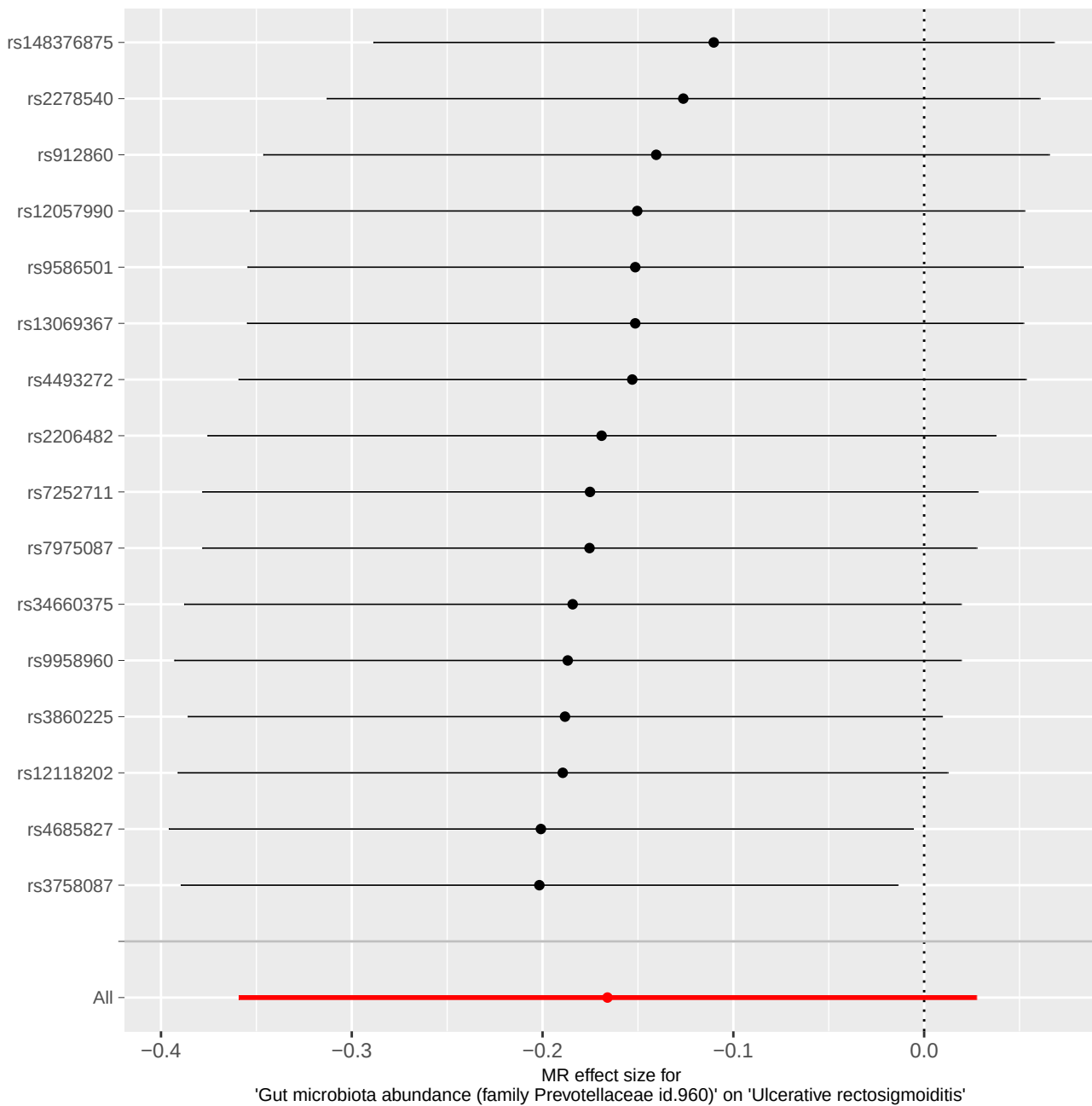


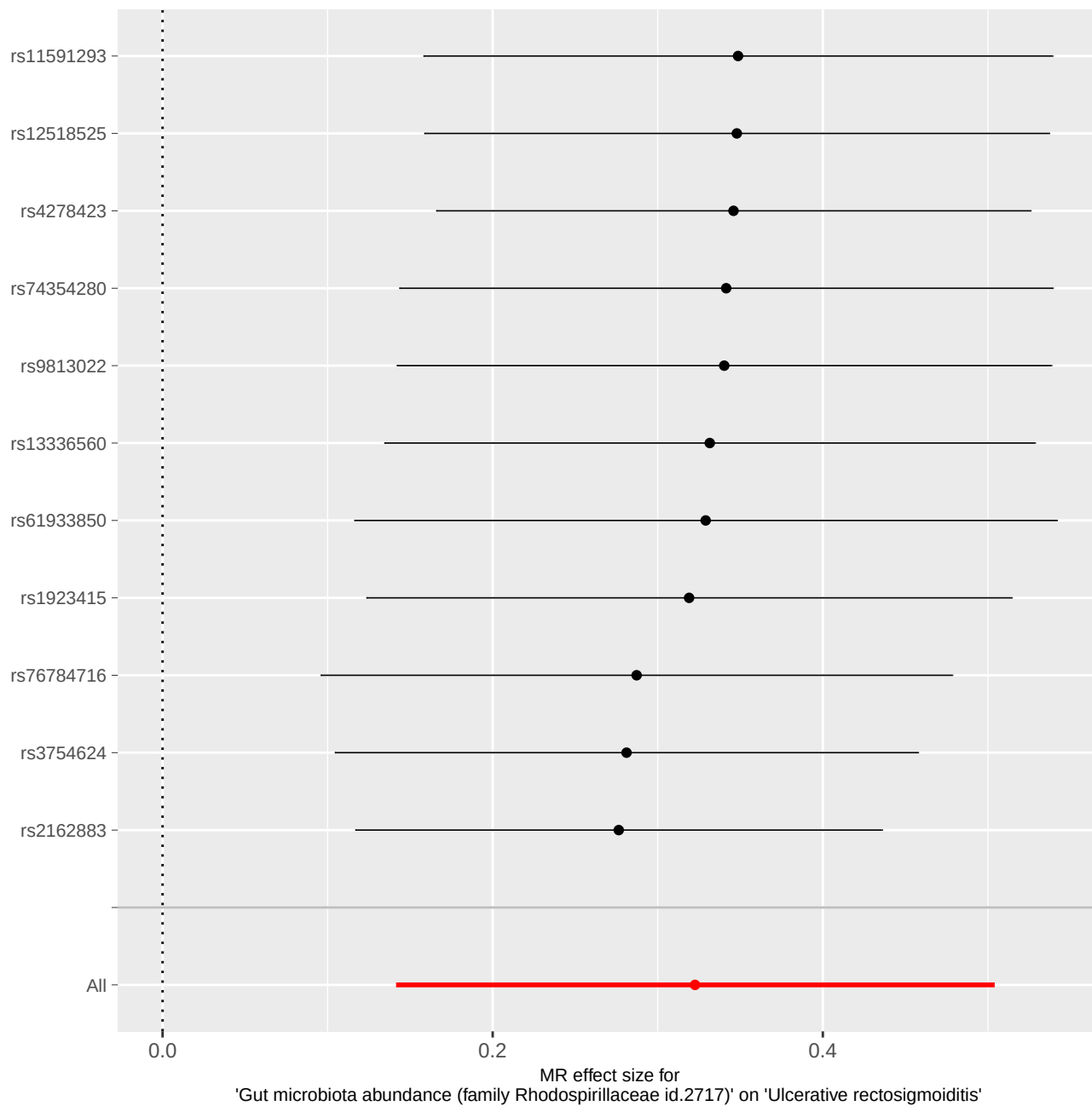


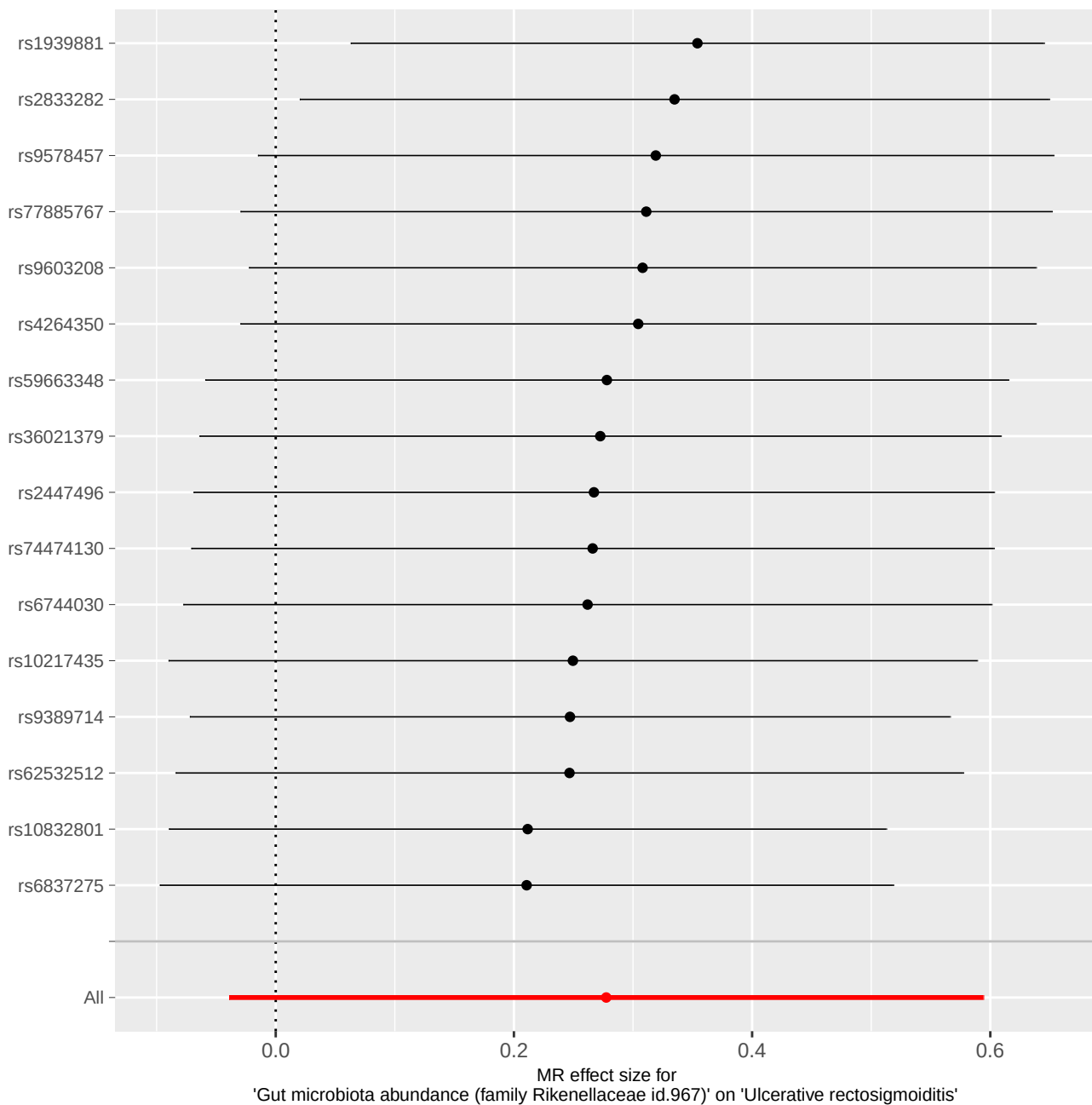


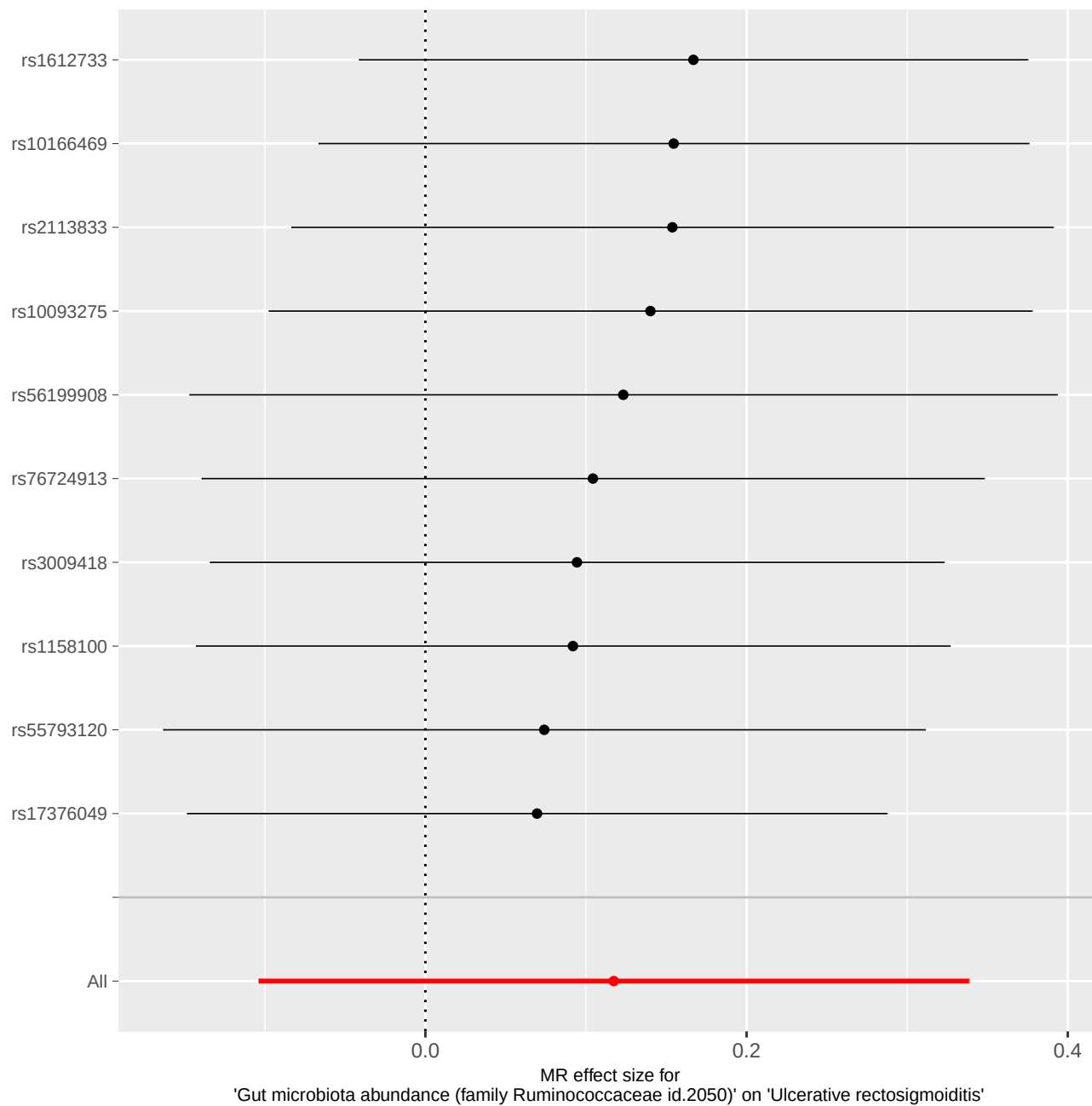


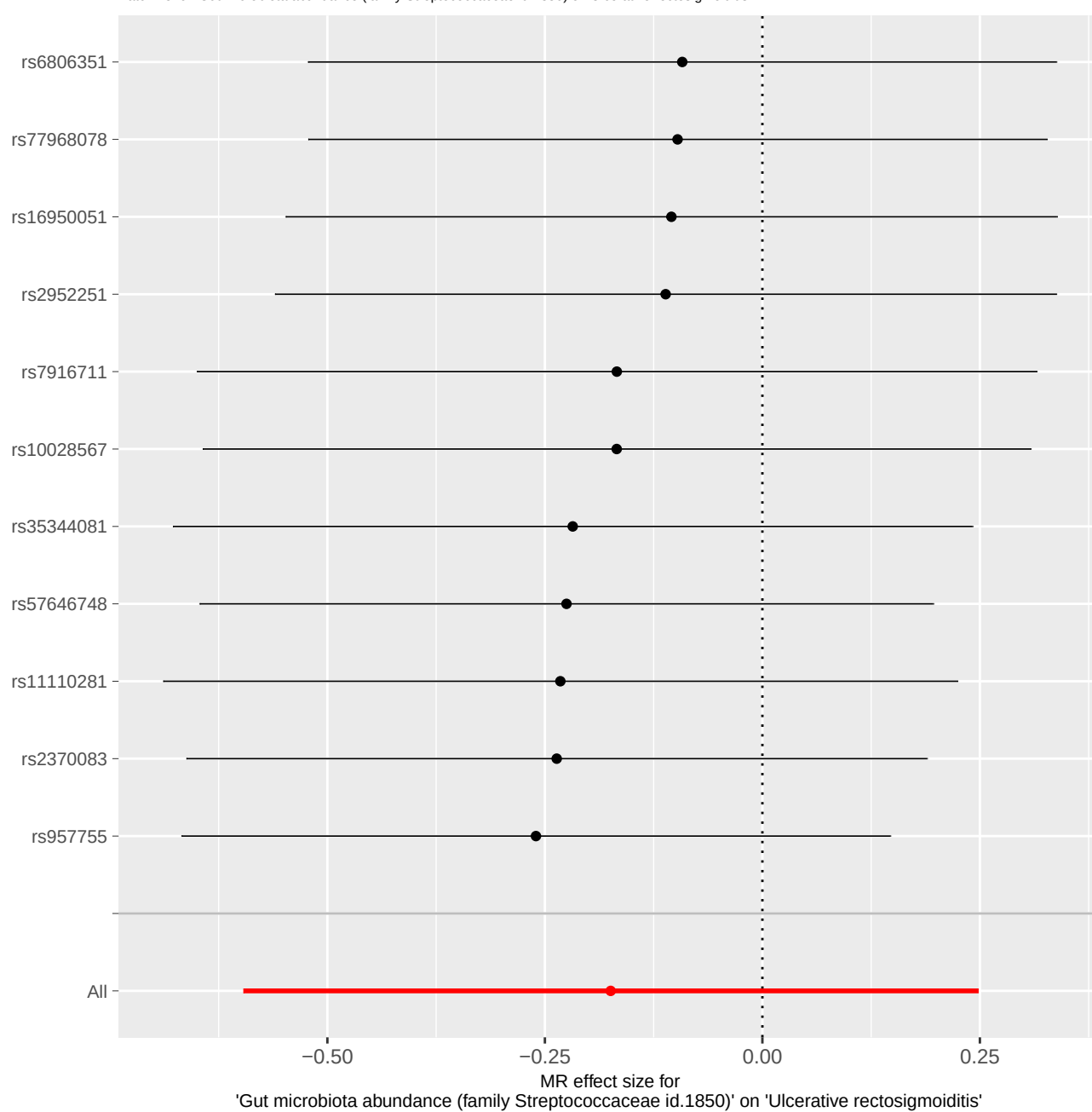


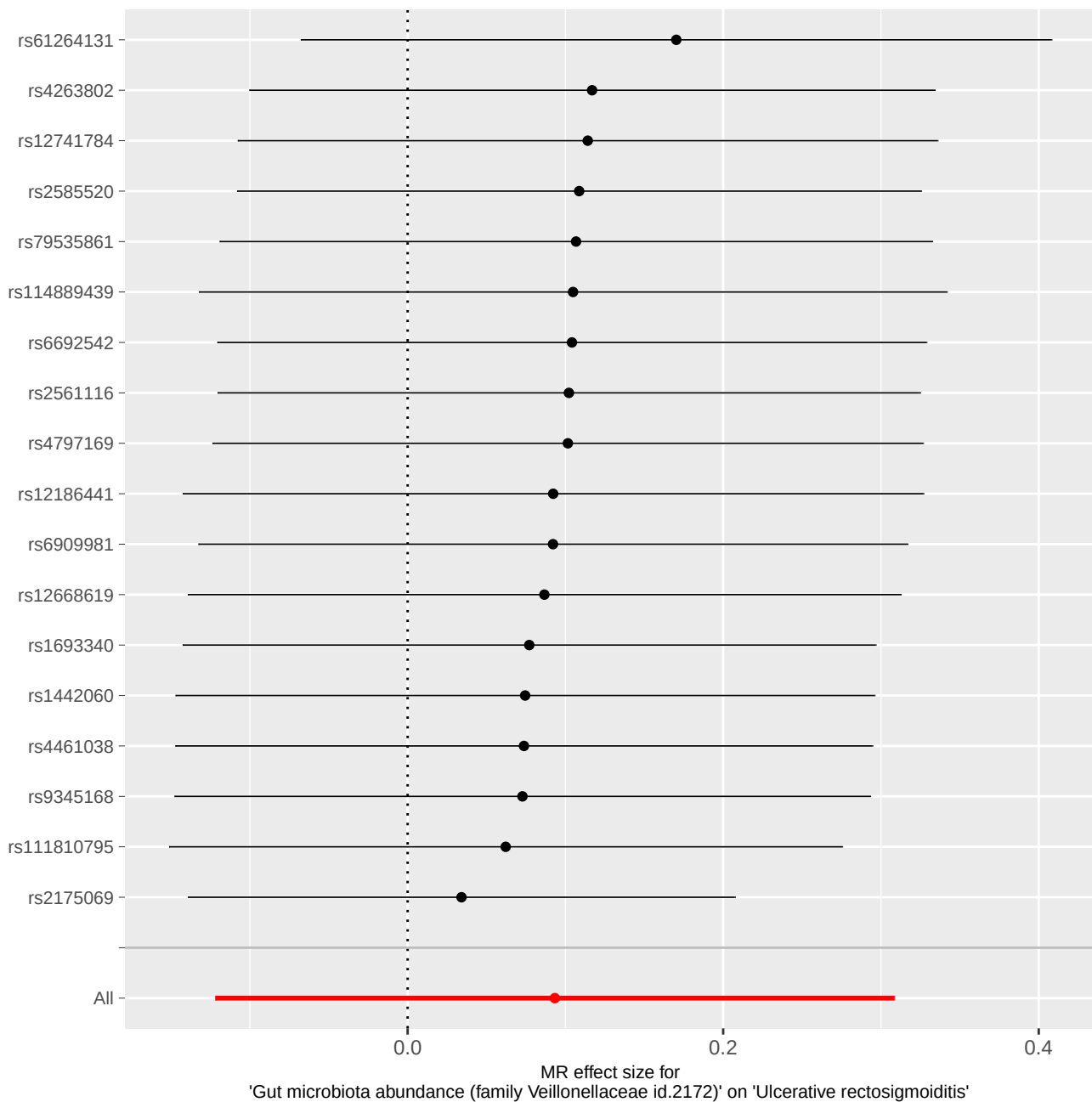


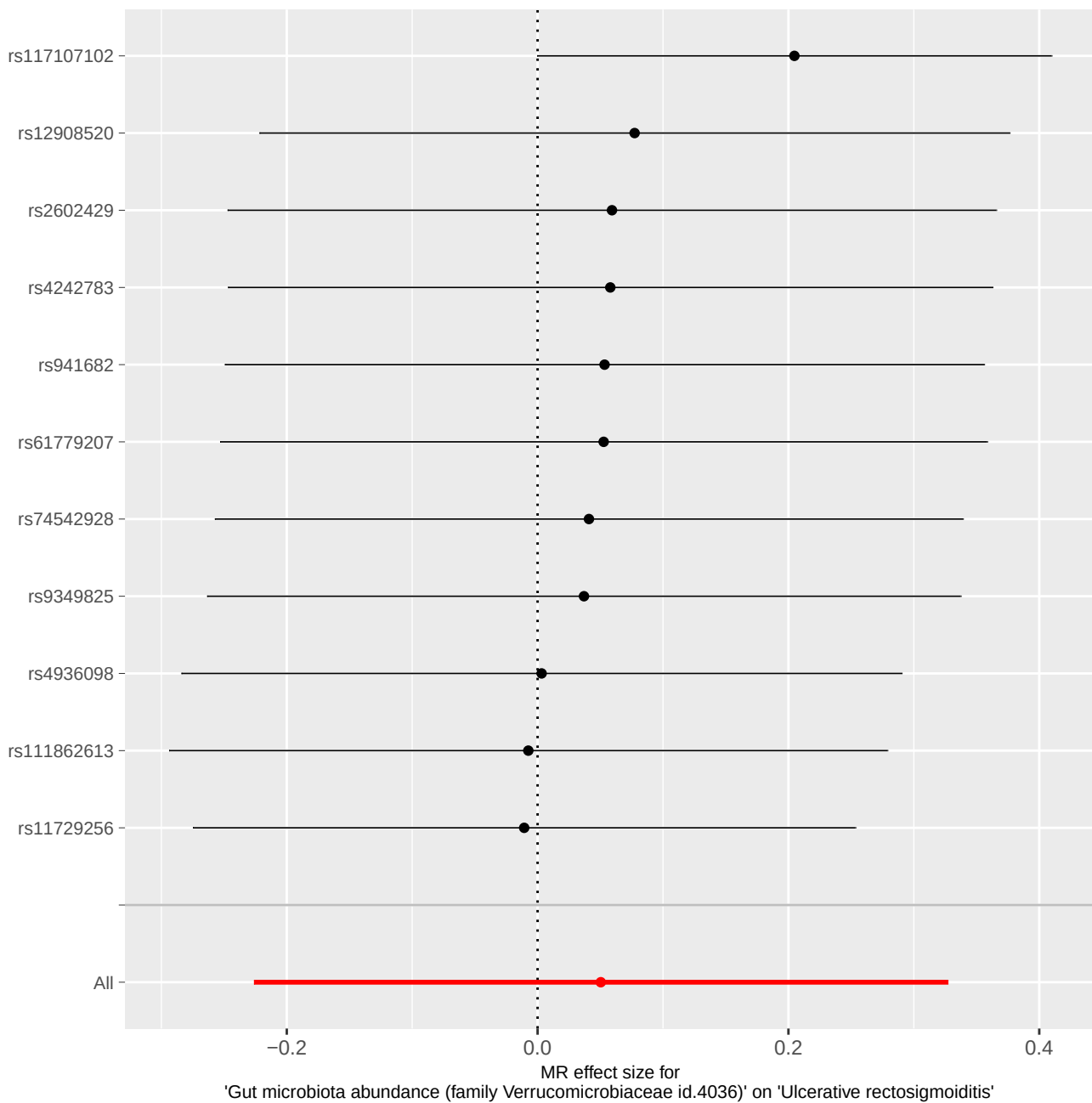


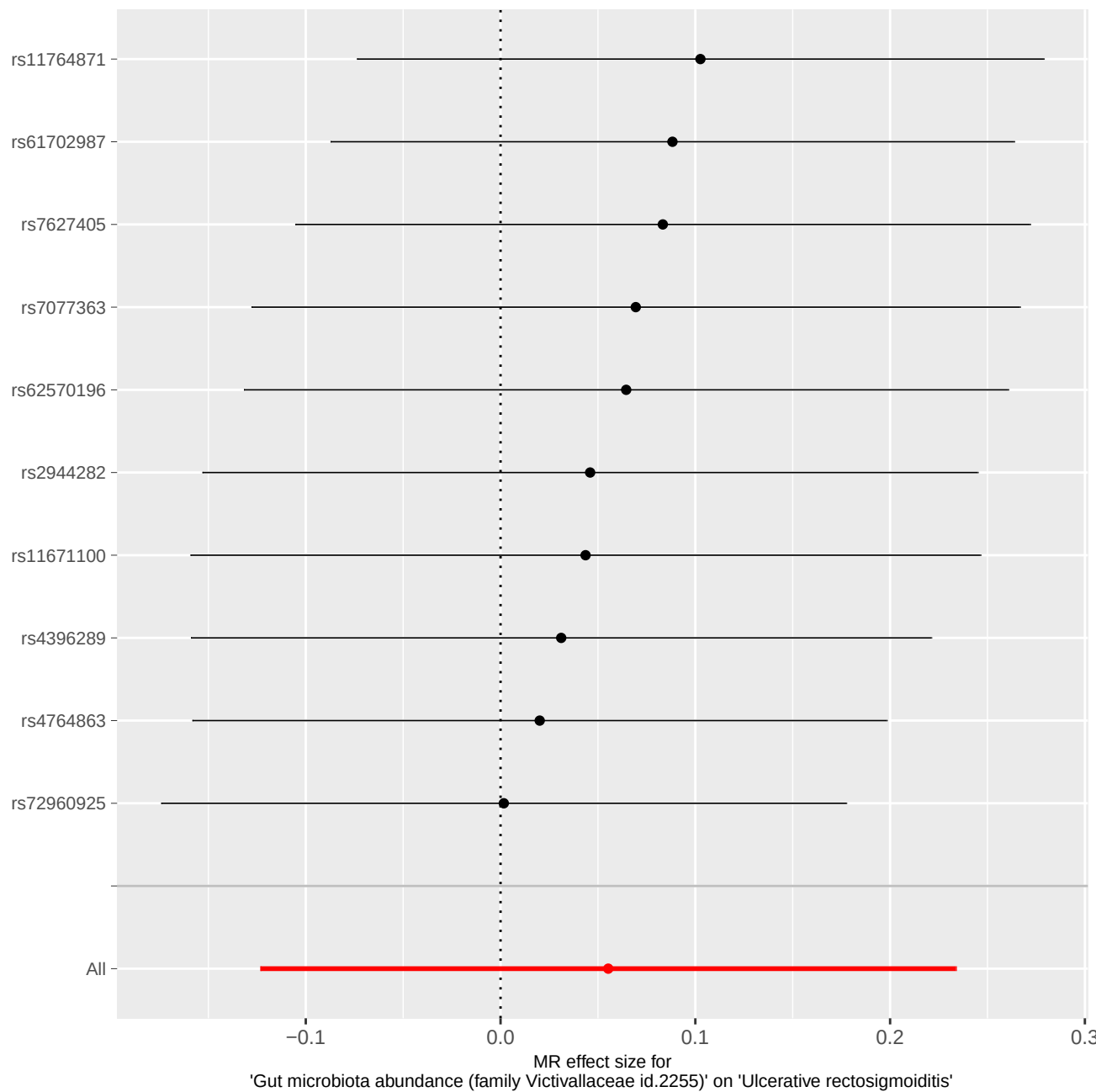


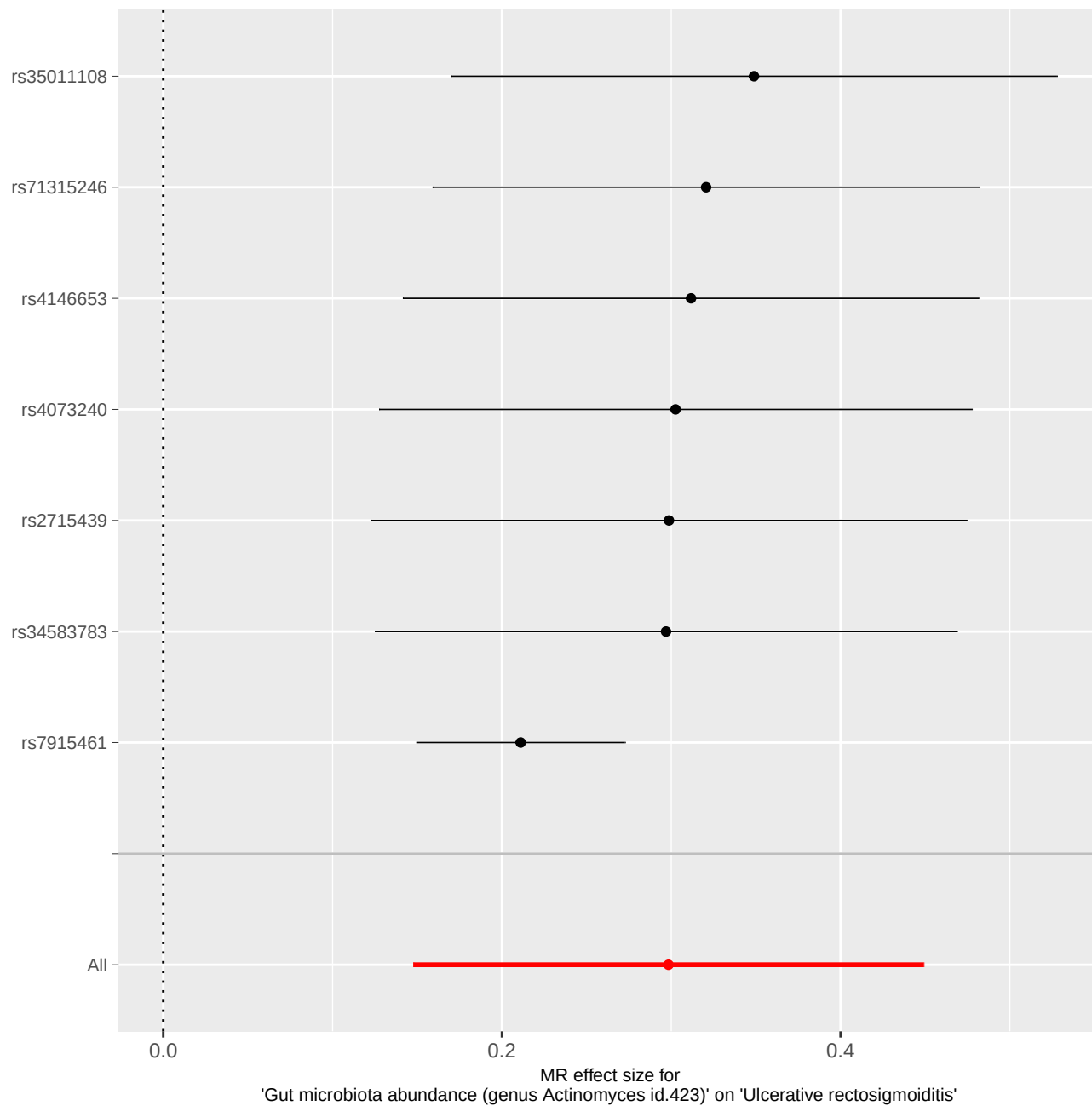


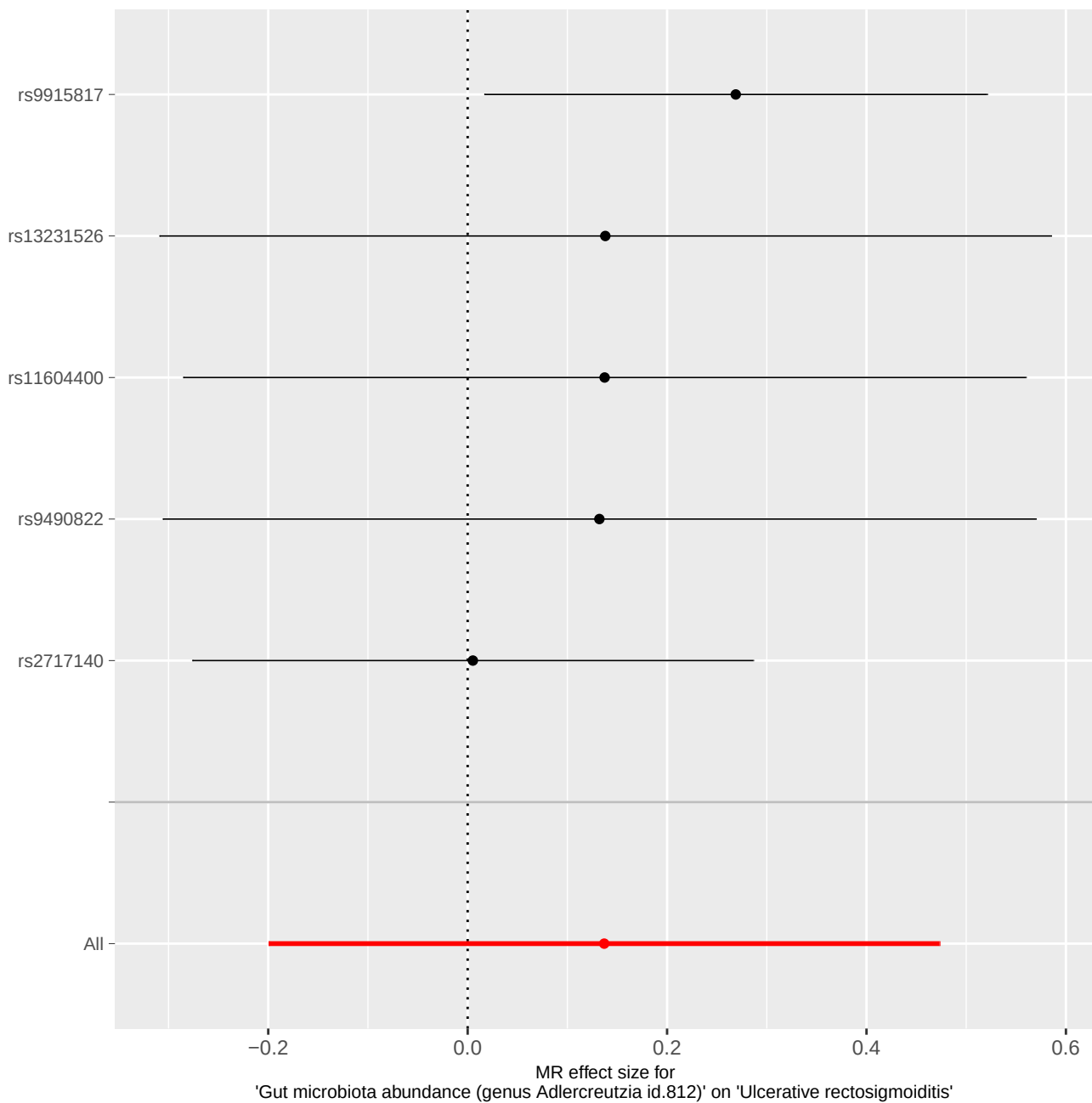


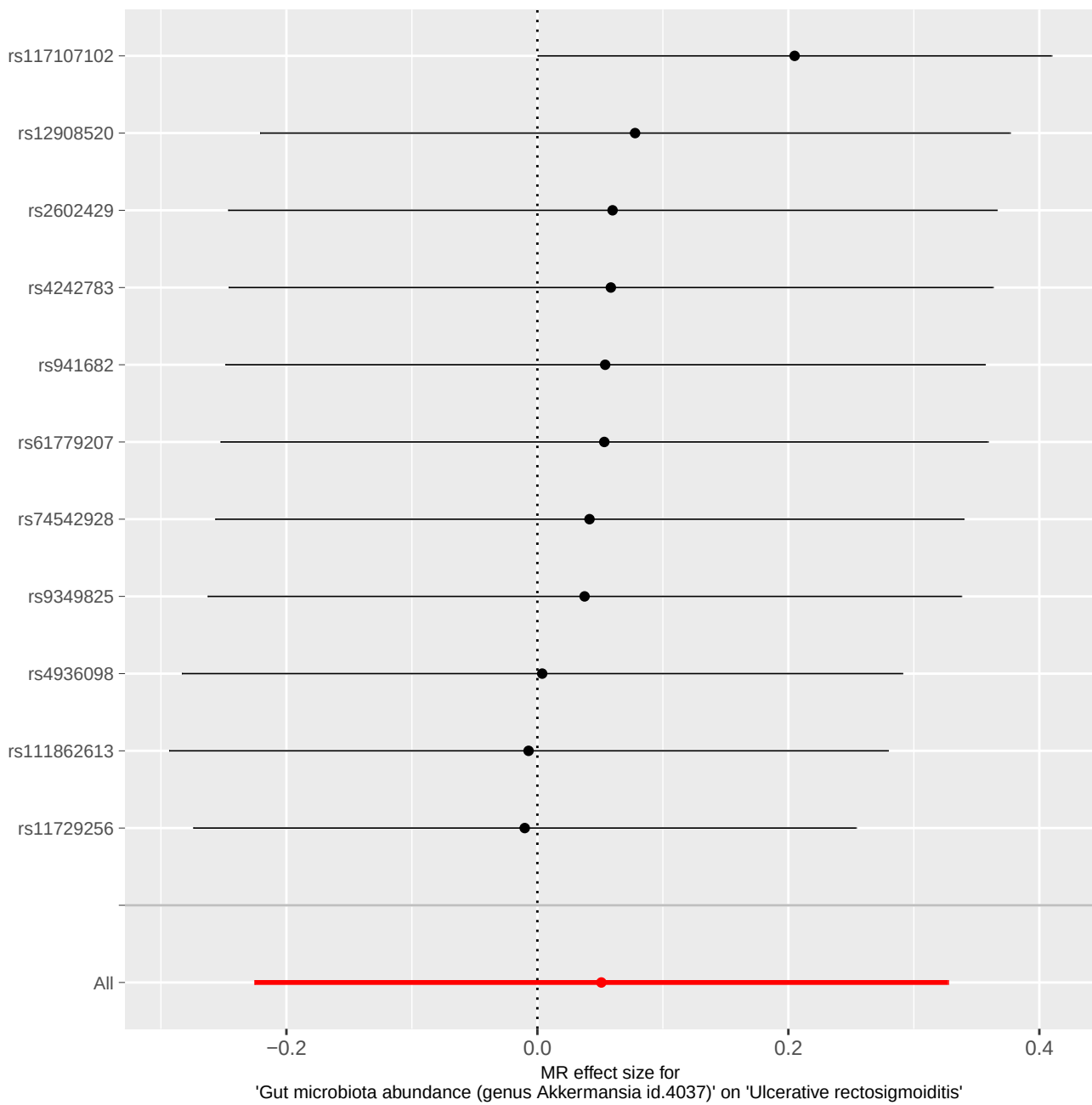


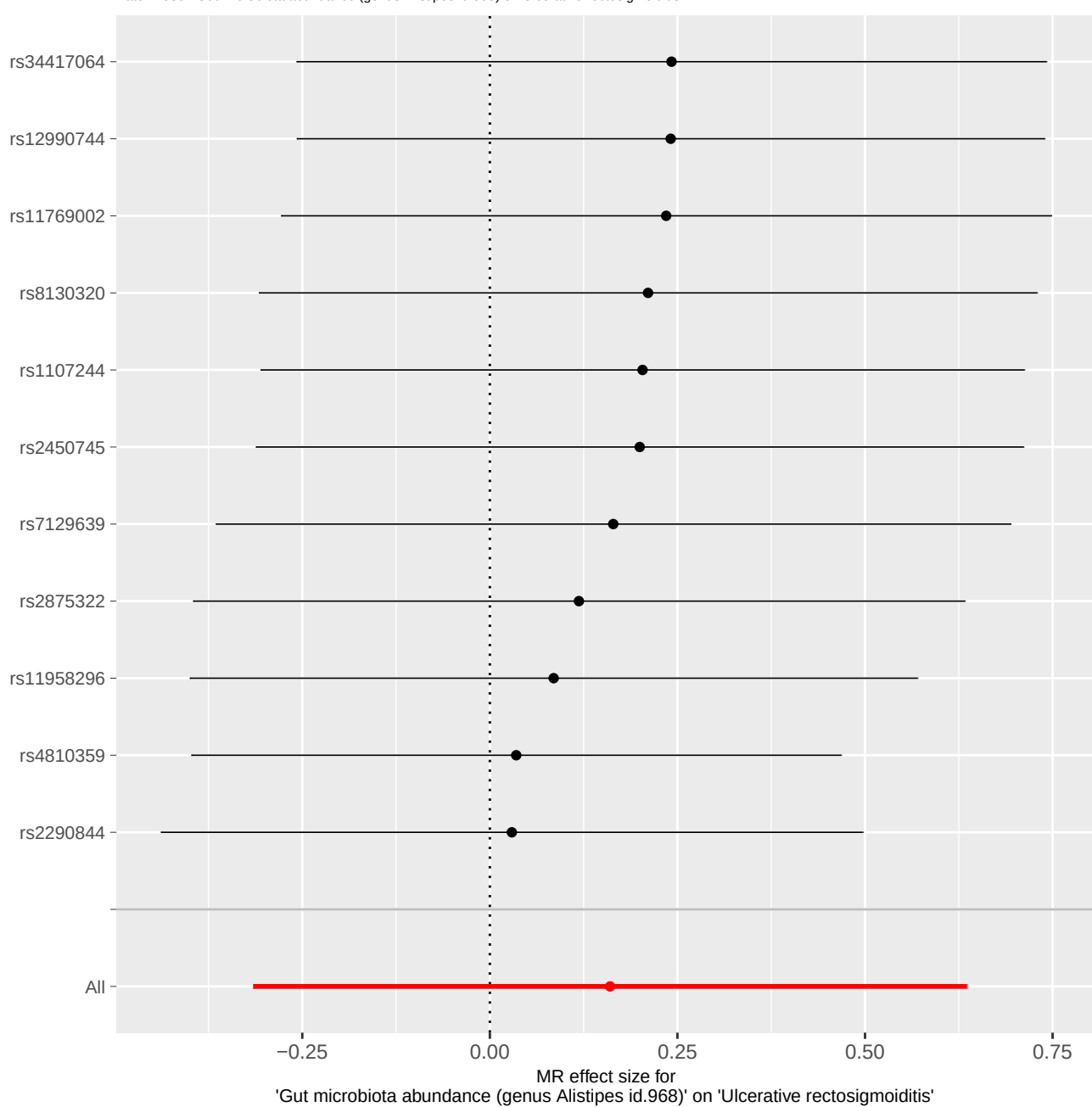


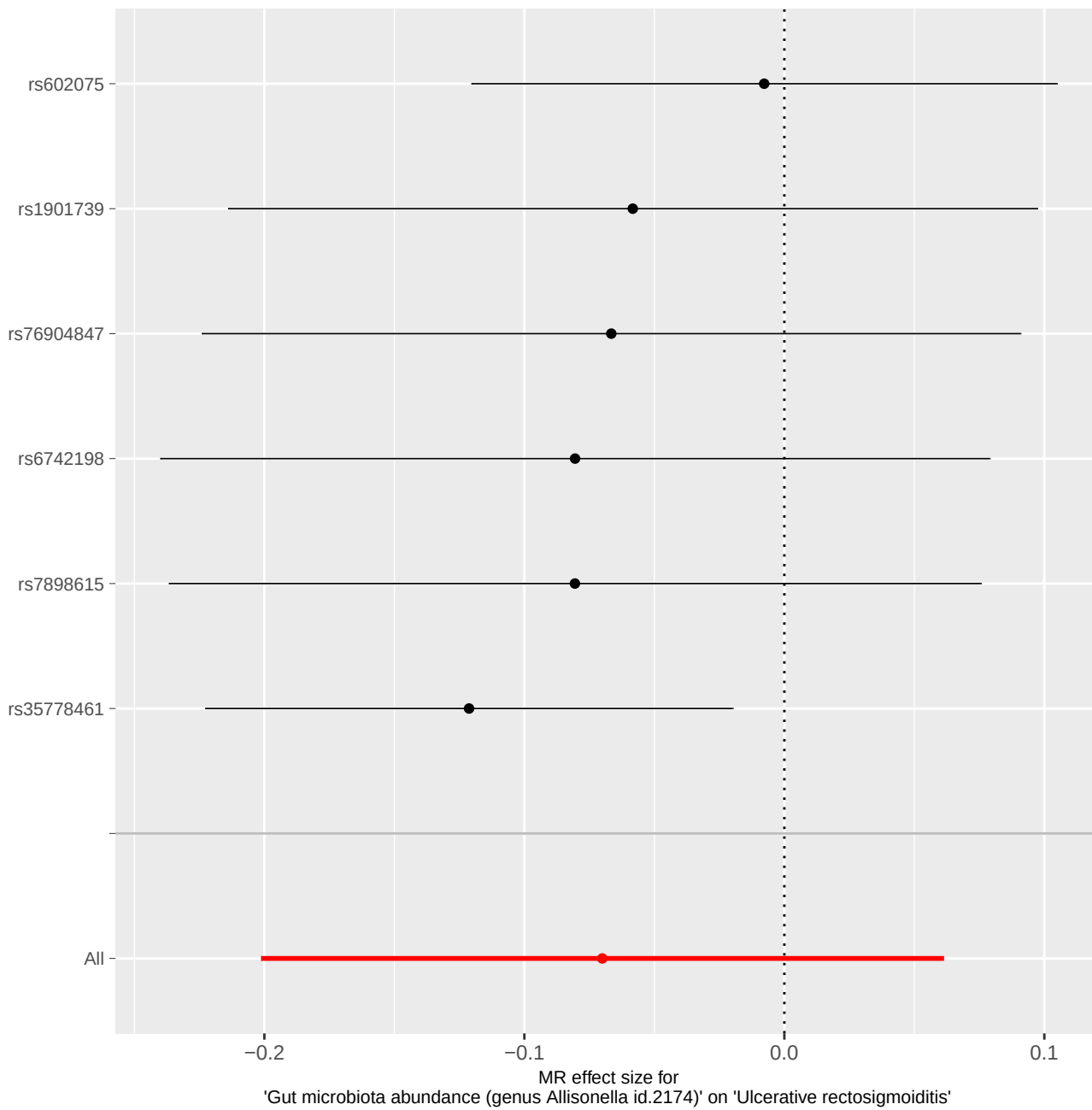


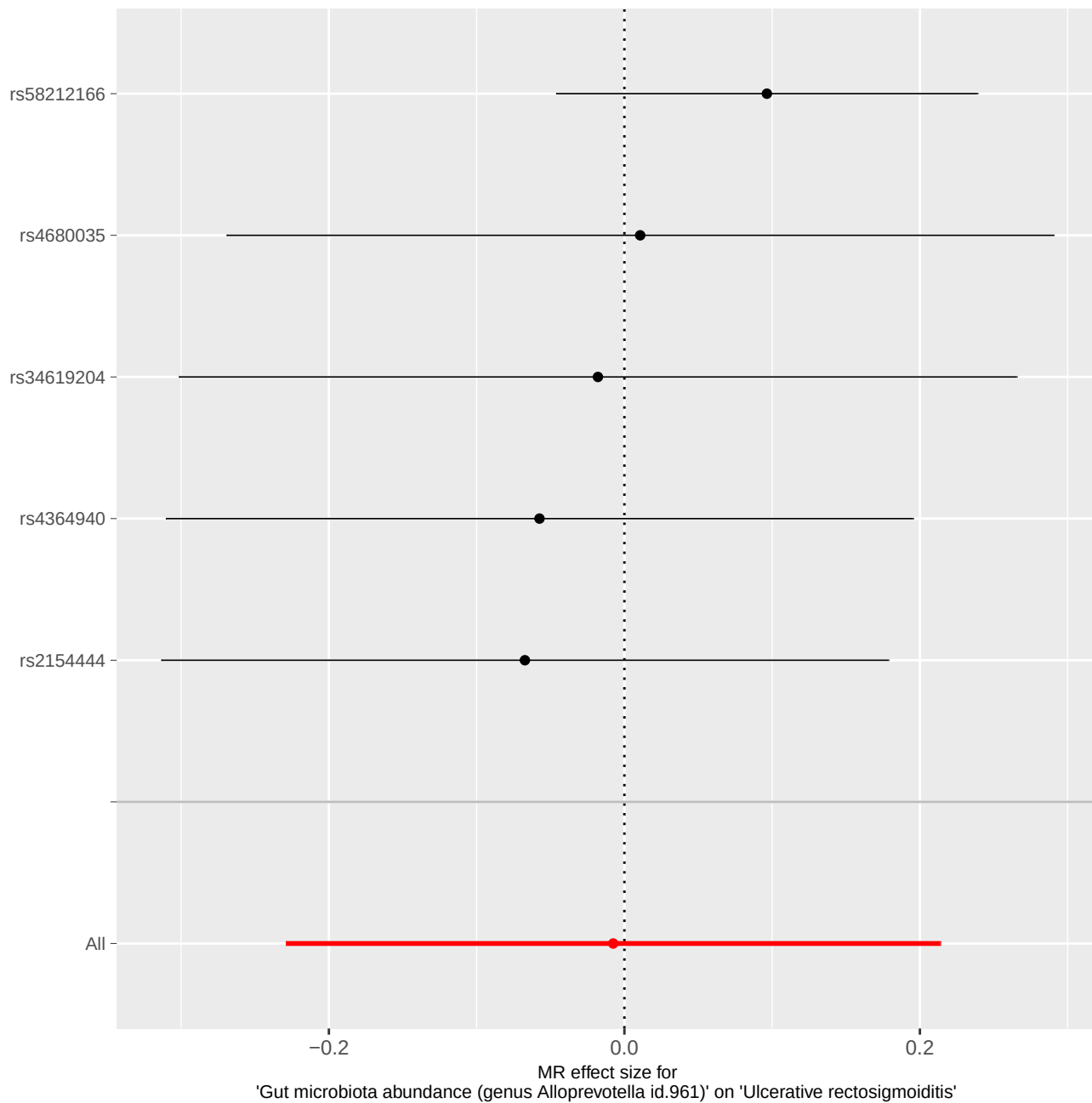


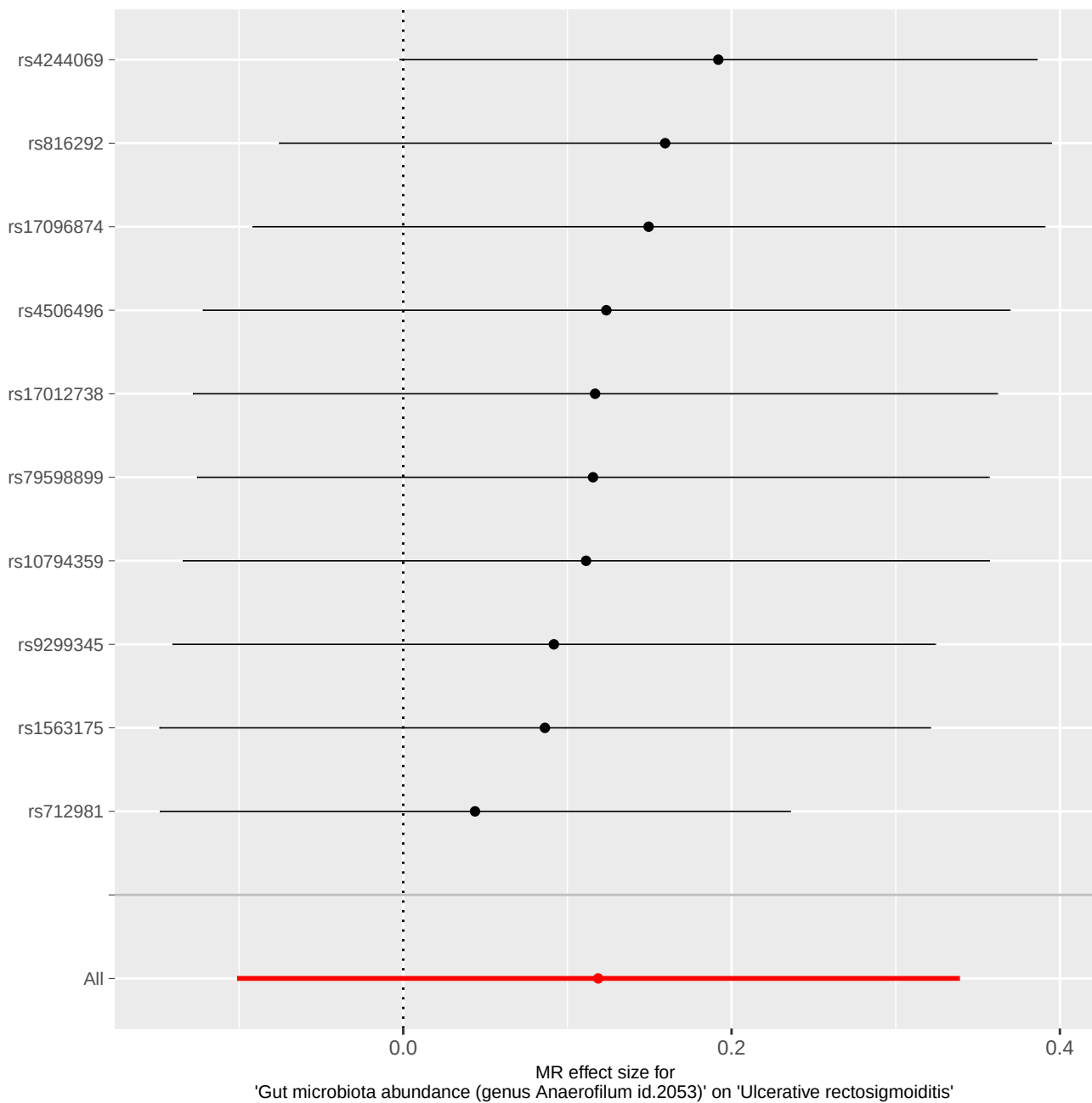


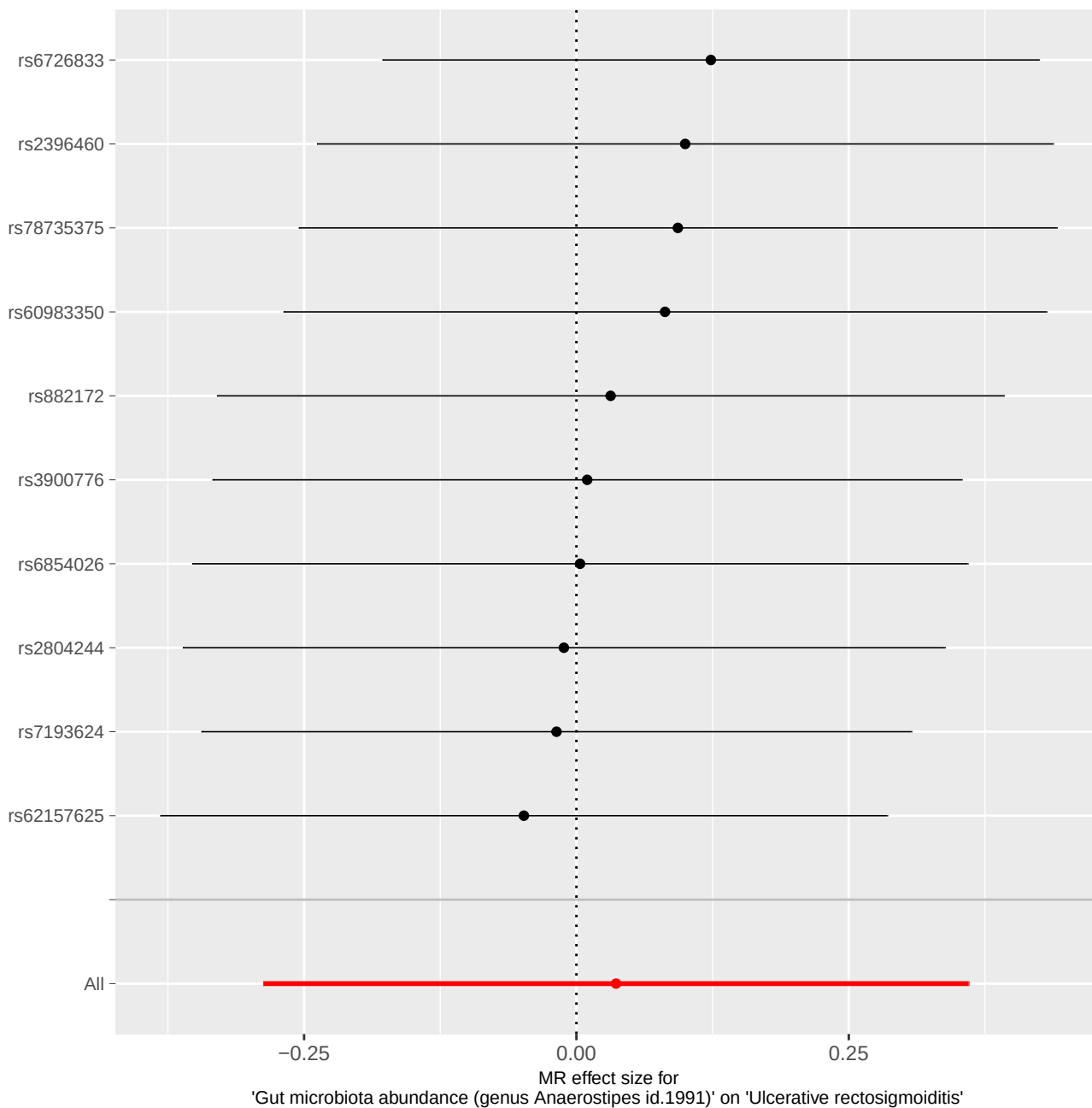


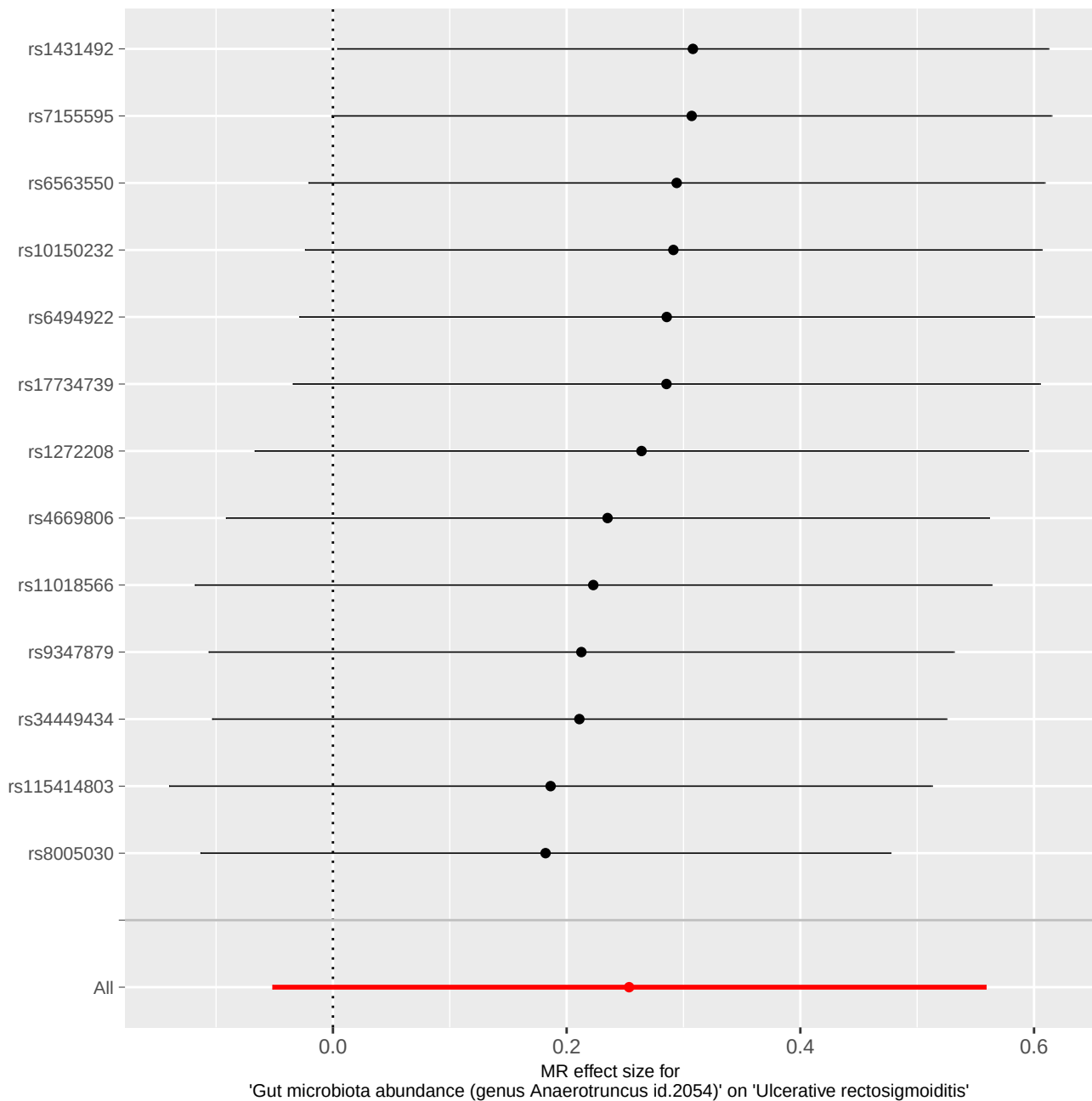




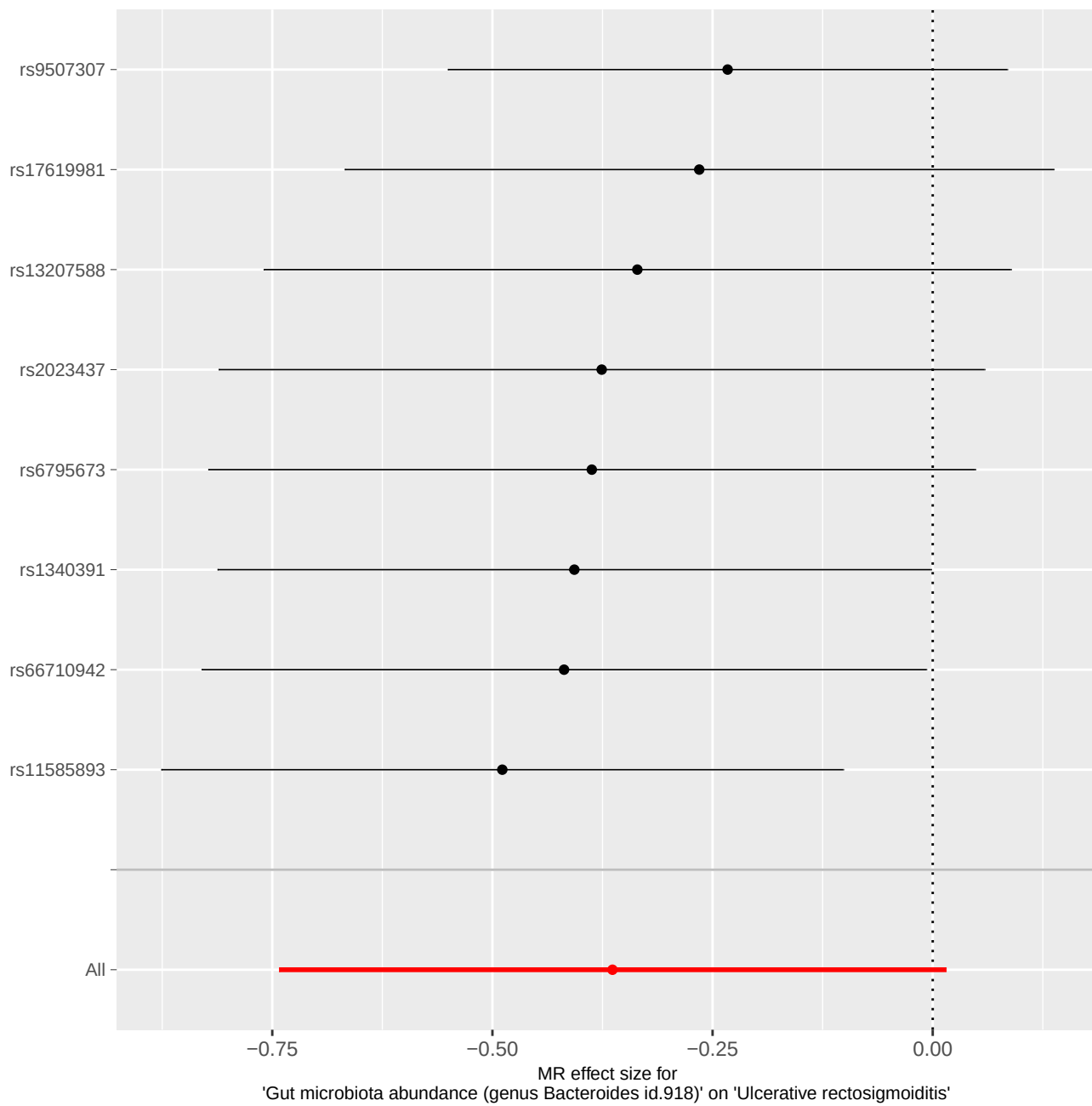


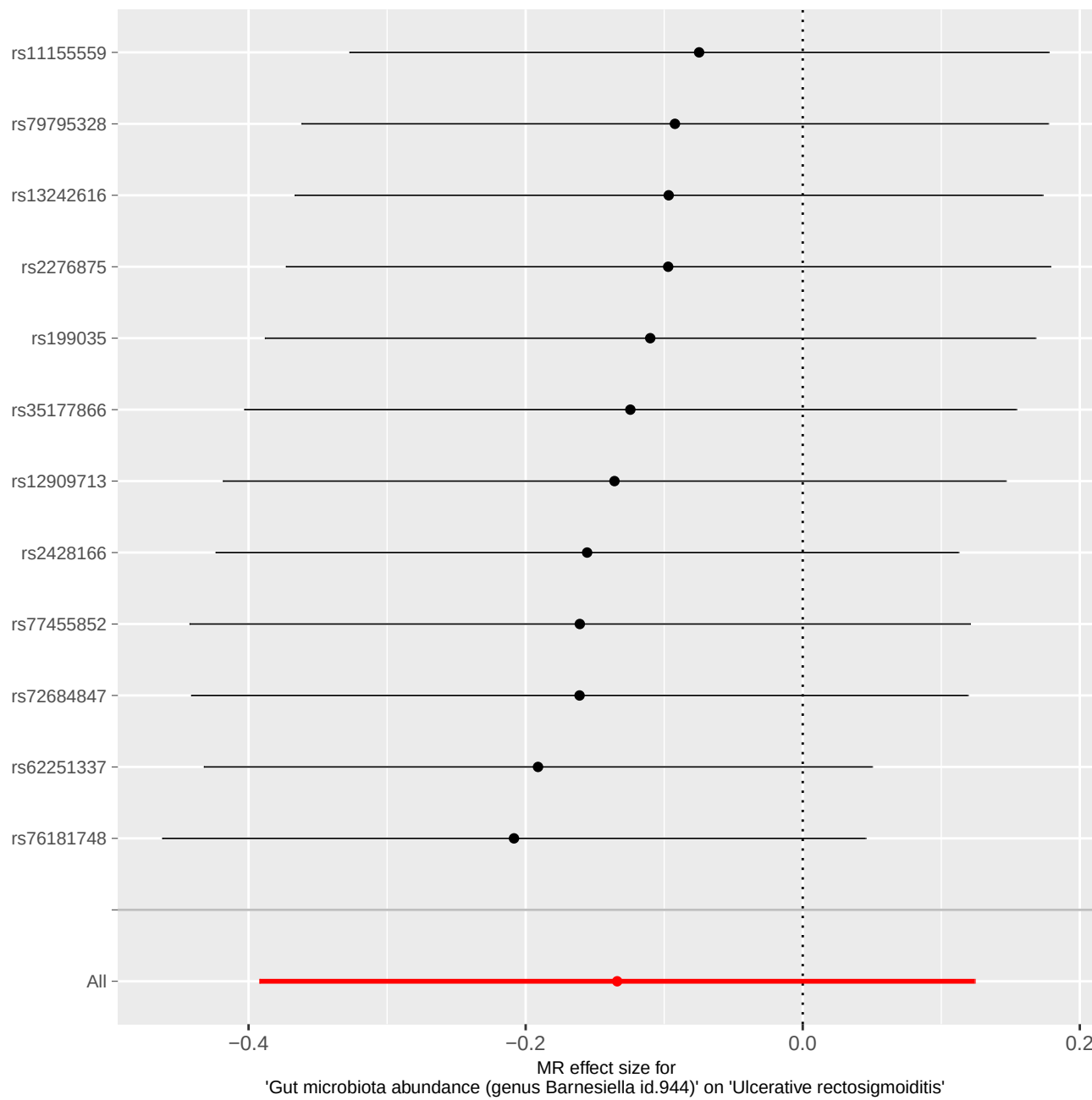


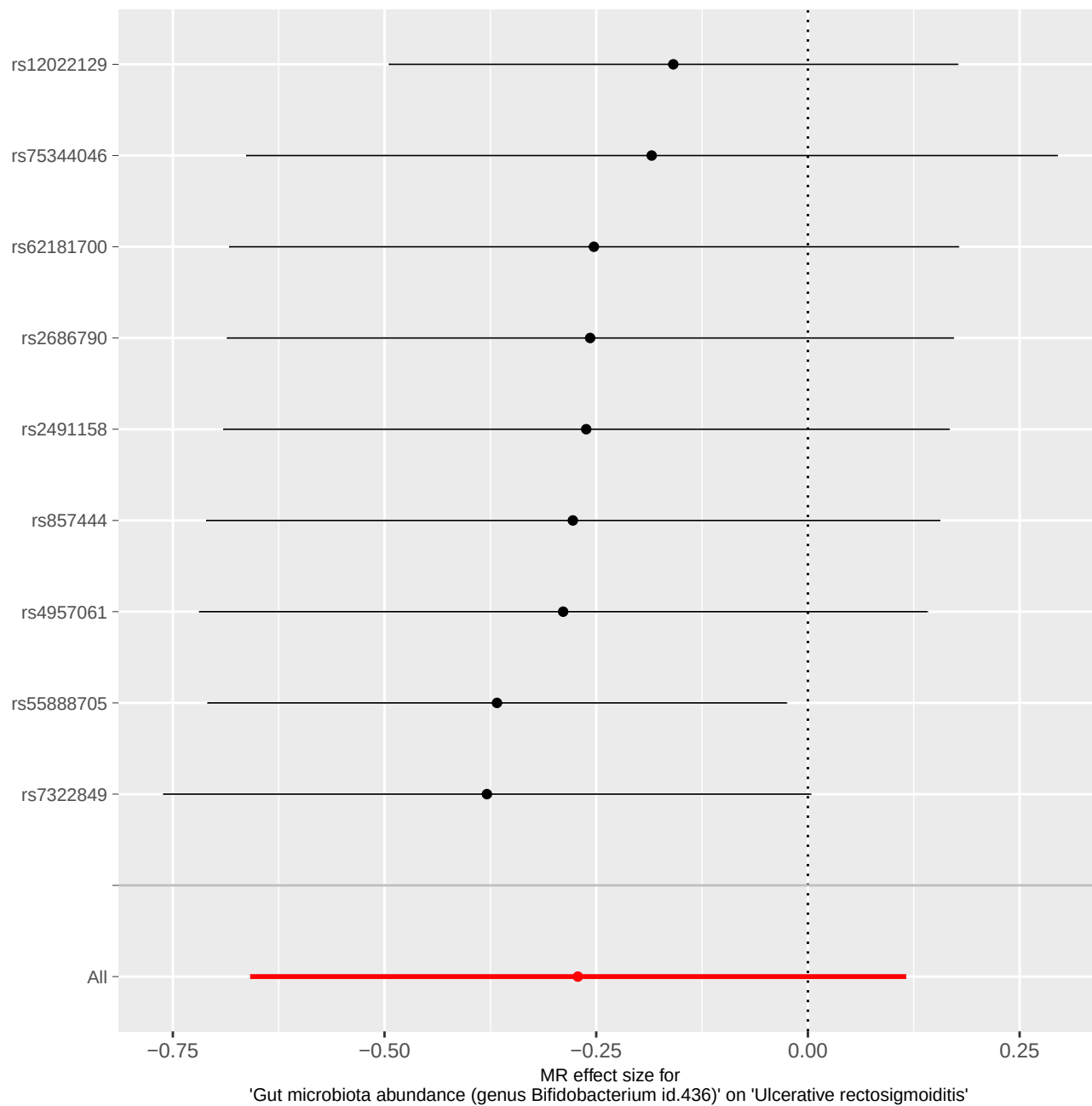


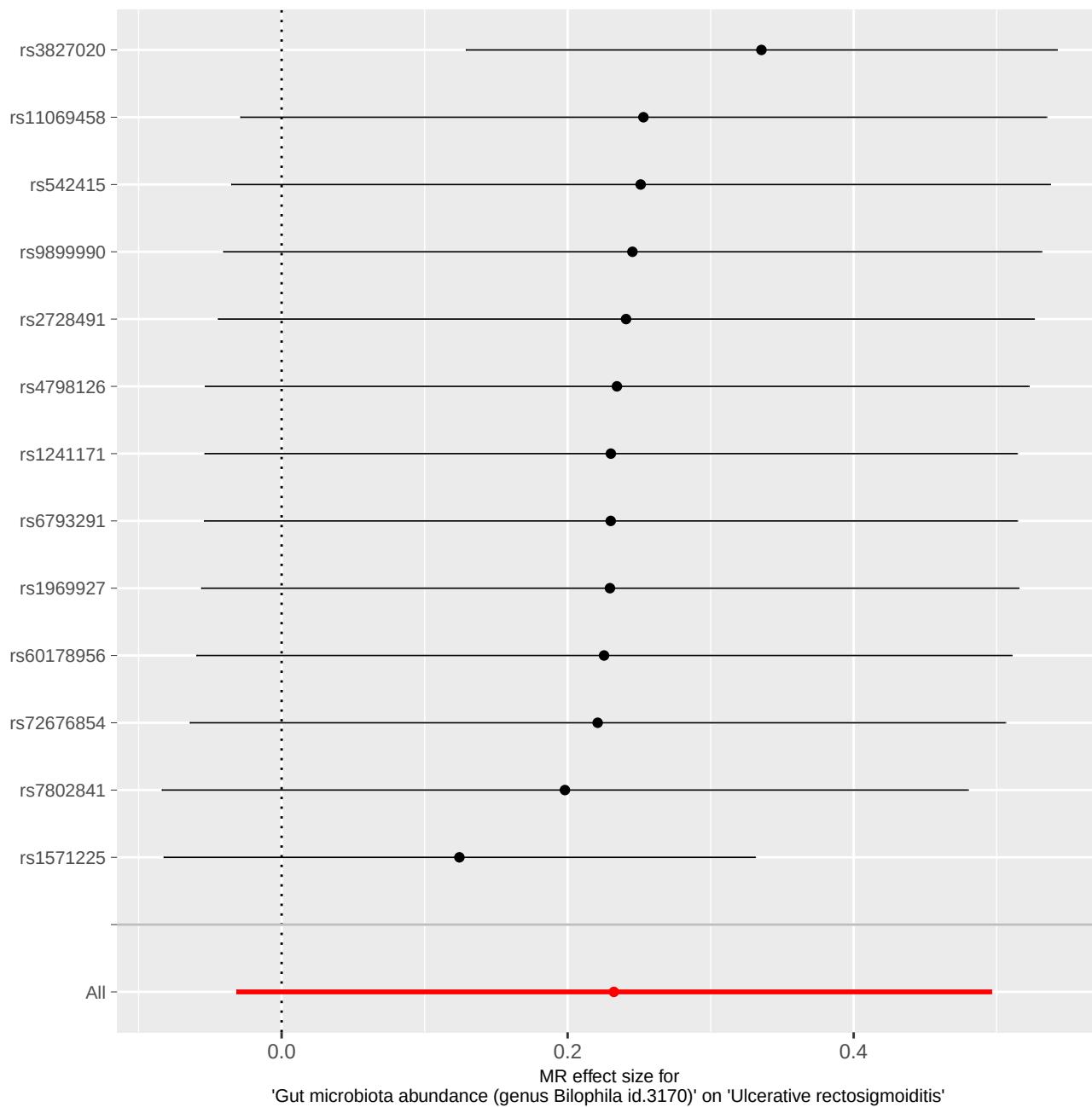


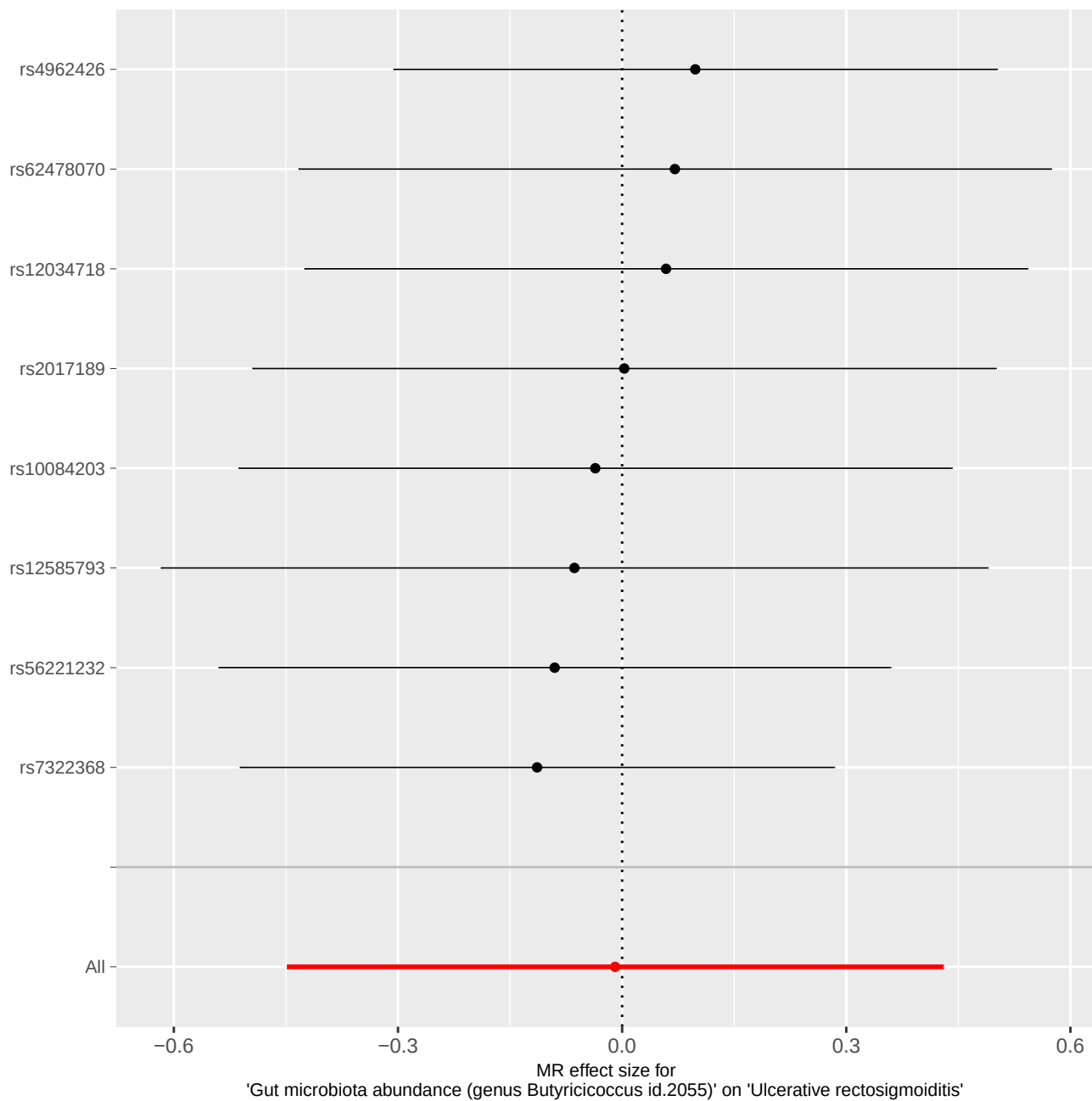
Batch 1542 : Gut microbiota abundance (genus Bacteroides id.918) on Ulcerative rectosigmoiditis

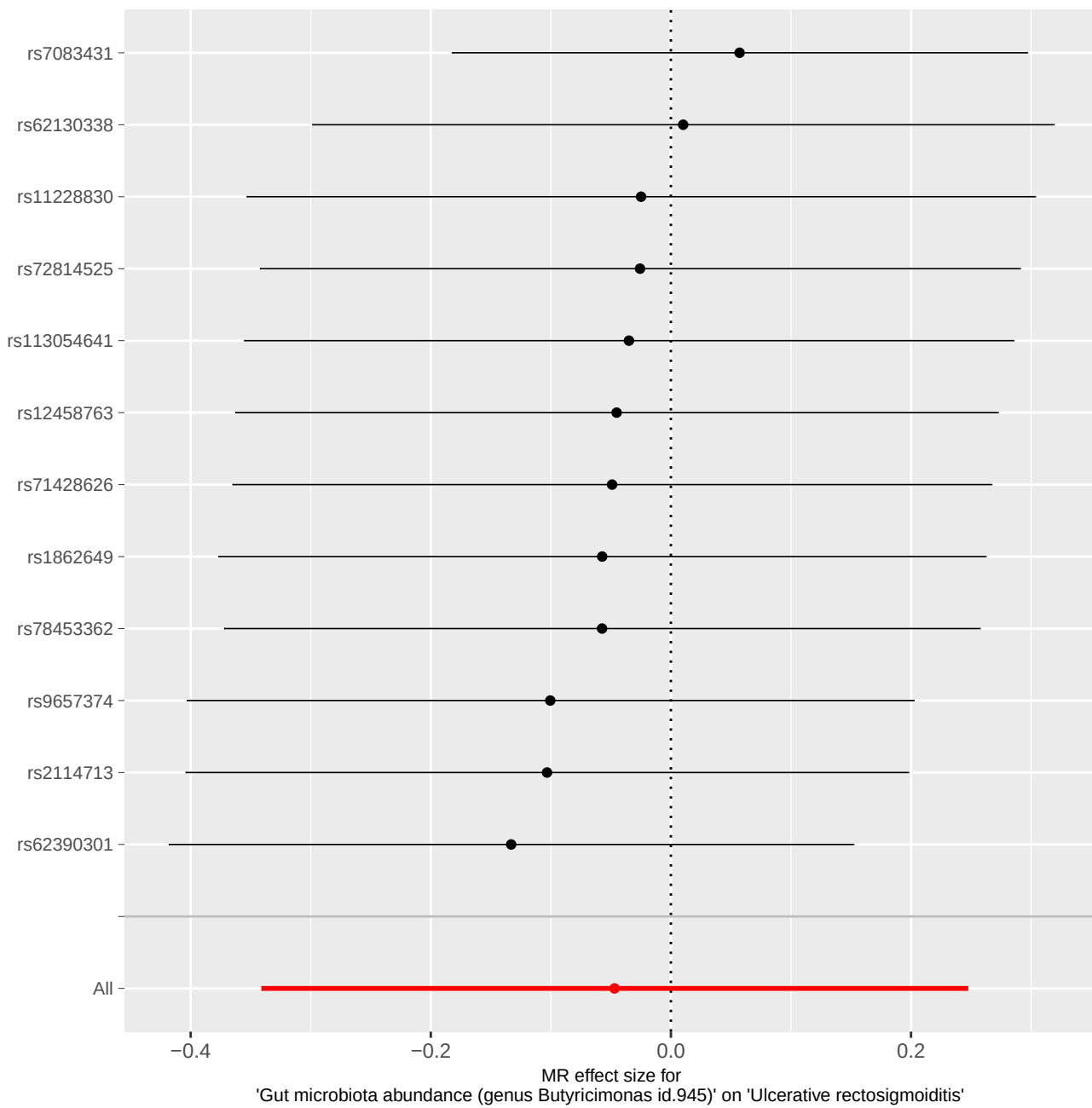


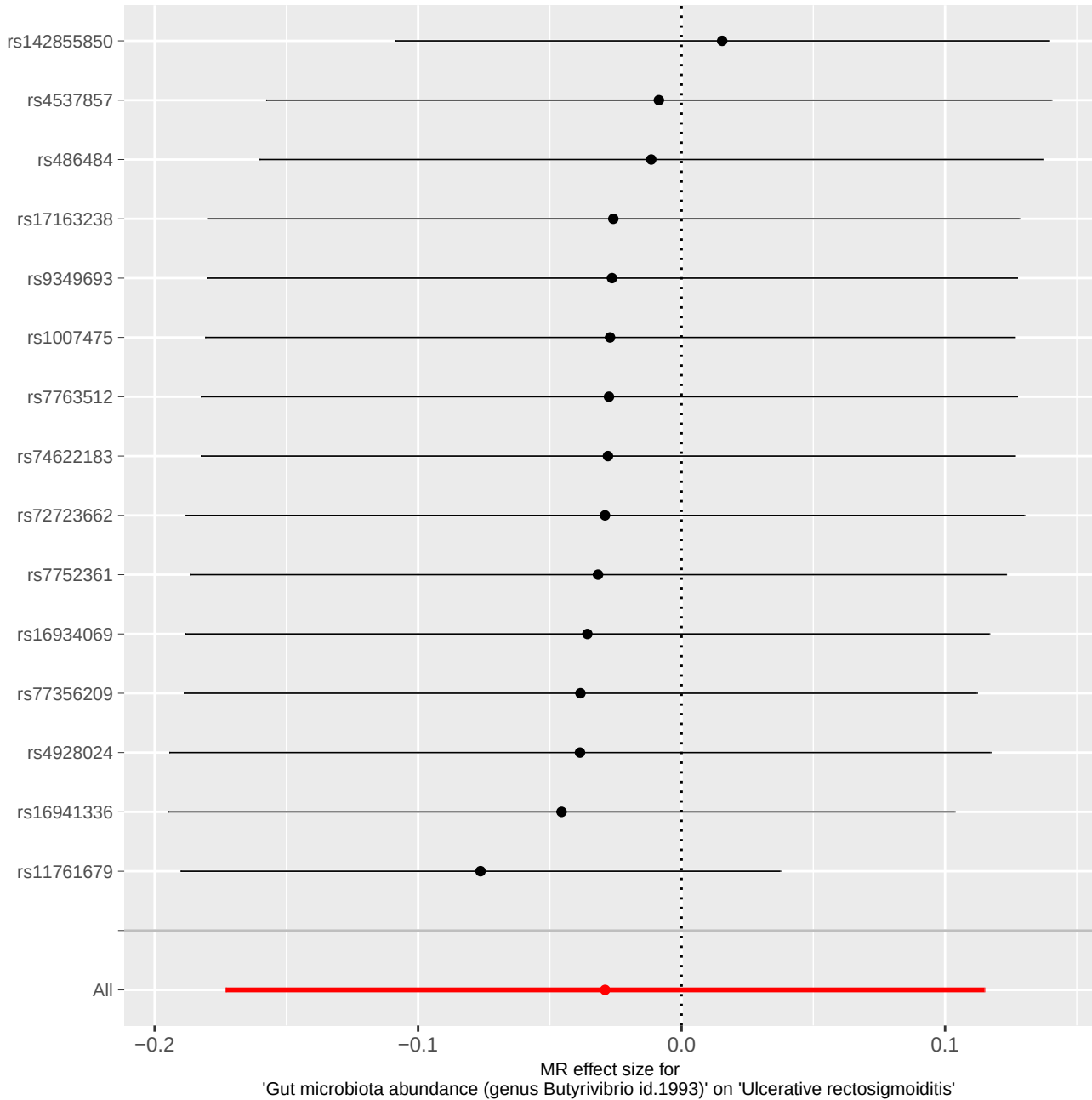


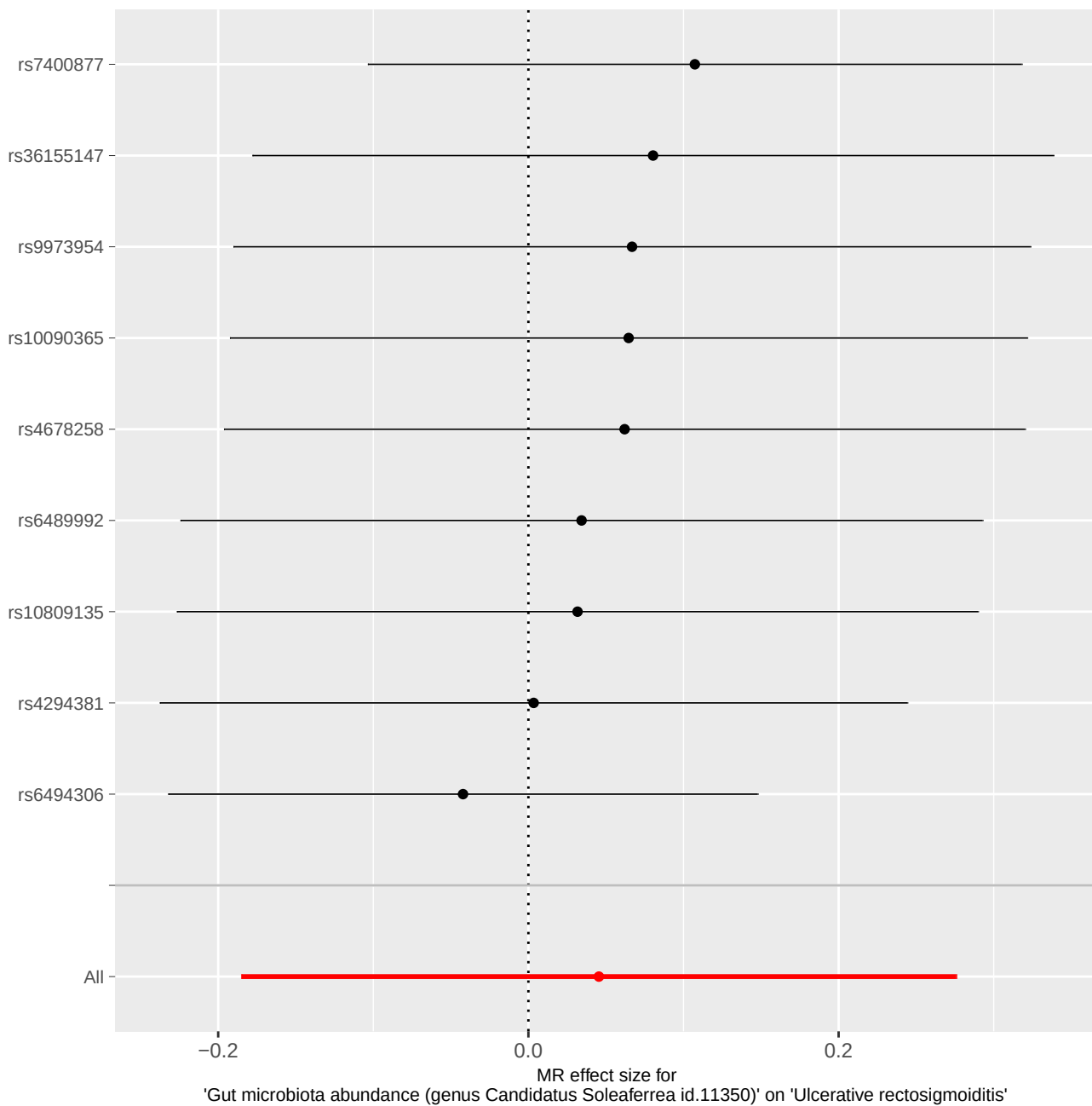


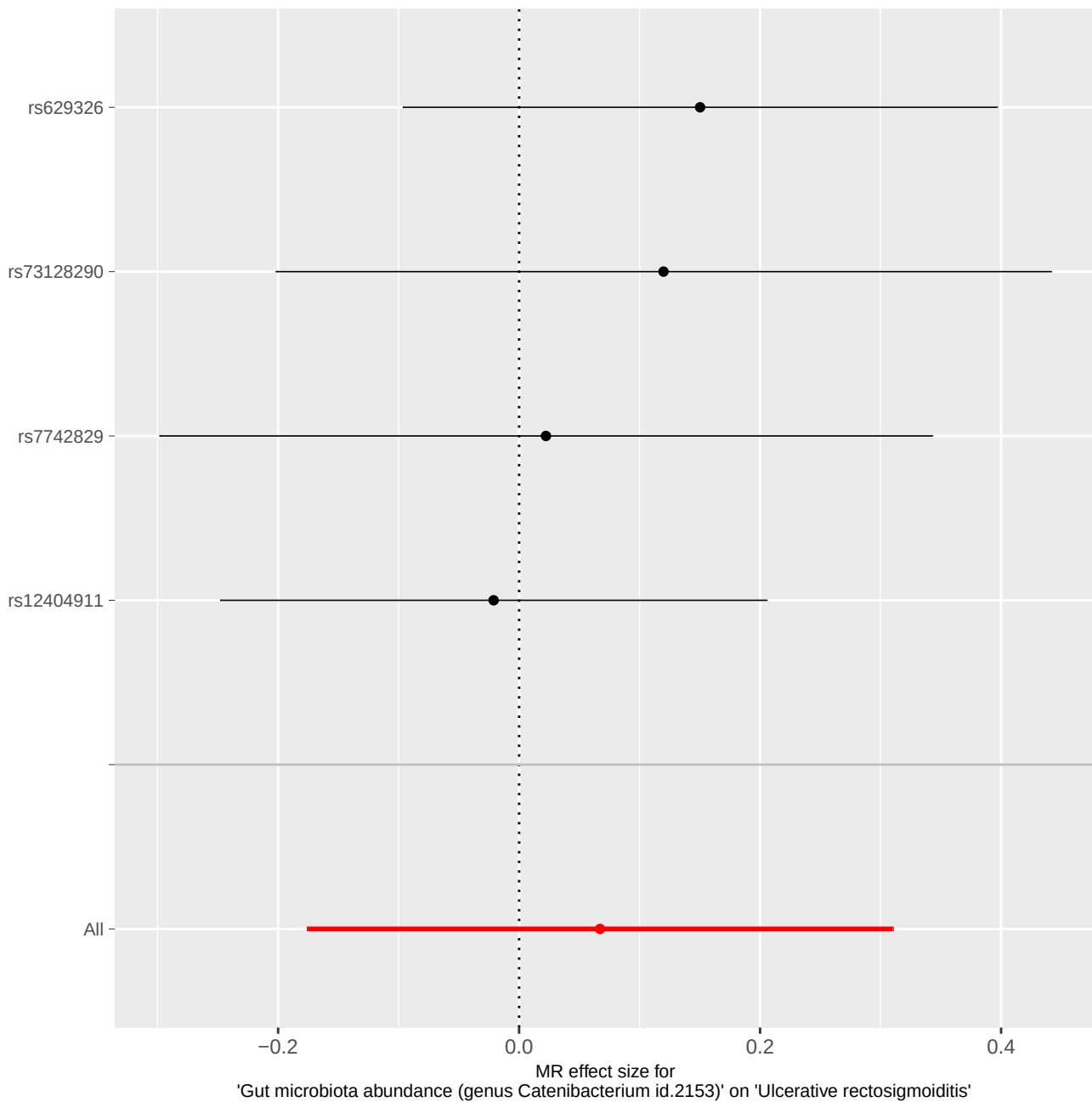


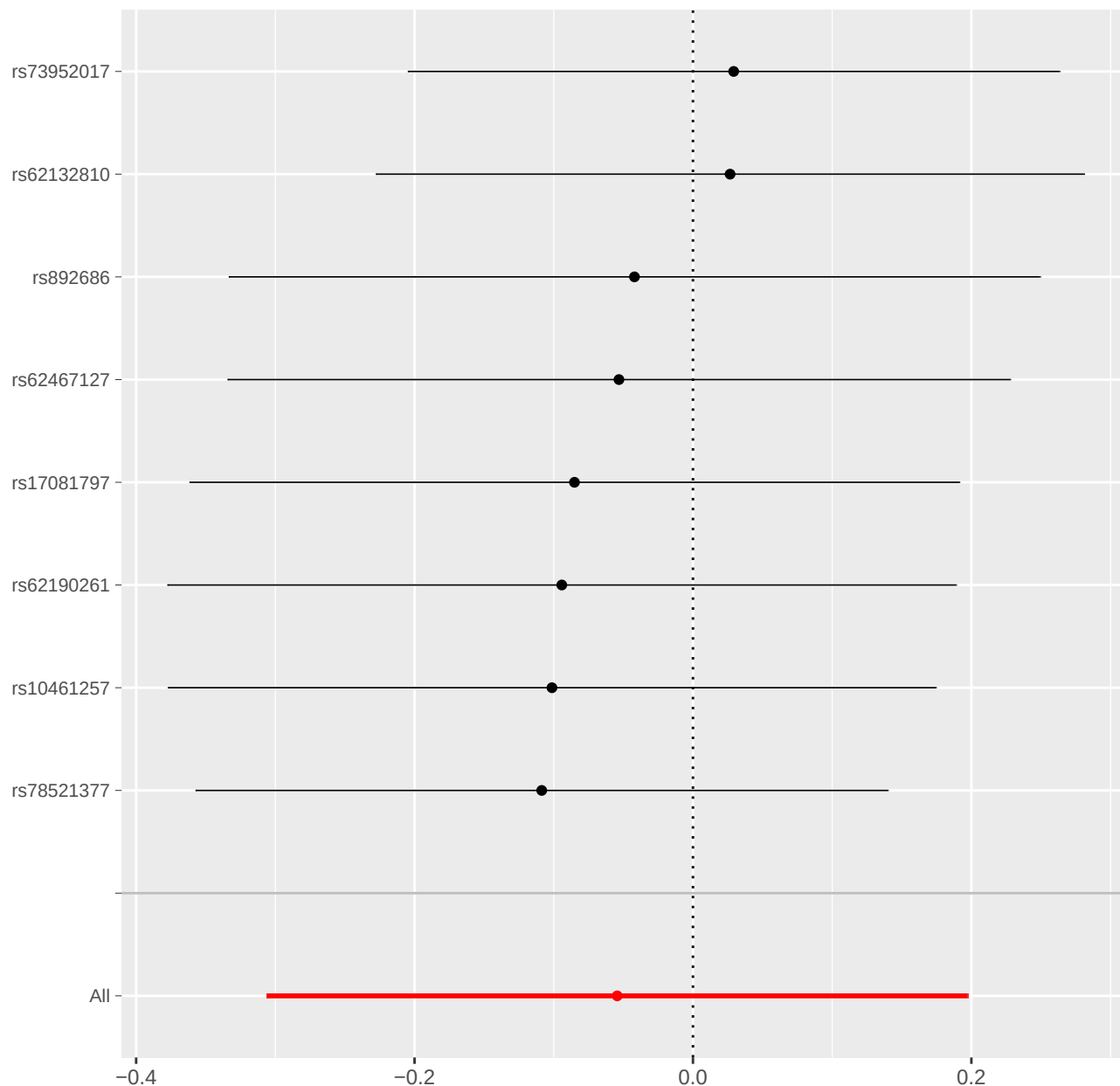






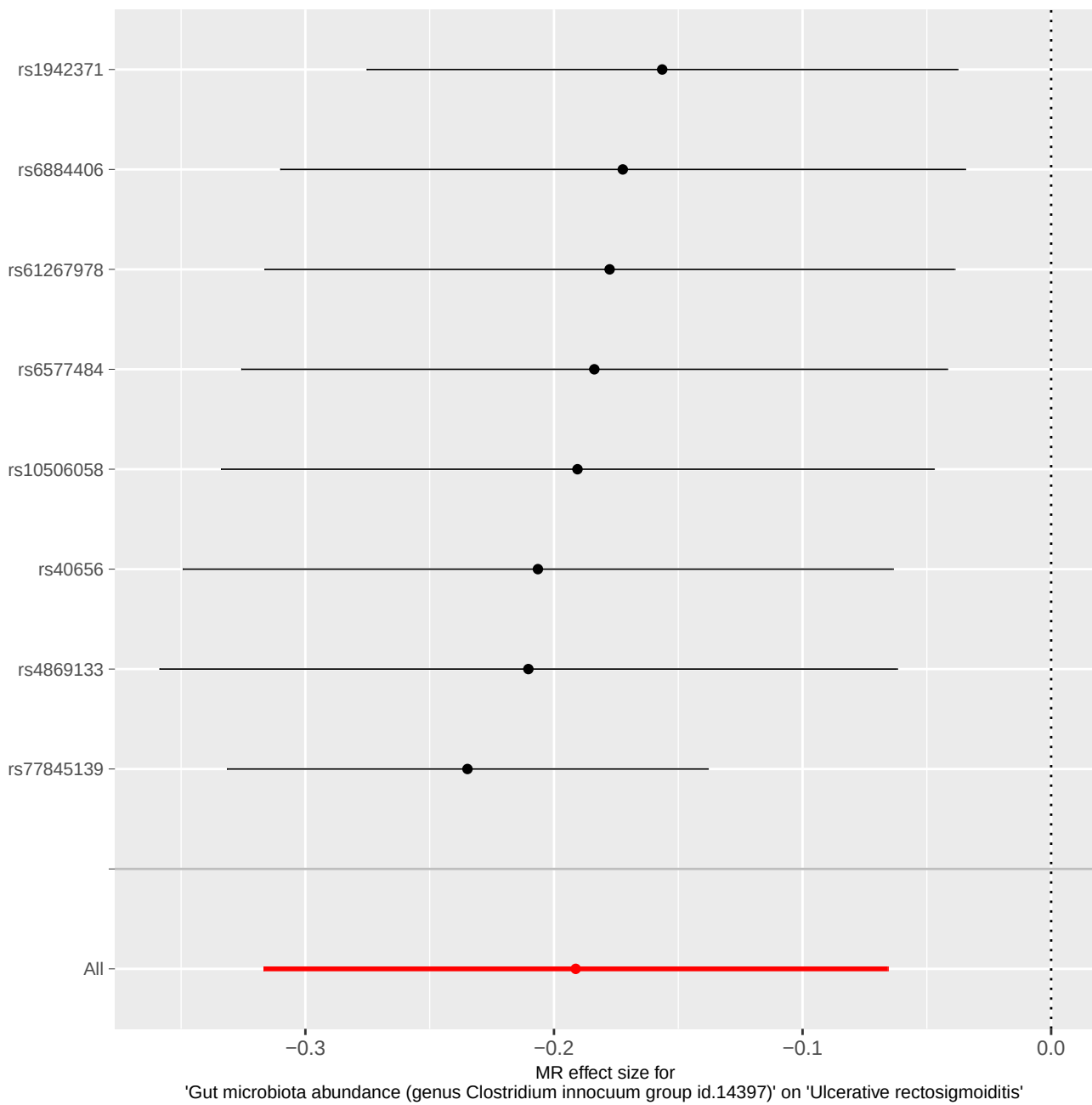


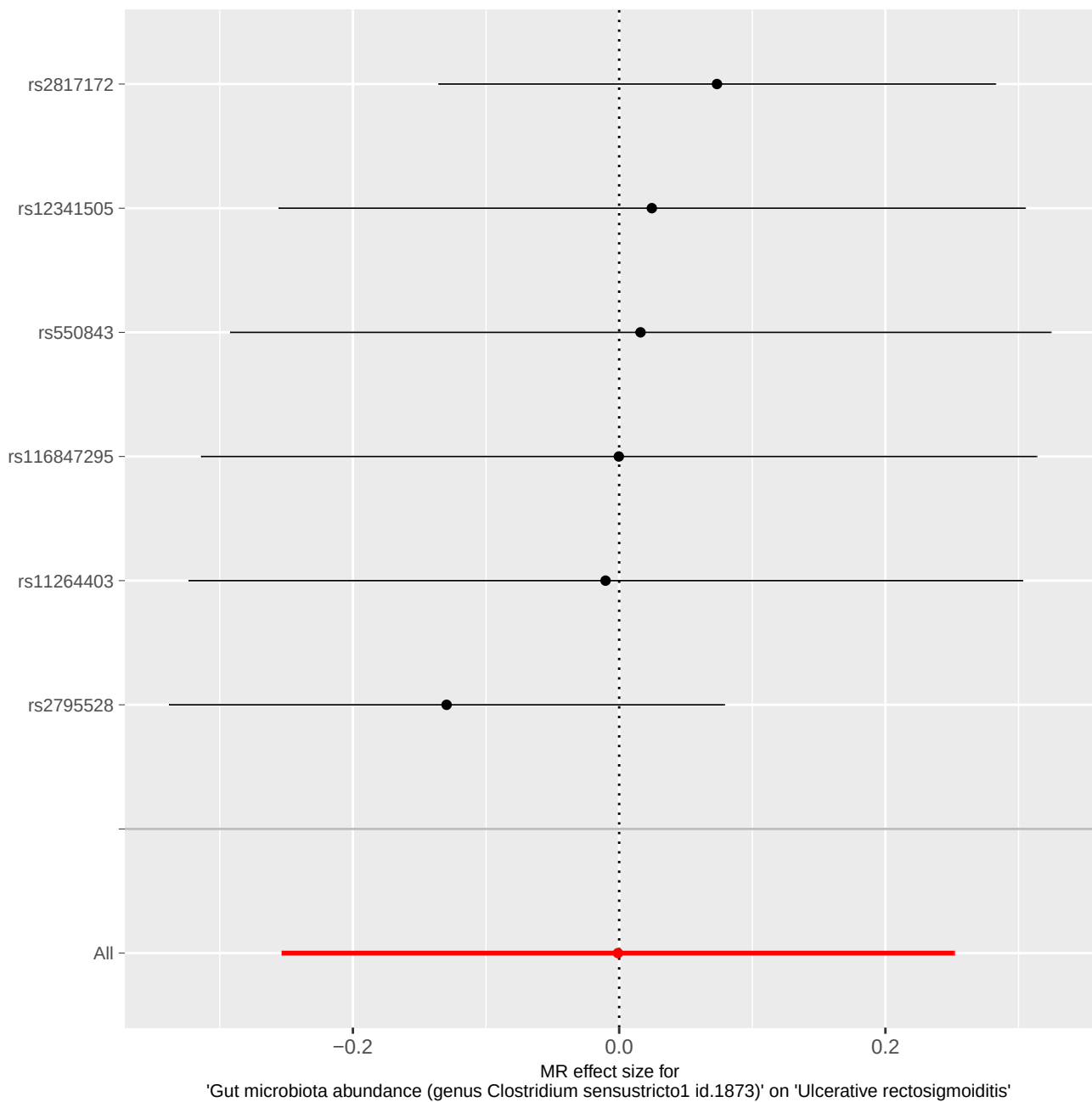


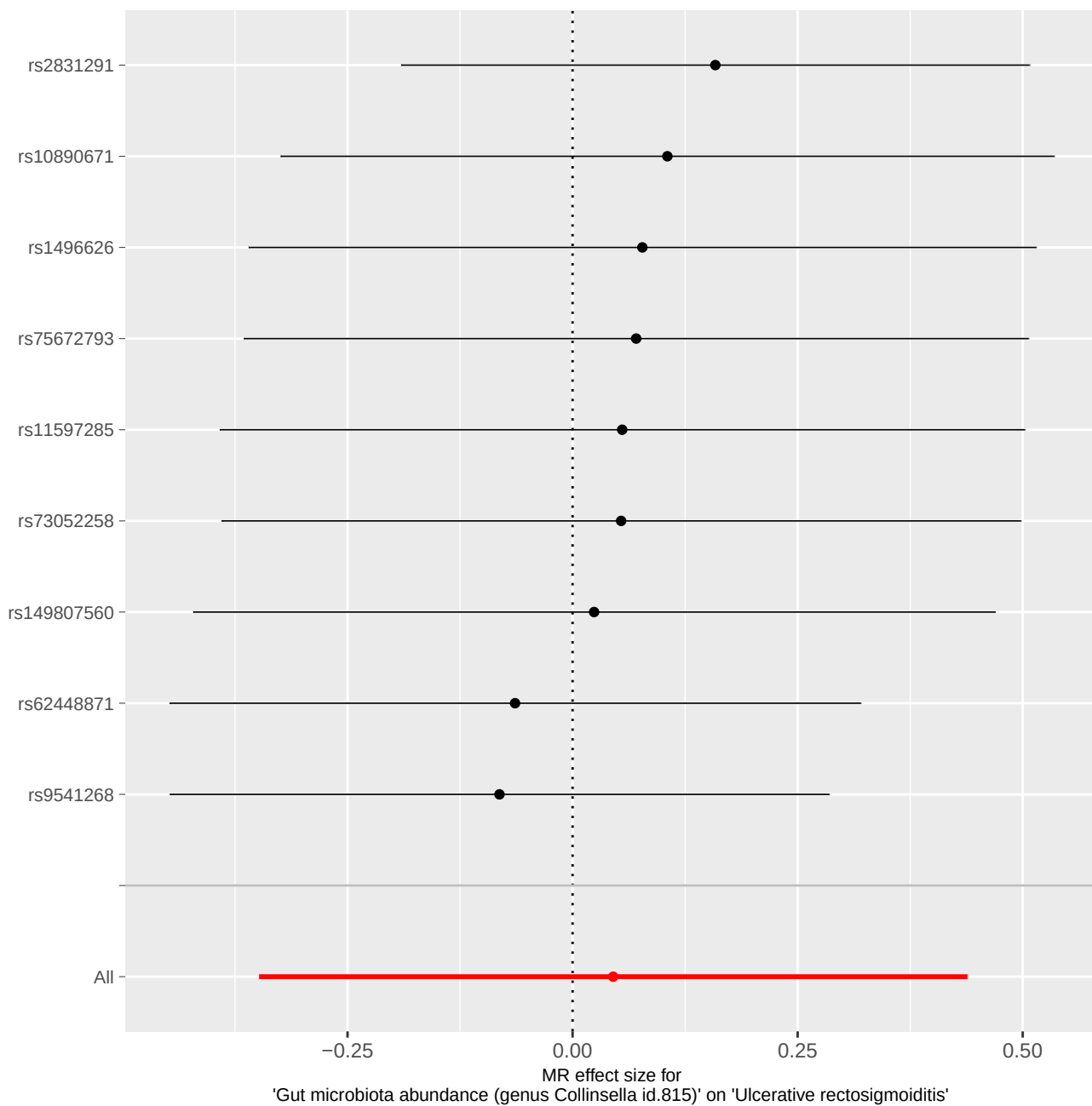


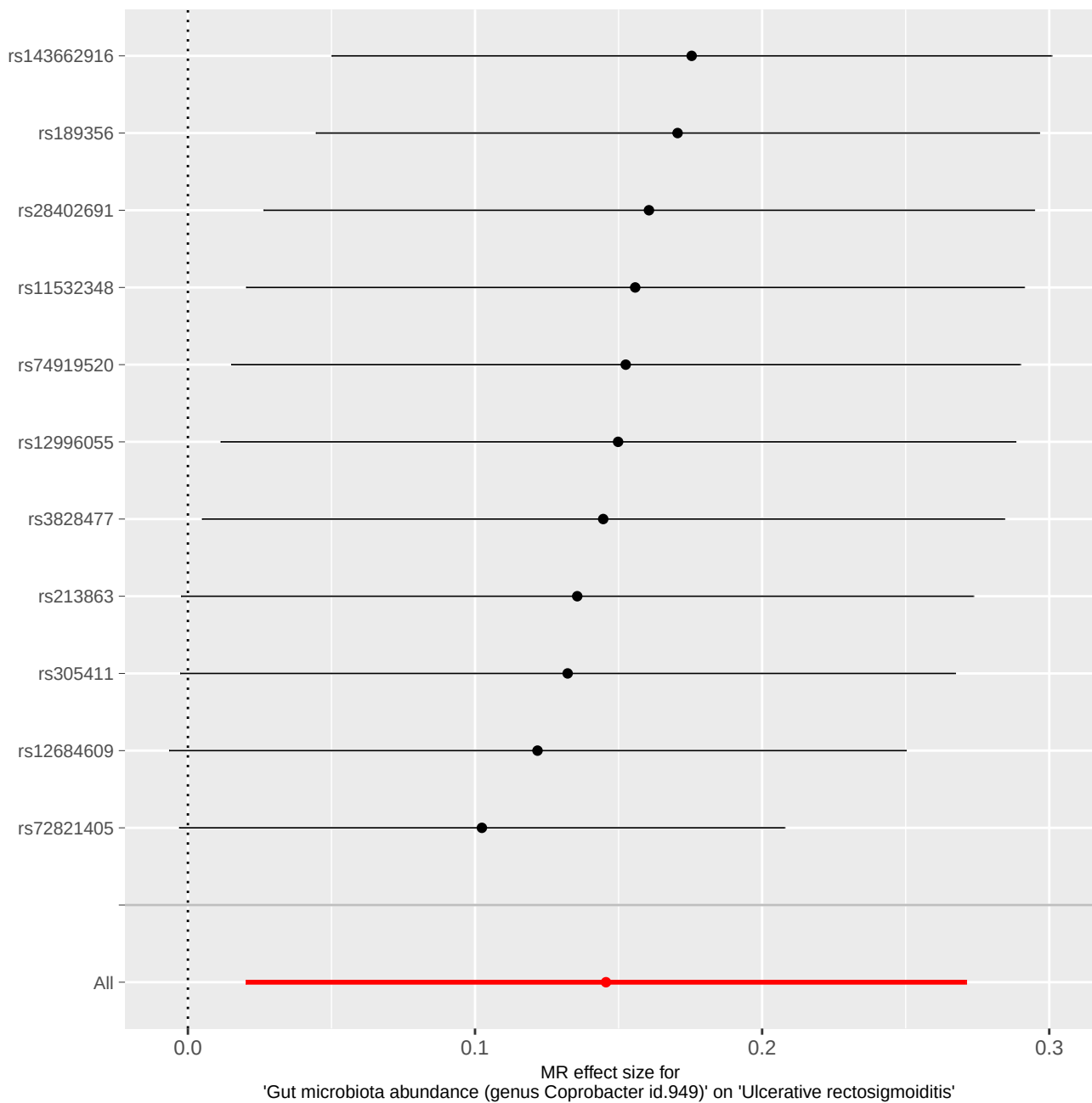
MR effect size for

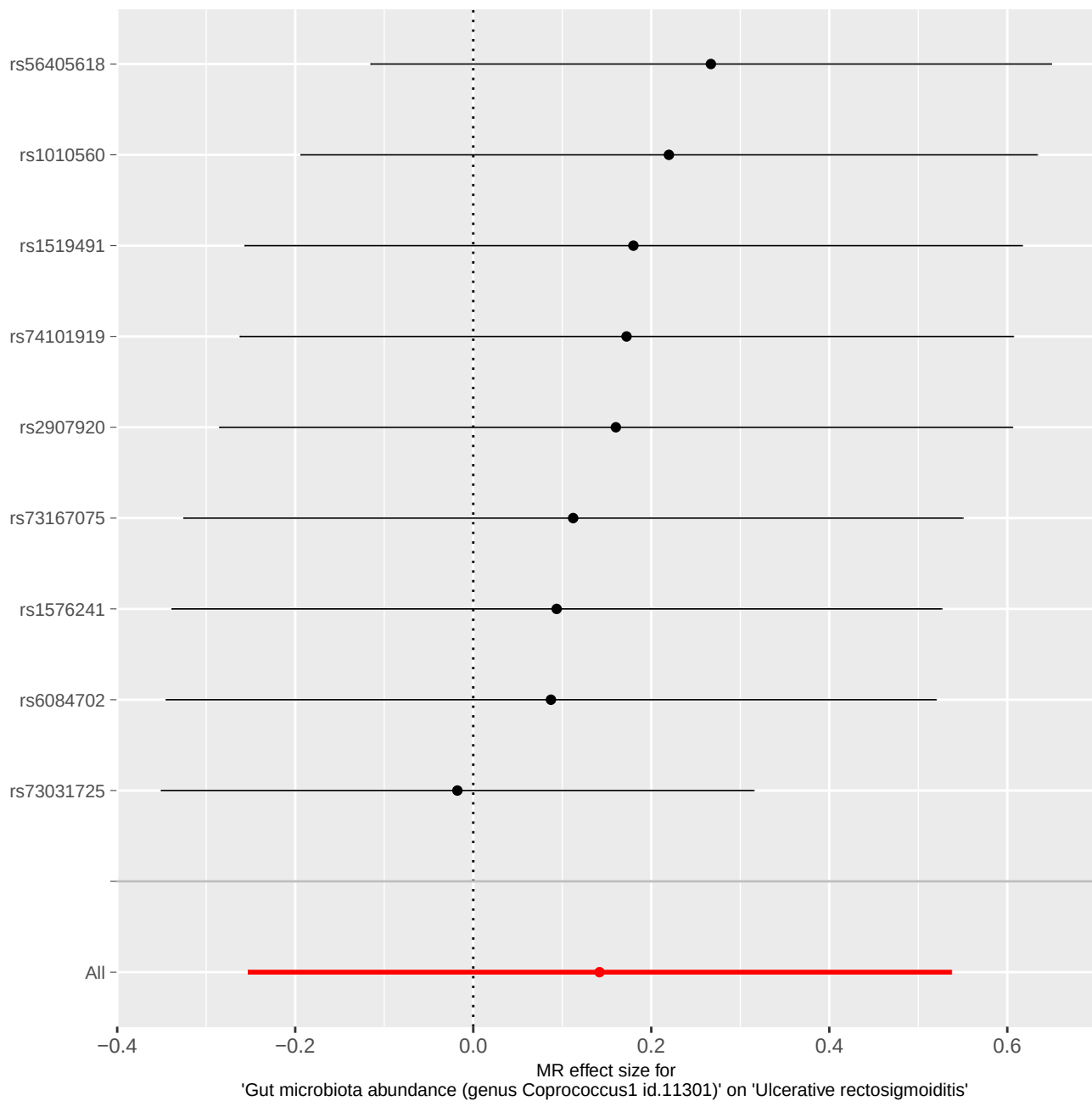
'Gut microbiota abundance (genus Christensenellaceae R 7group id.11283)' on 'Ulcerative rectosigmoiditis'

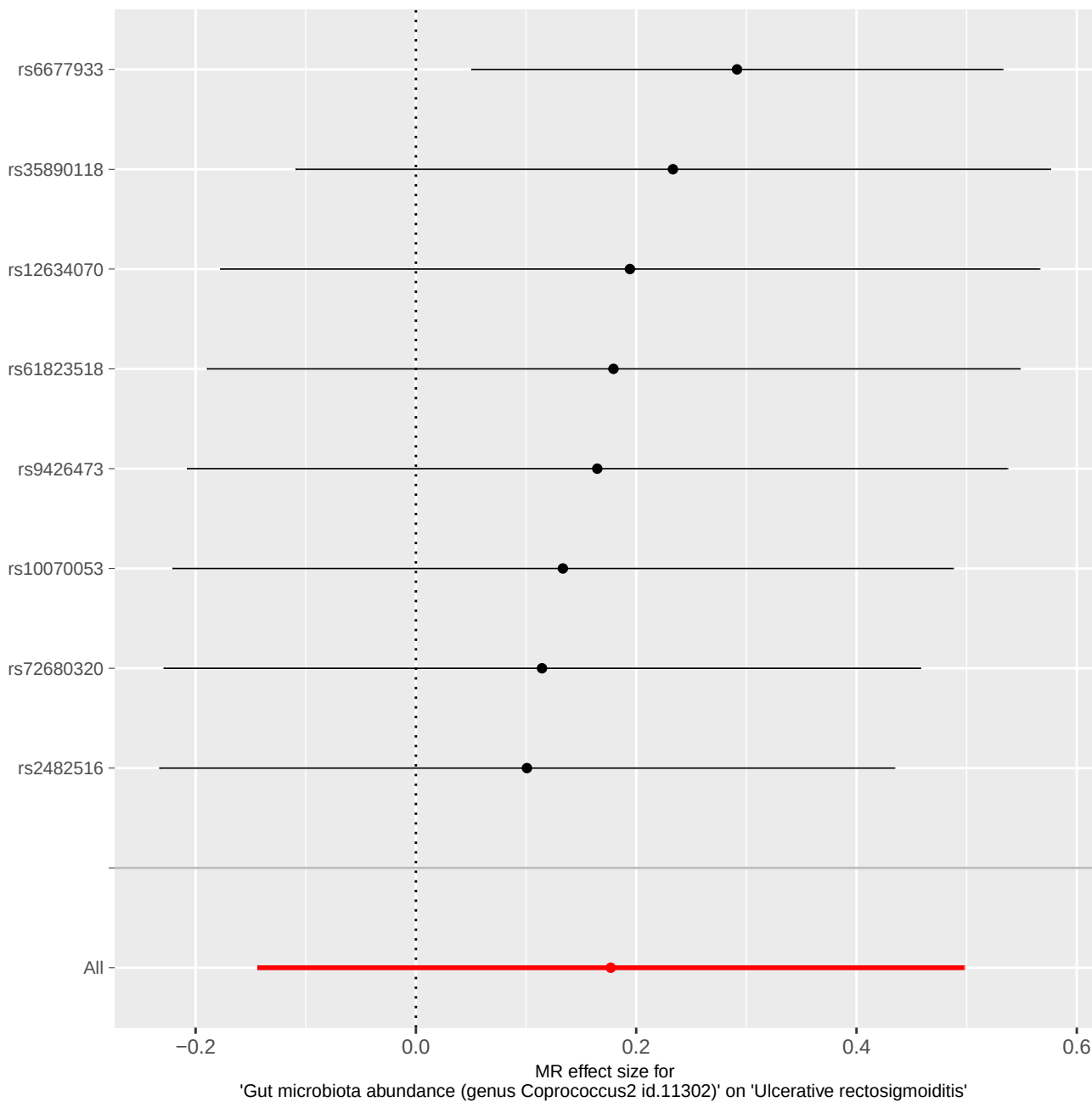


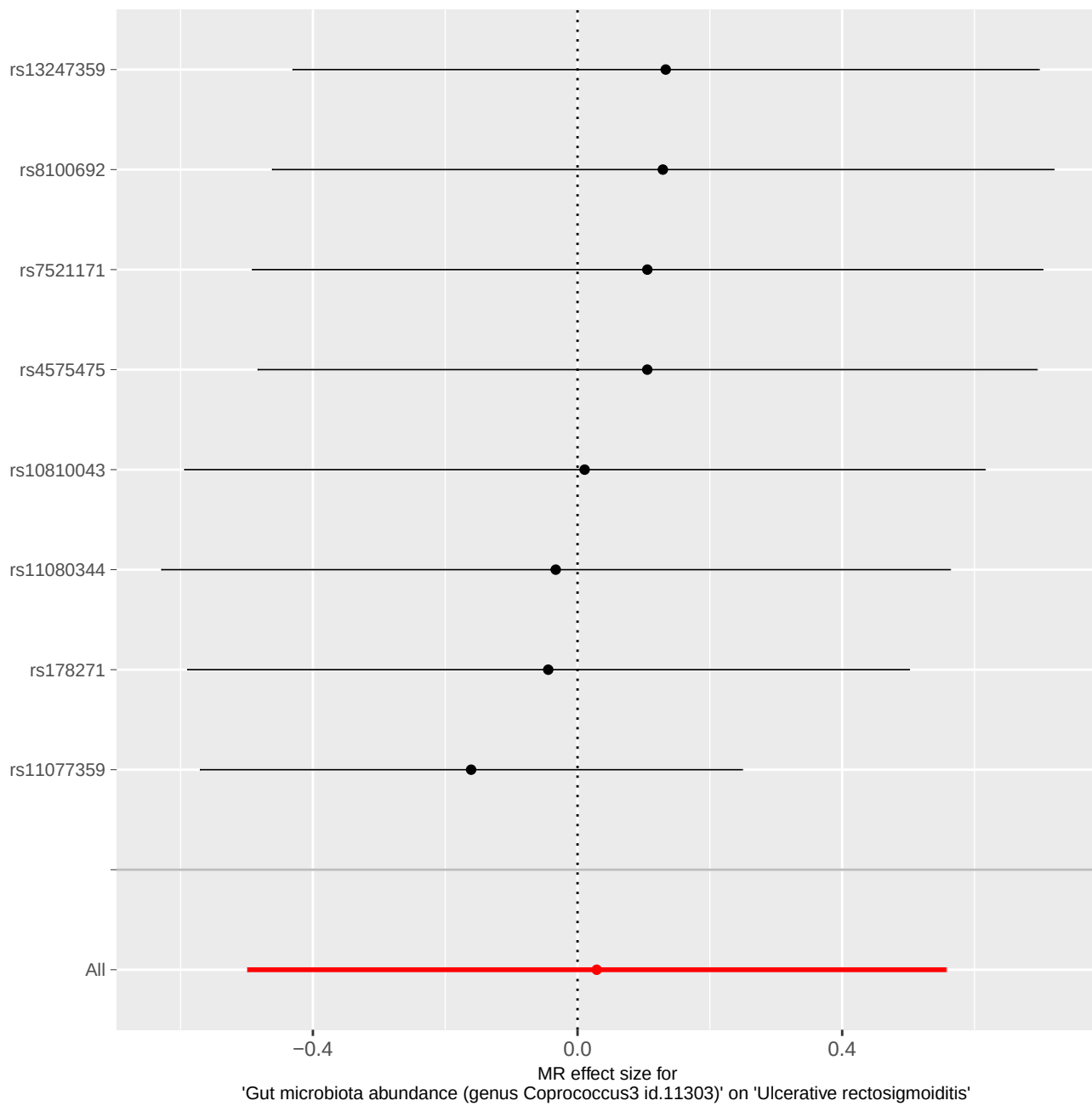


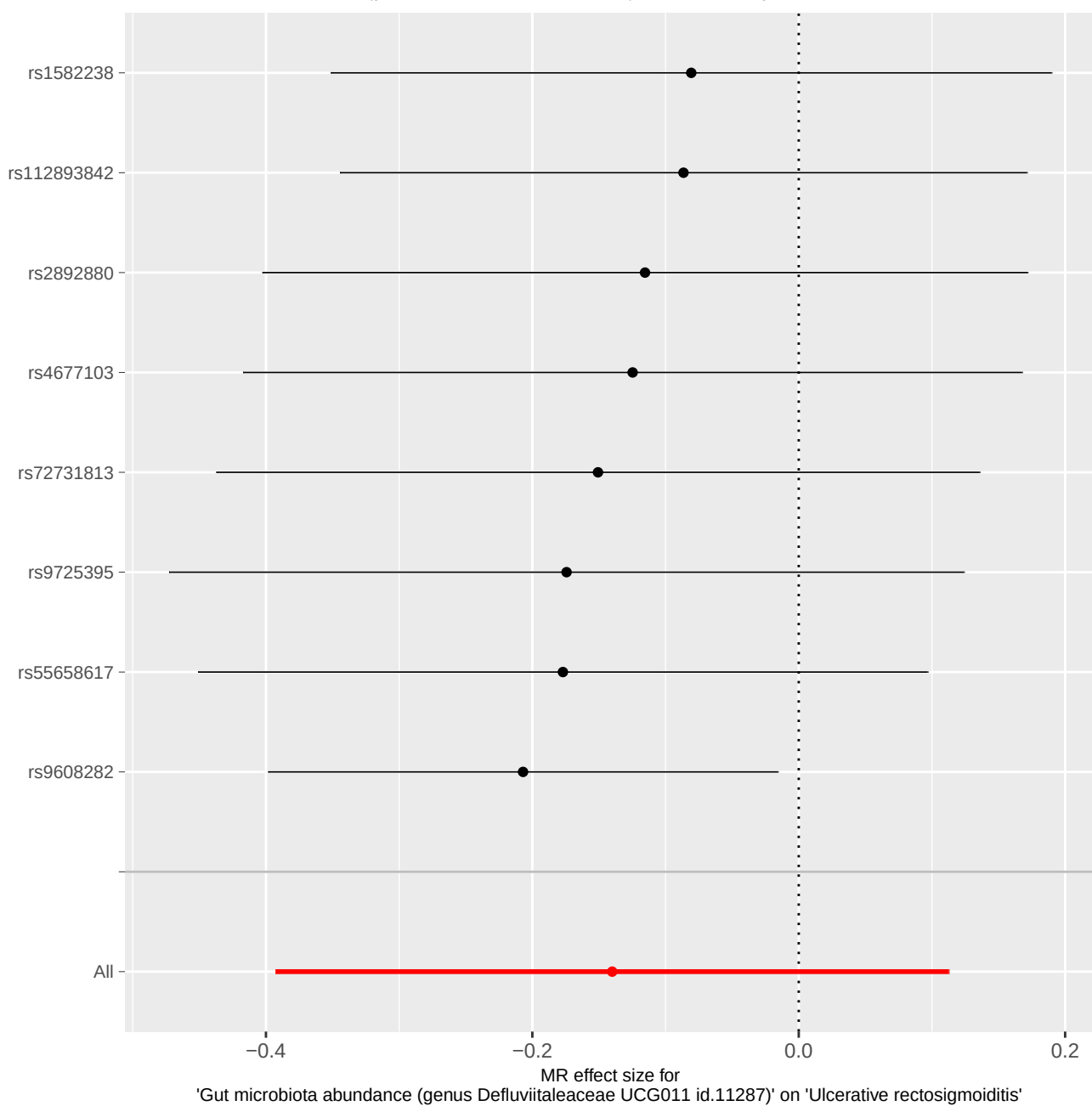


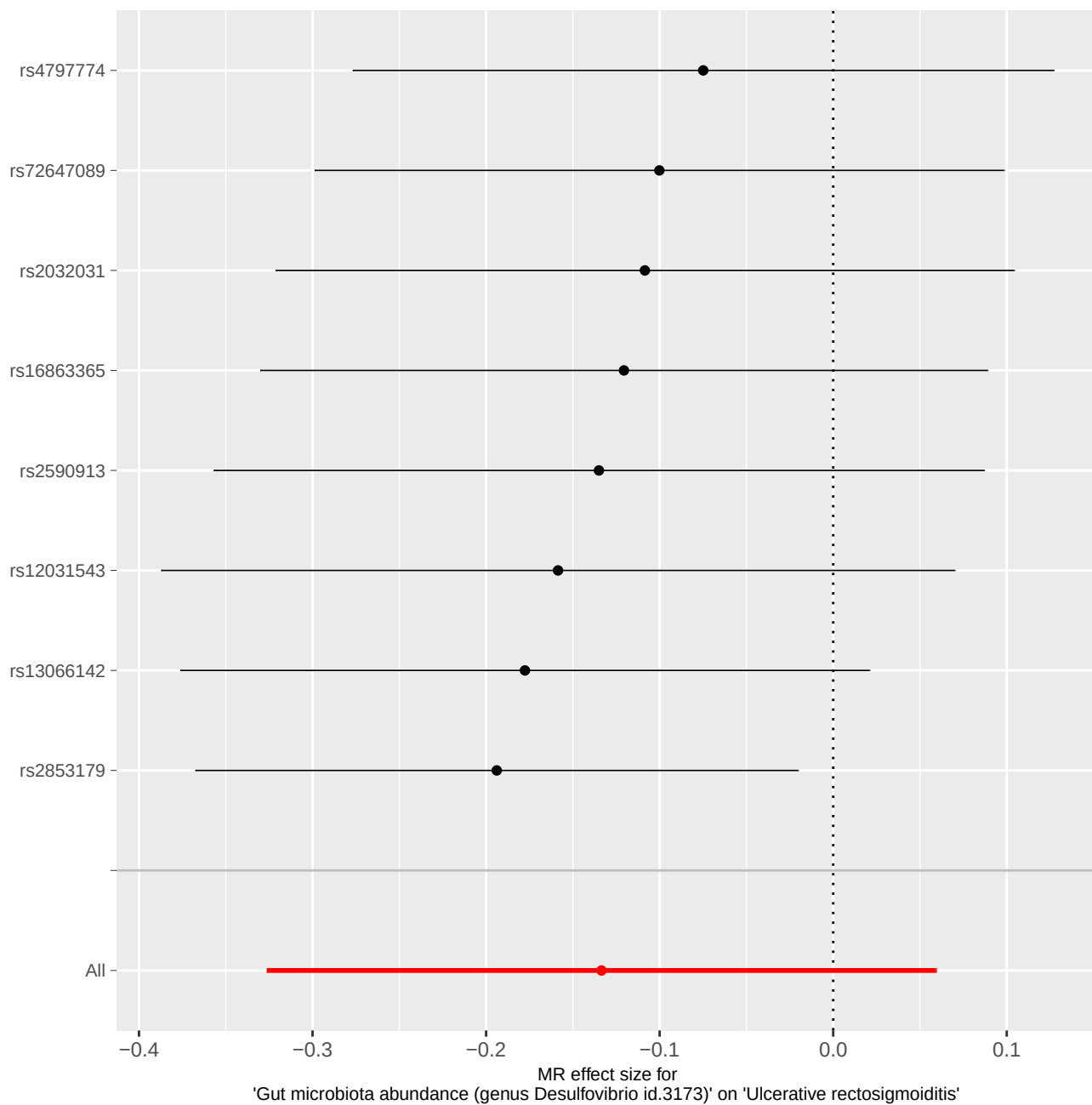


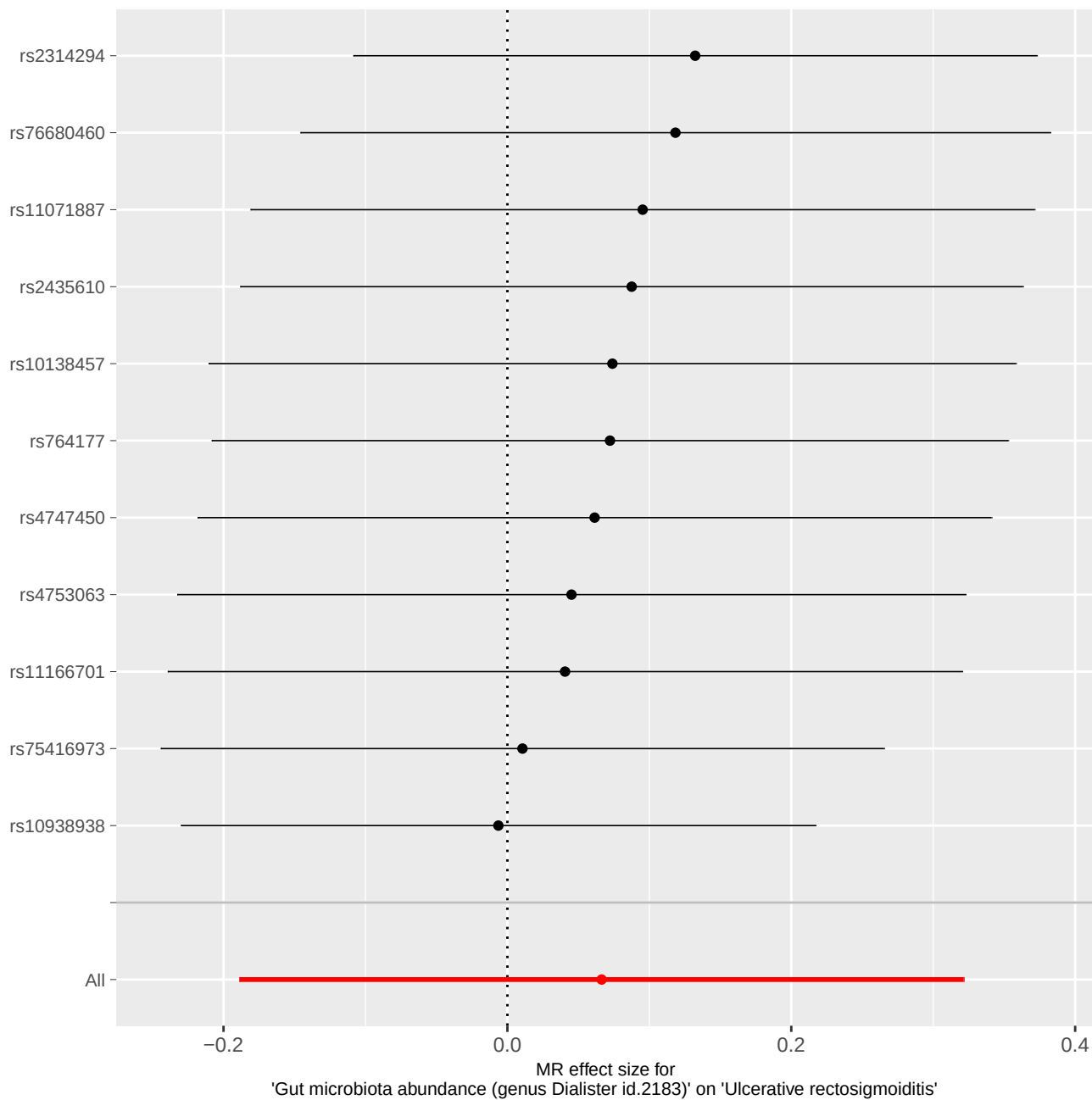


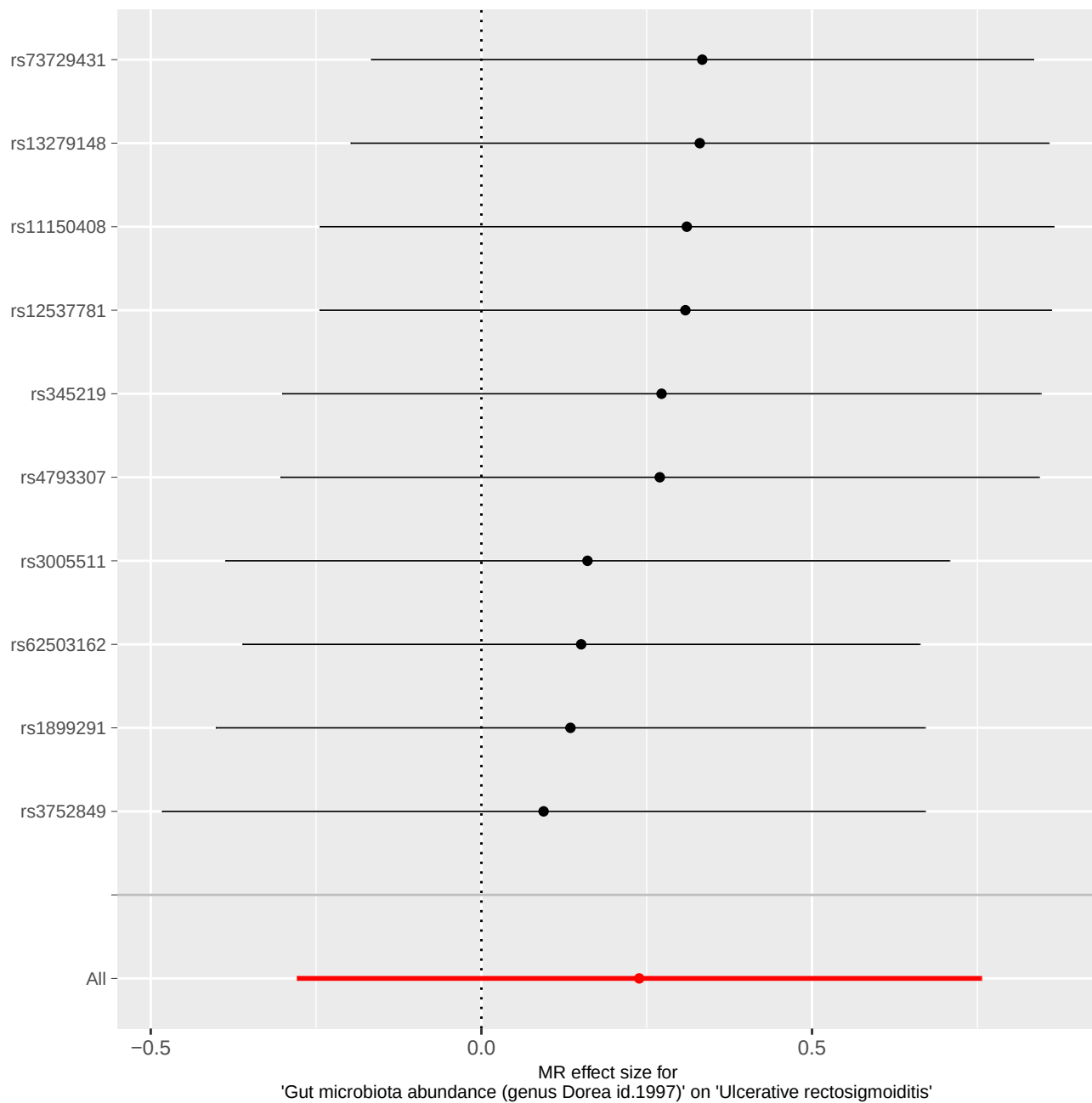


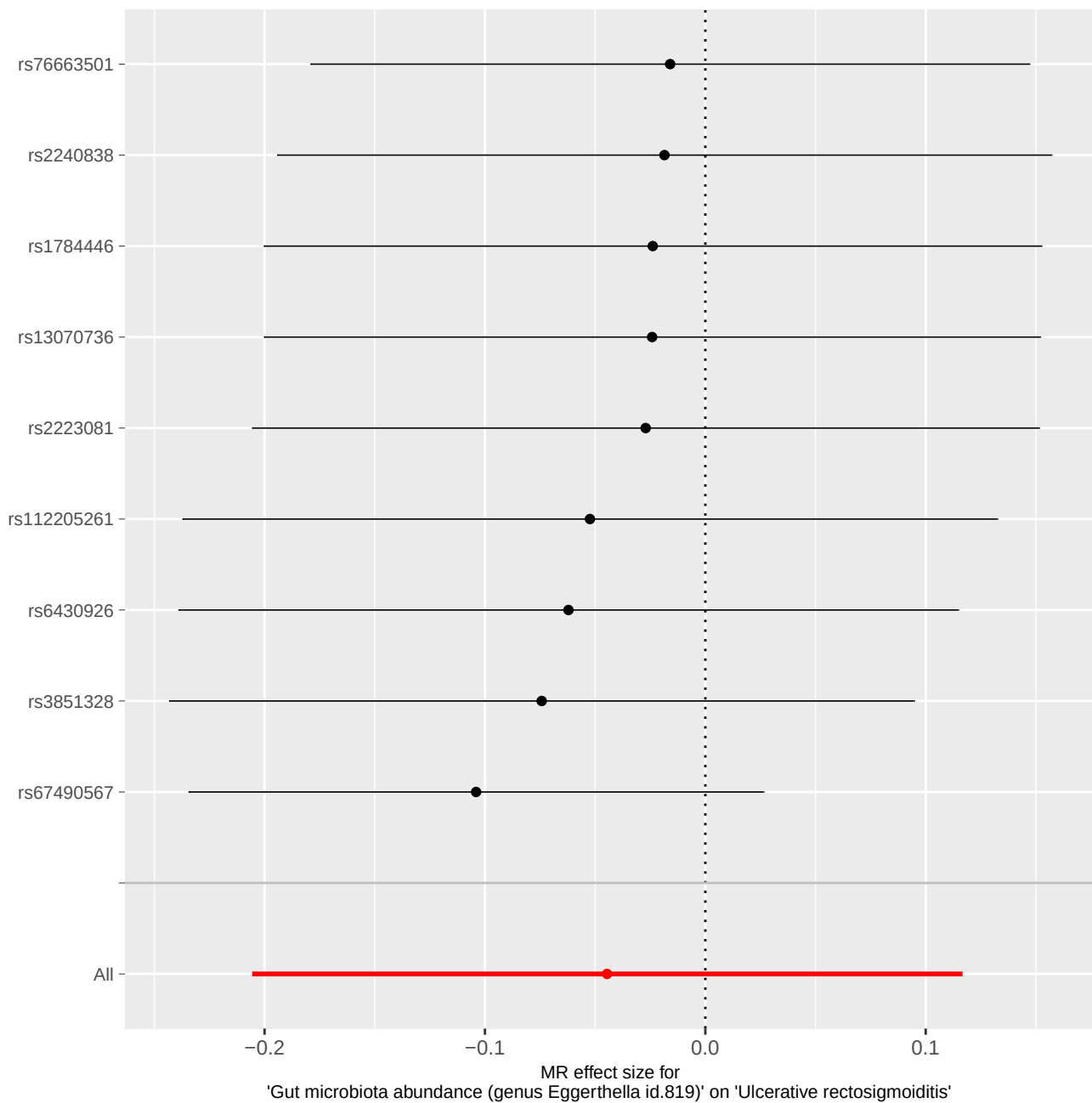


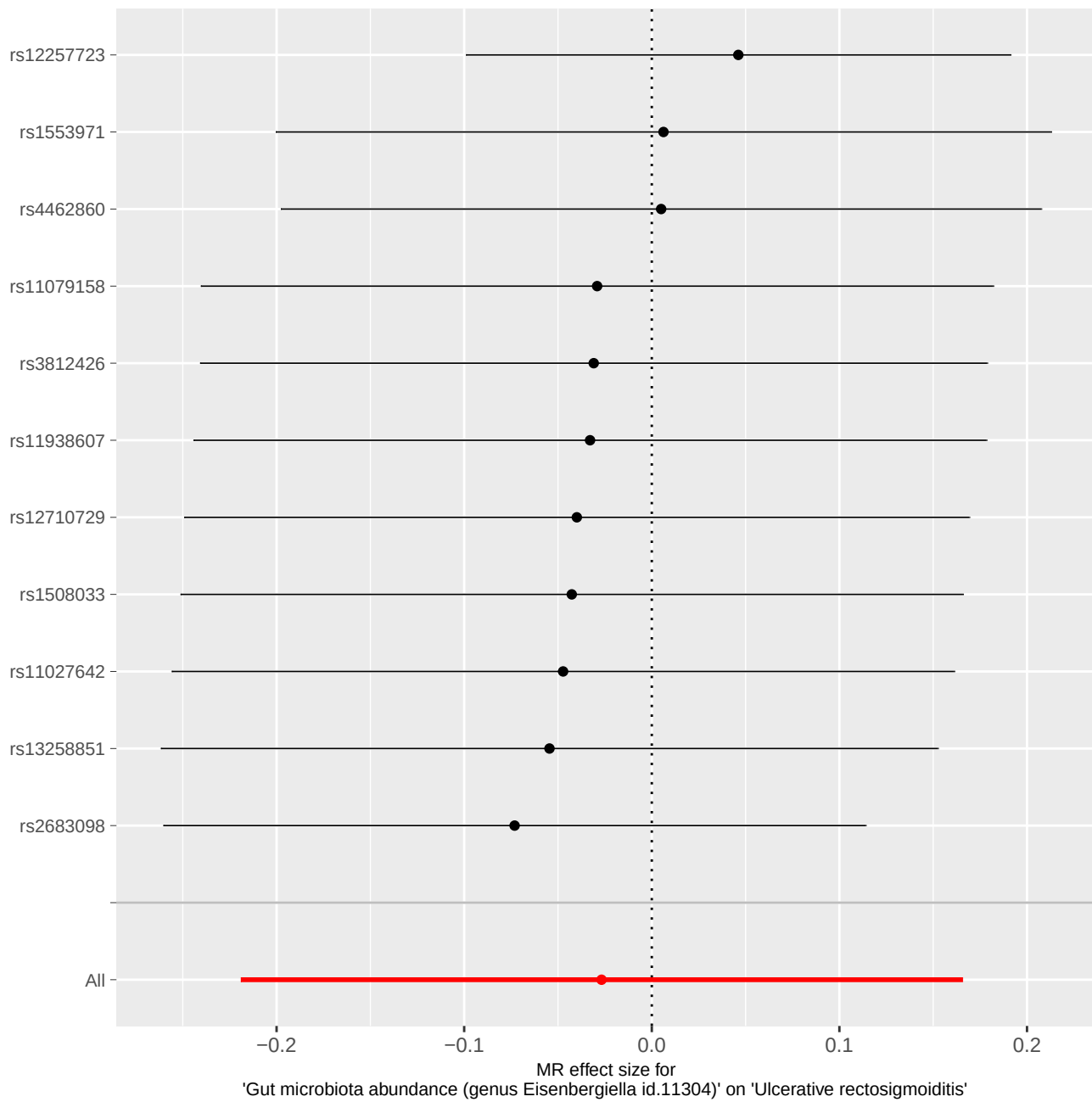


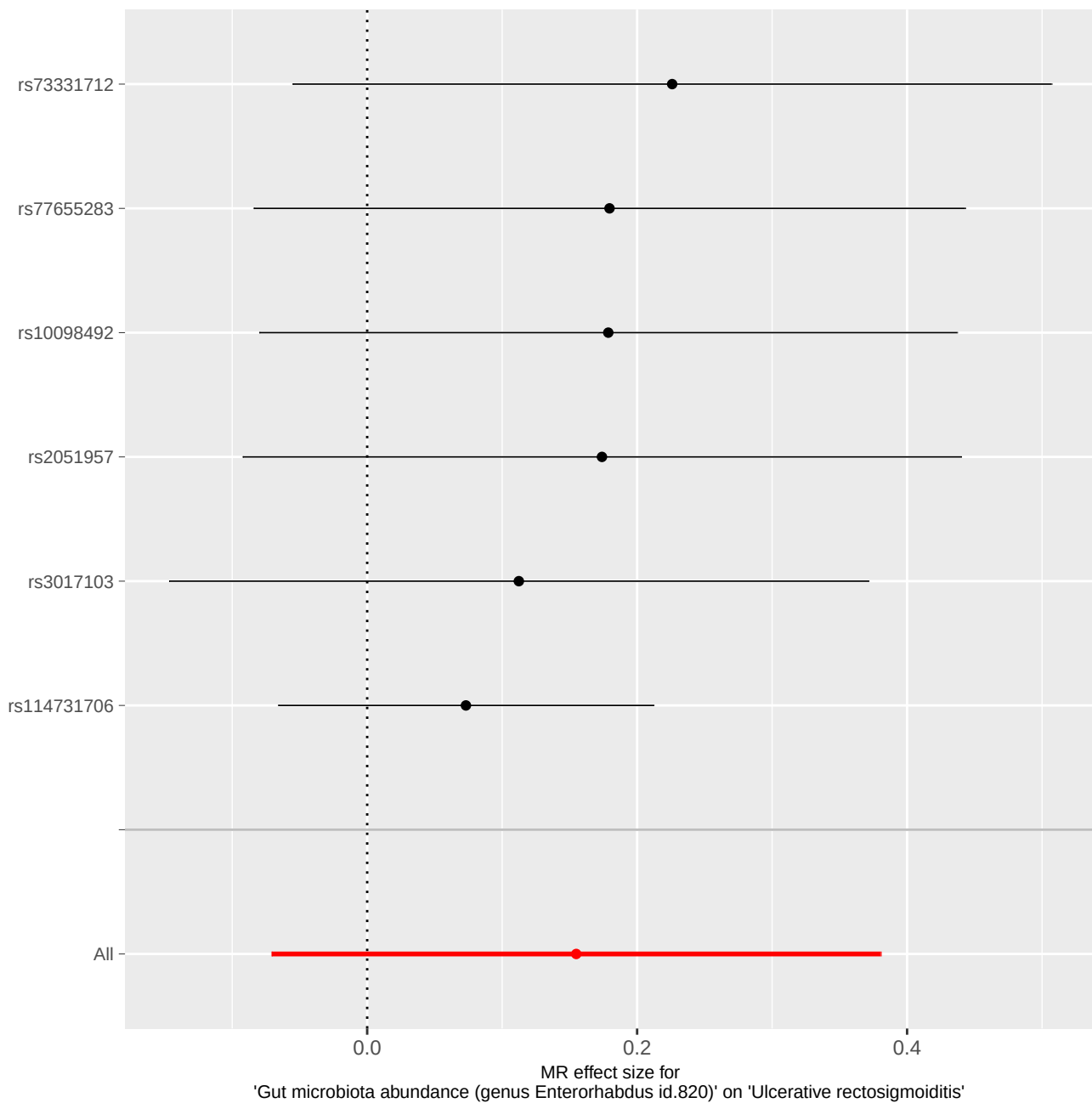


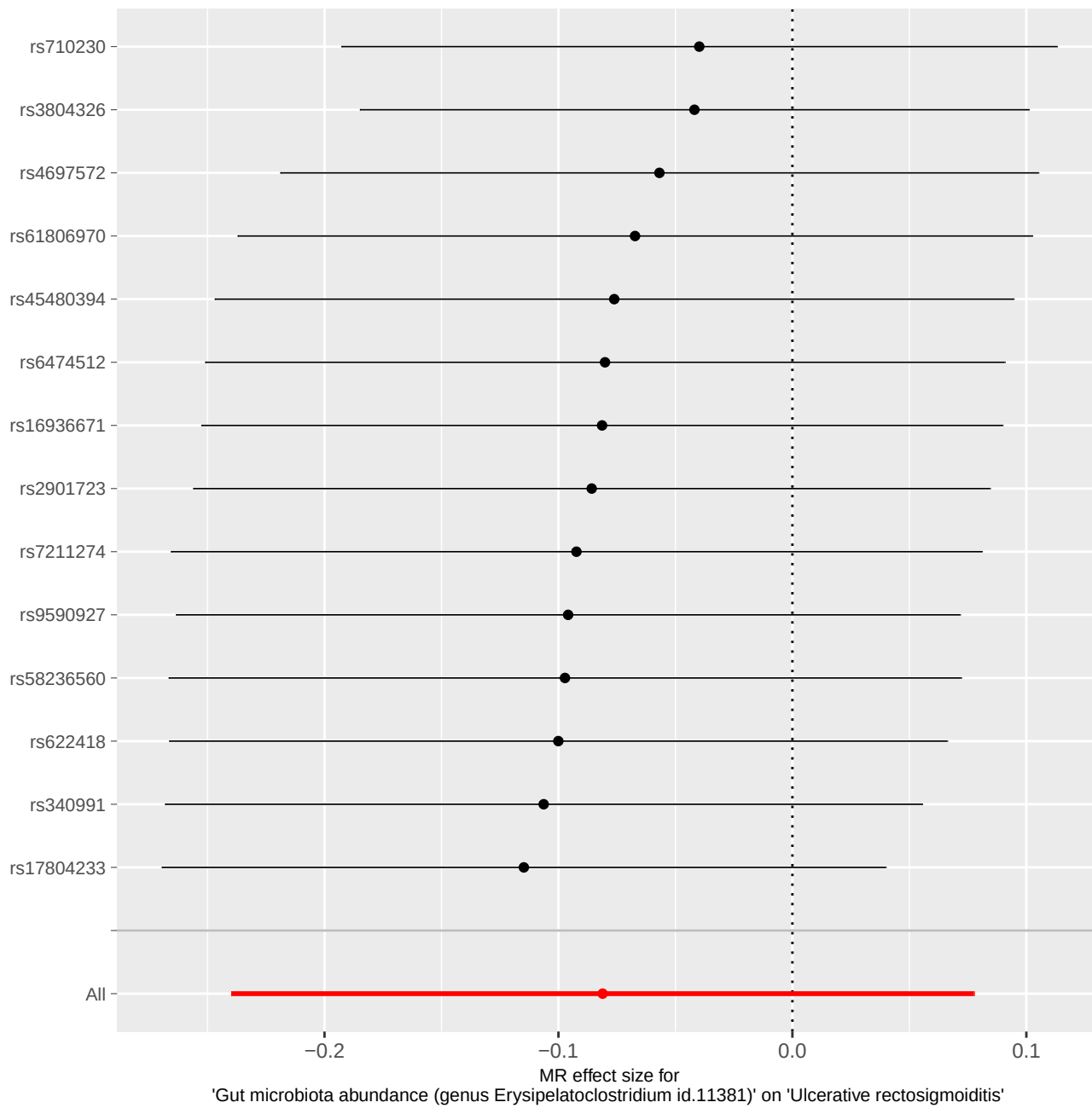


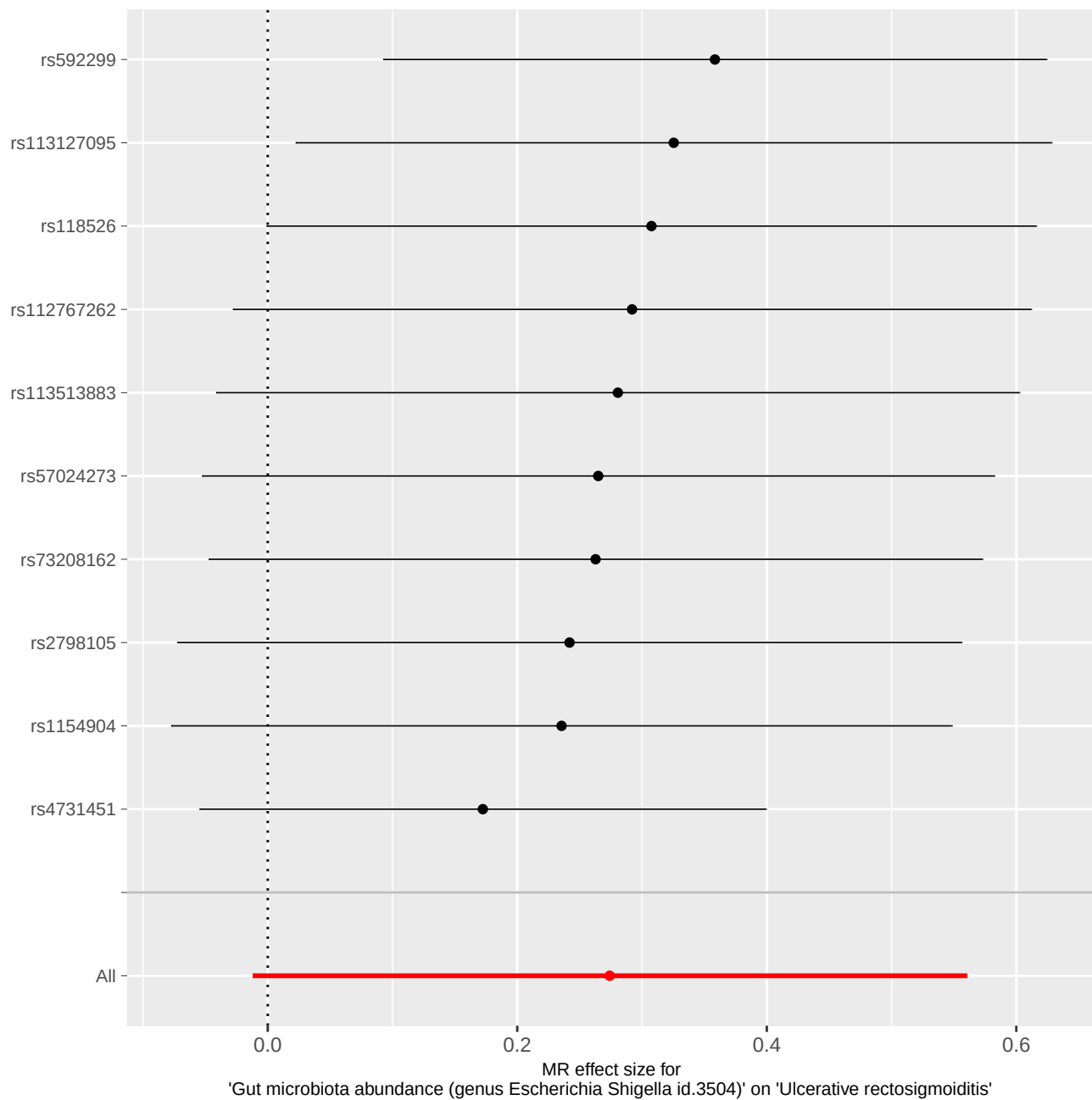


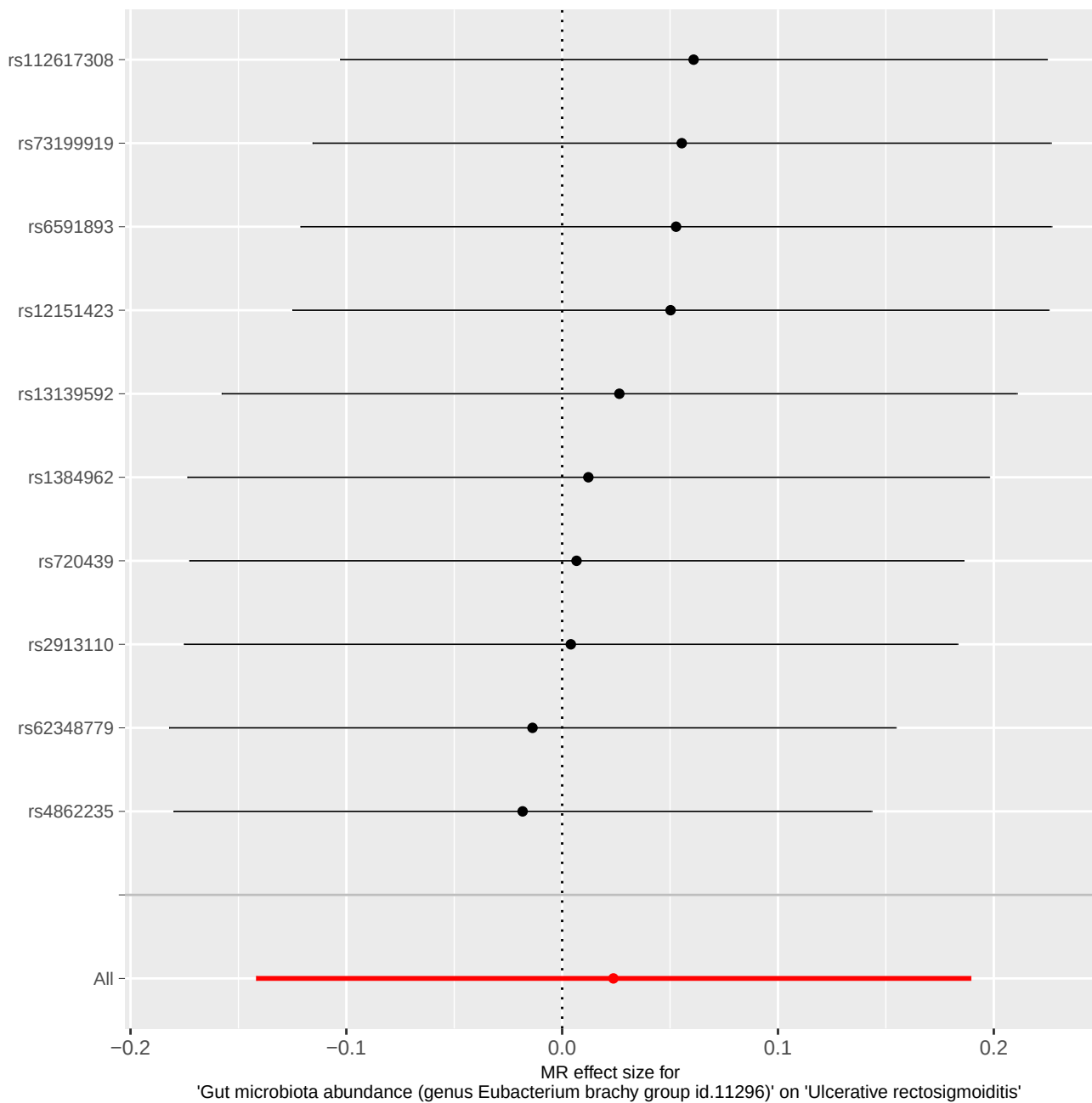


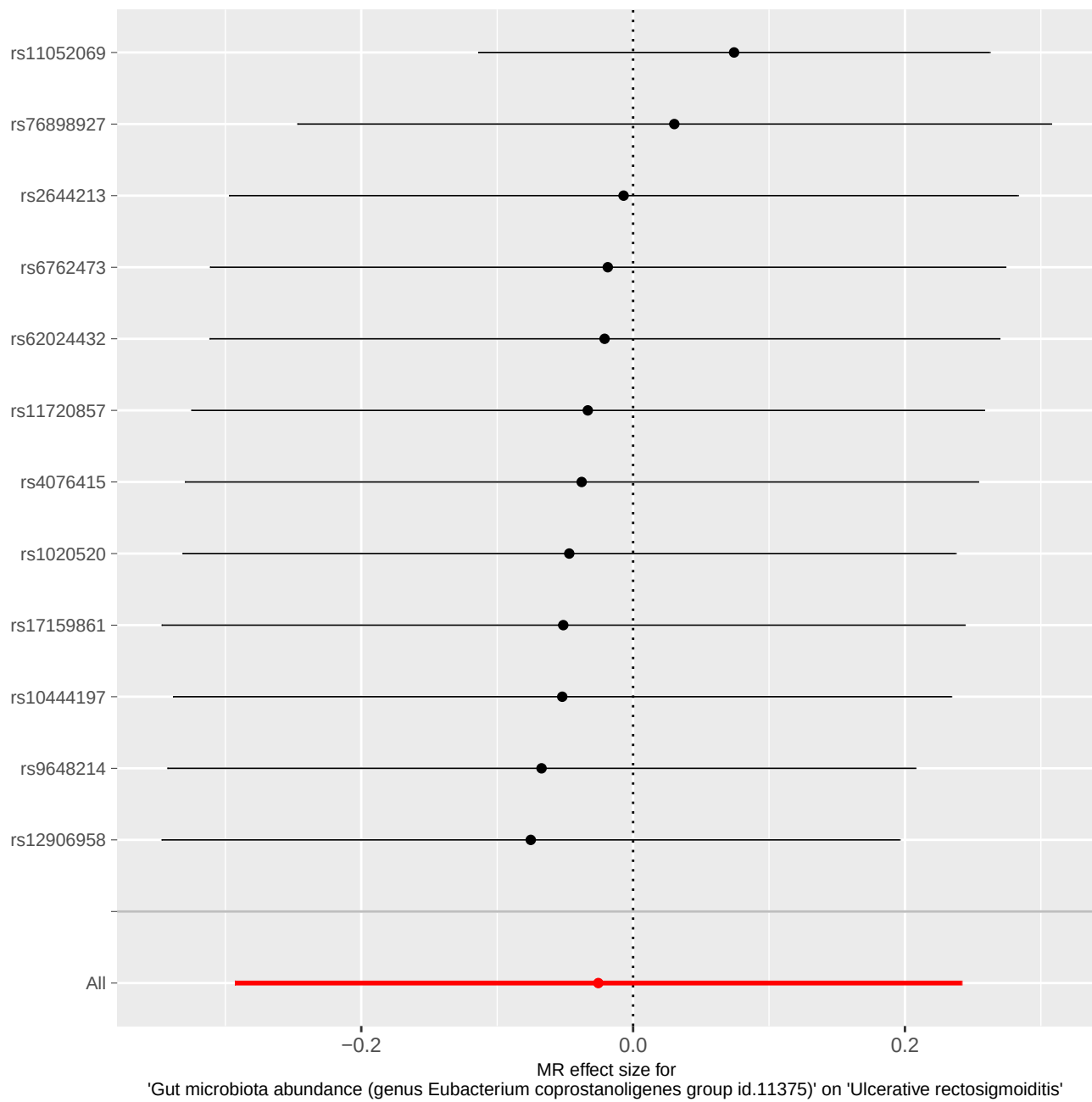


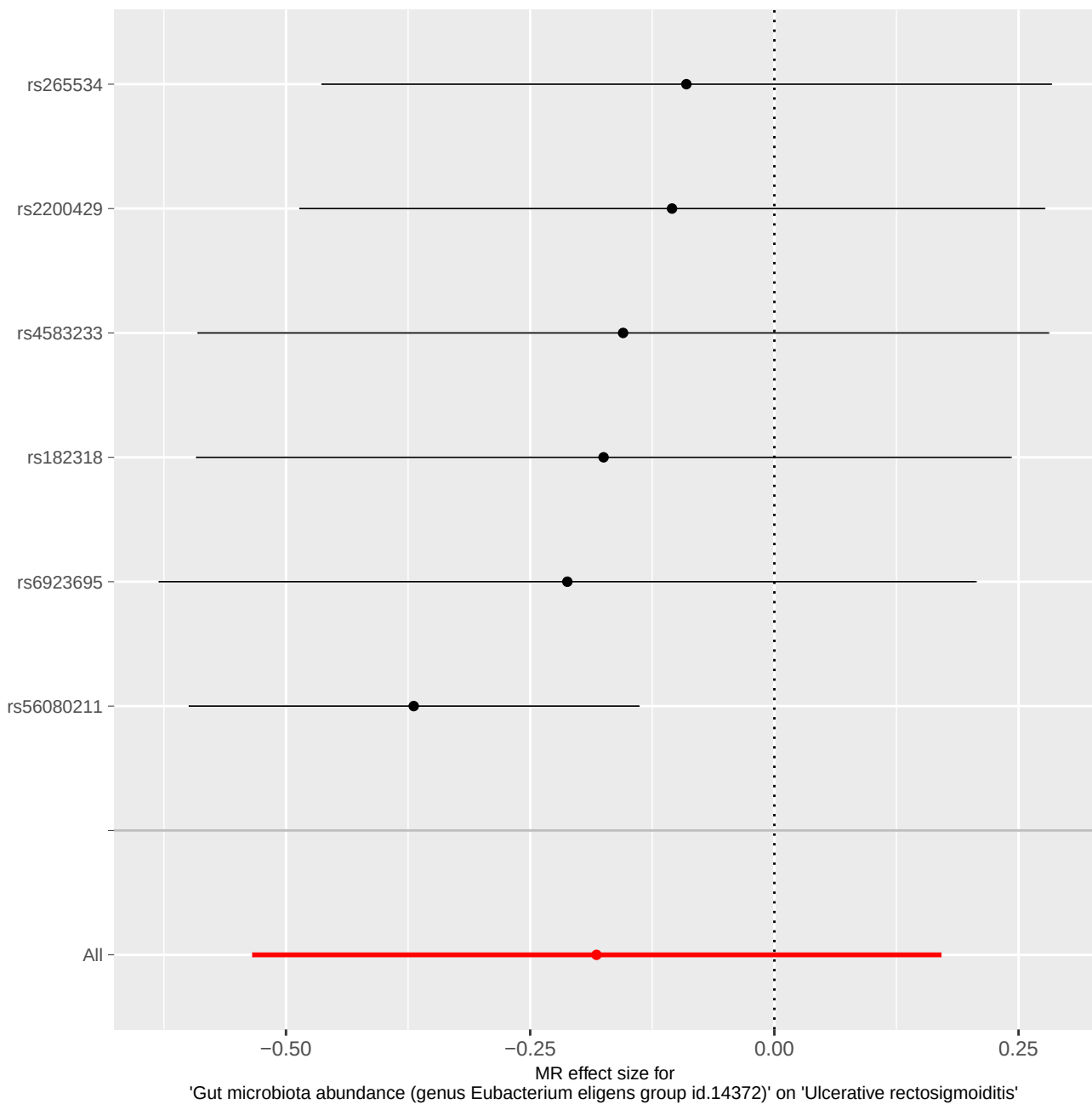


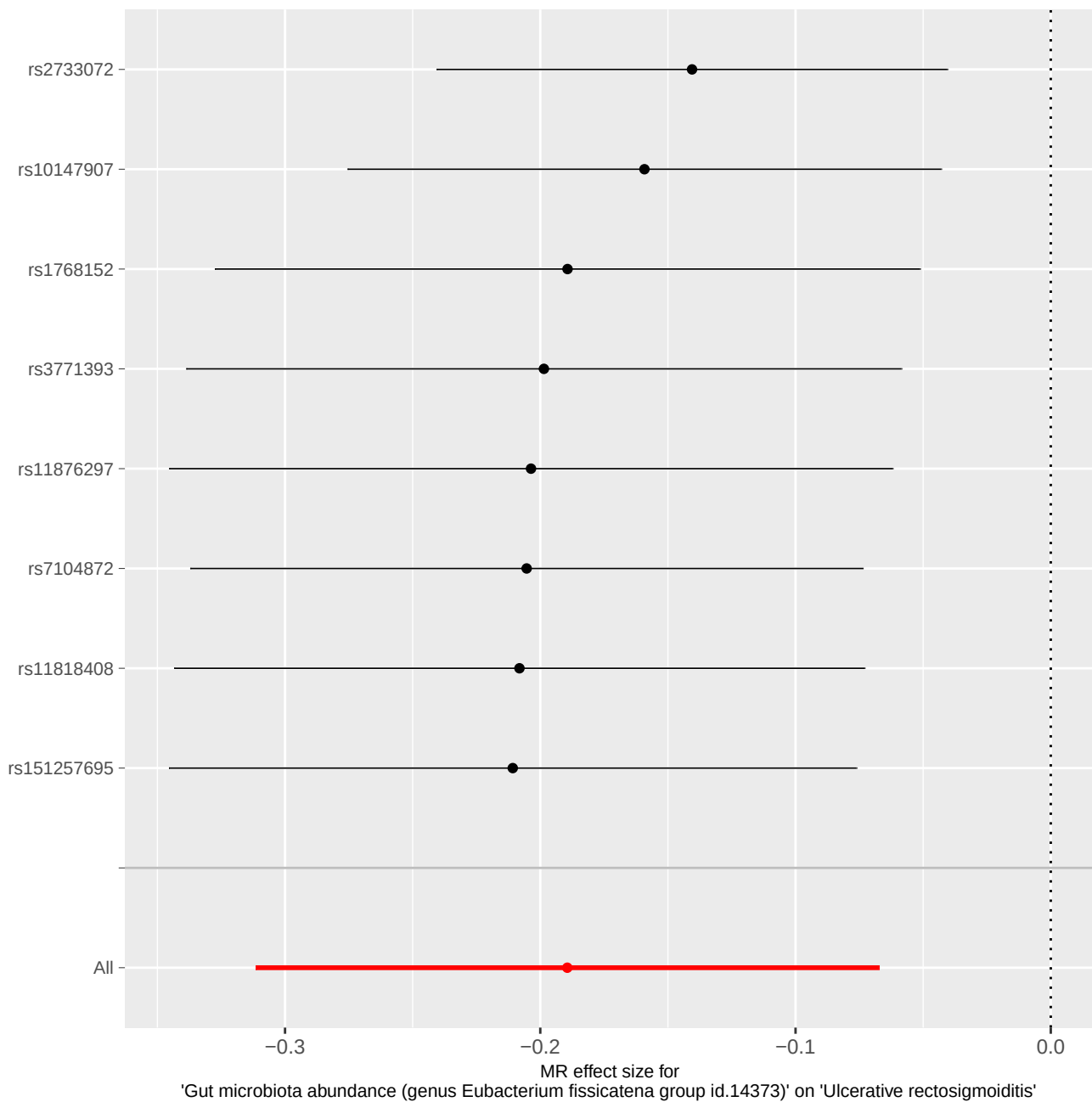


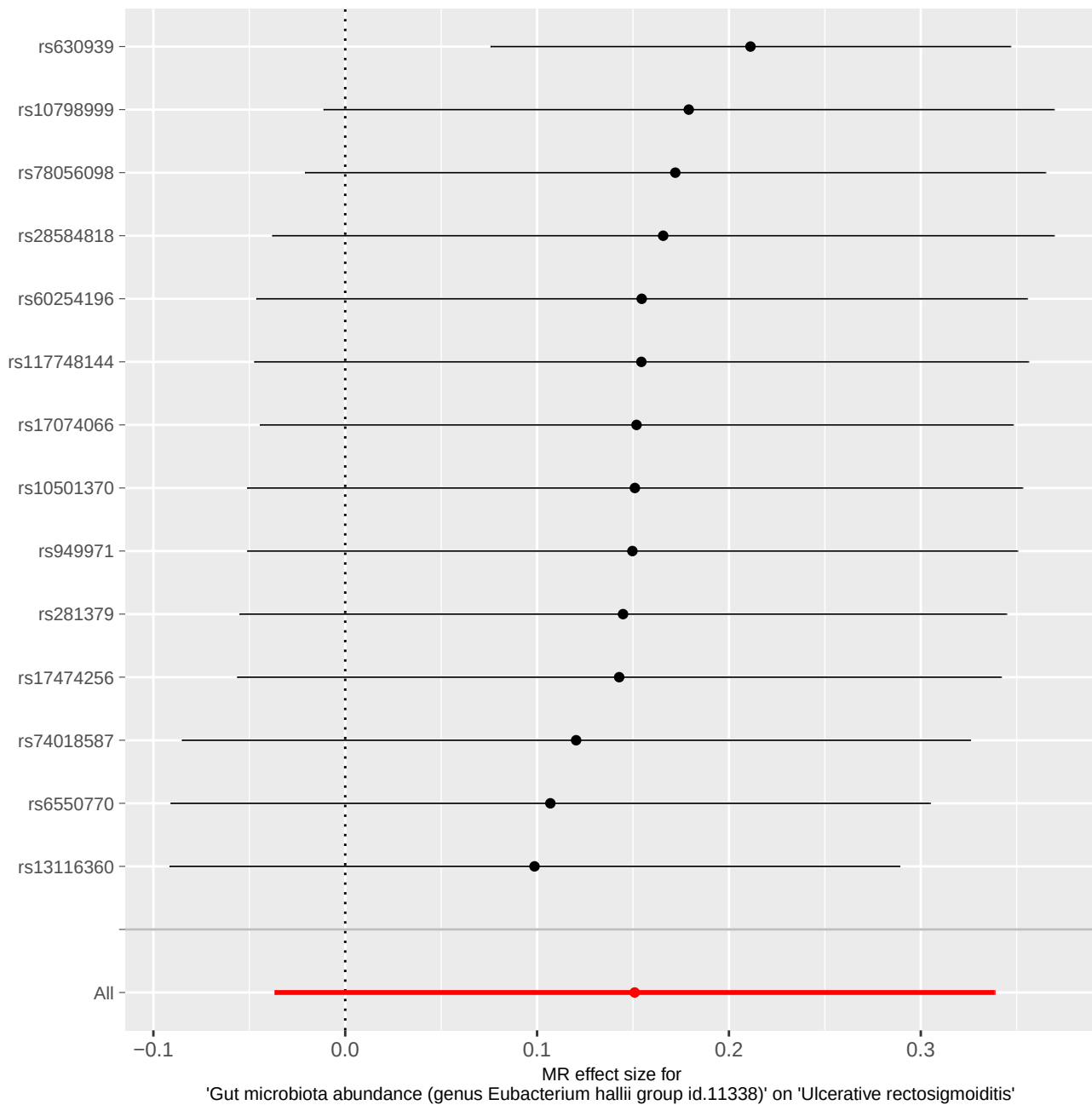


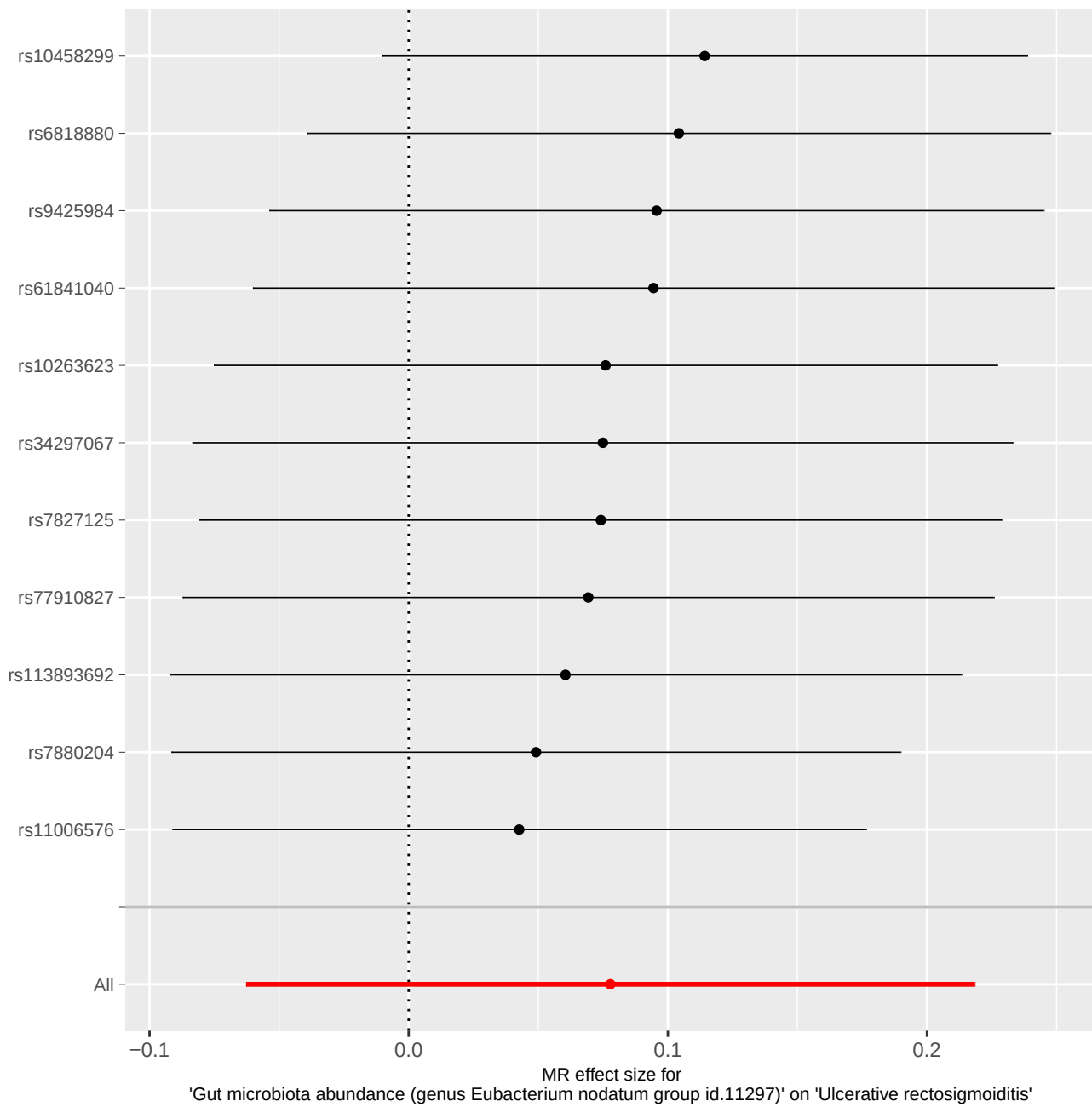


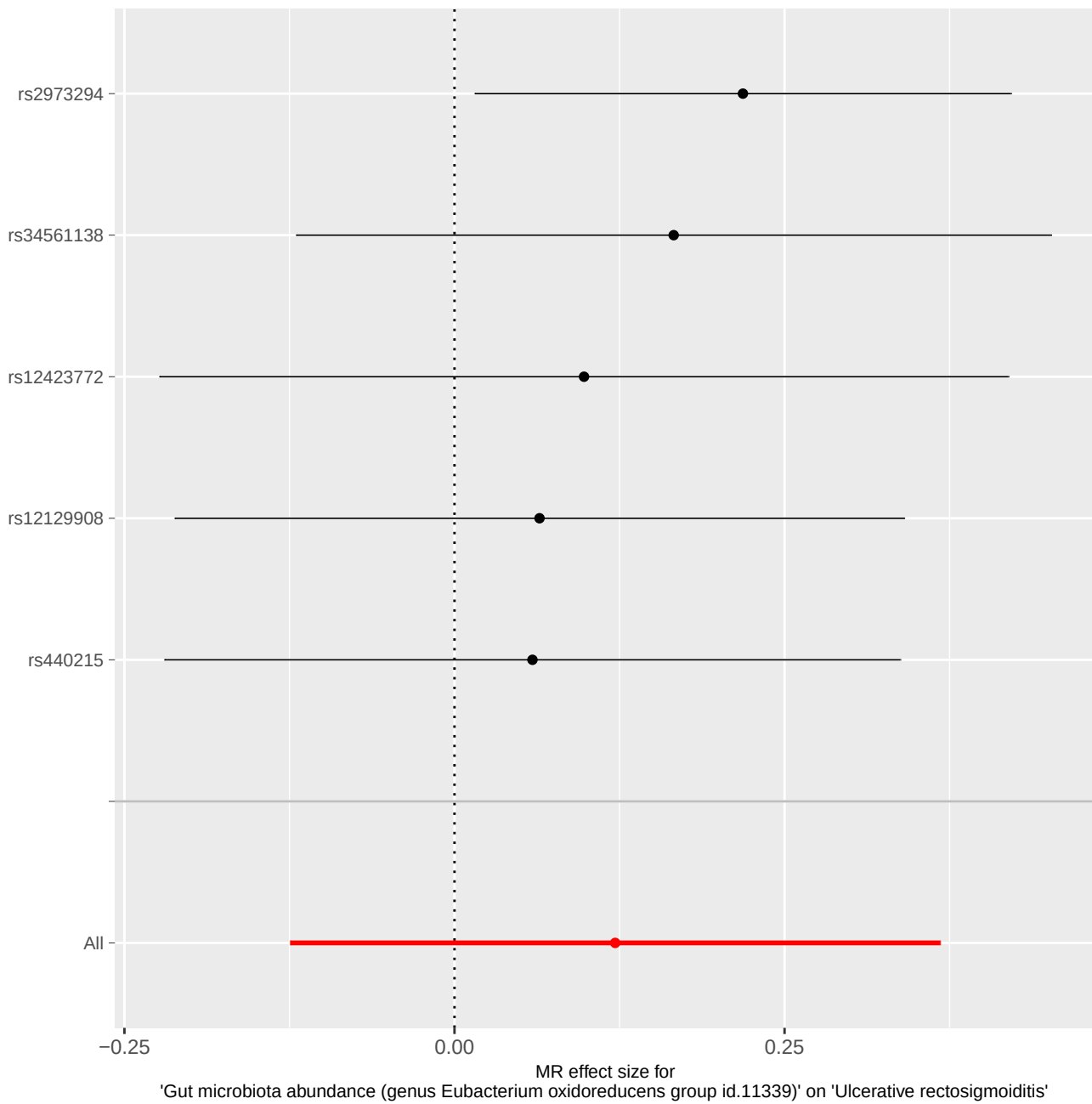




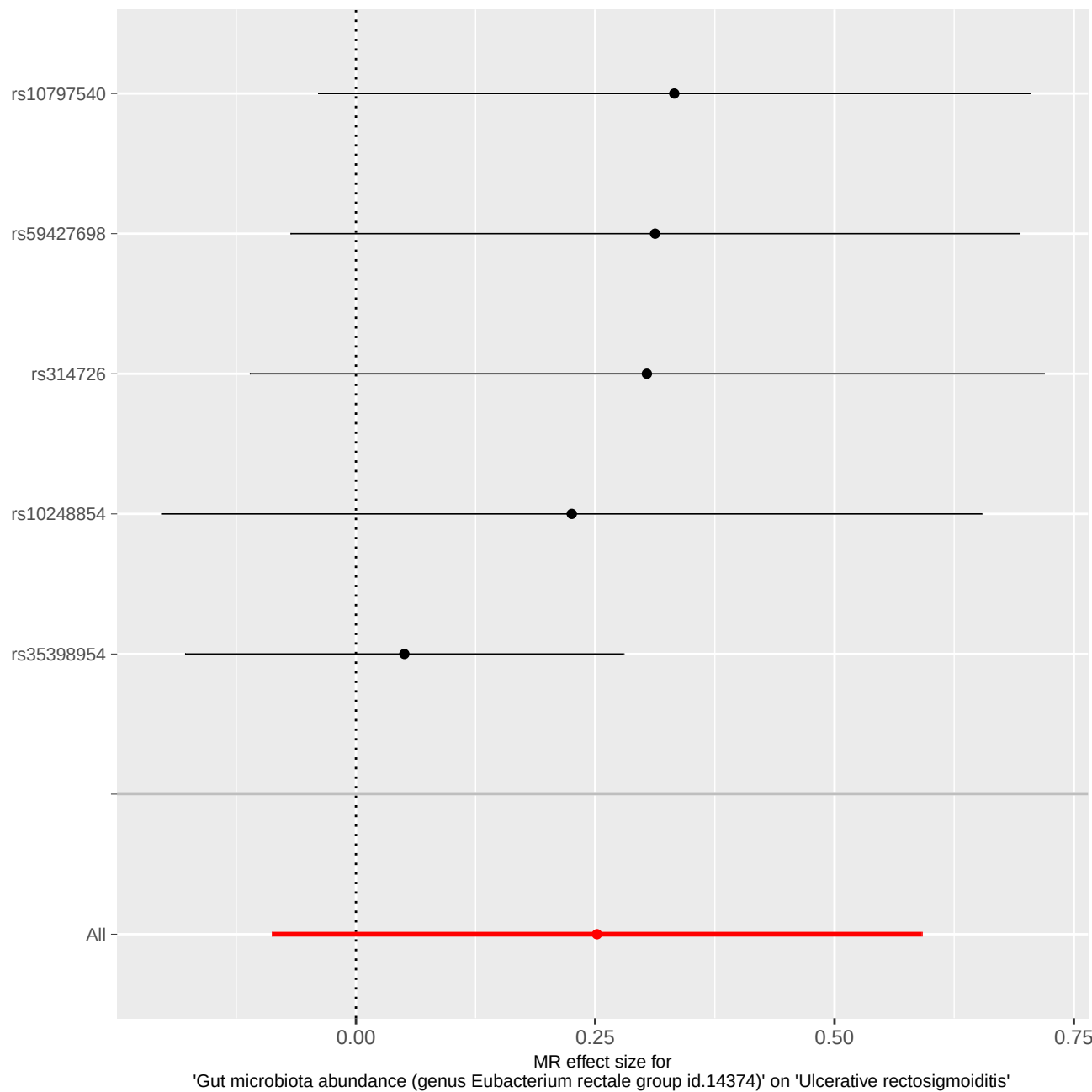


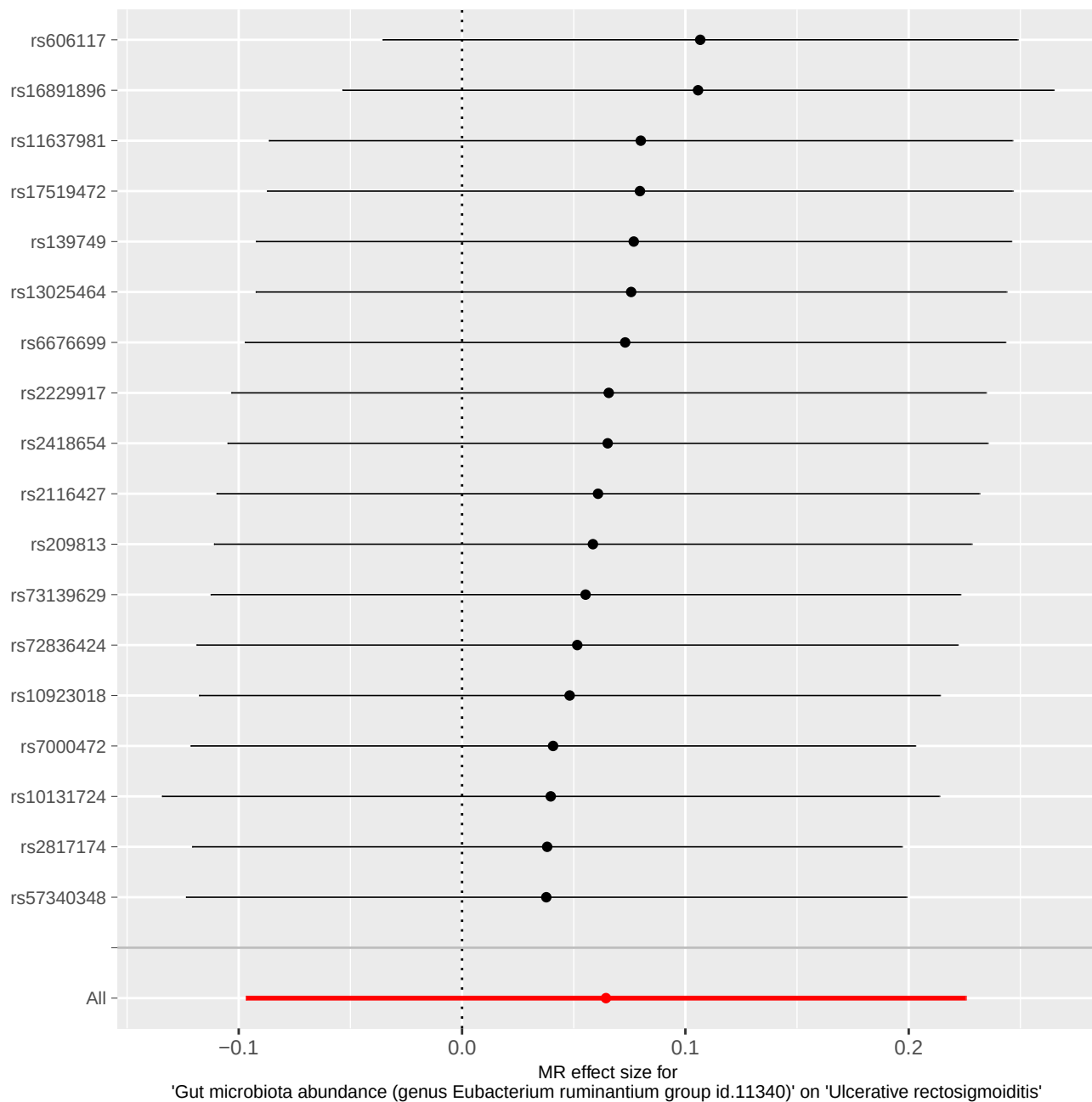




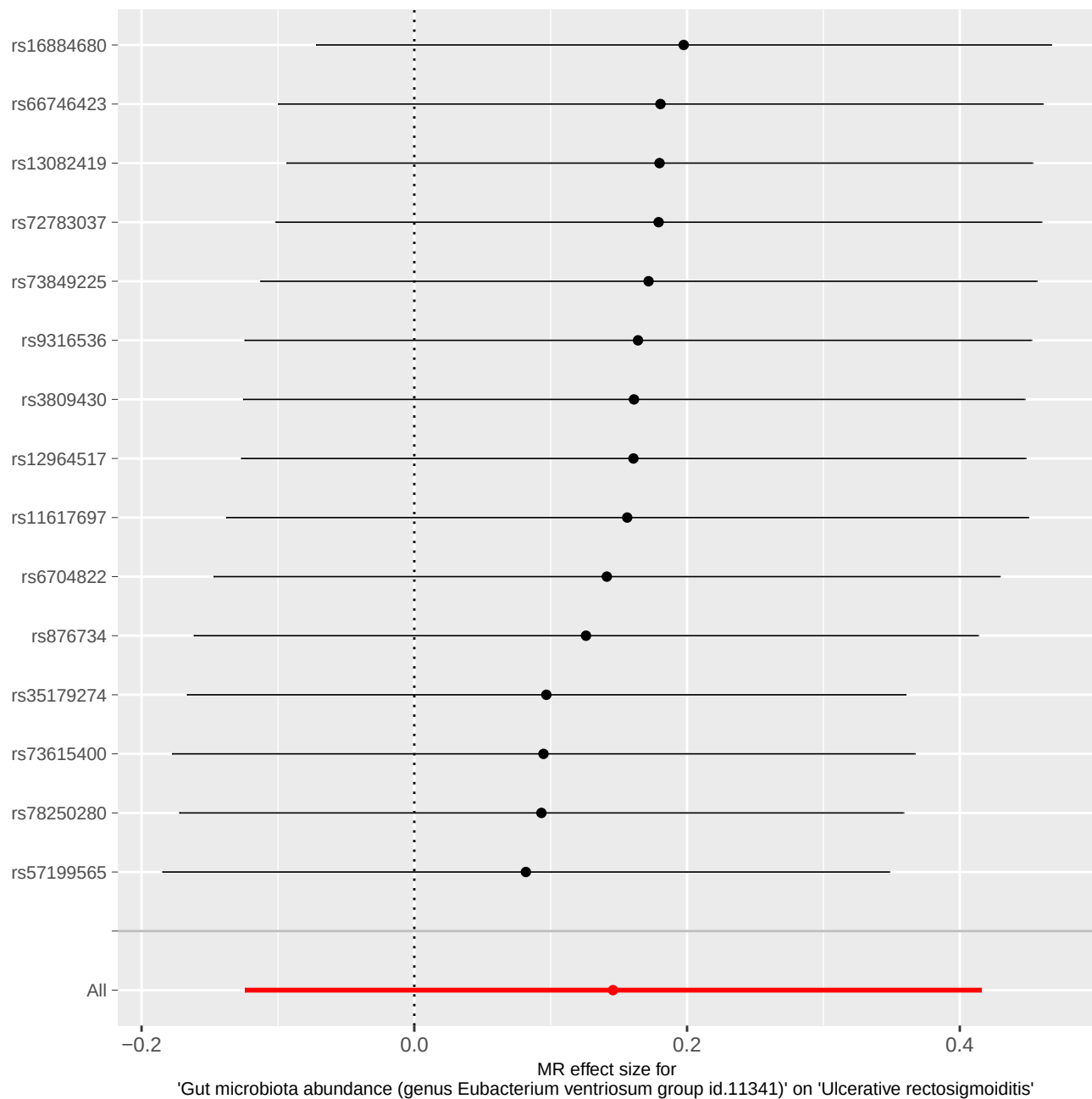


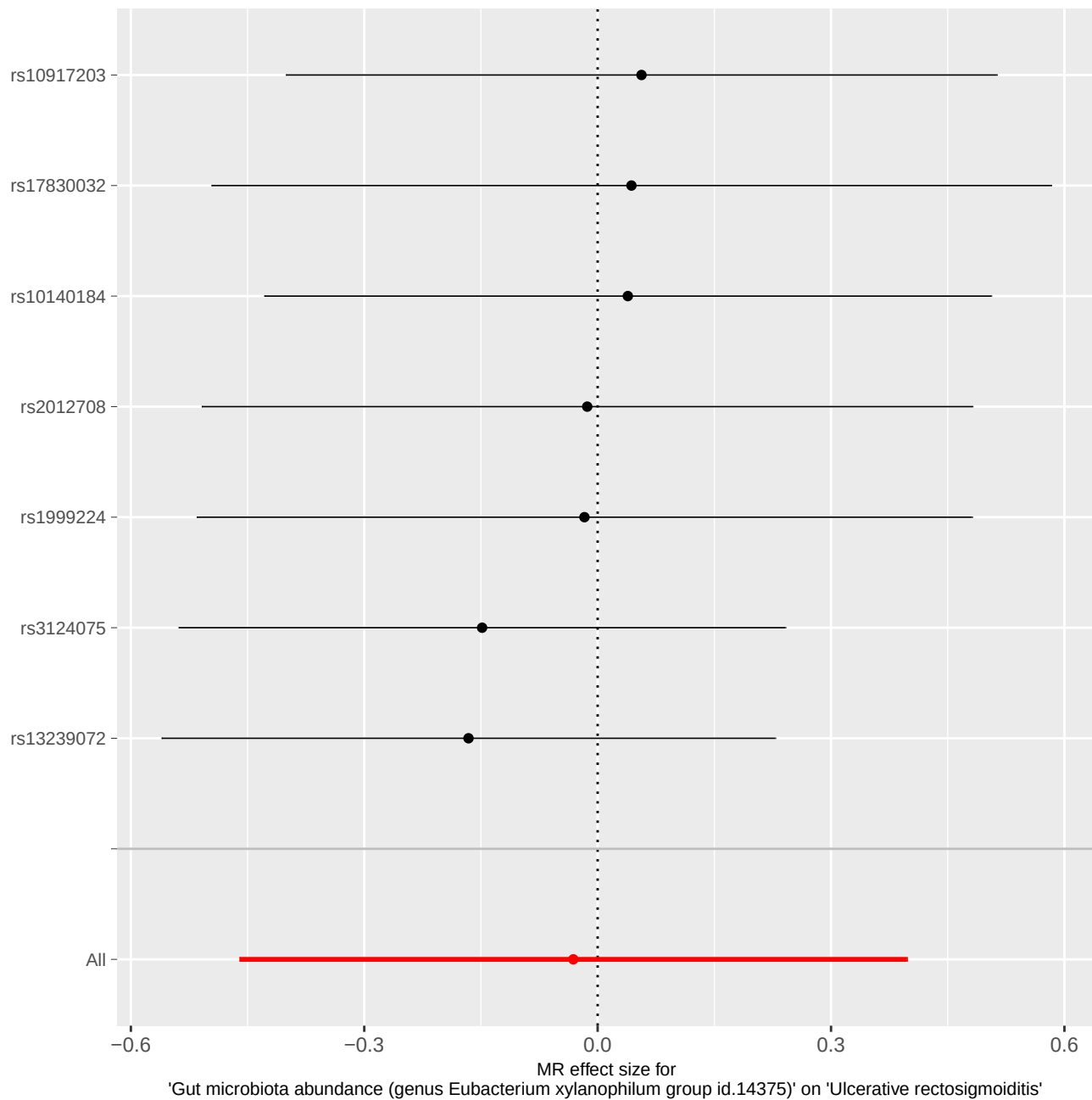
MR effect size for
'Gut microbiota abundance (genus Eubacterium oxidoreducens group id.11339)' on 'Ulcerative rectosigmoiditis'

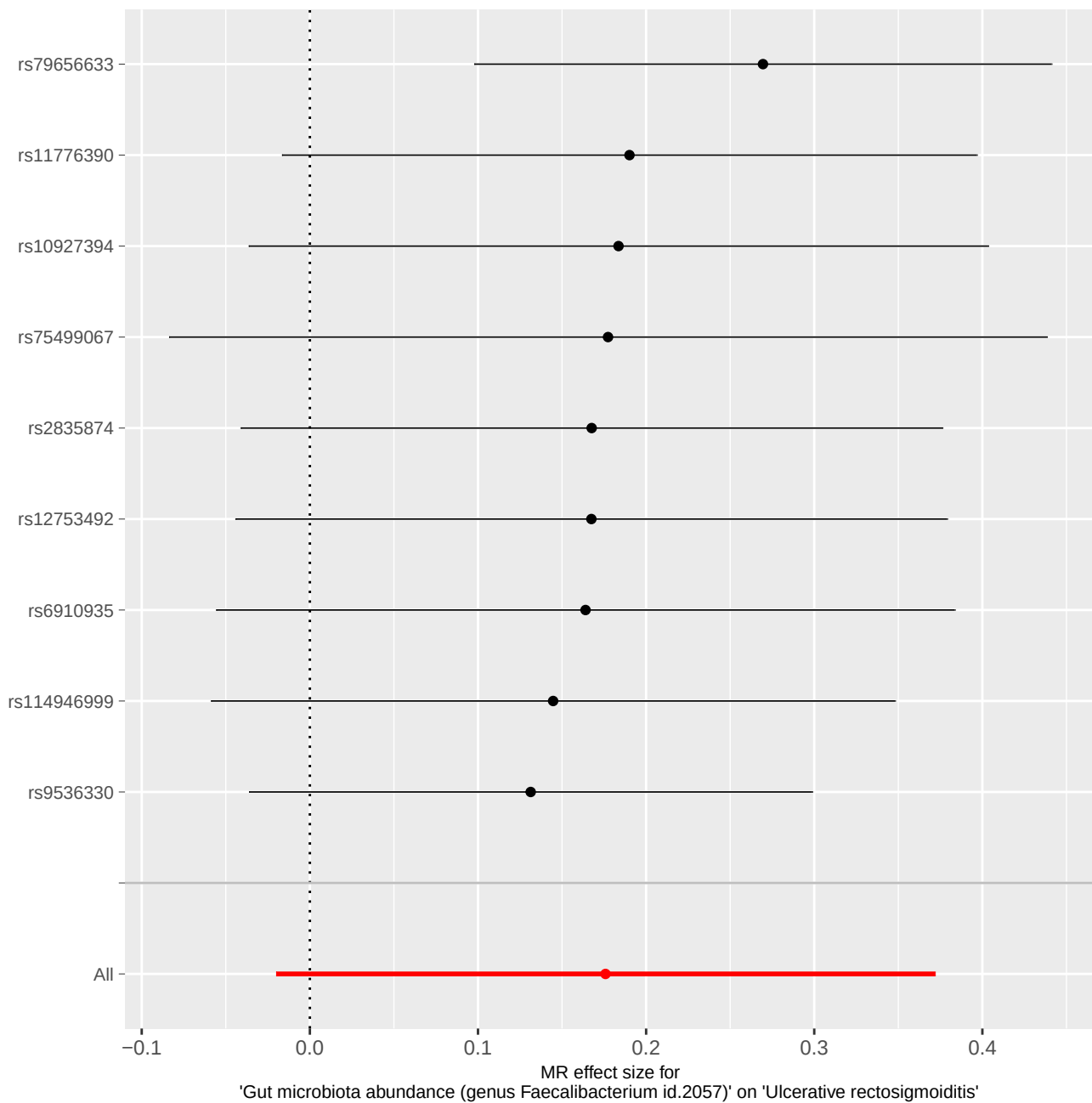


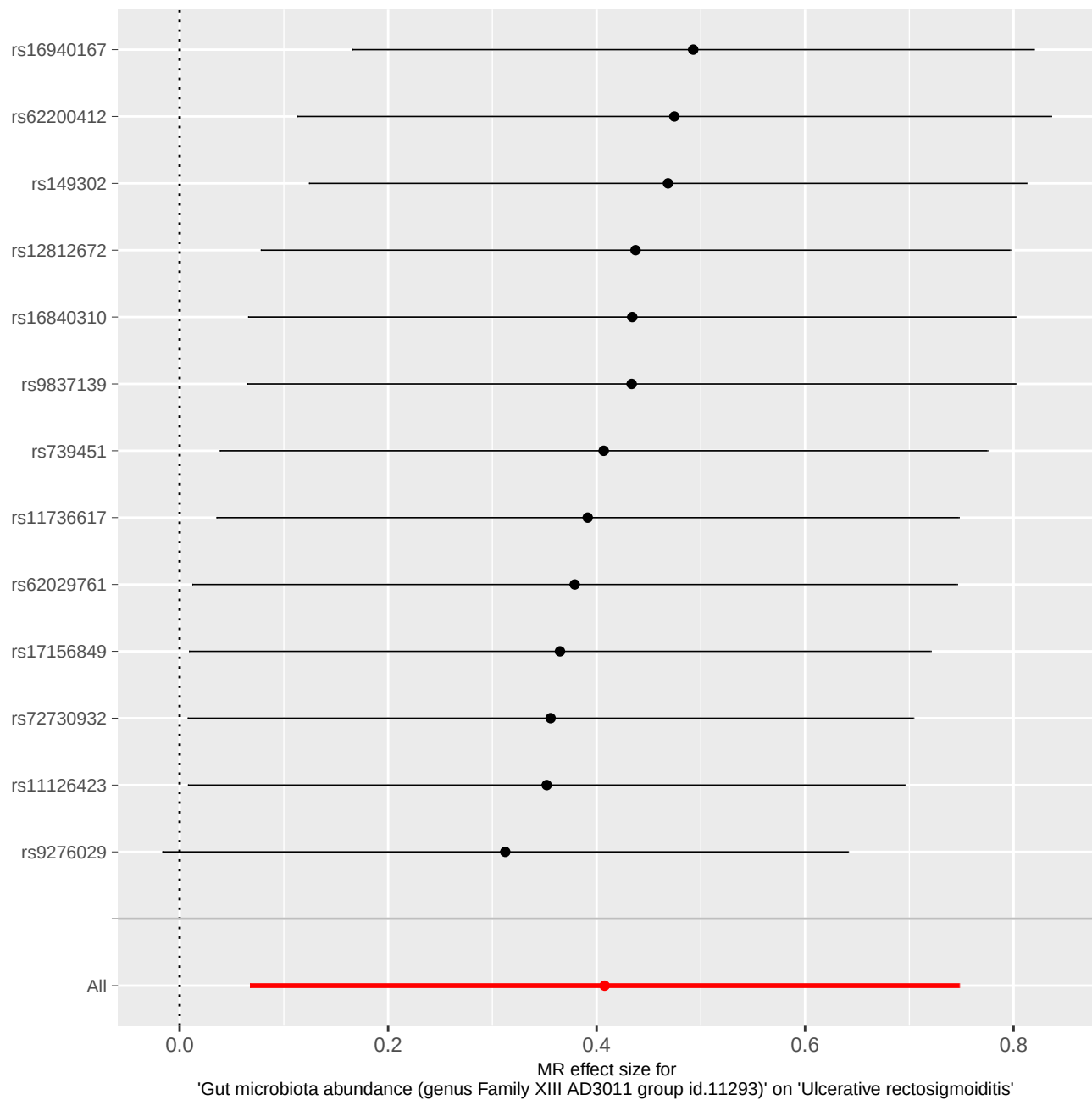


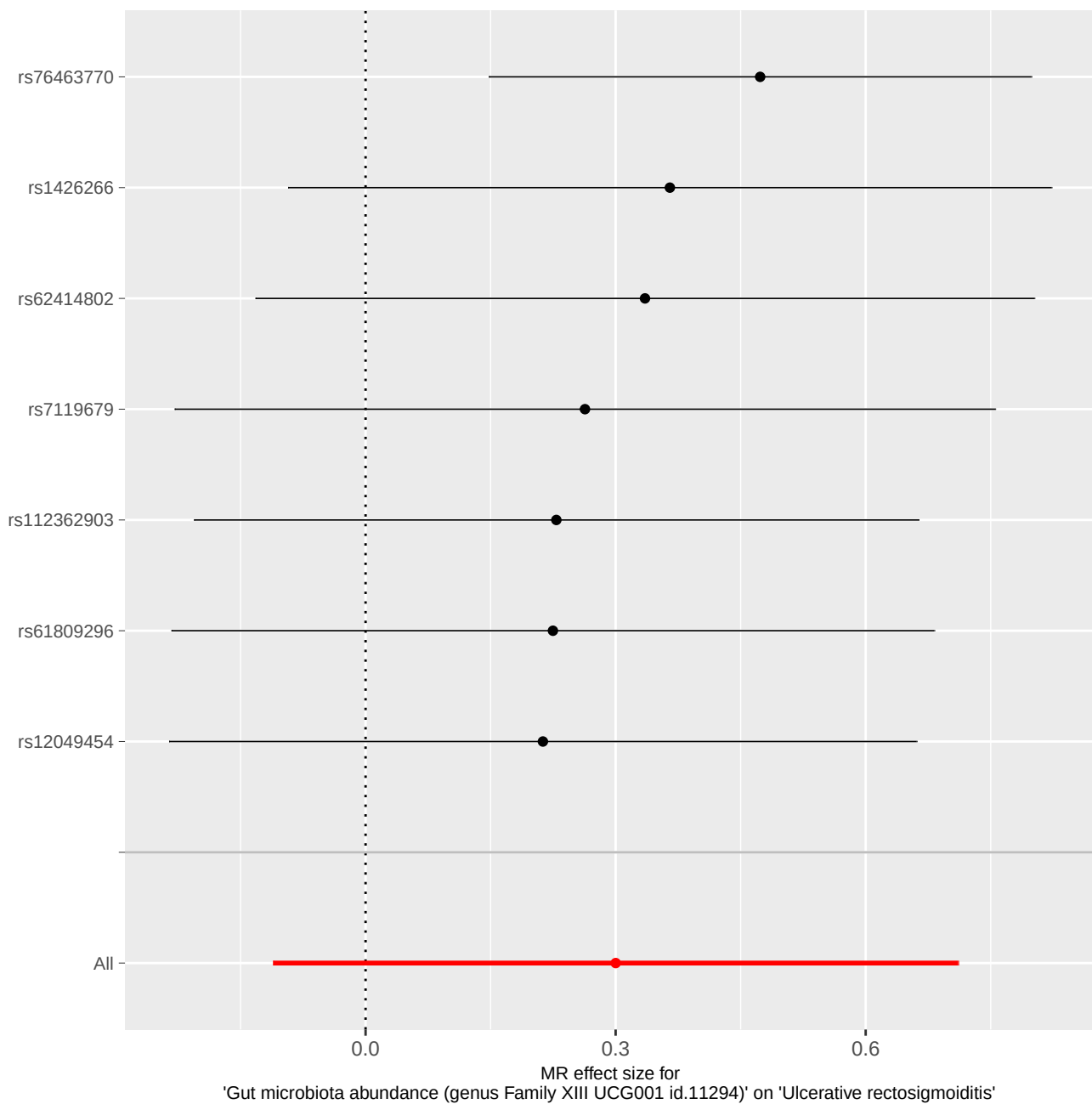
MR effect size for
'Gut microbiota abundance (genus Eubacterium ruminantium group id.11340)' on 'Ulcerative rectosigmoiditis'

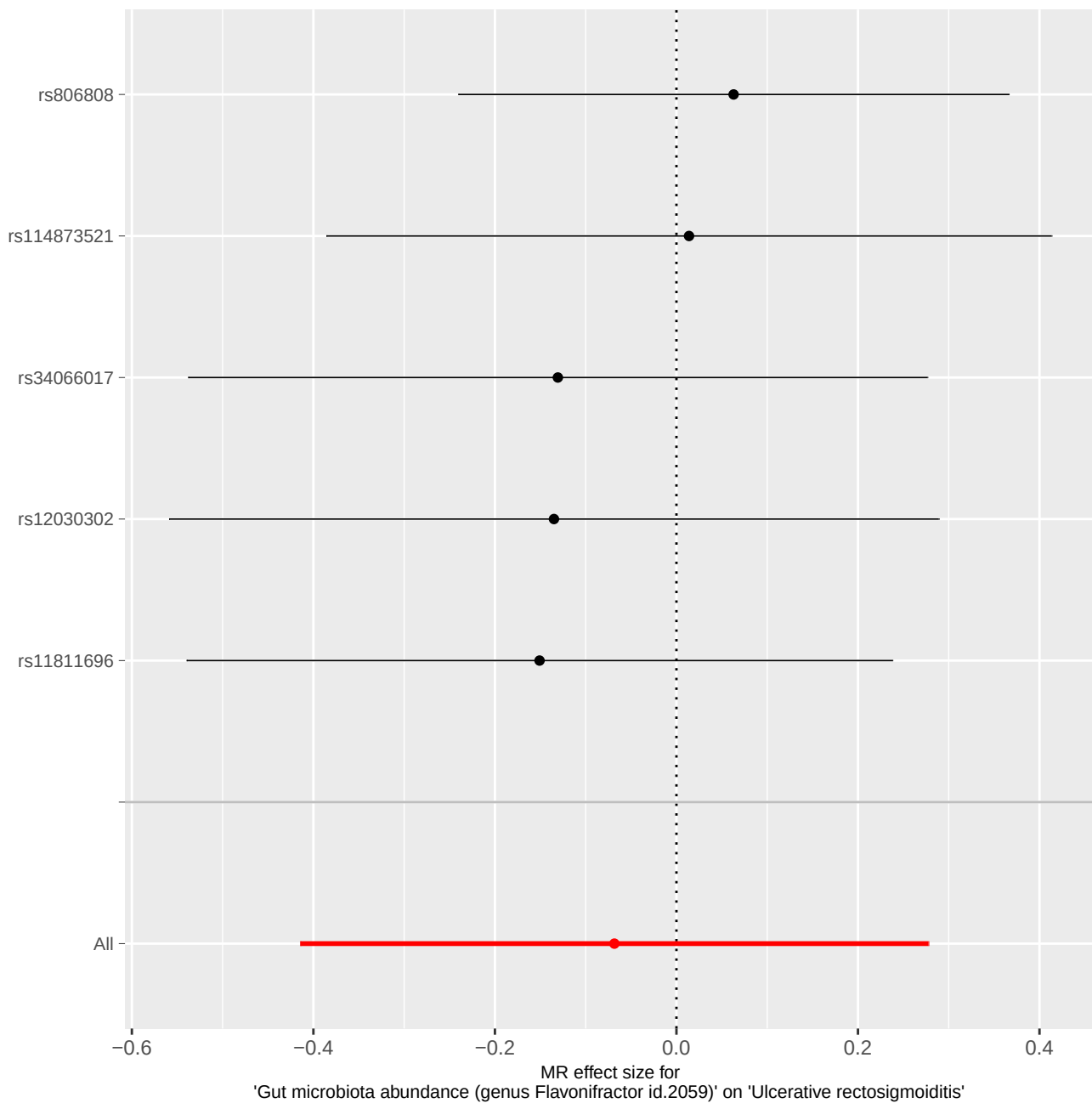


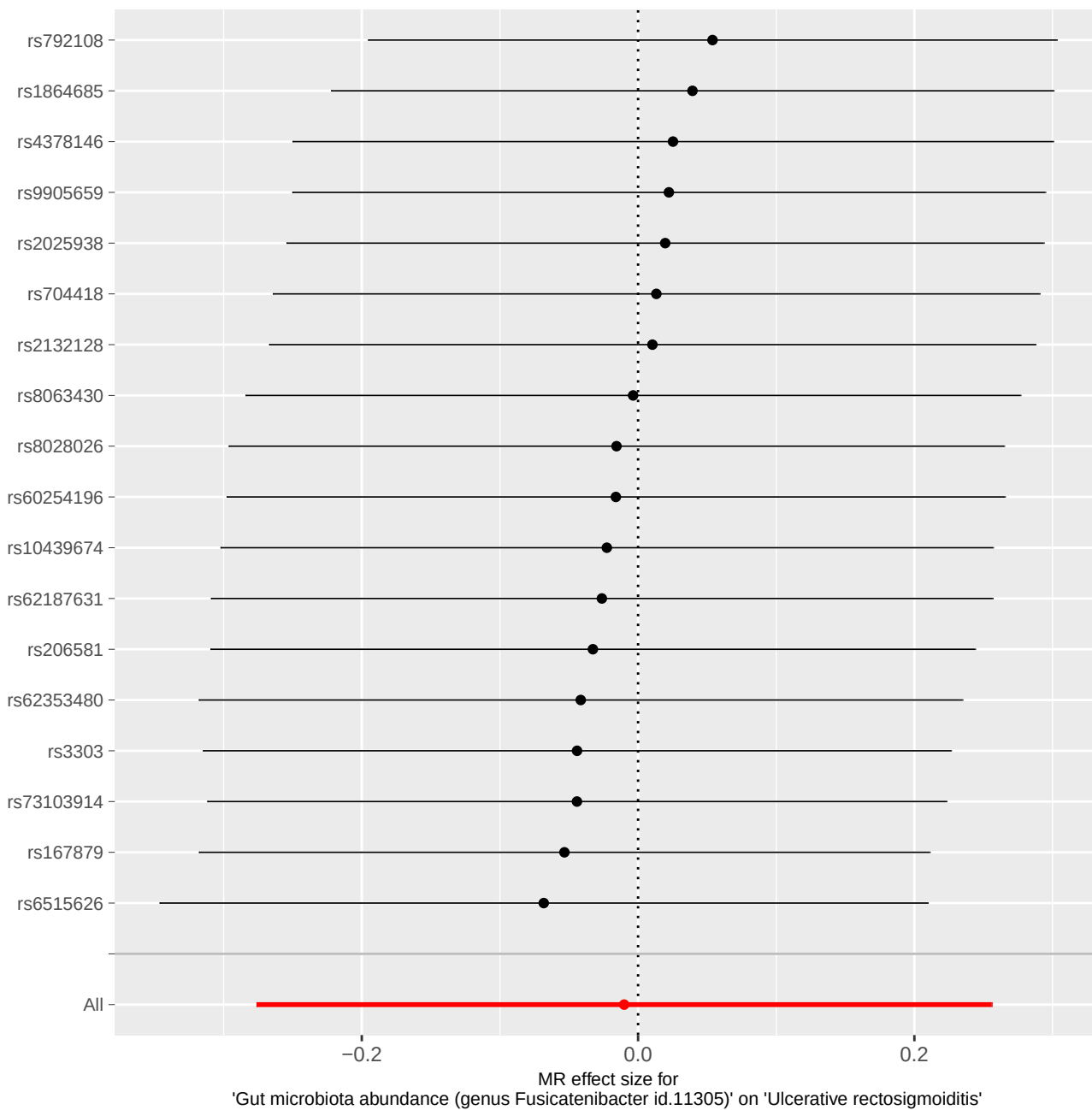






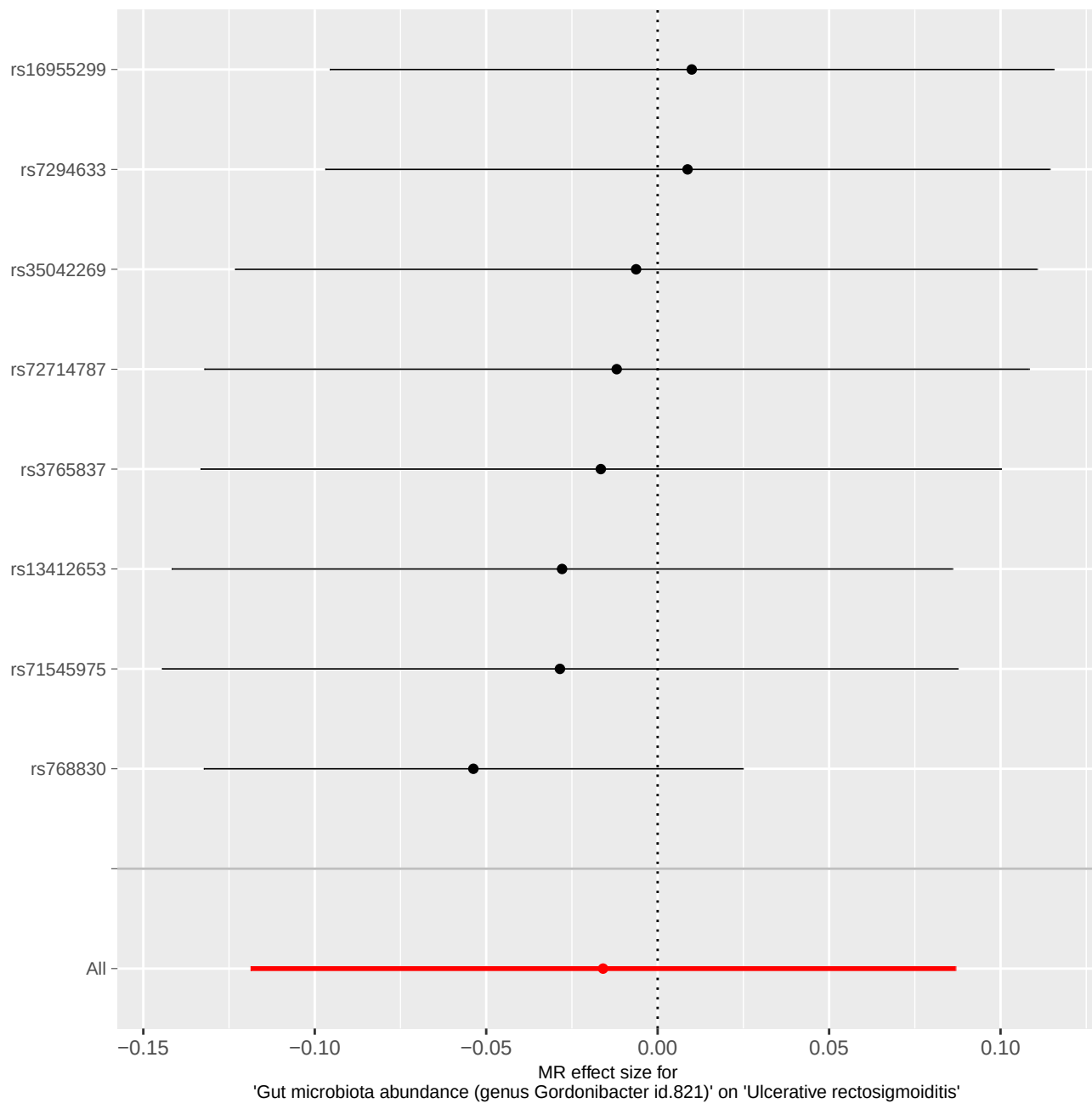


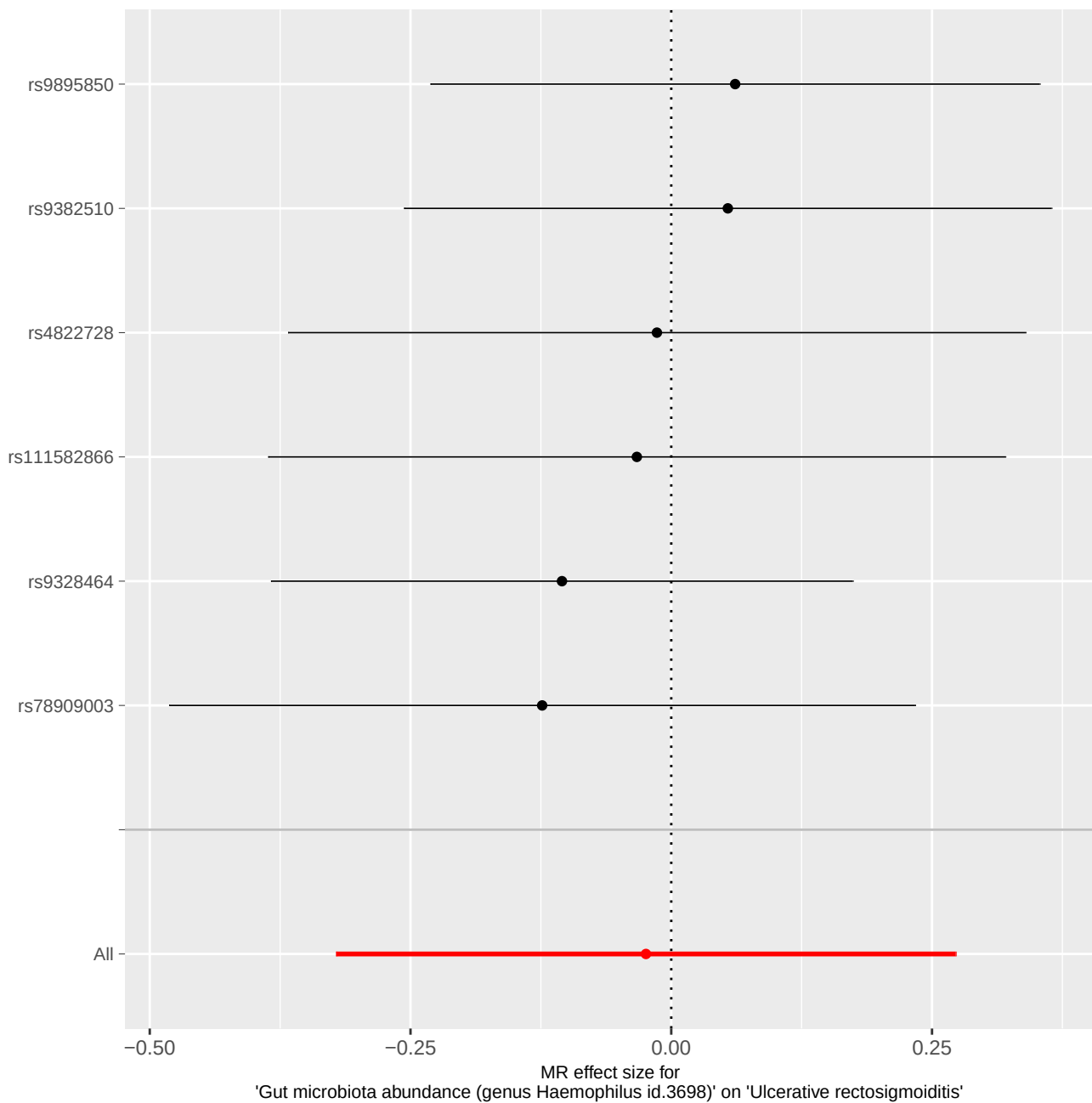


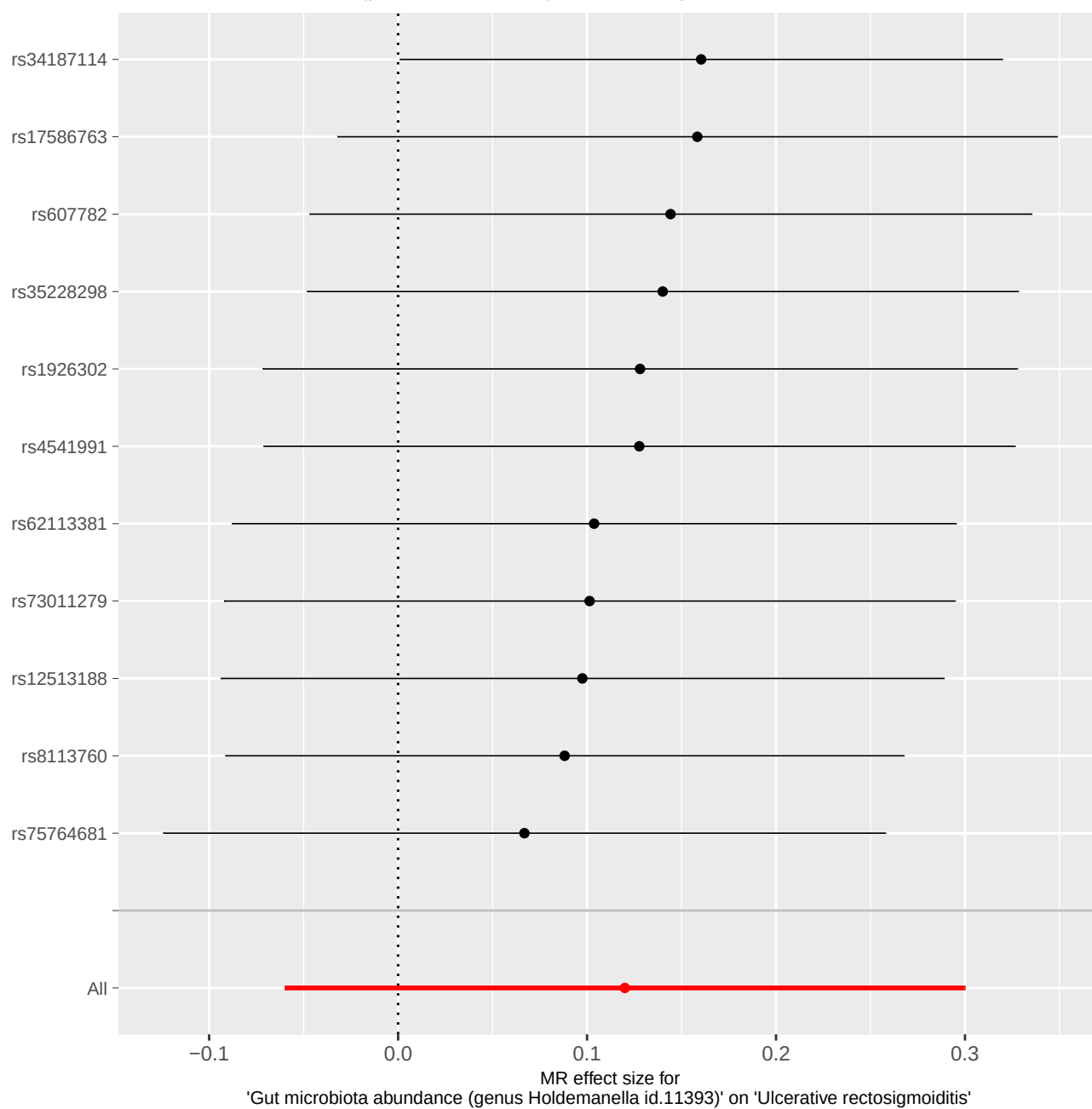


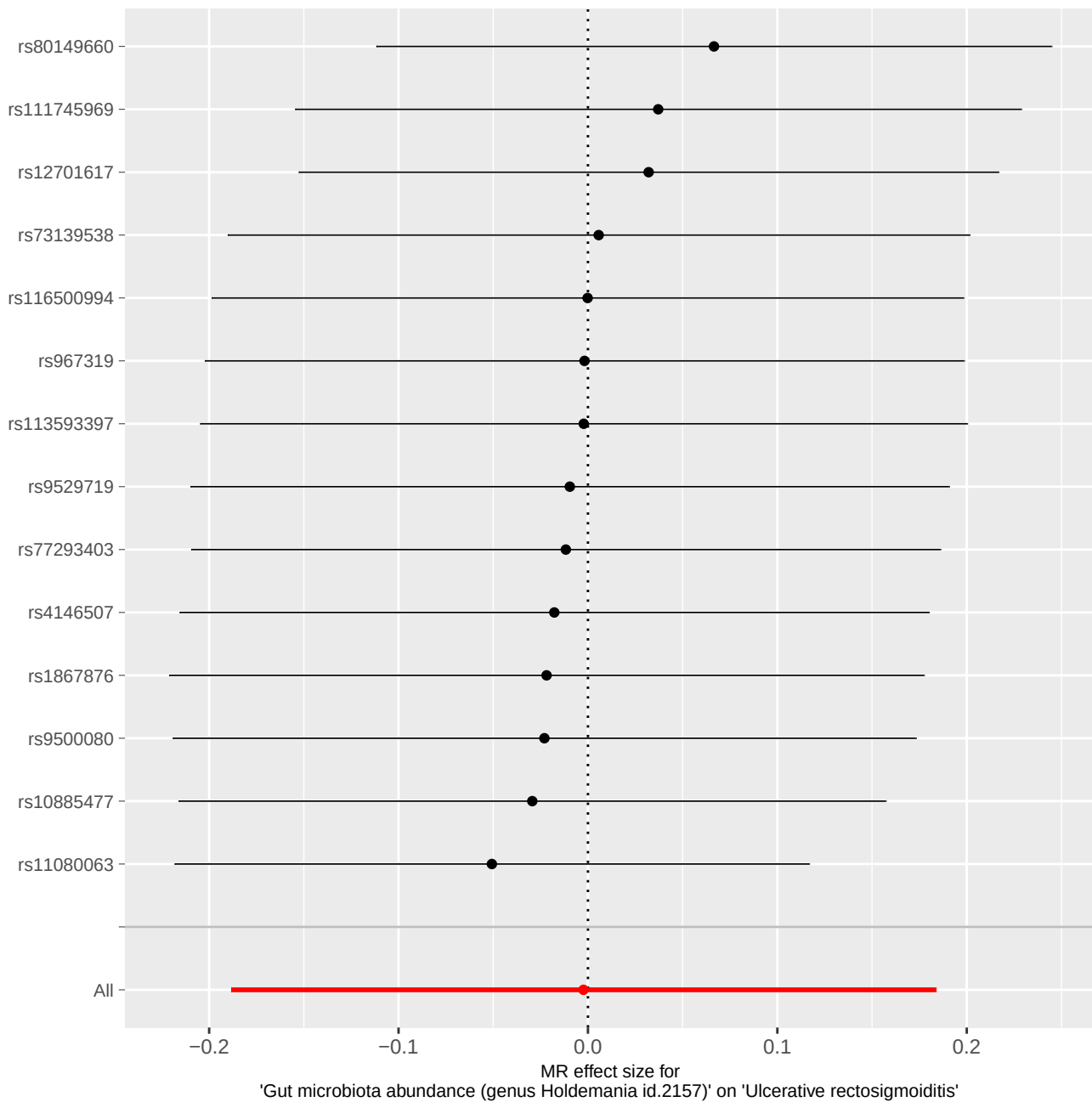
MR effect size for

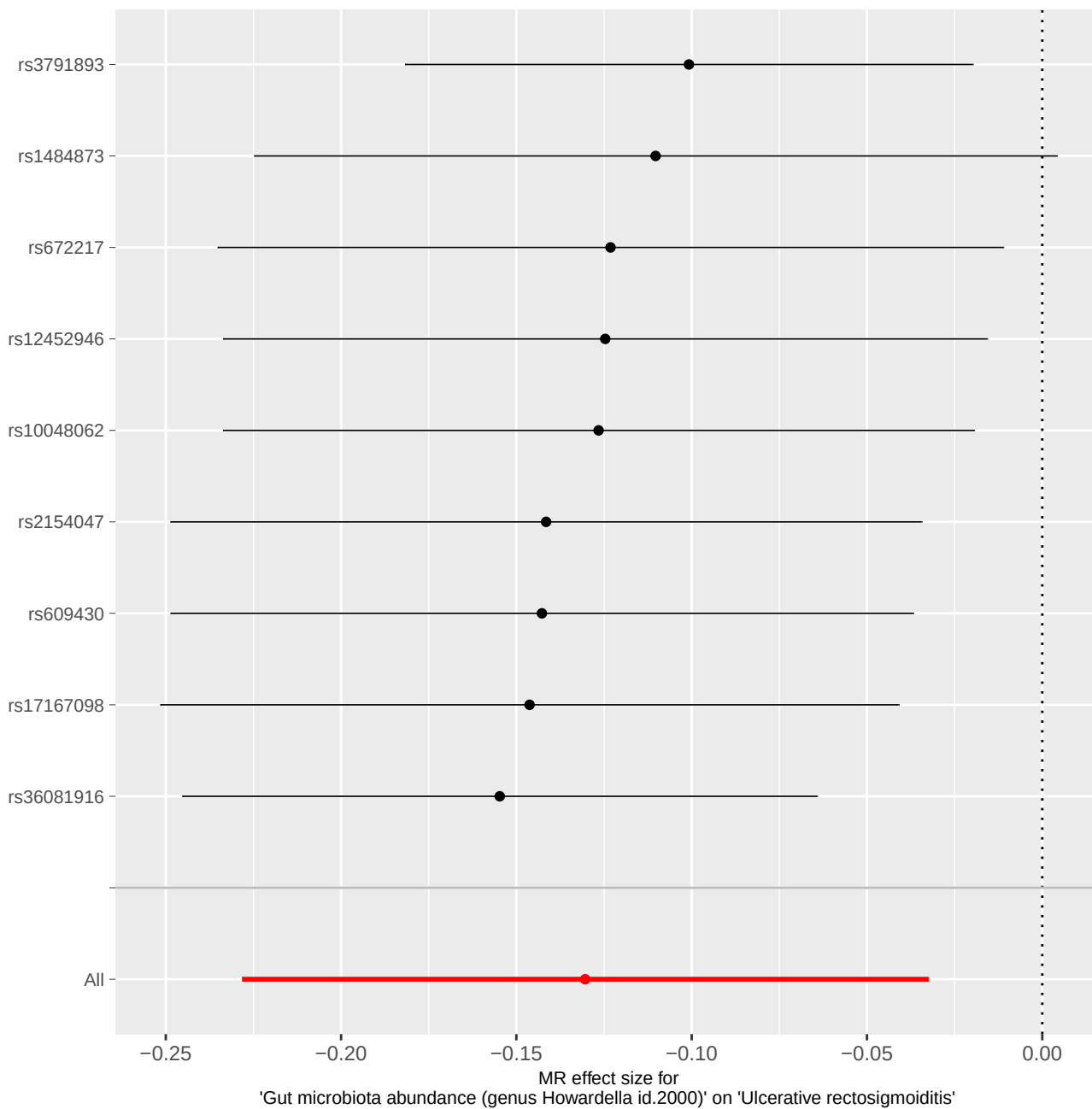
'Gut microbiota abundance (genus Fusicatenibacter id.11305)' on 'Ulcerative rectosigmoiditis'



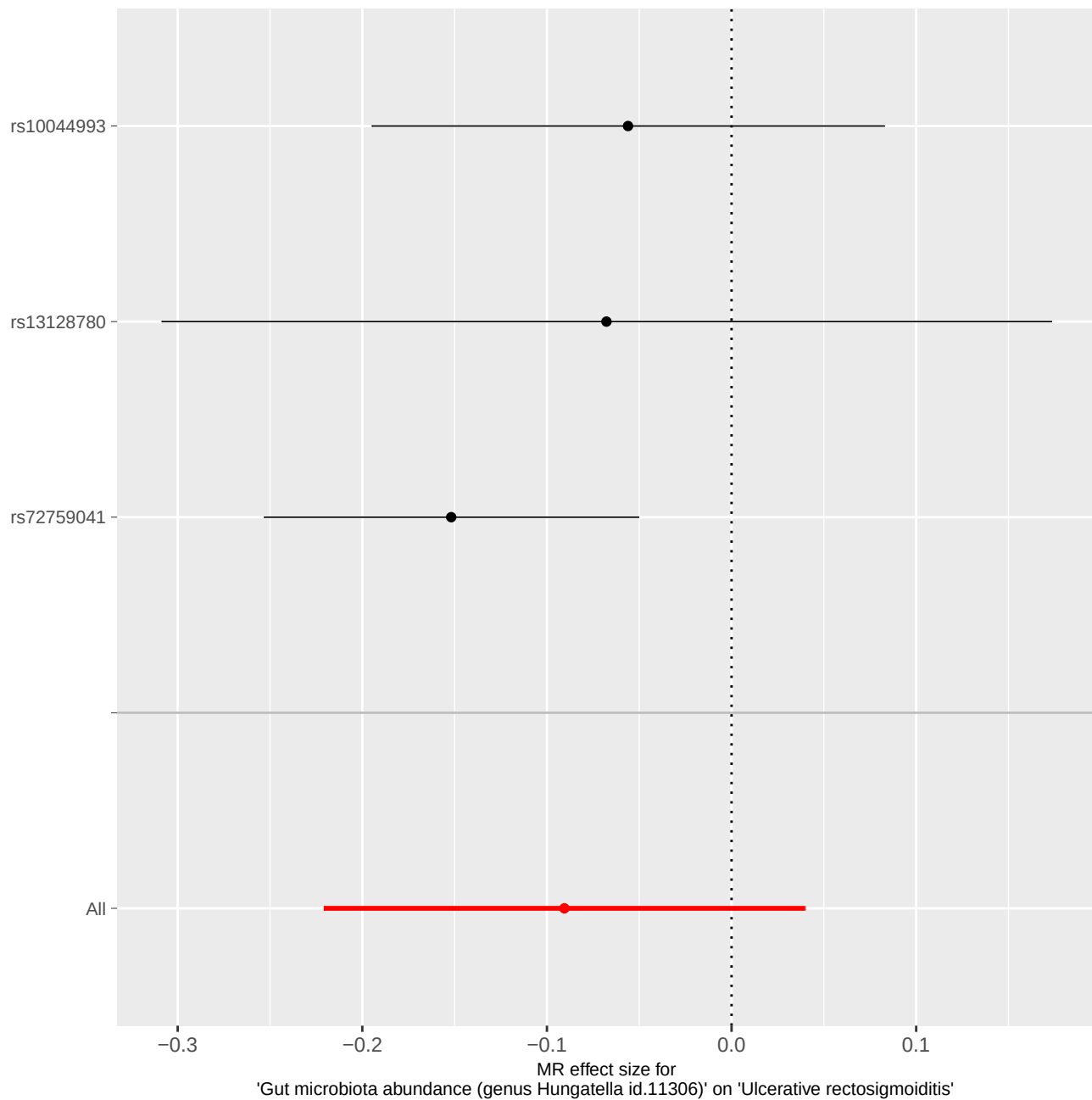


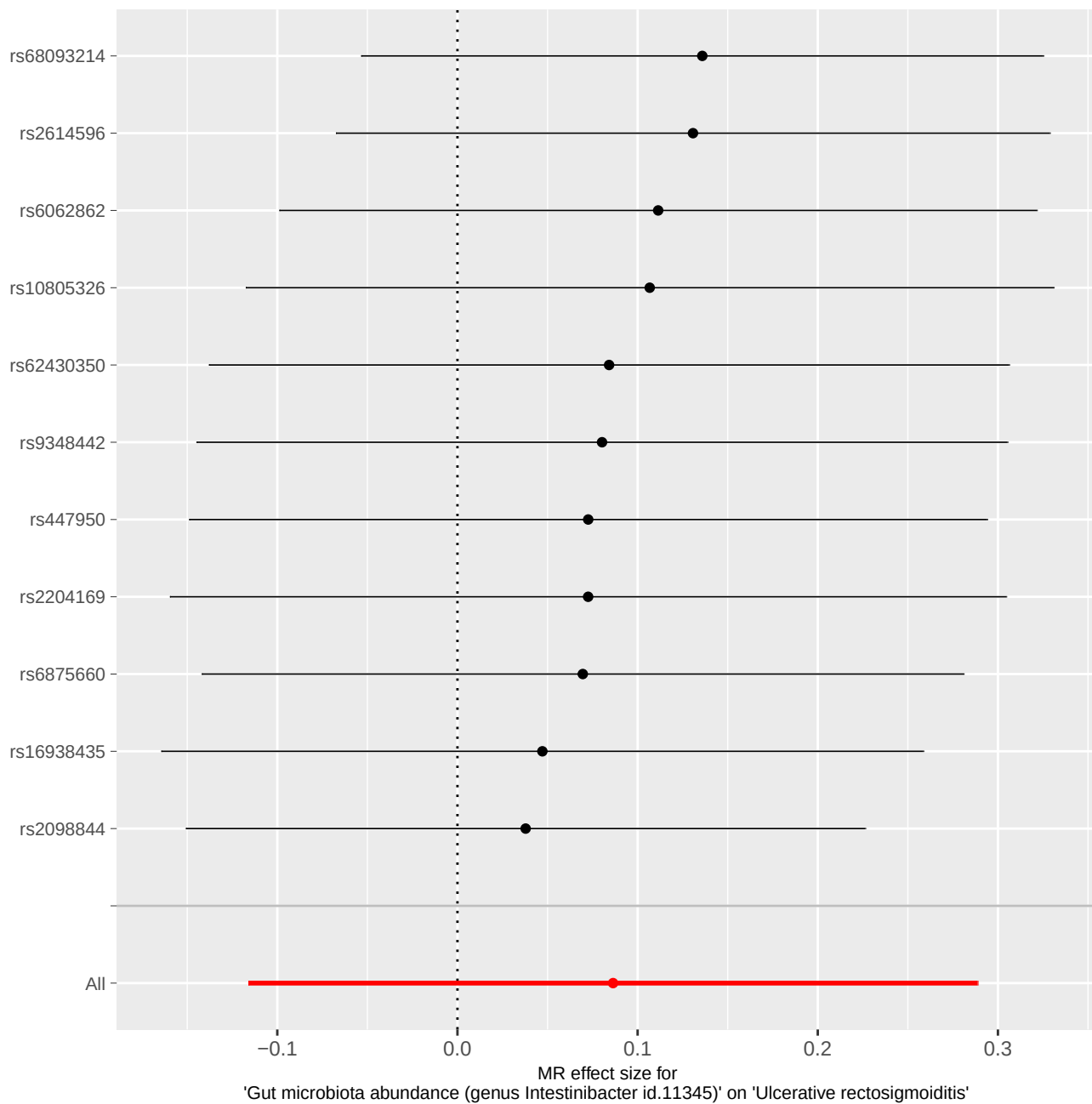


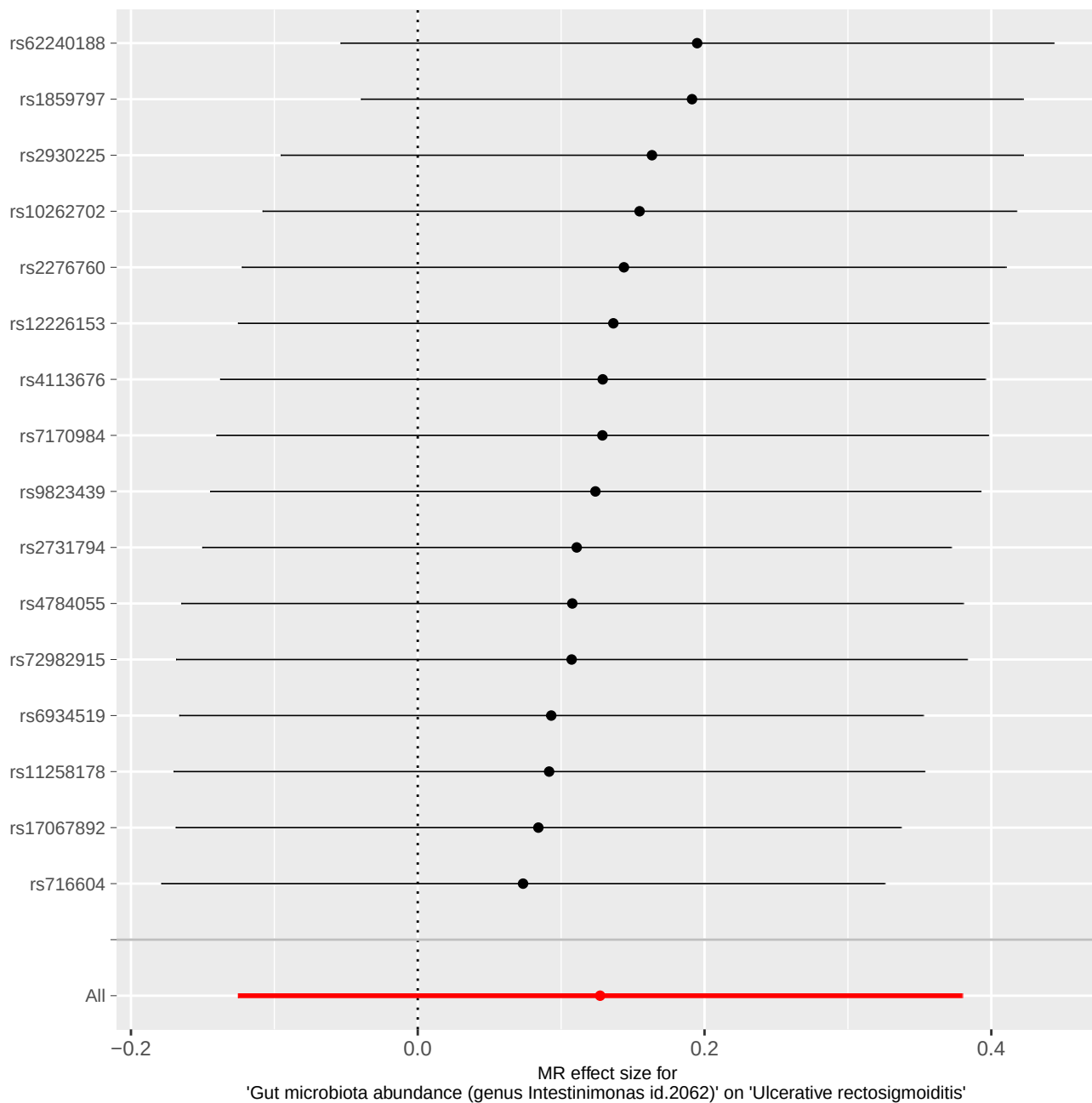




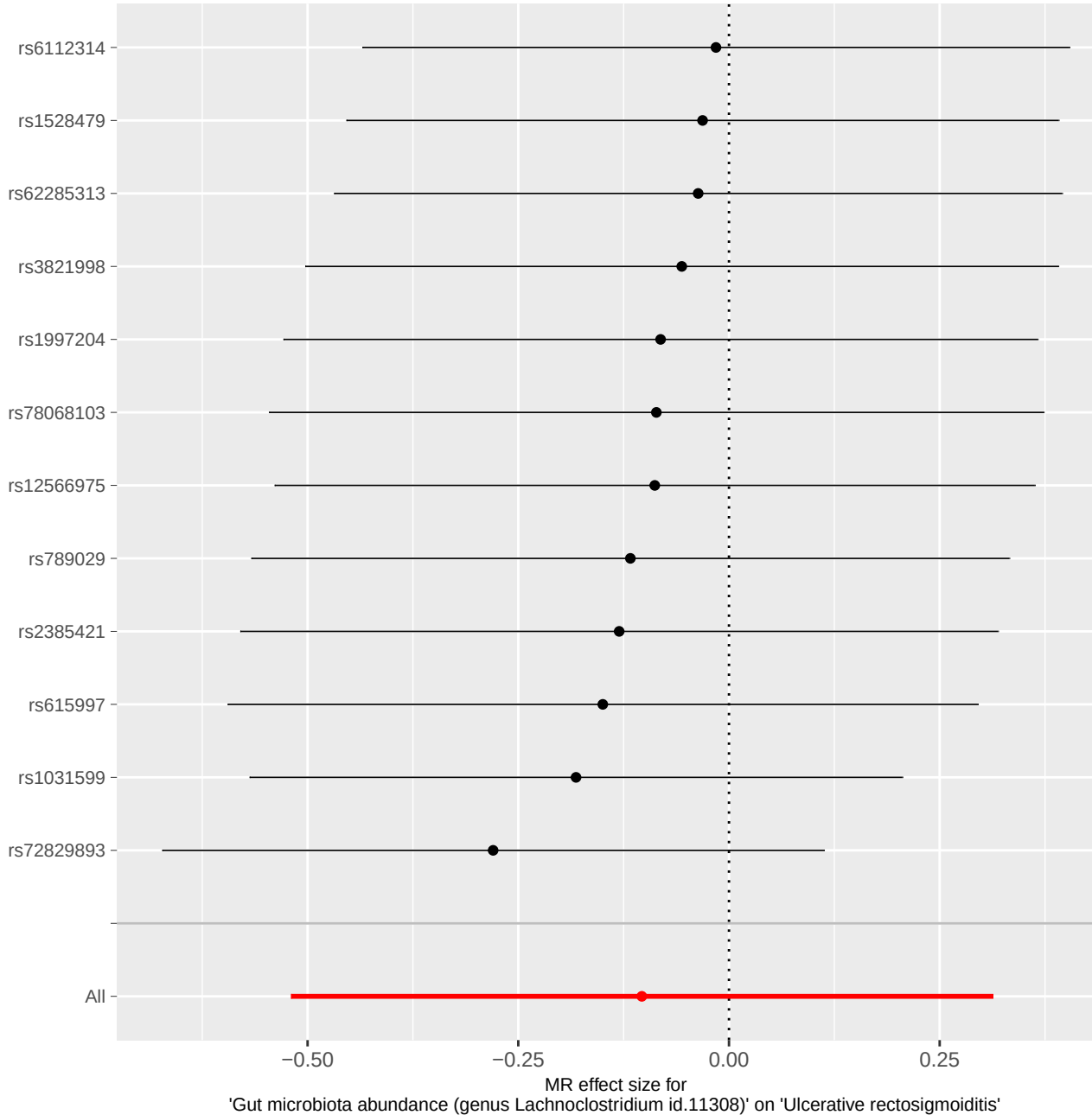
MR effect size for
'Gut microbiota abundance (genus Howardella id.2000)' on 'Ulcerative rectosigmoiditis'

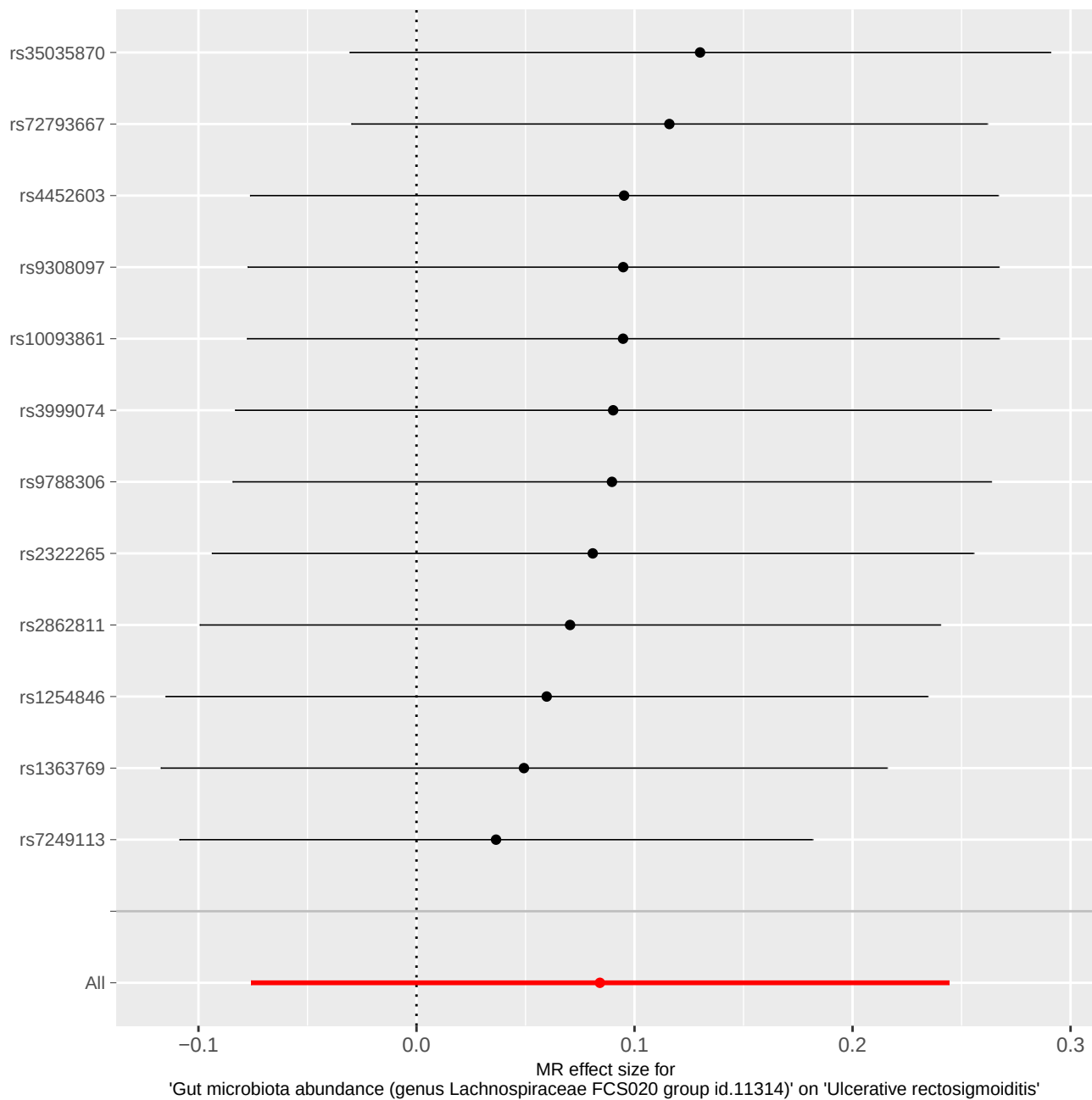


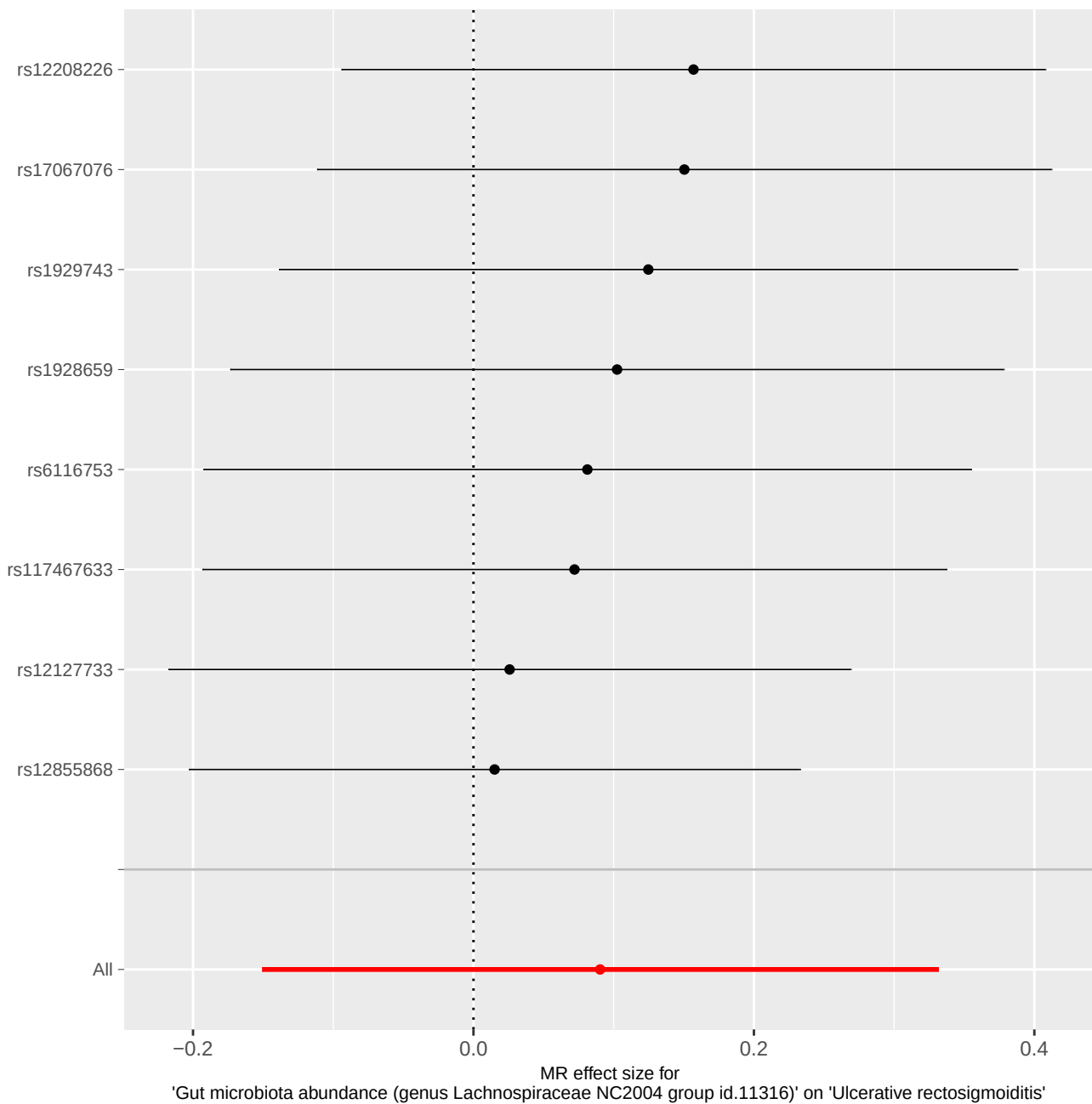


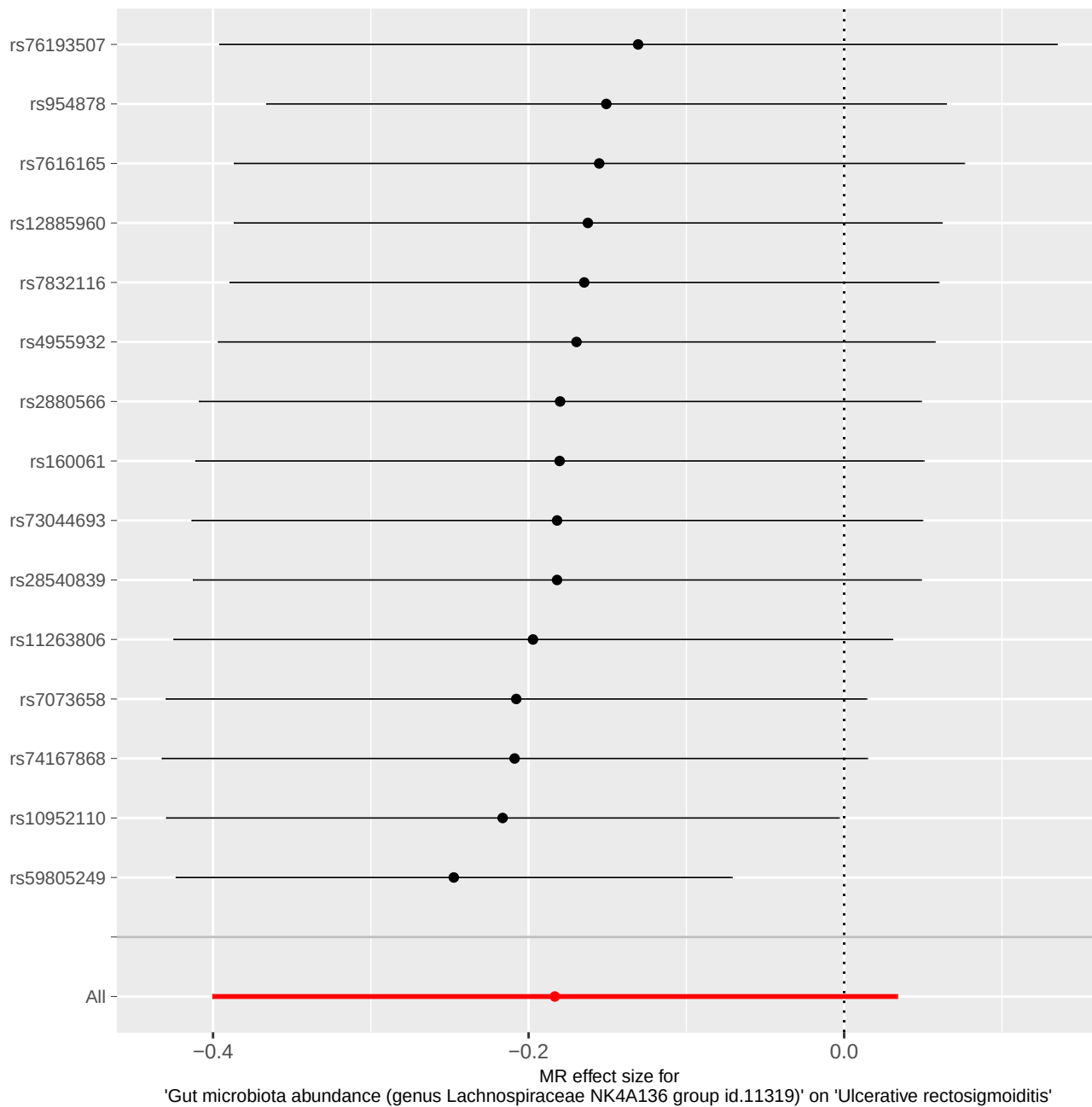


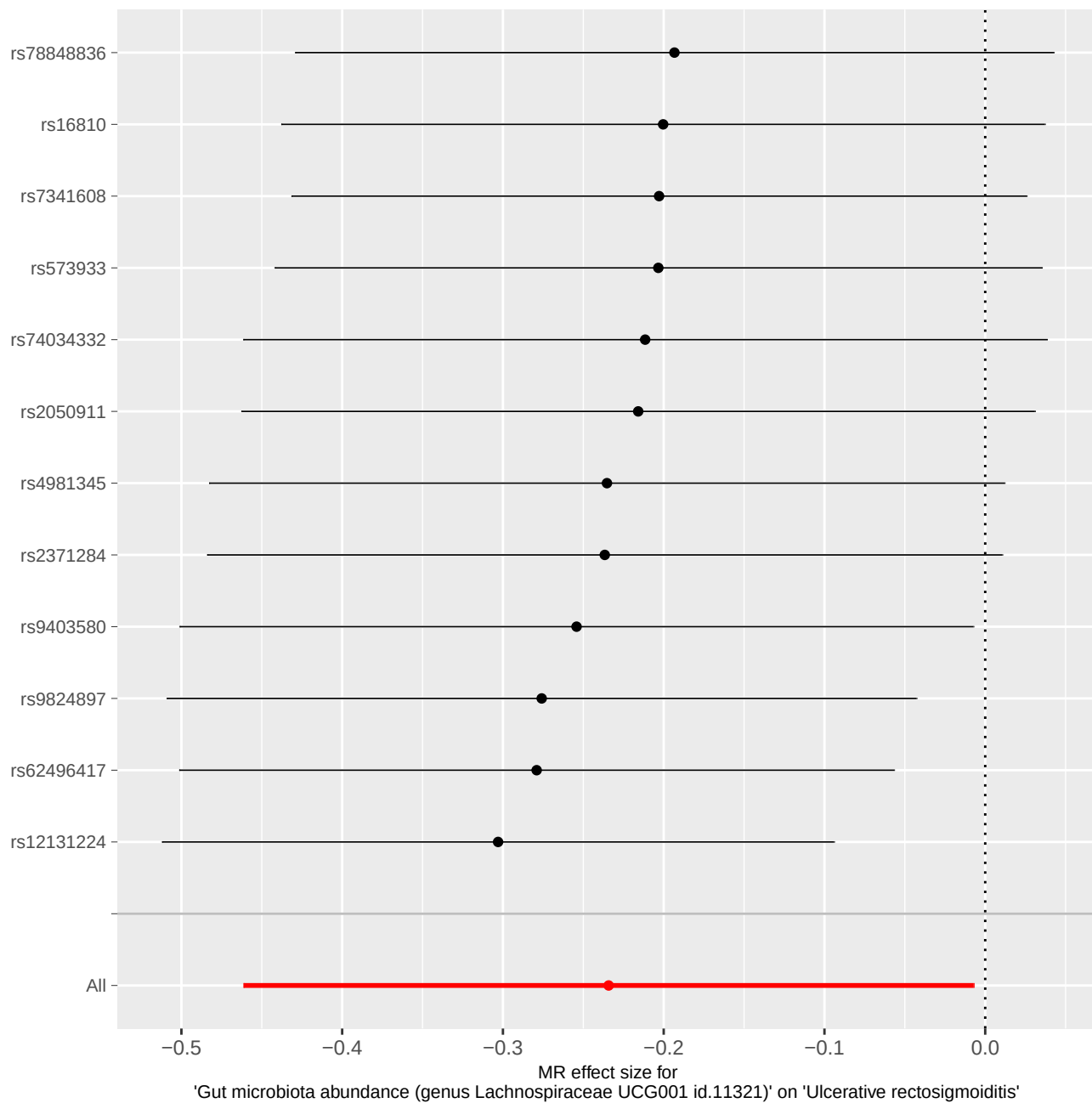
Batch 1594 : Gut microbiota abundance (genus Lachnoclostridium id.11308) on Ulcerative rectosigmoiditis

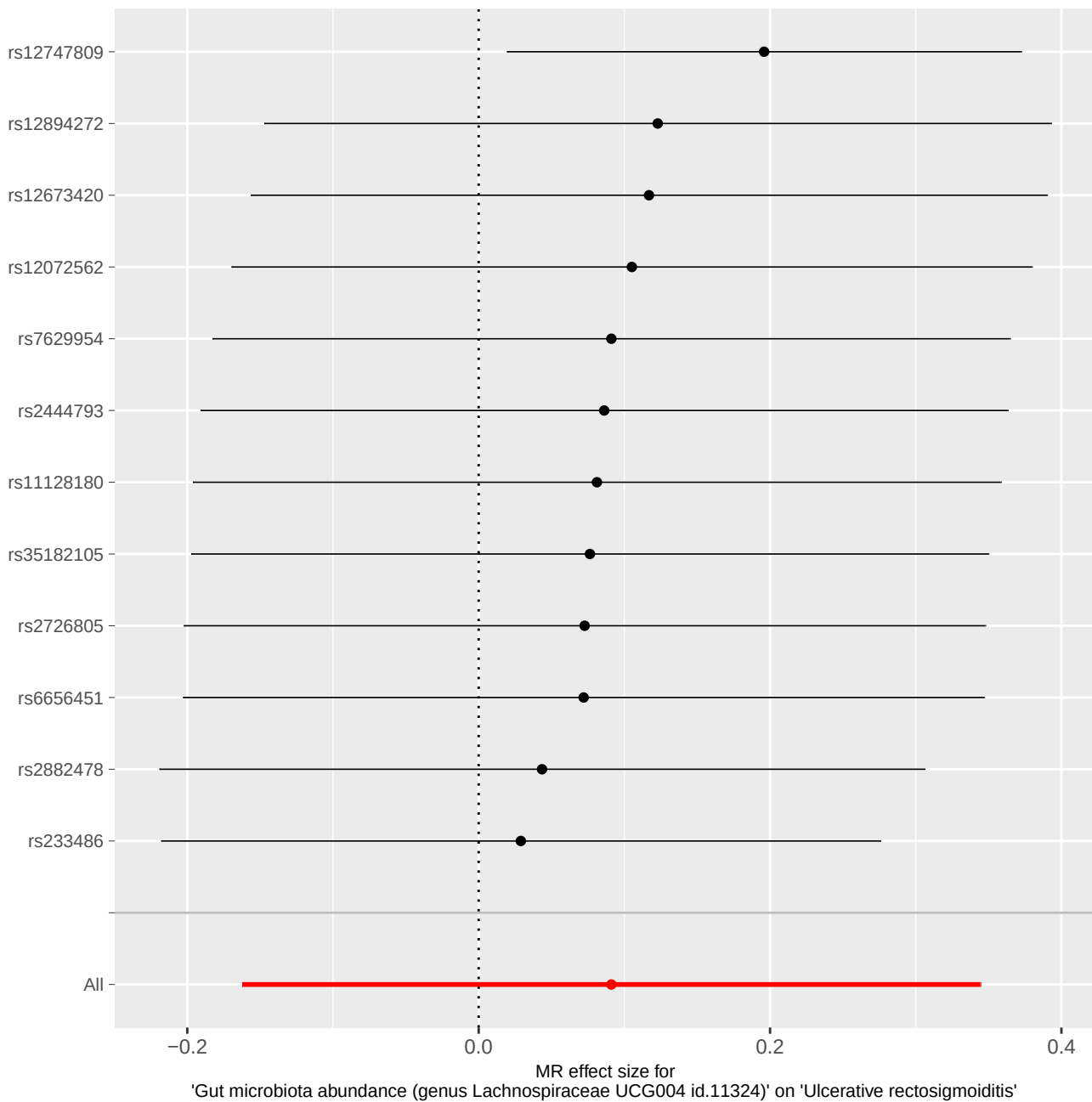


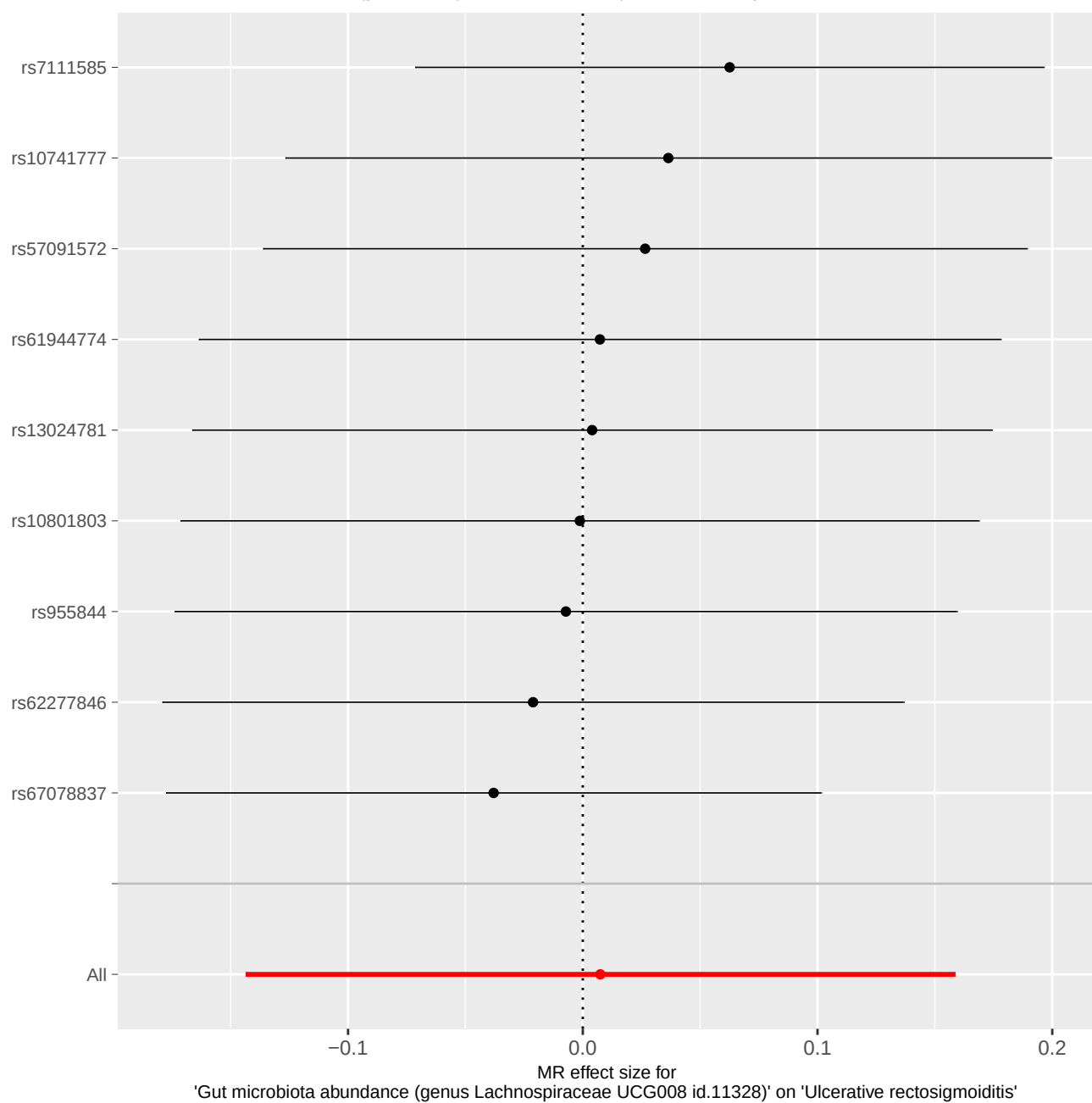


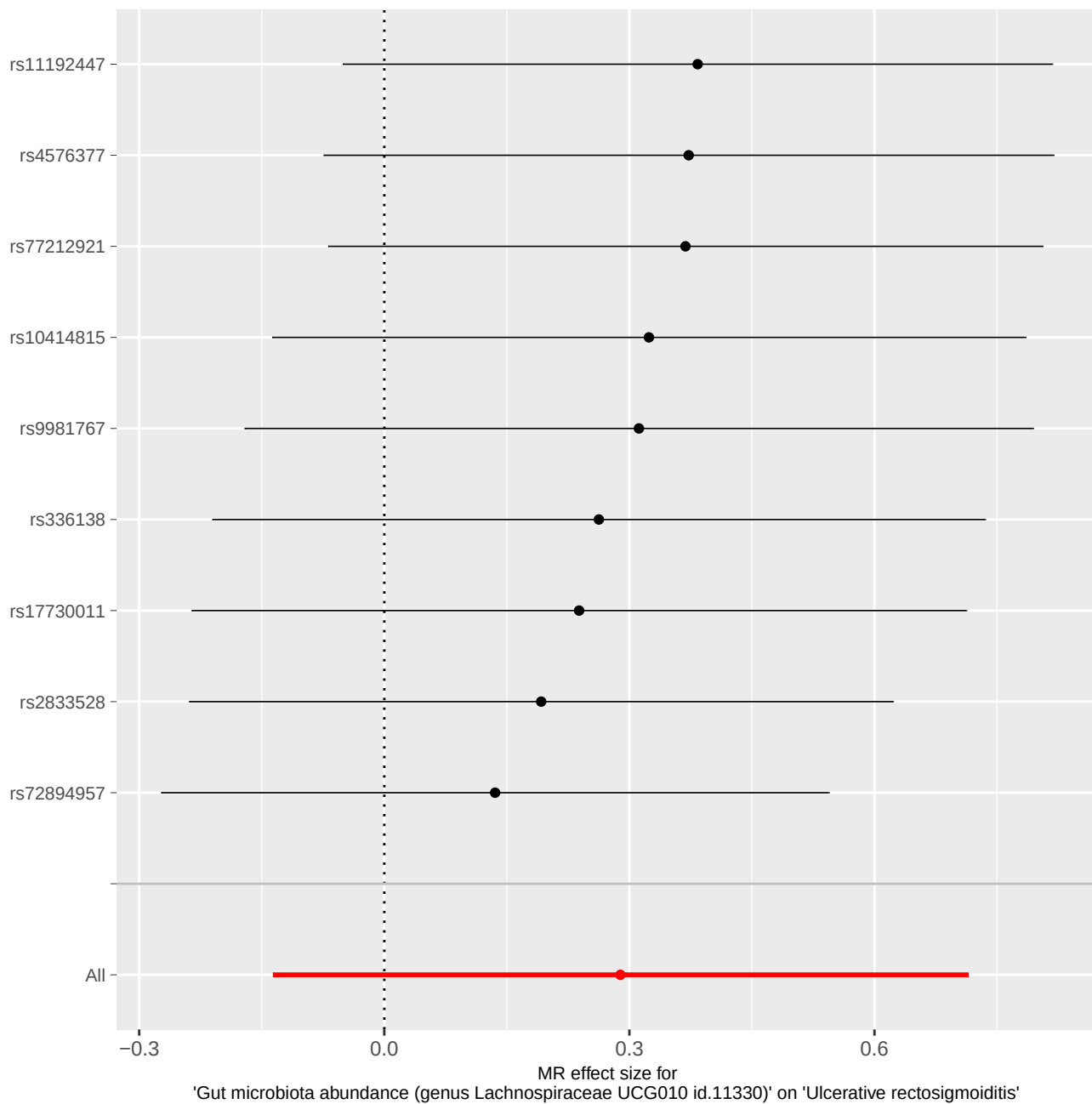


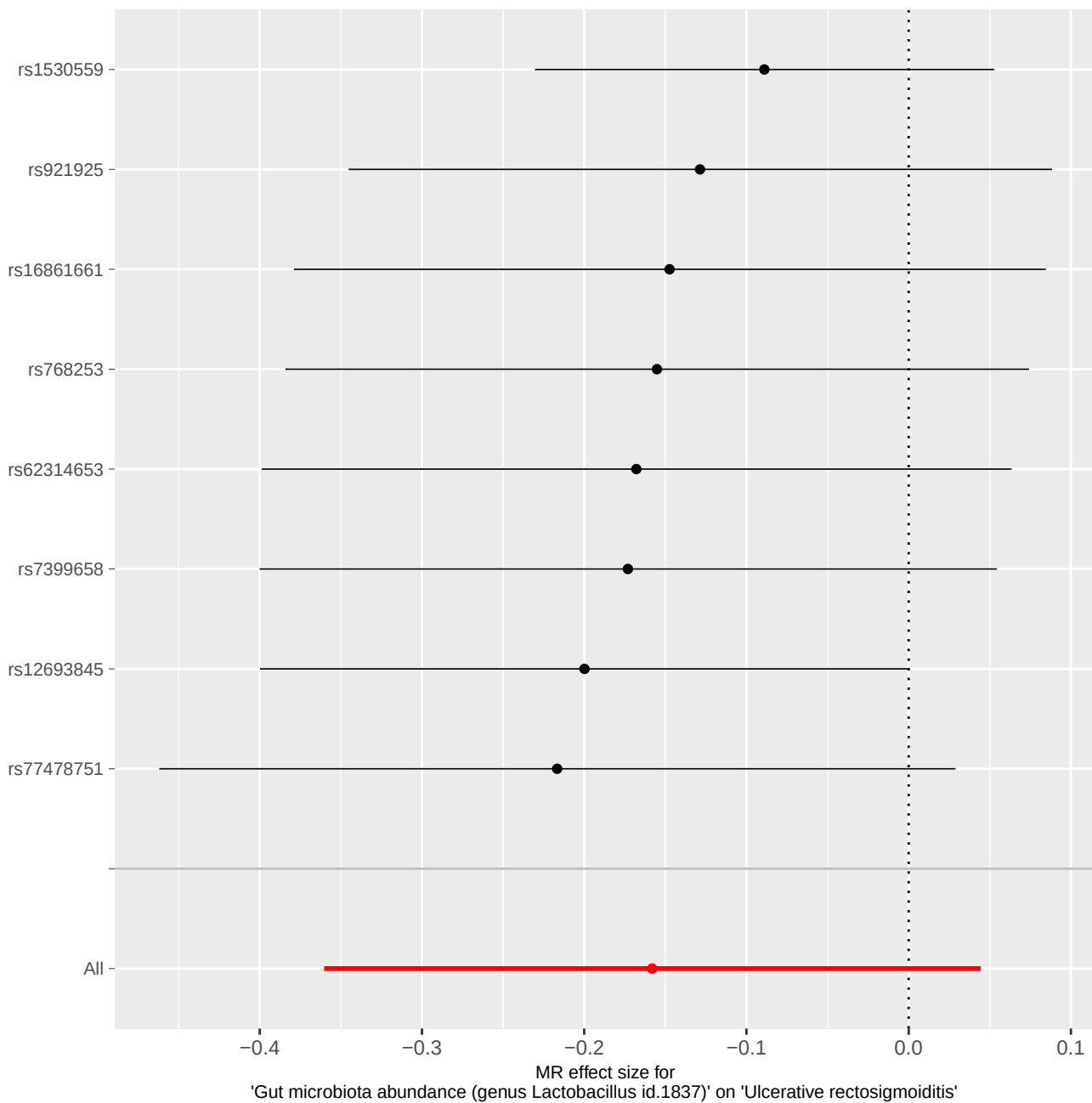


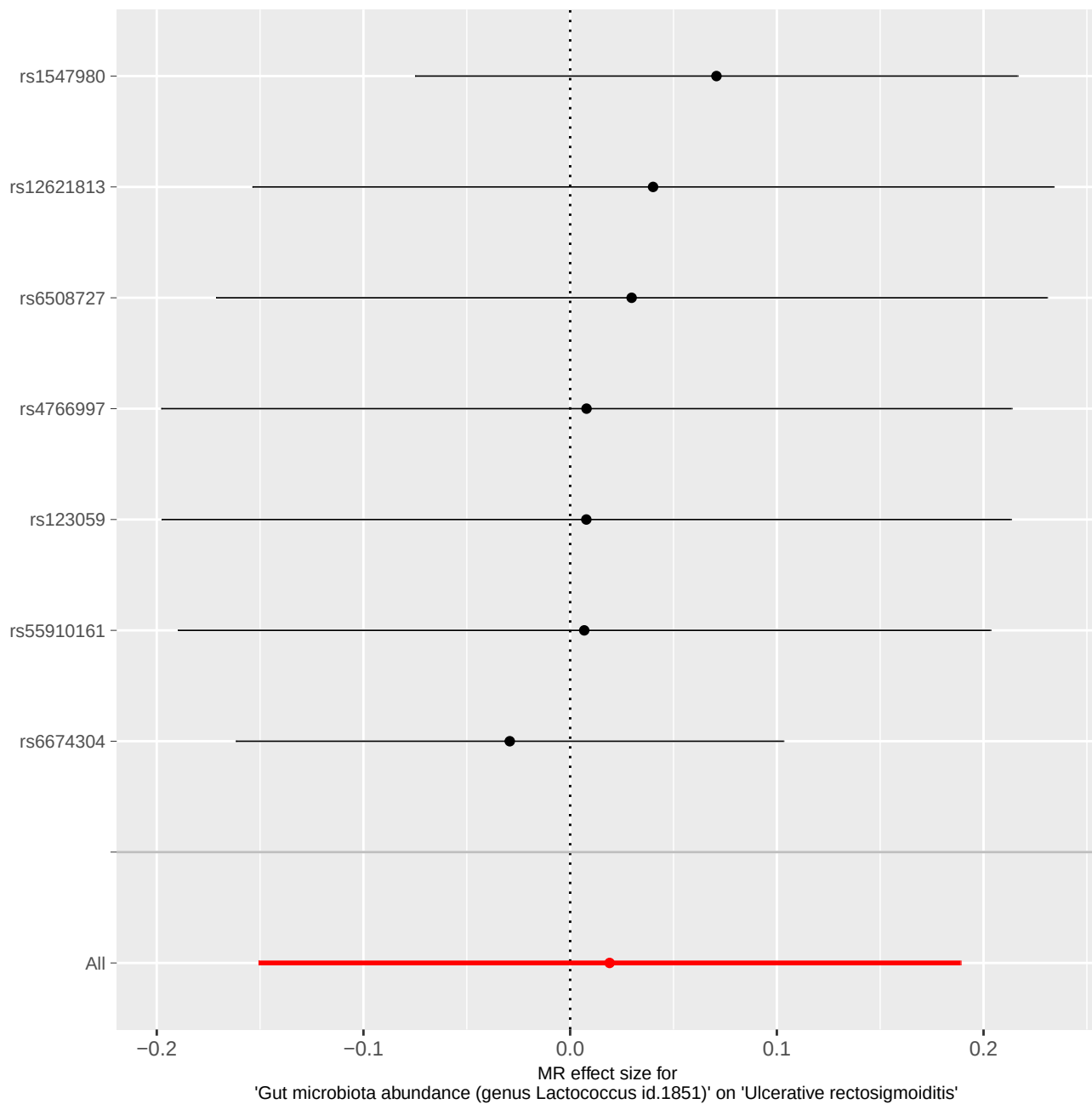


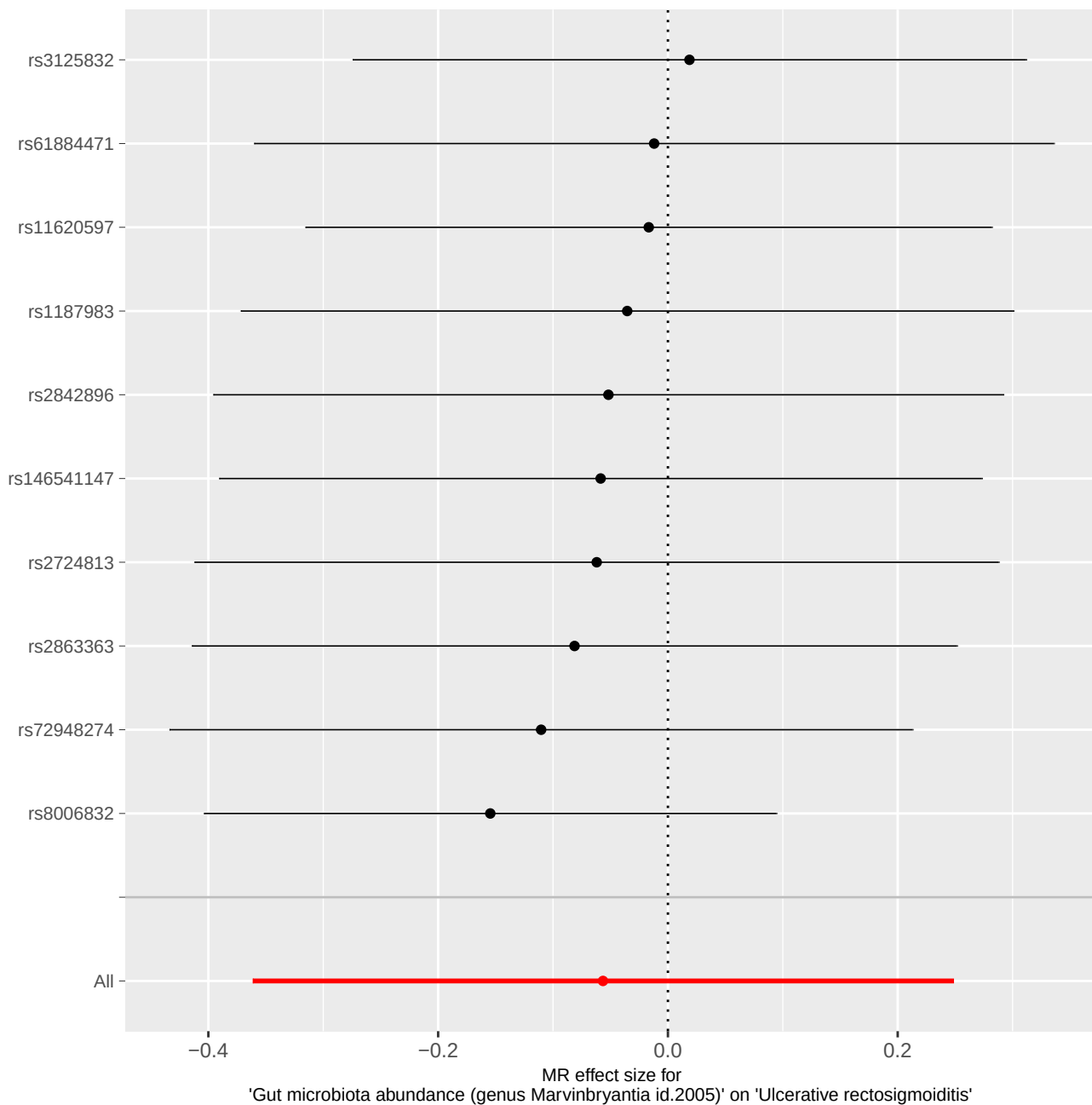


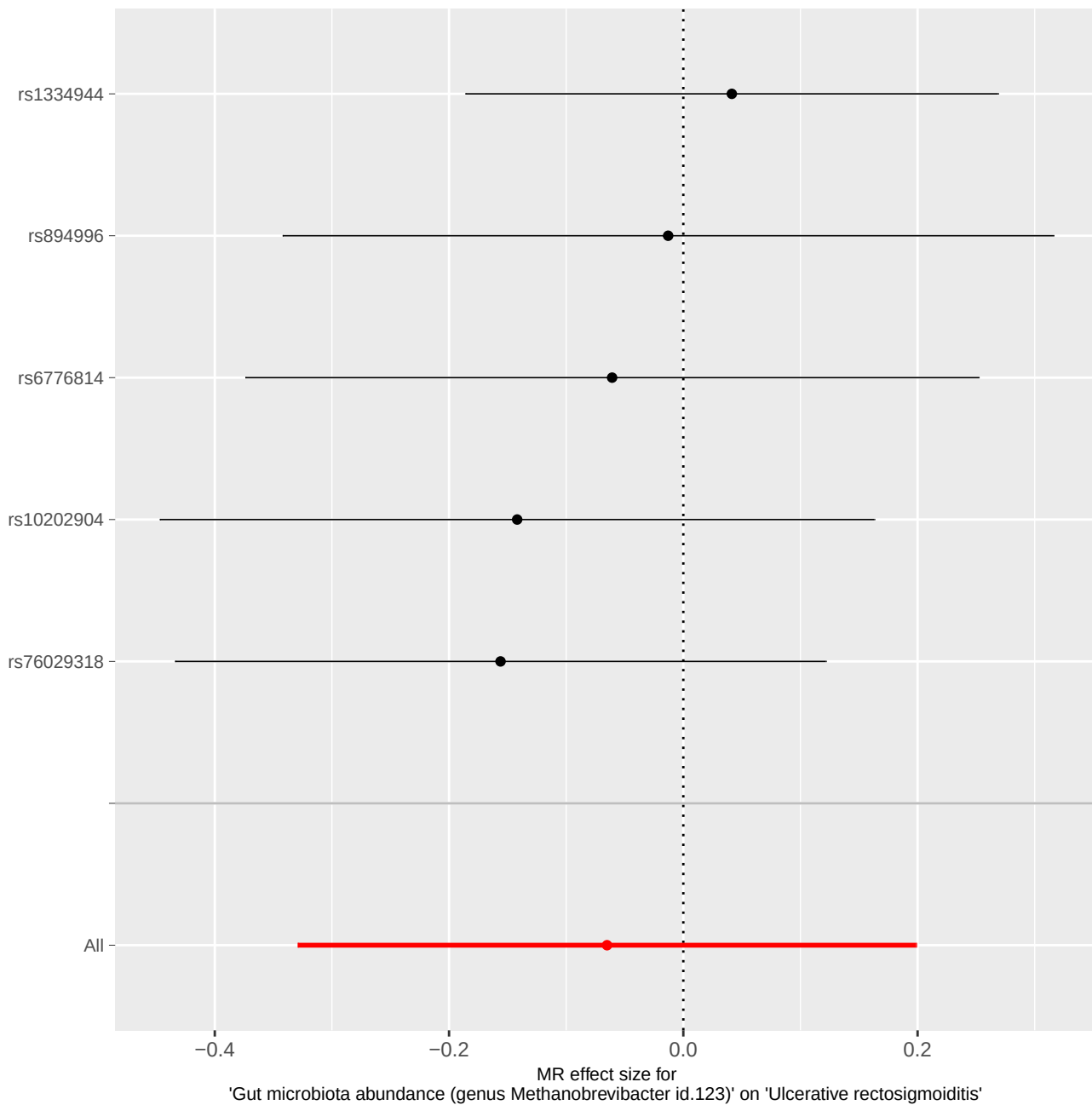


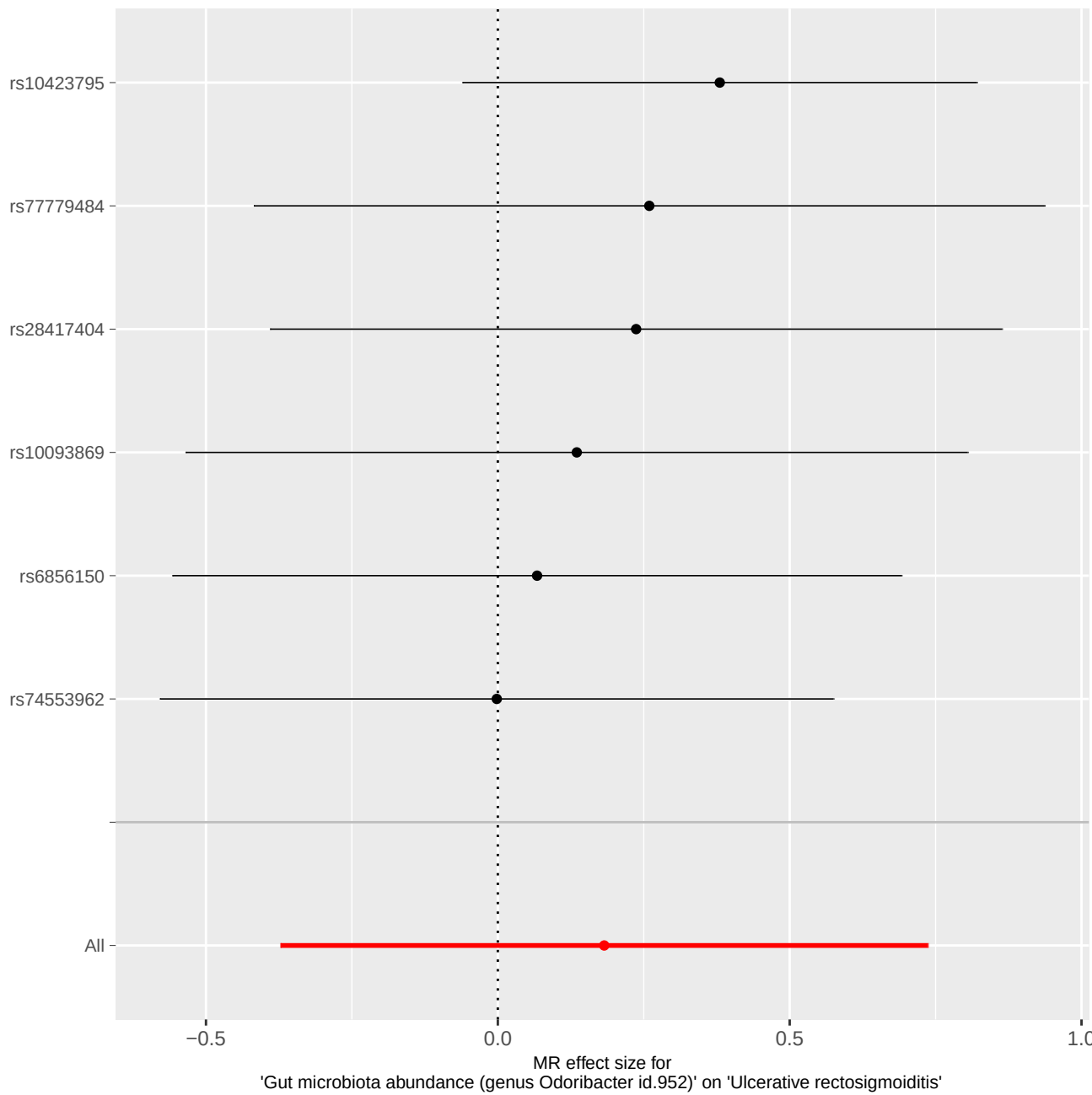


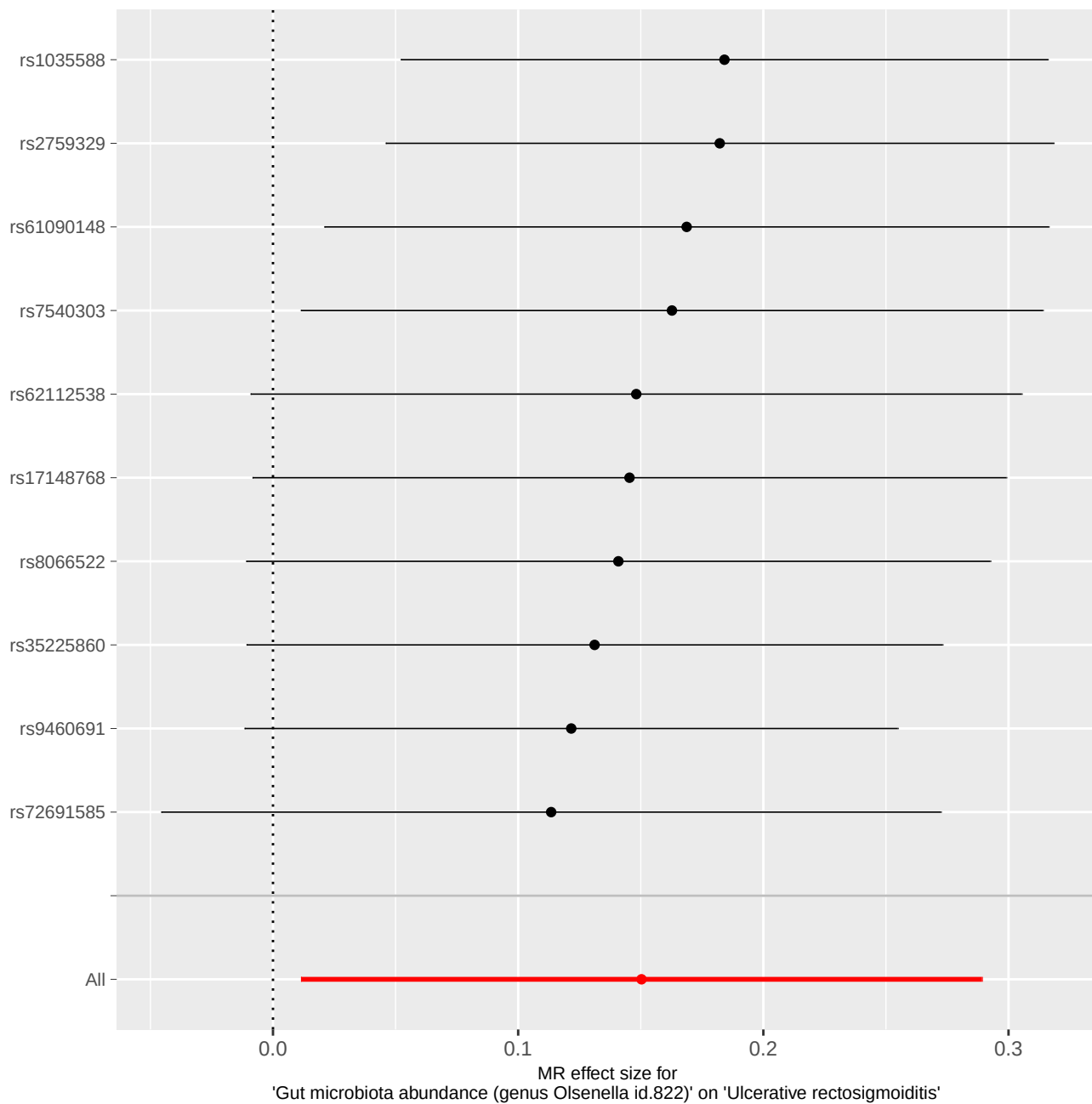


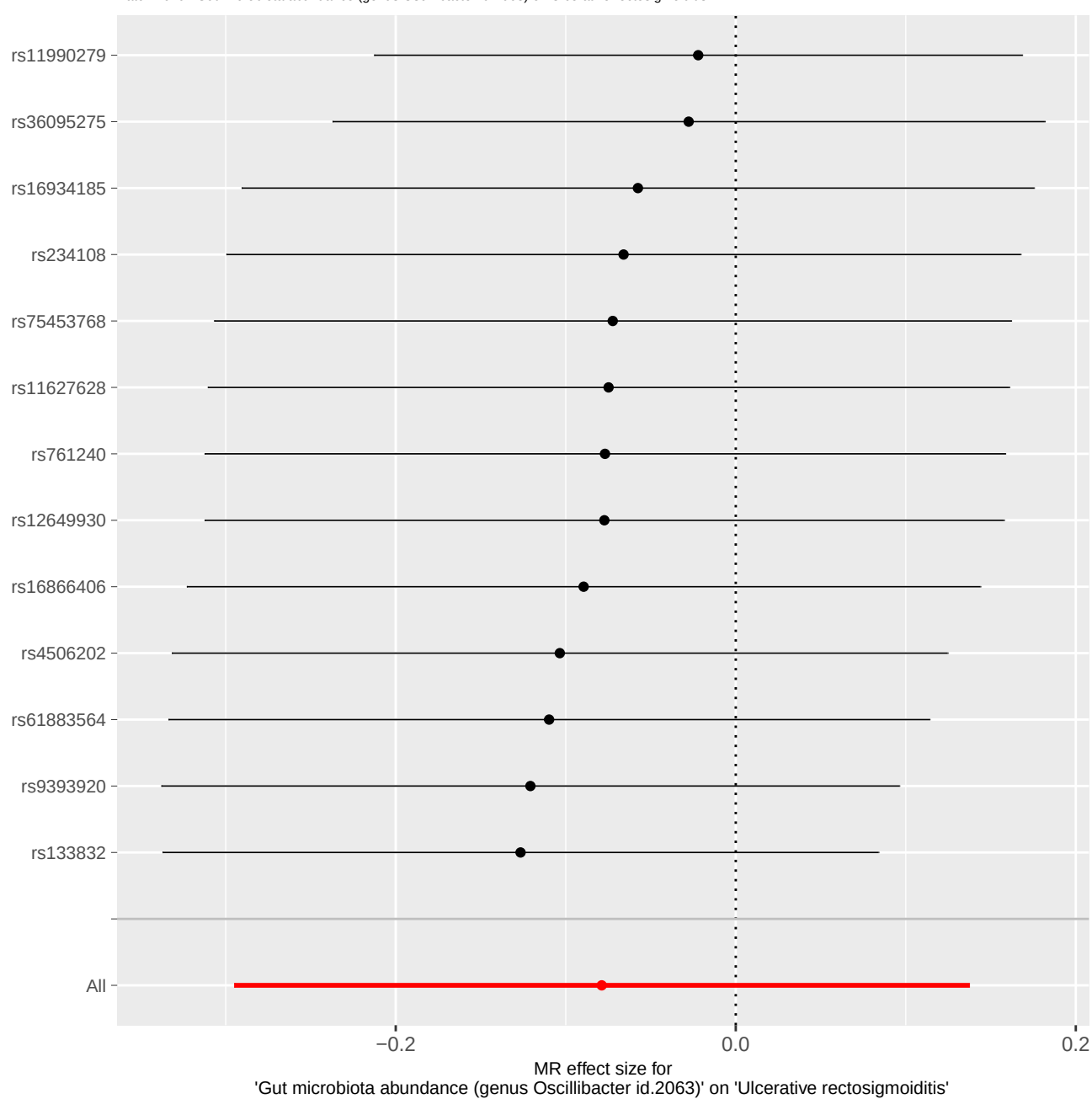




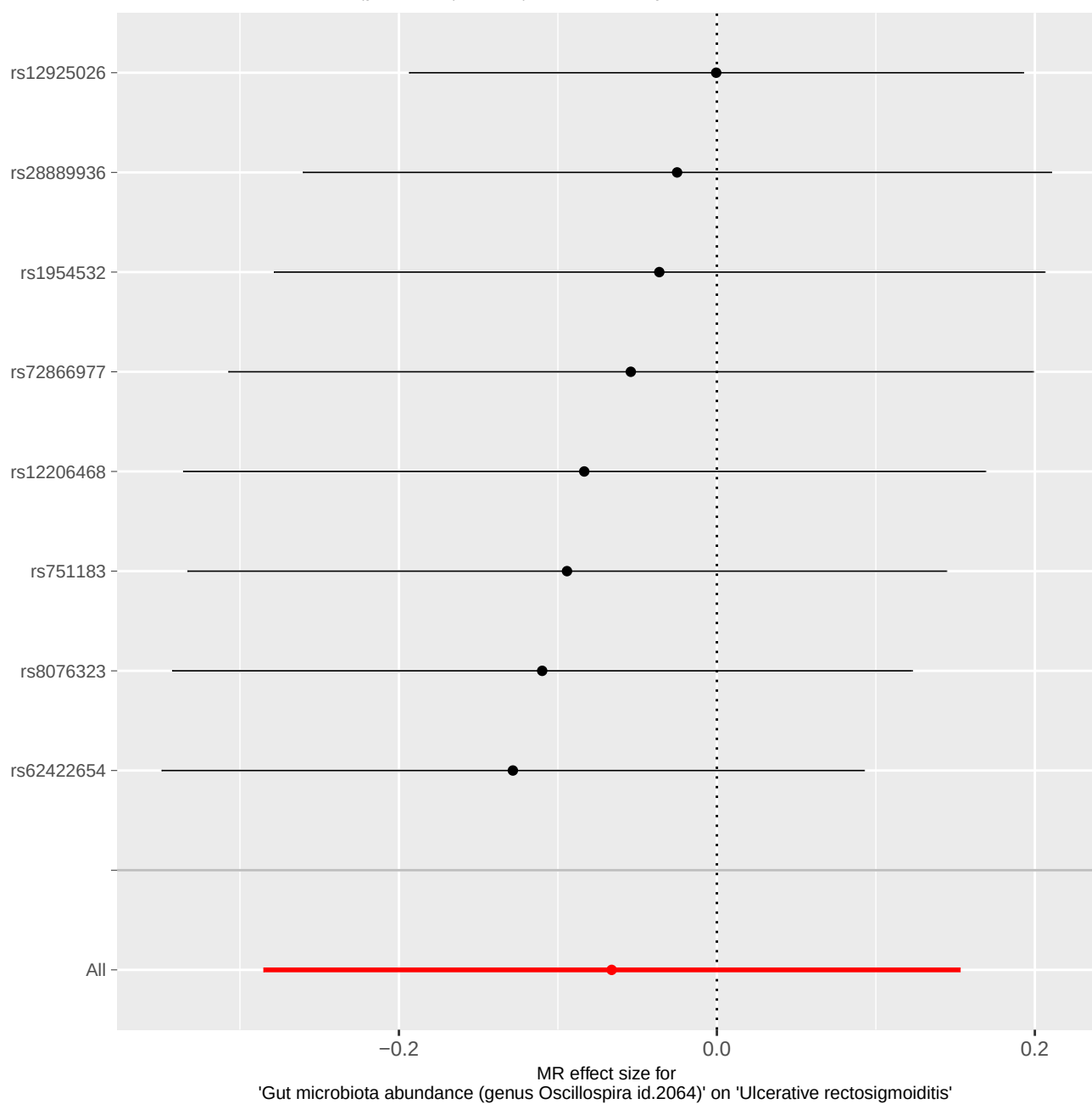


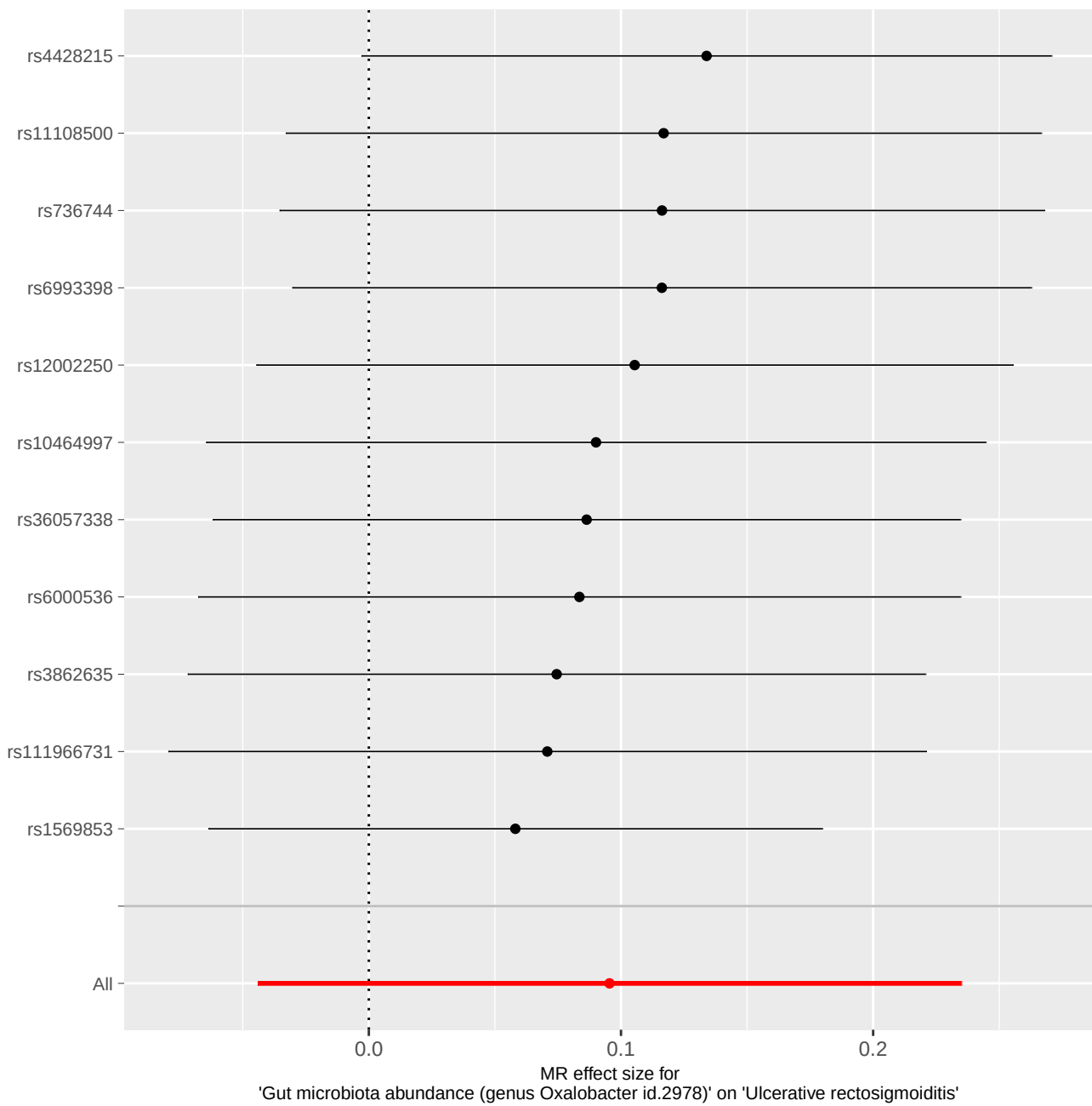


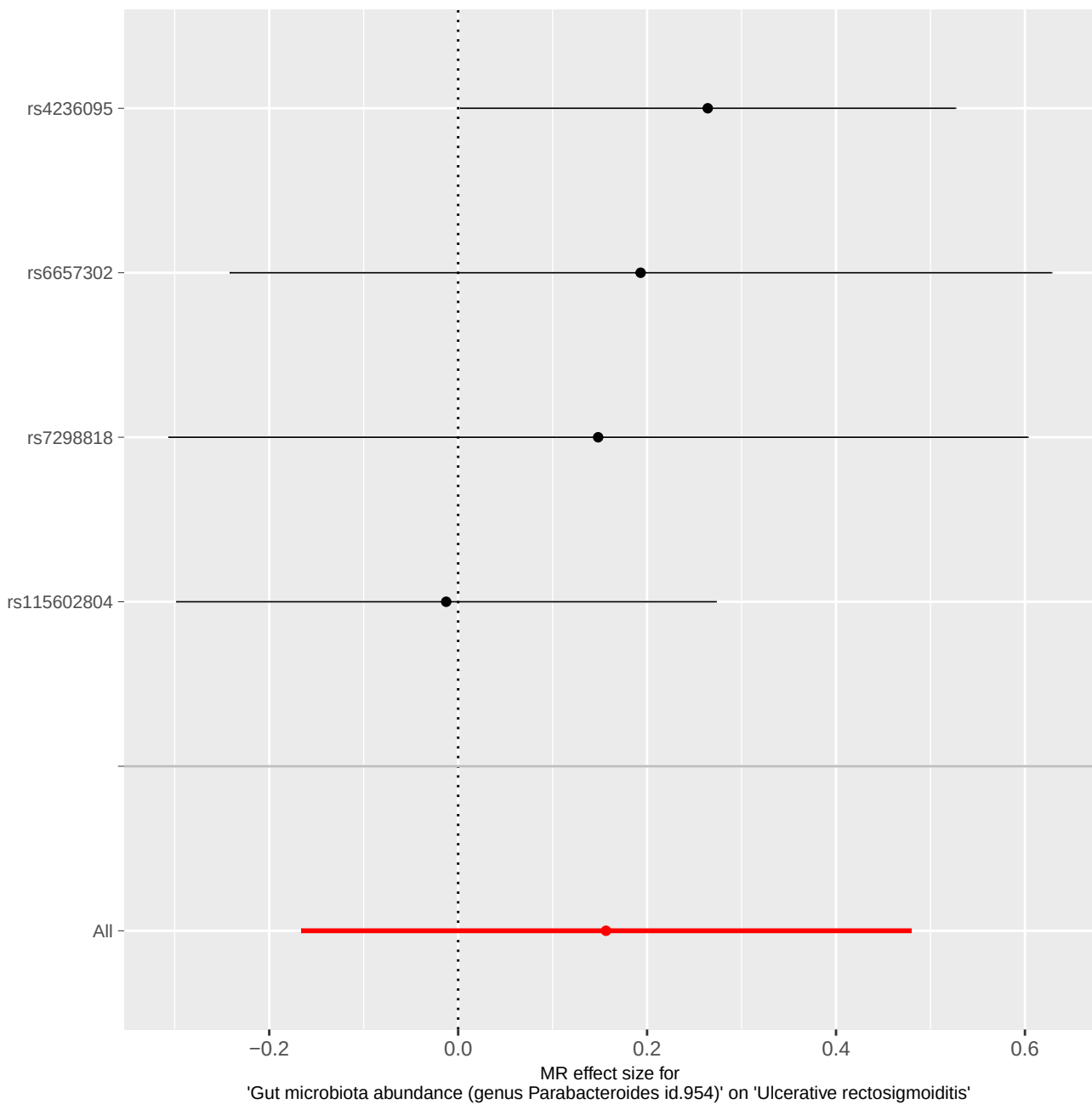


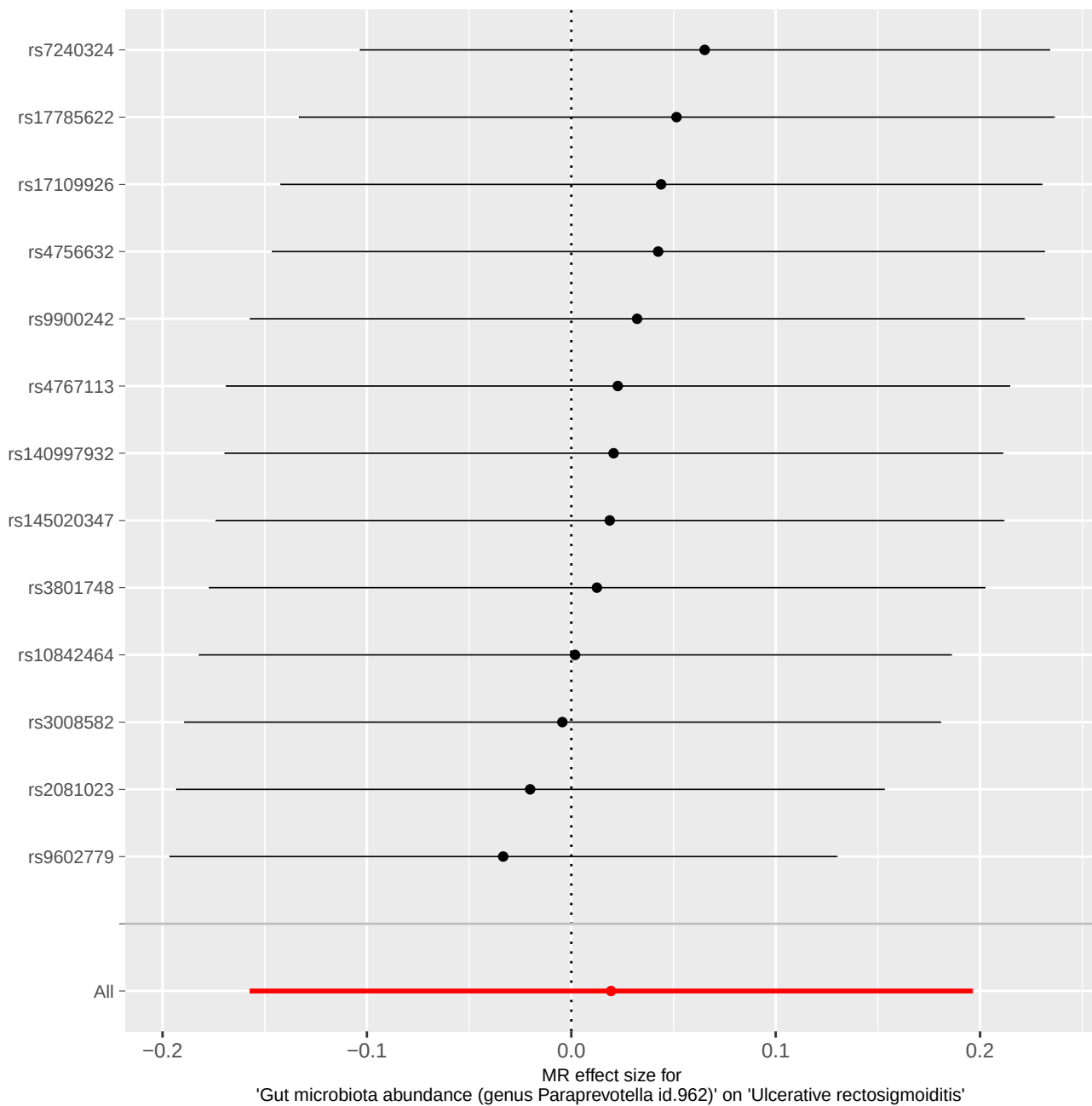


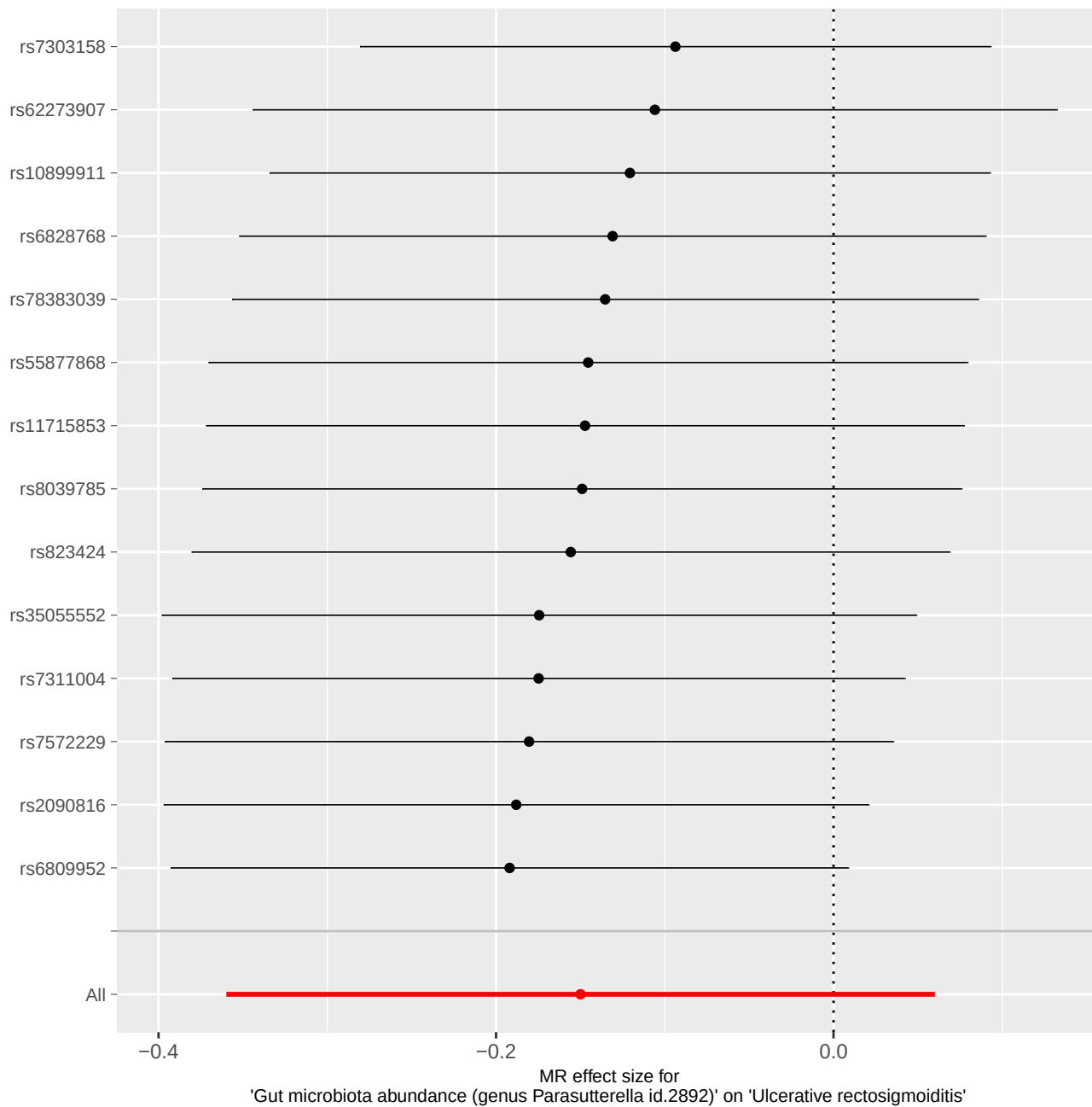
MR effect size for
'Gut microbiota abundance (genus Oscillibacter id.2063) on 'Ulcerative rectosigmoiditis'

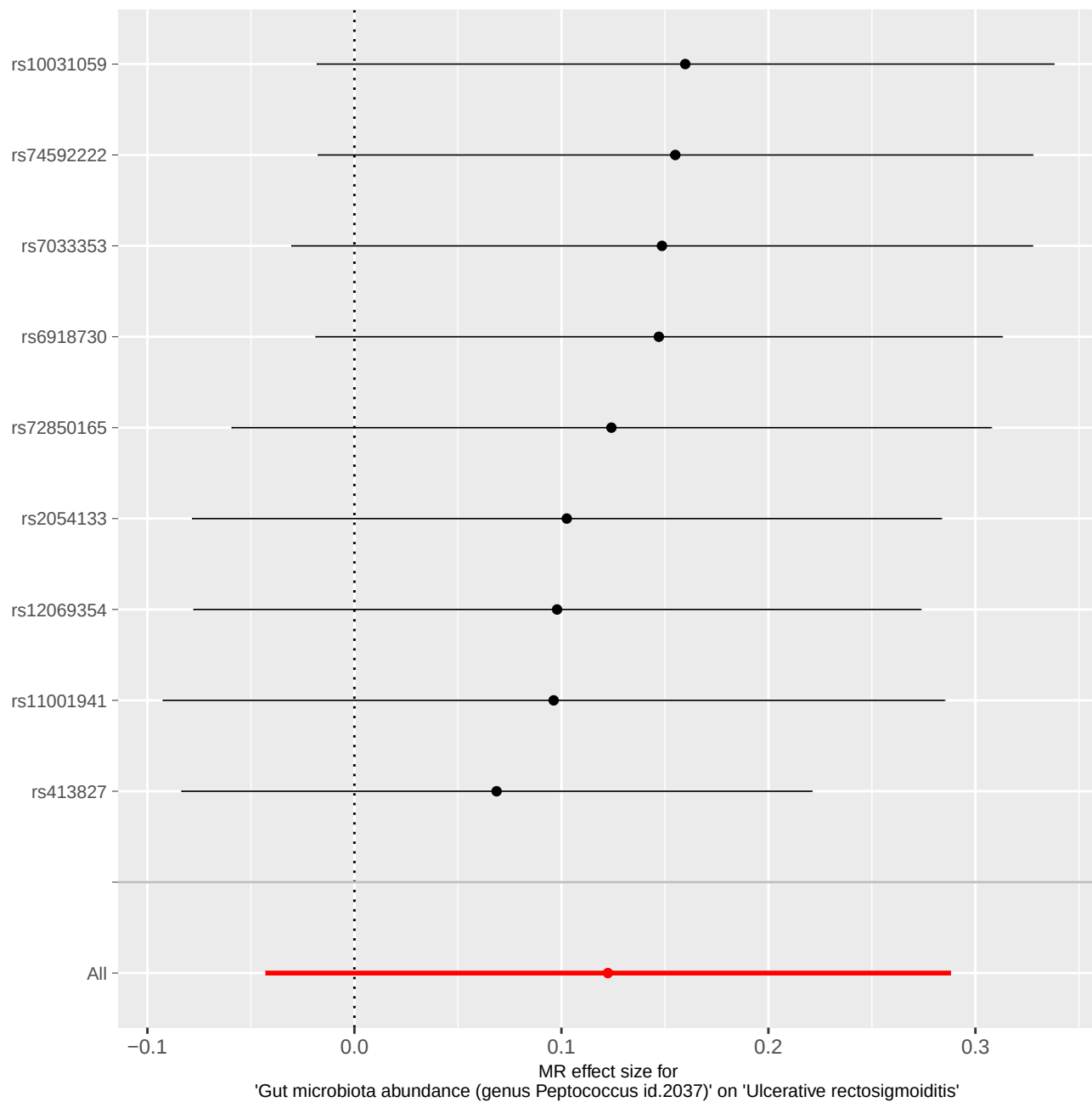


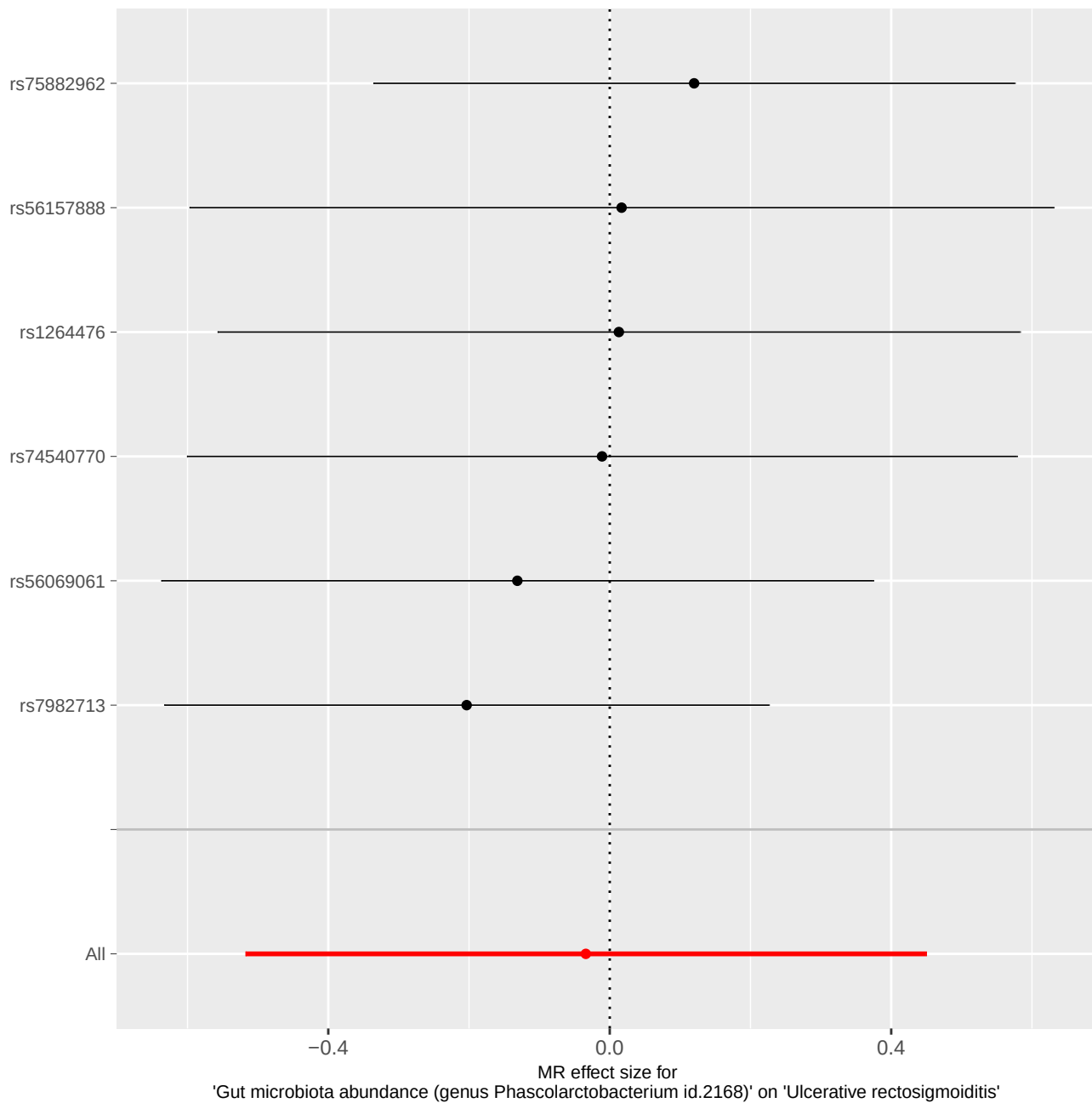


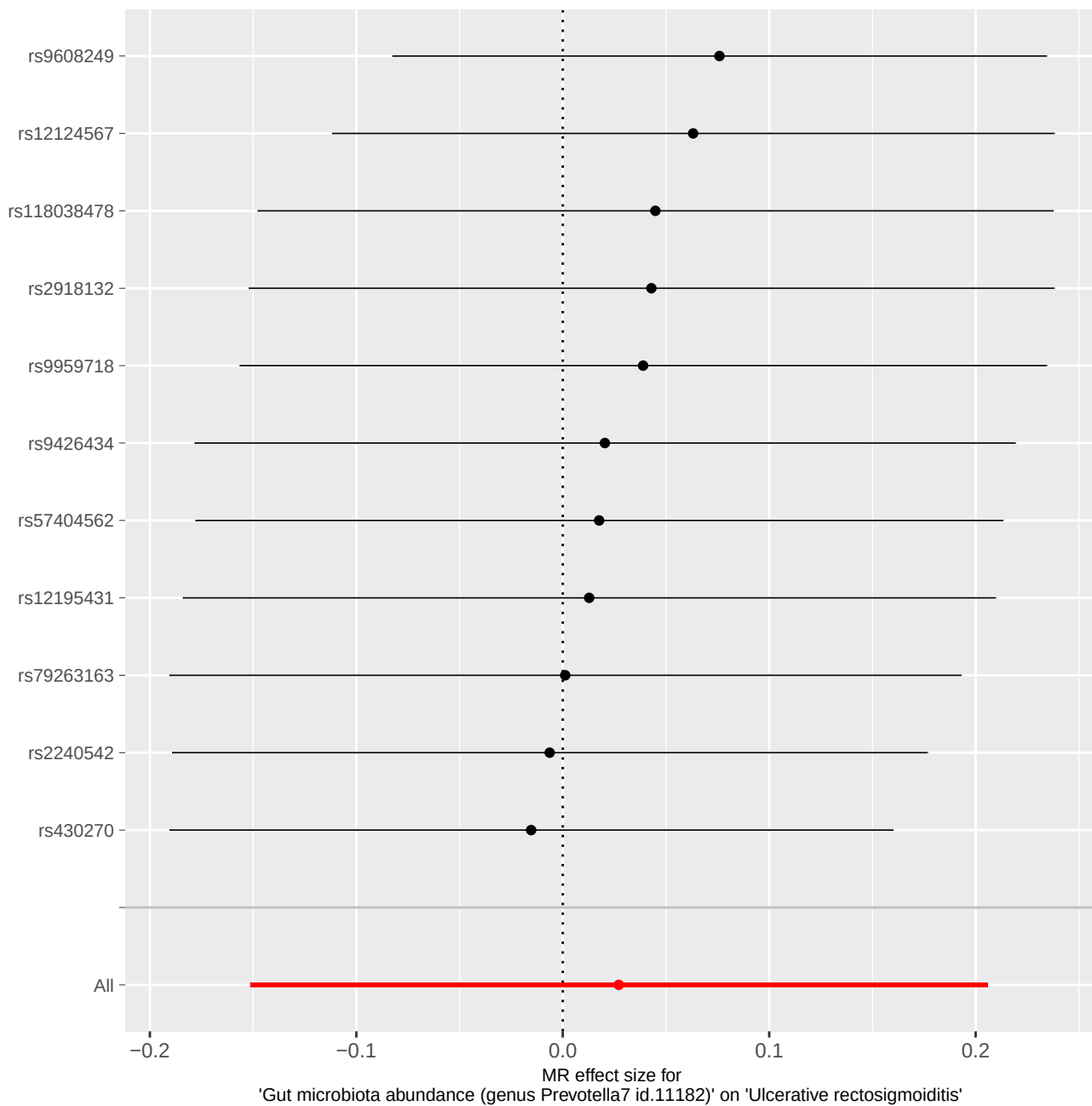


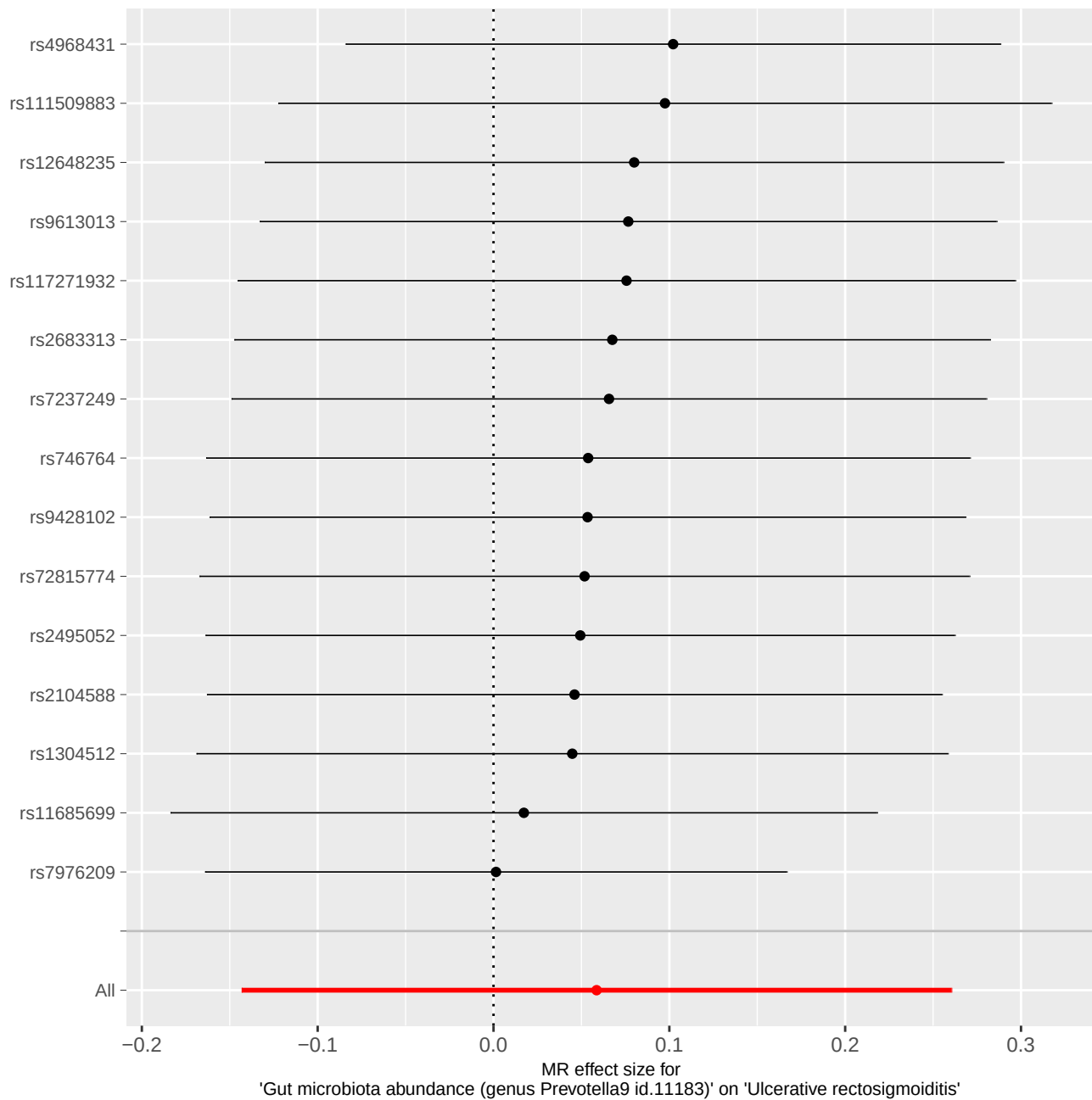


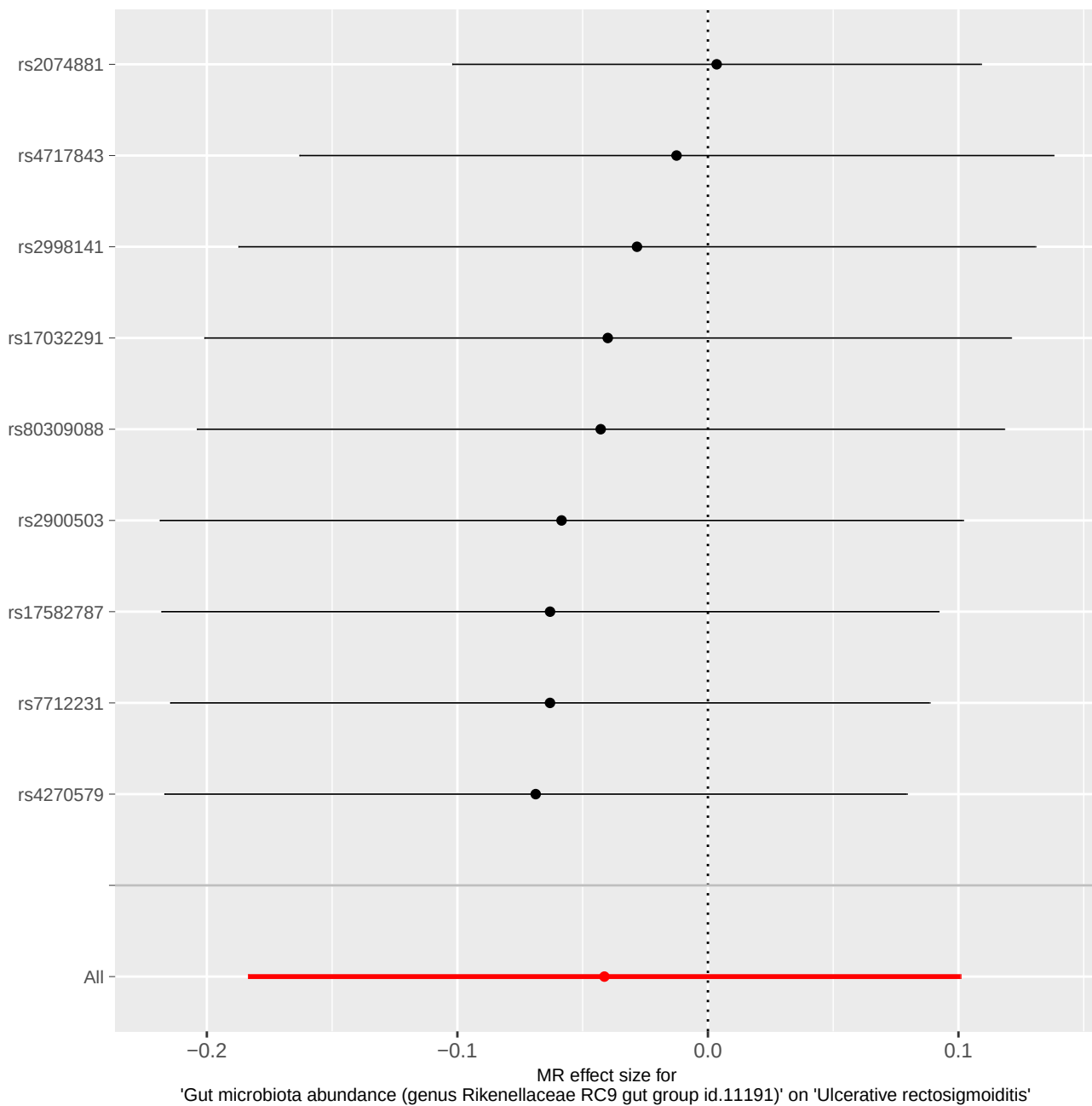


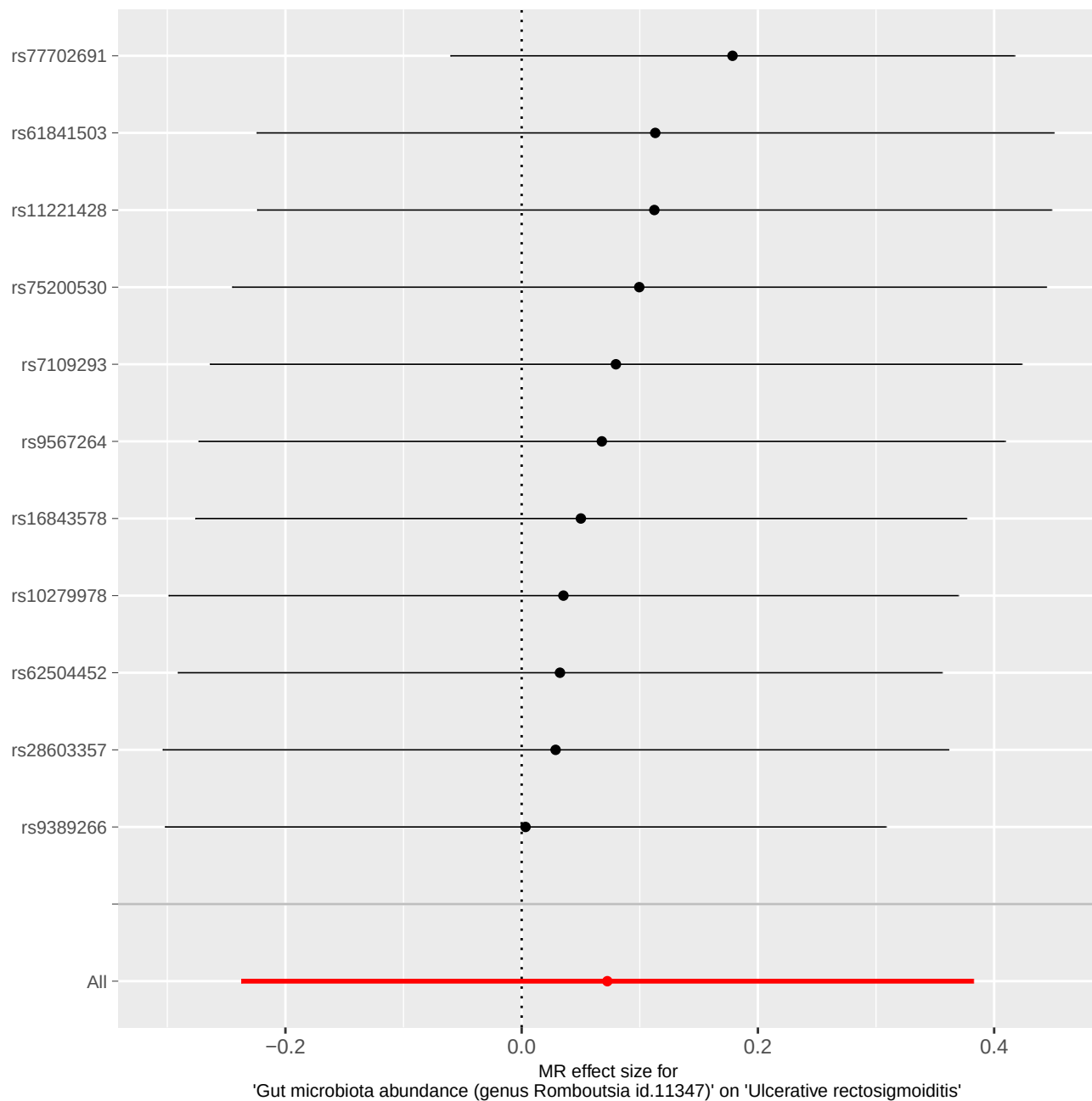


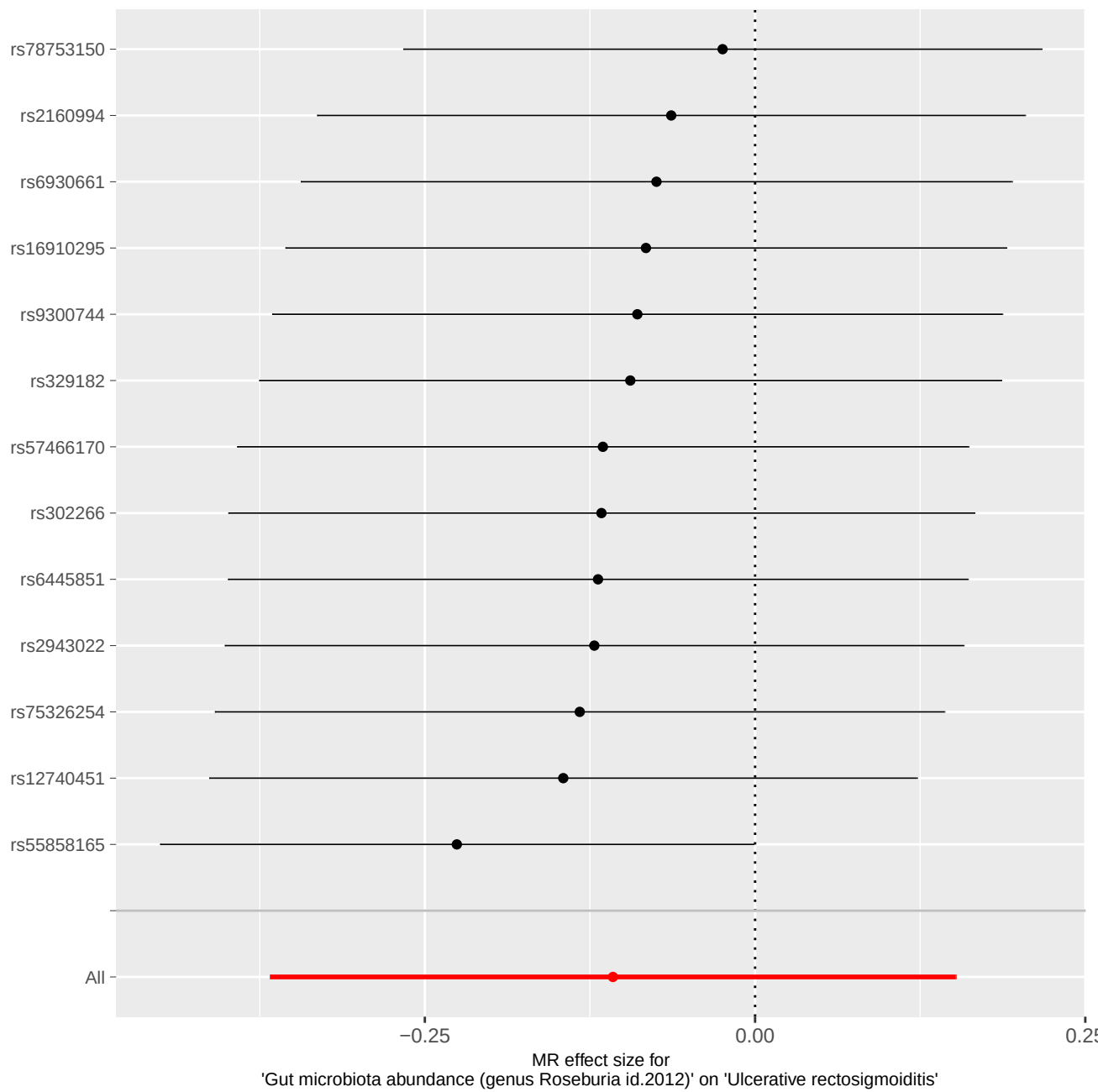




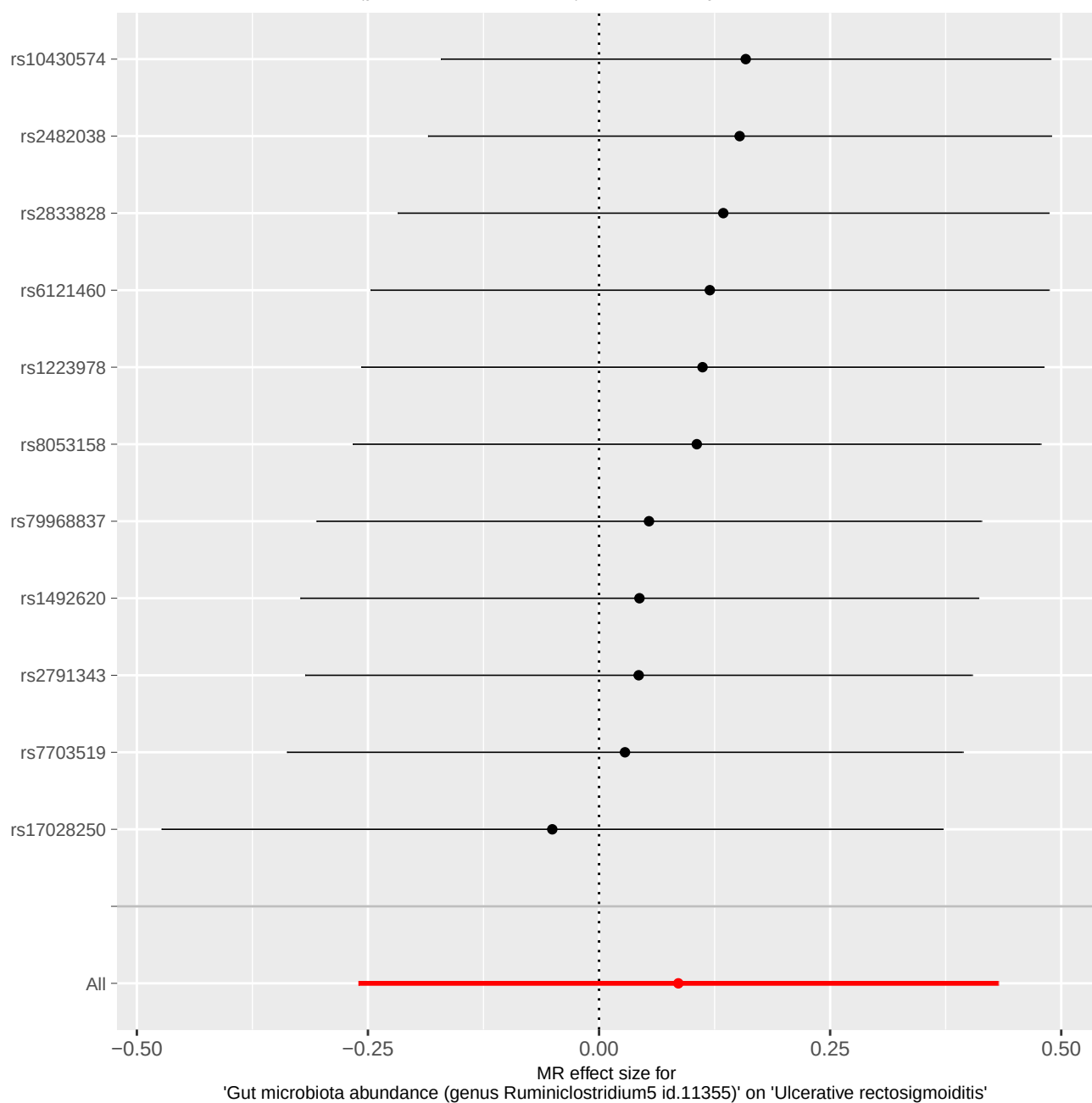


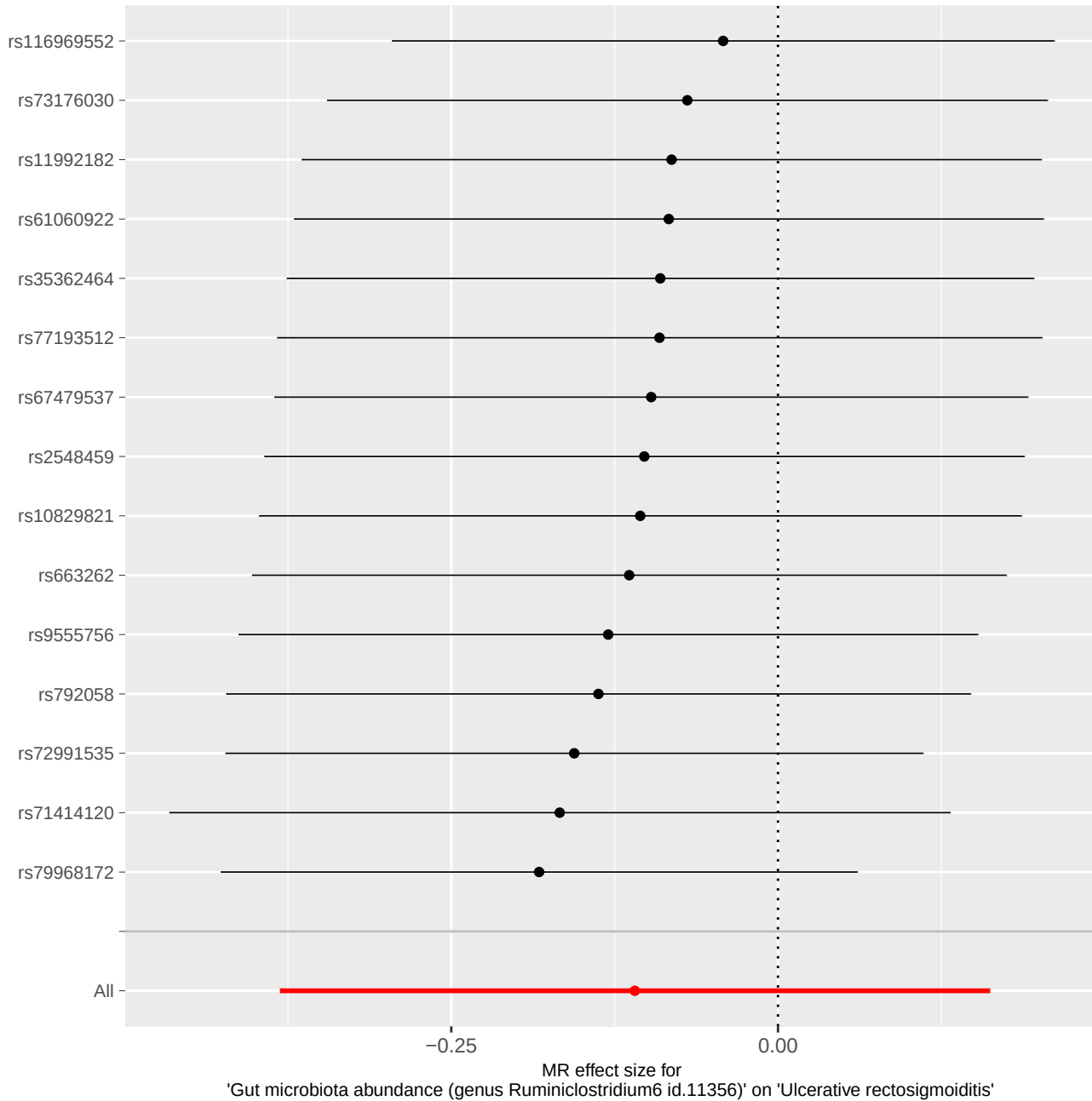


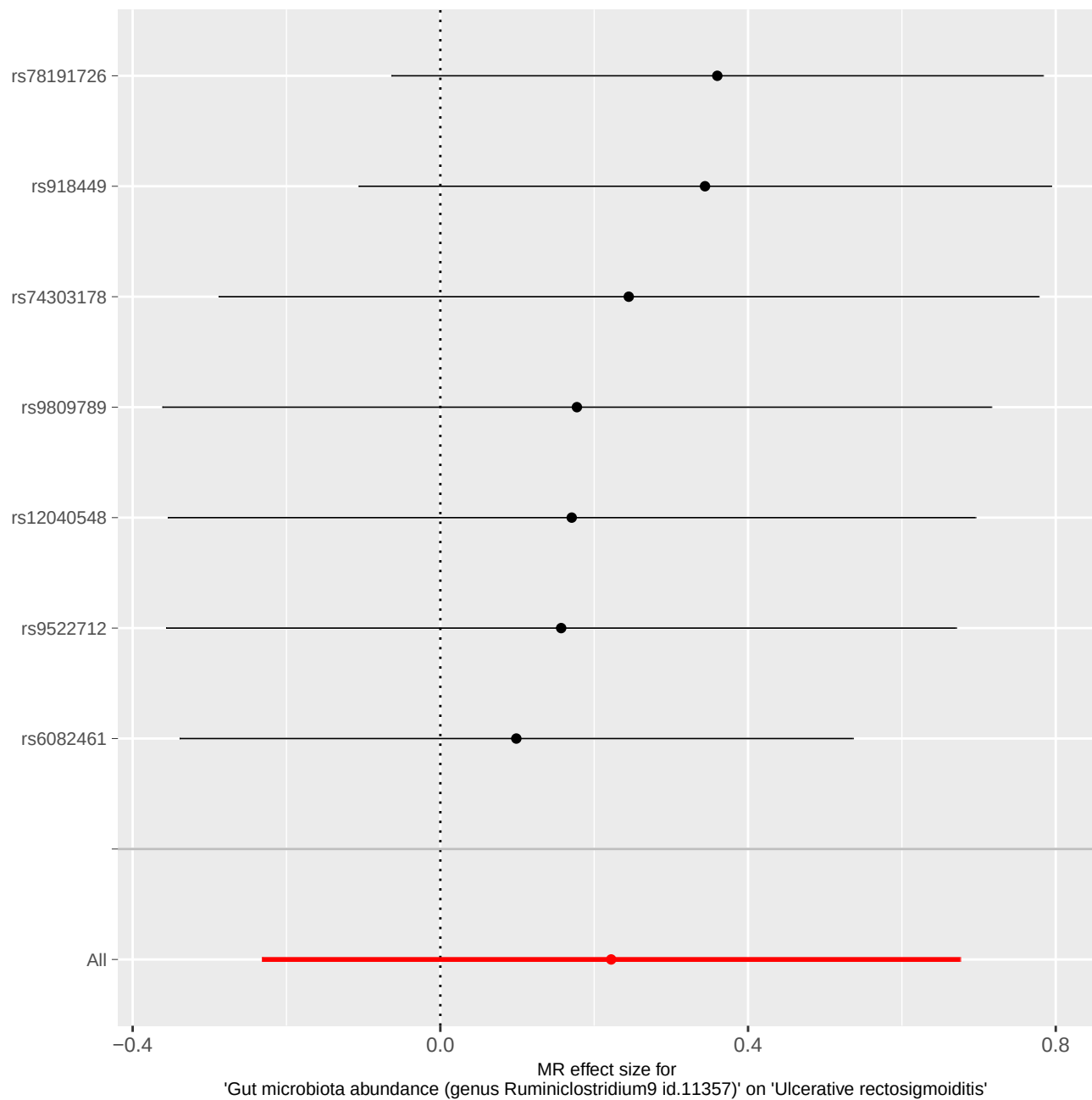


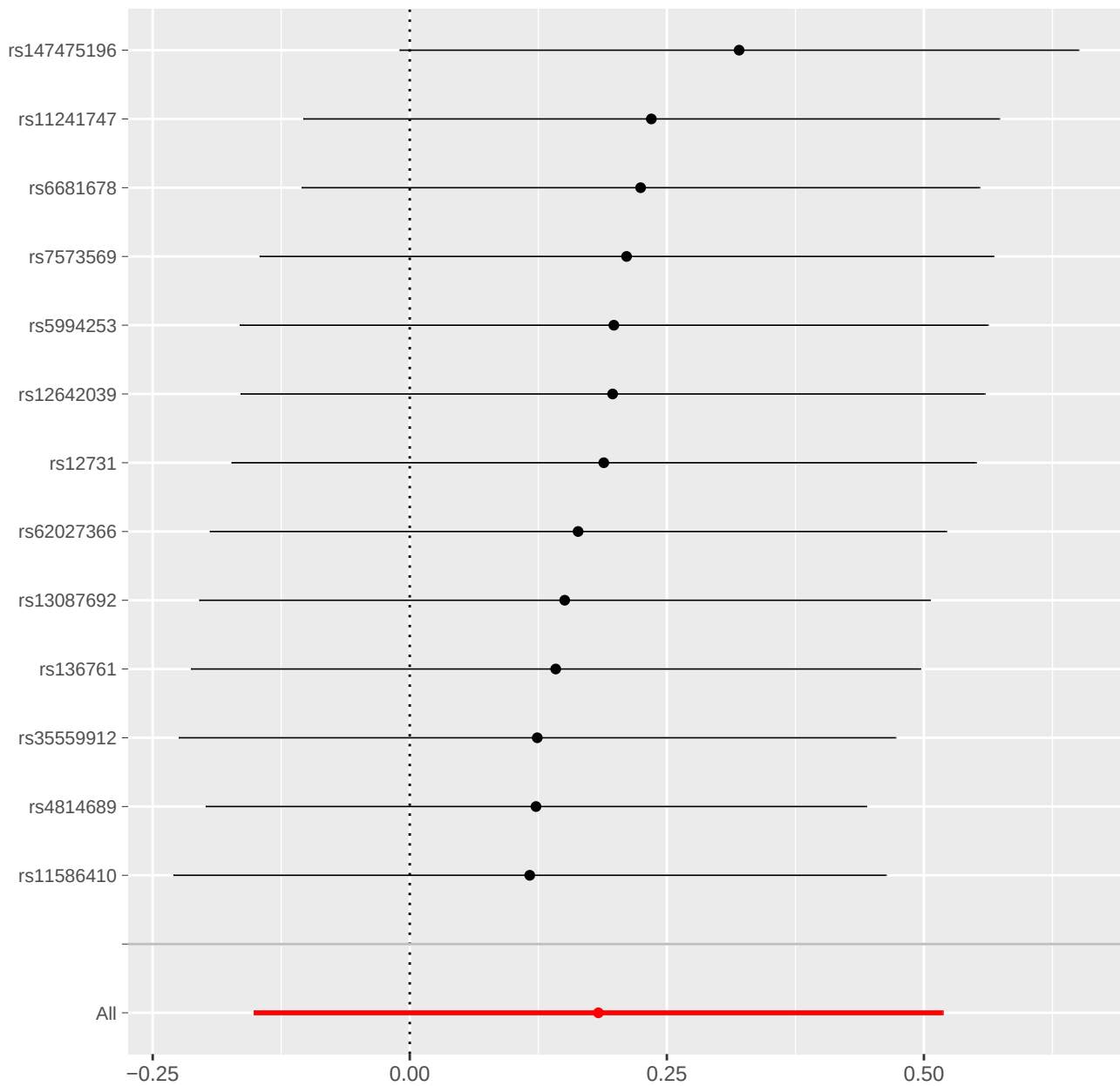


Batch 1623 : Gut microbiota abundance (genus Ruminiclostridium5 id.11355) on Ulcerative rectosigmoiditis

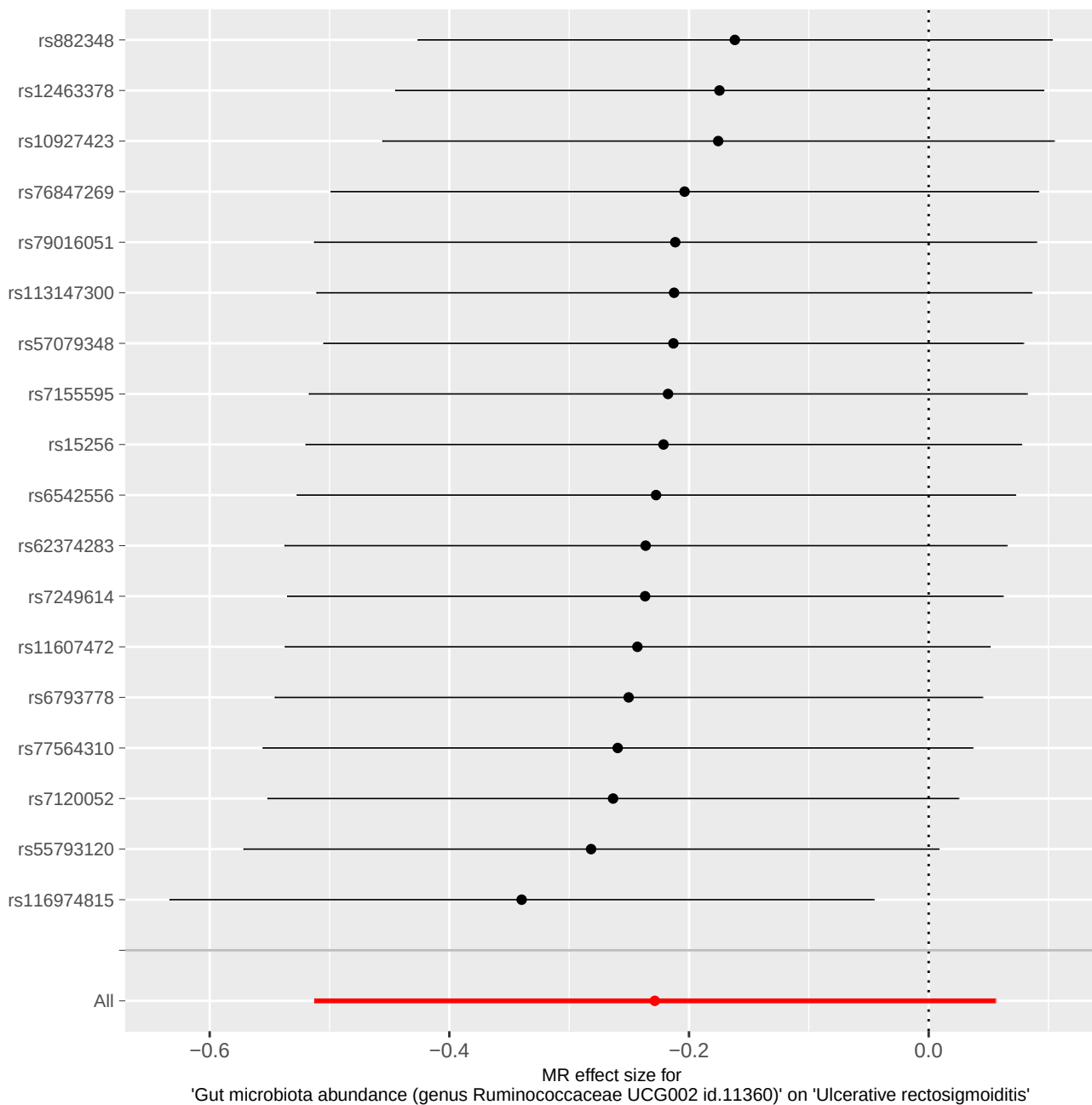


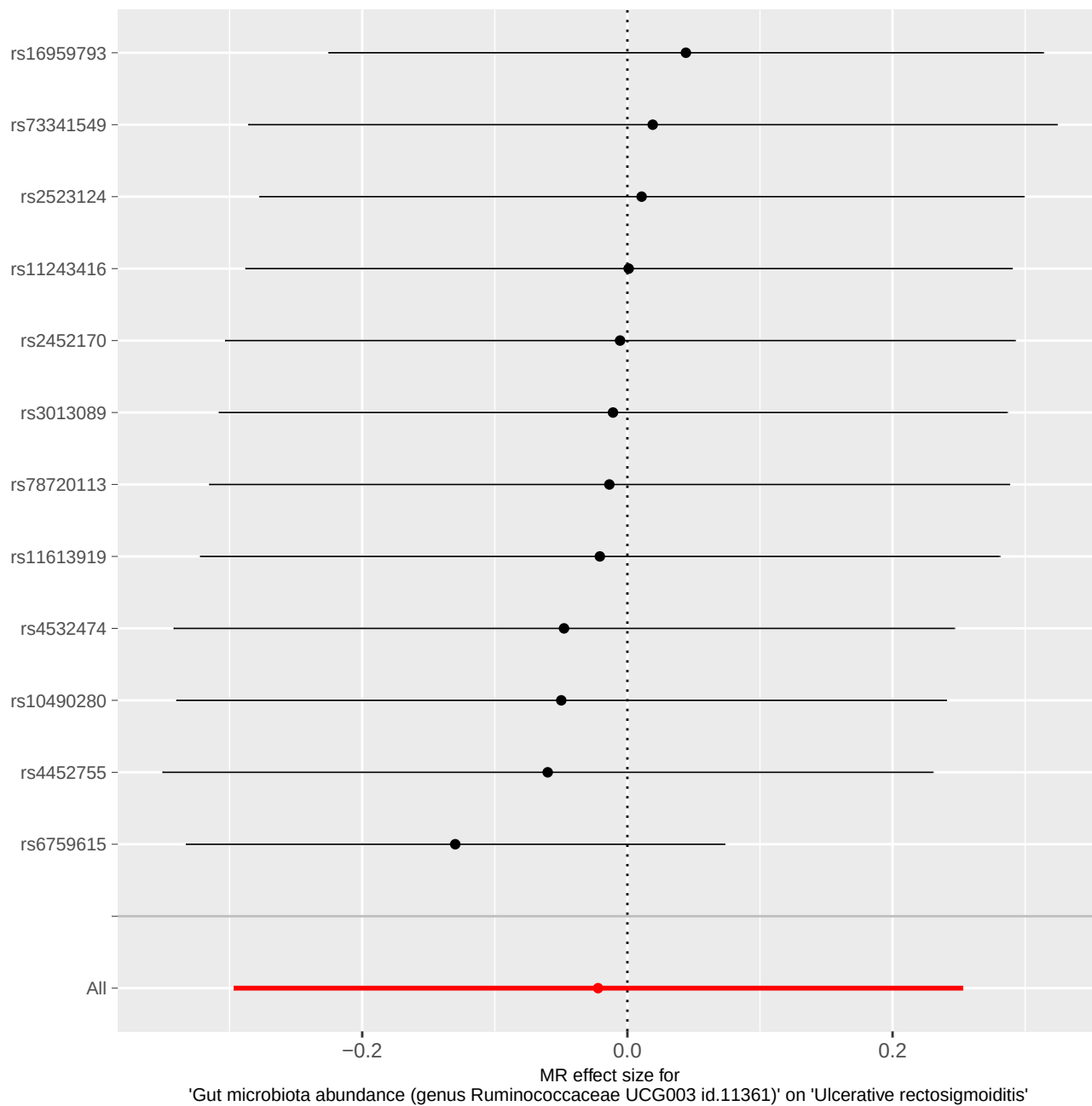


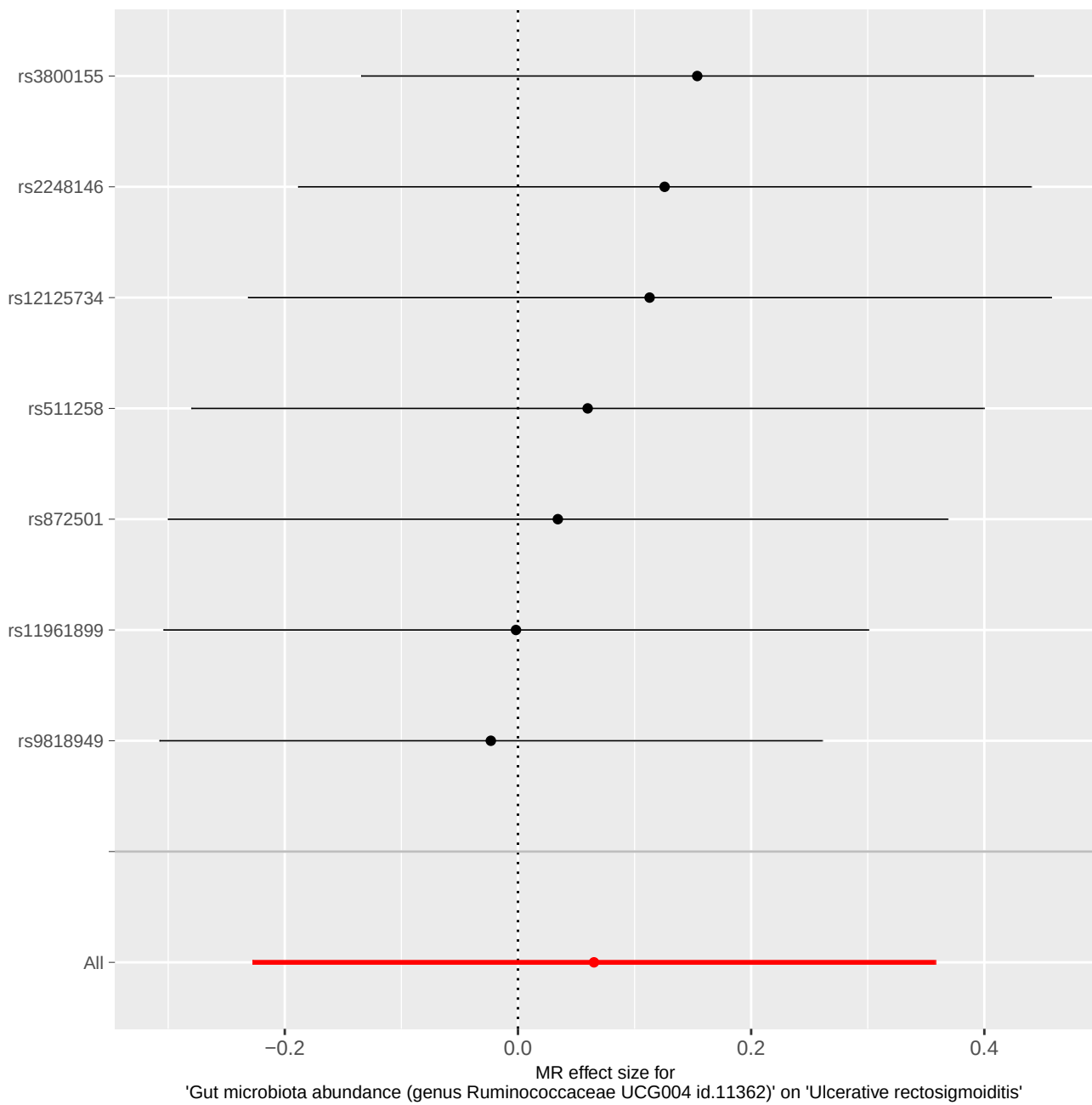


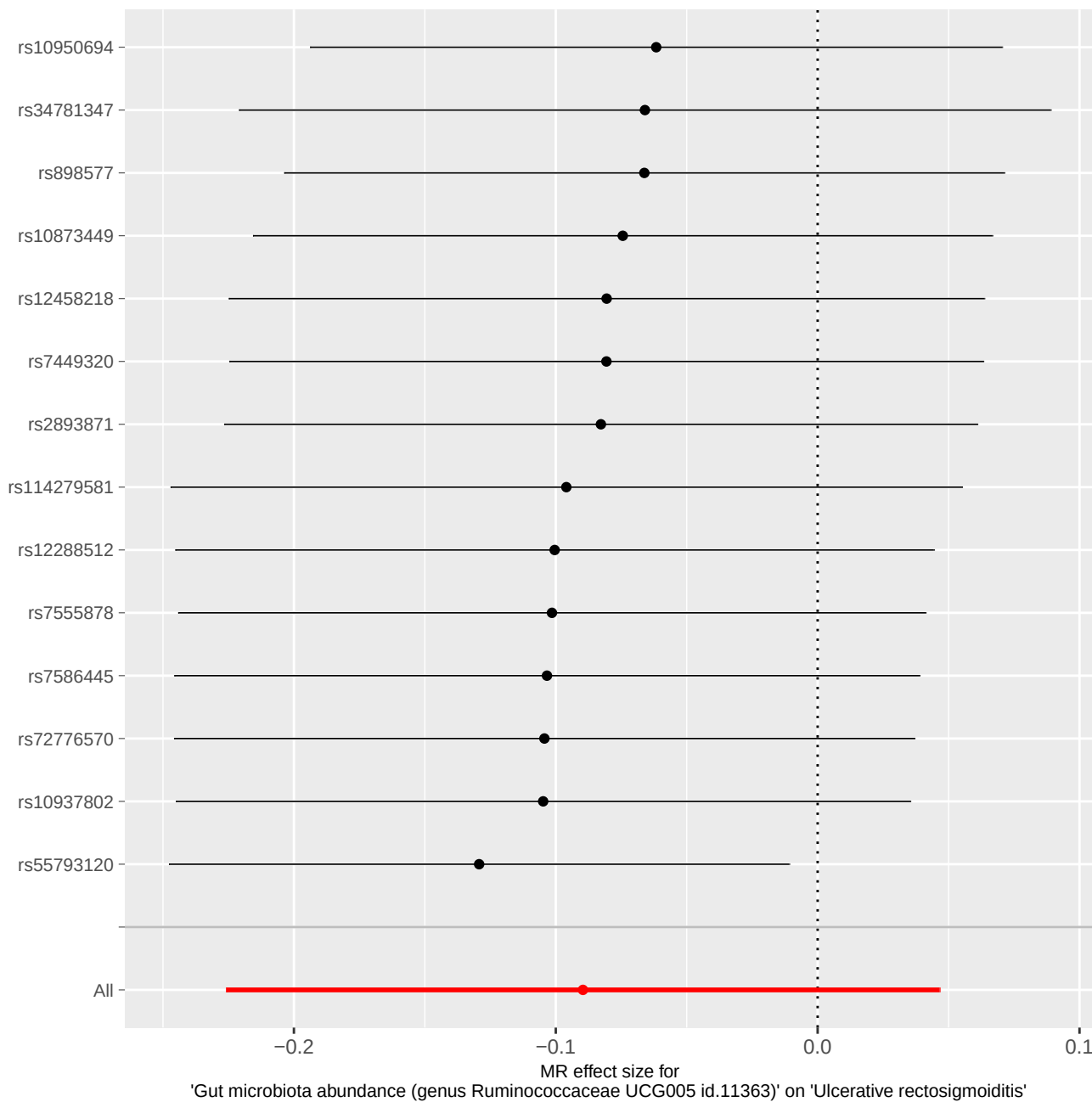


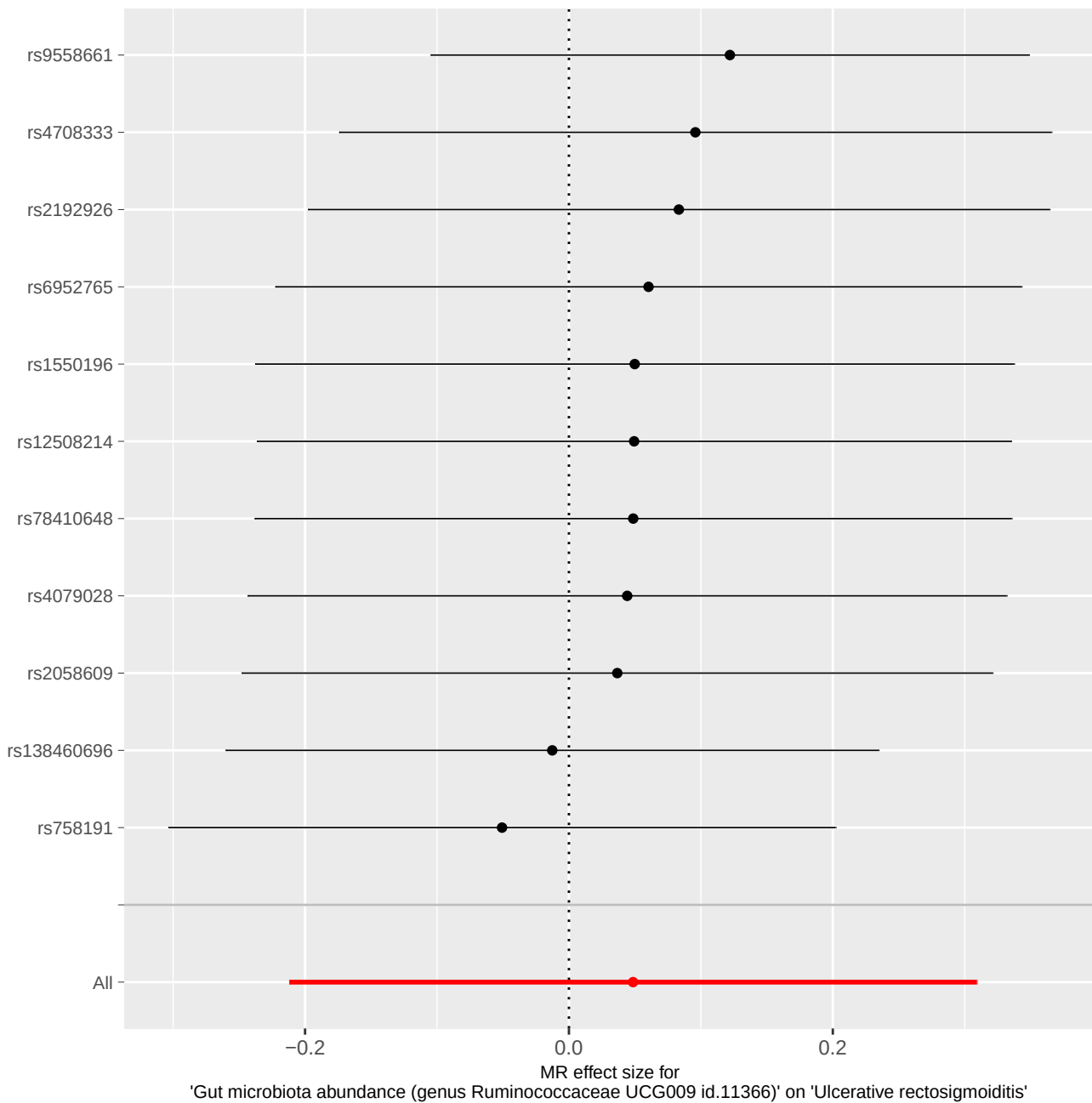
MR effect size for
'Gut microbiota abundance (genus Ruminococcaceae NK4A214 group id.11358)' on 'Ulcerative rectosigmoiditis'

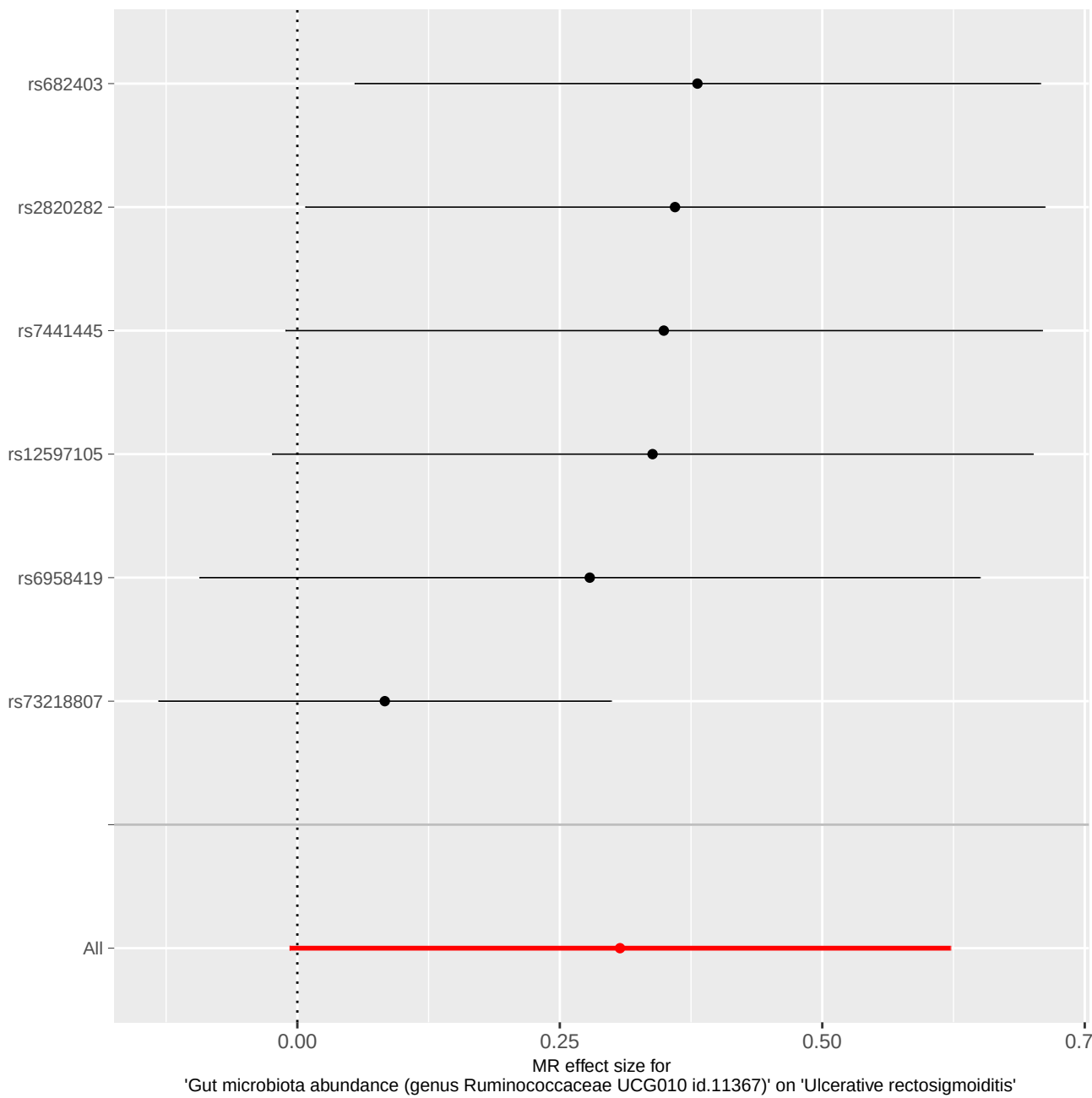


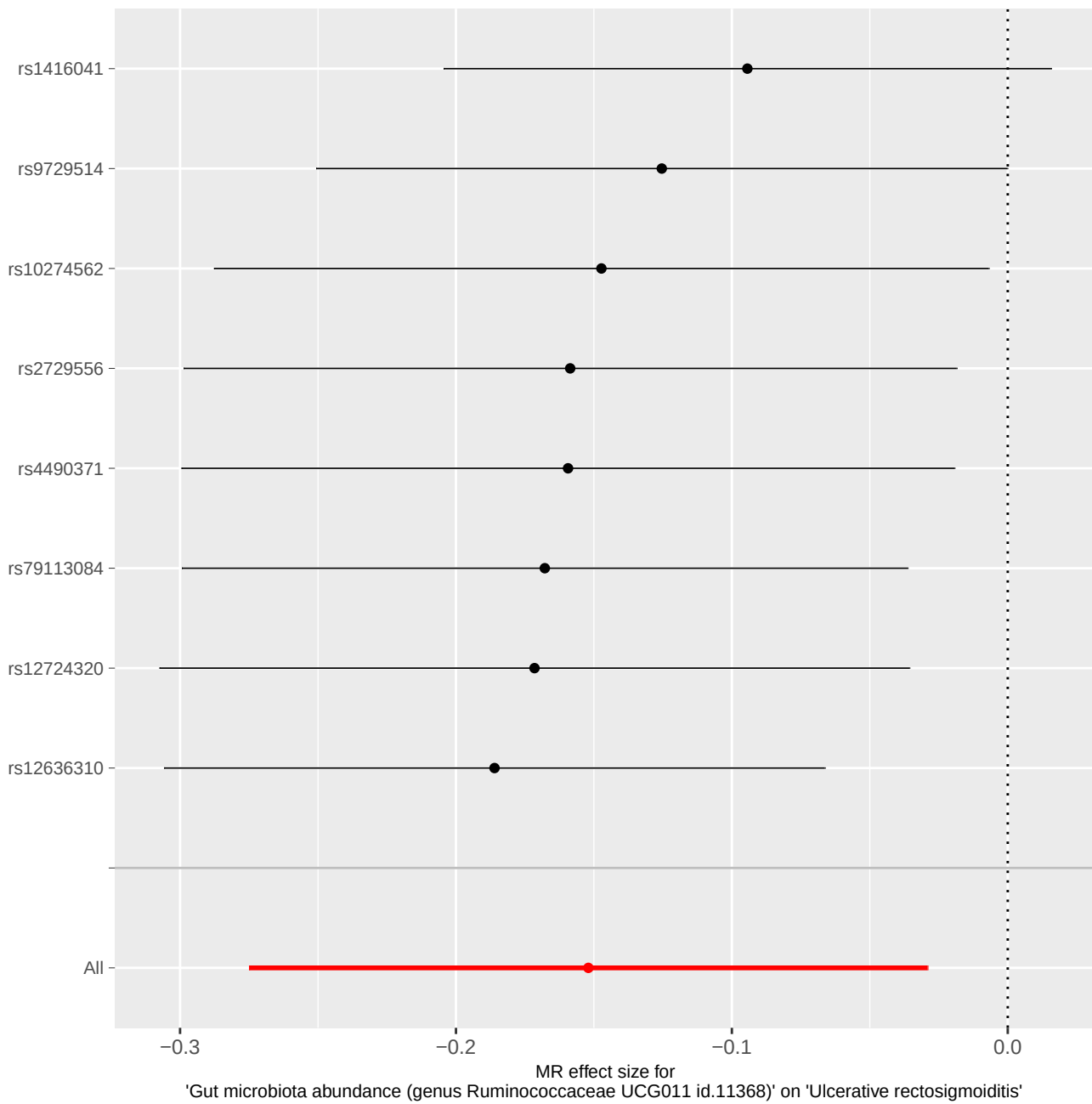


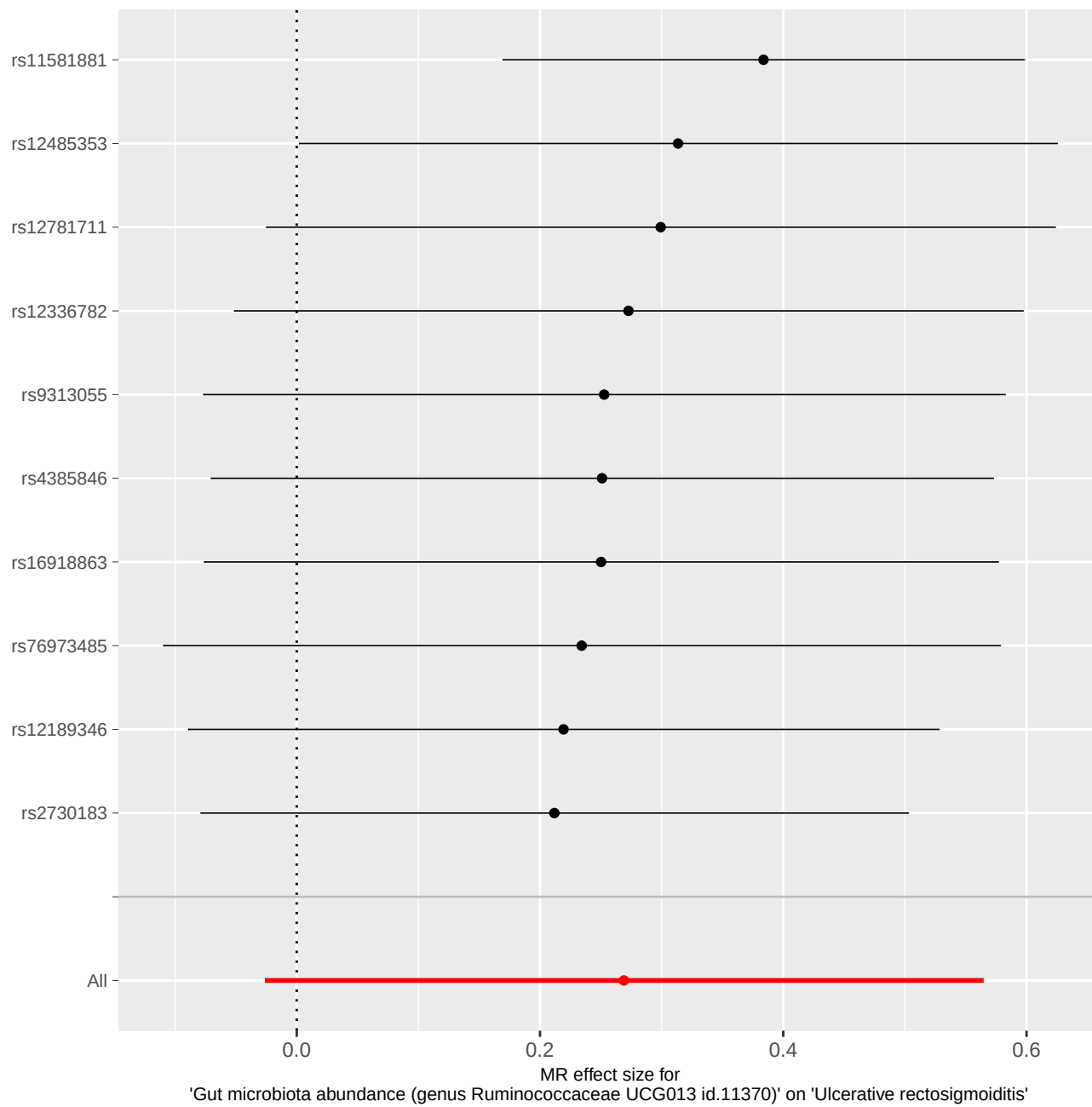


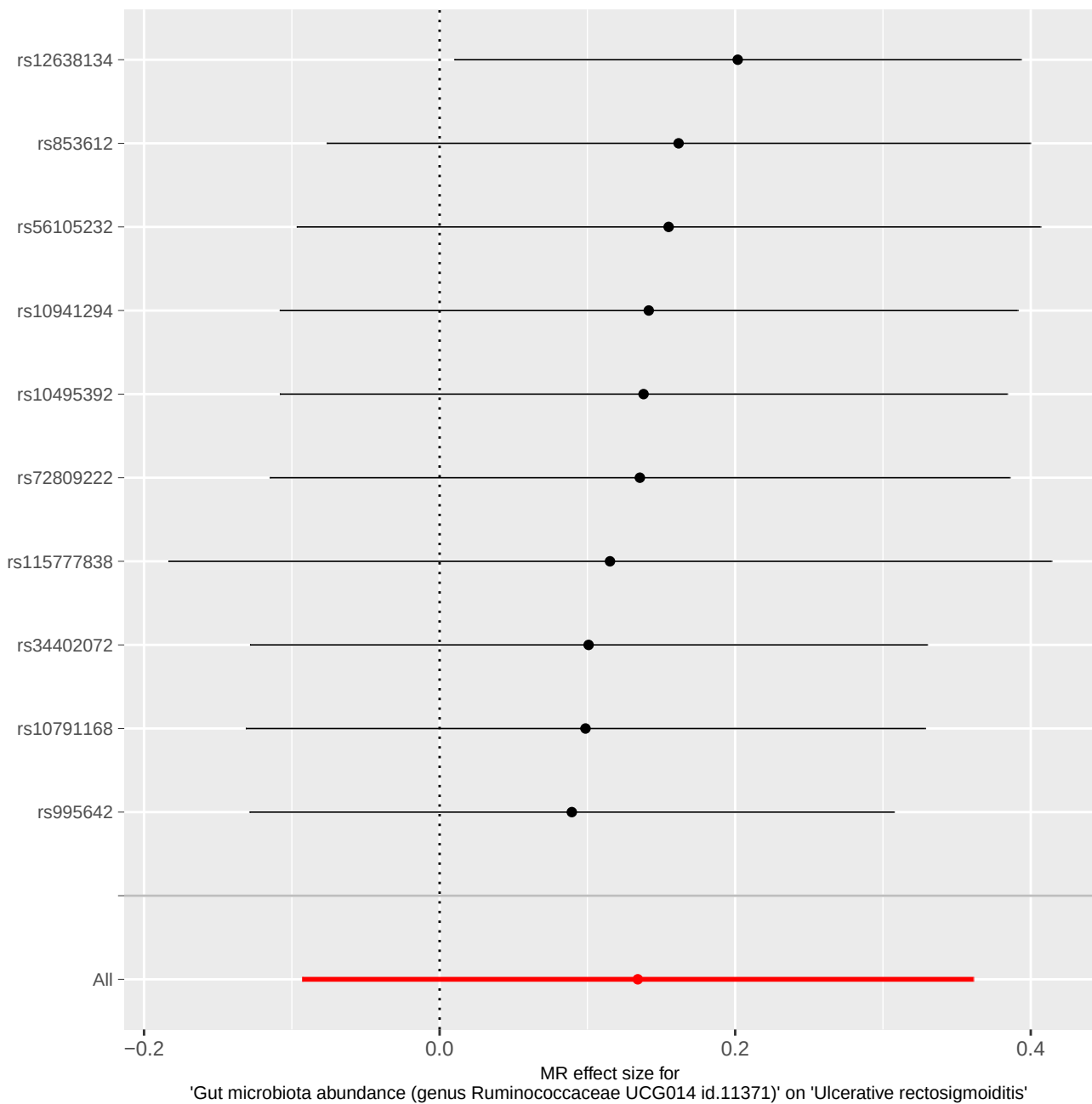


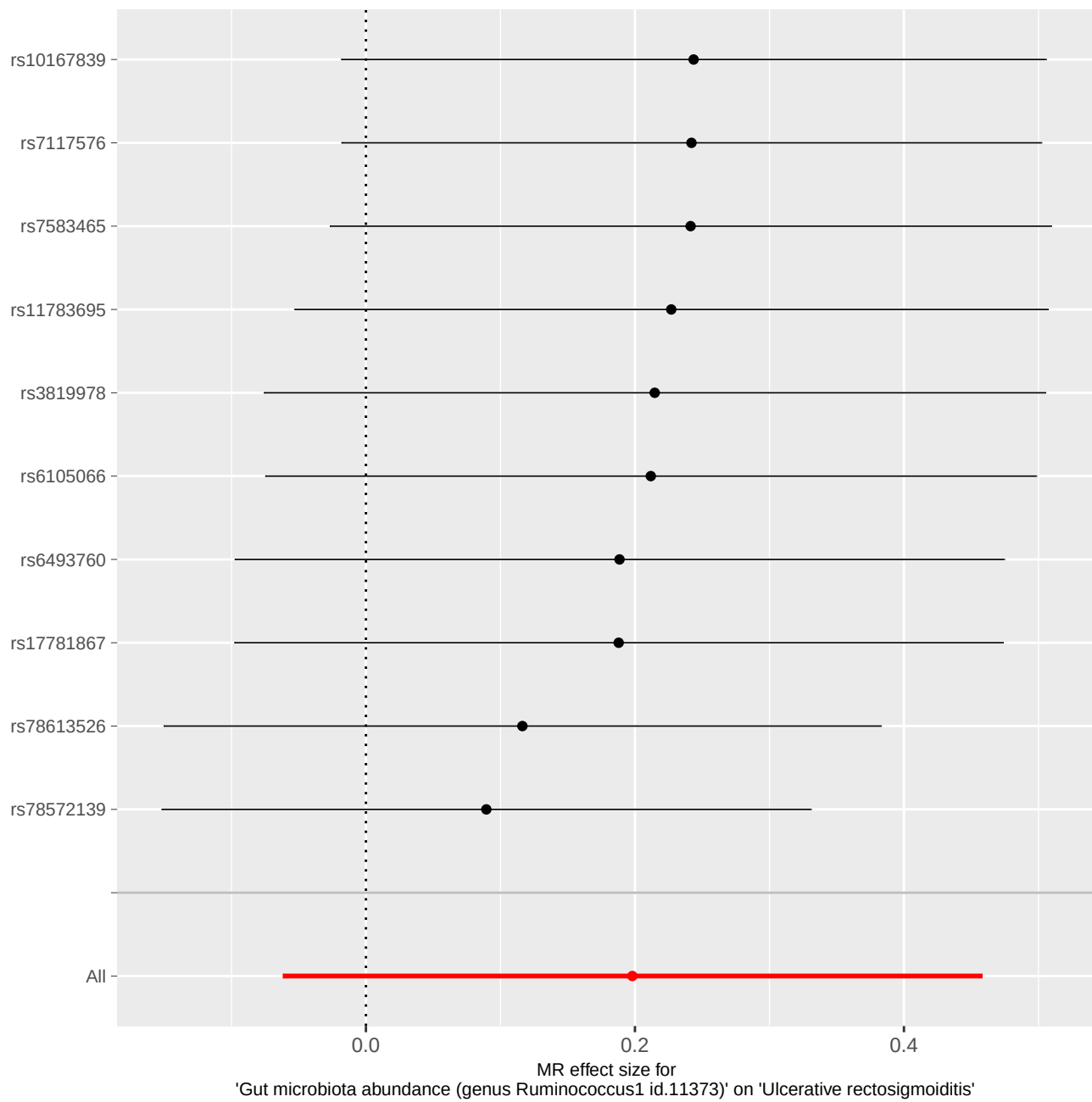


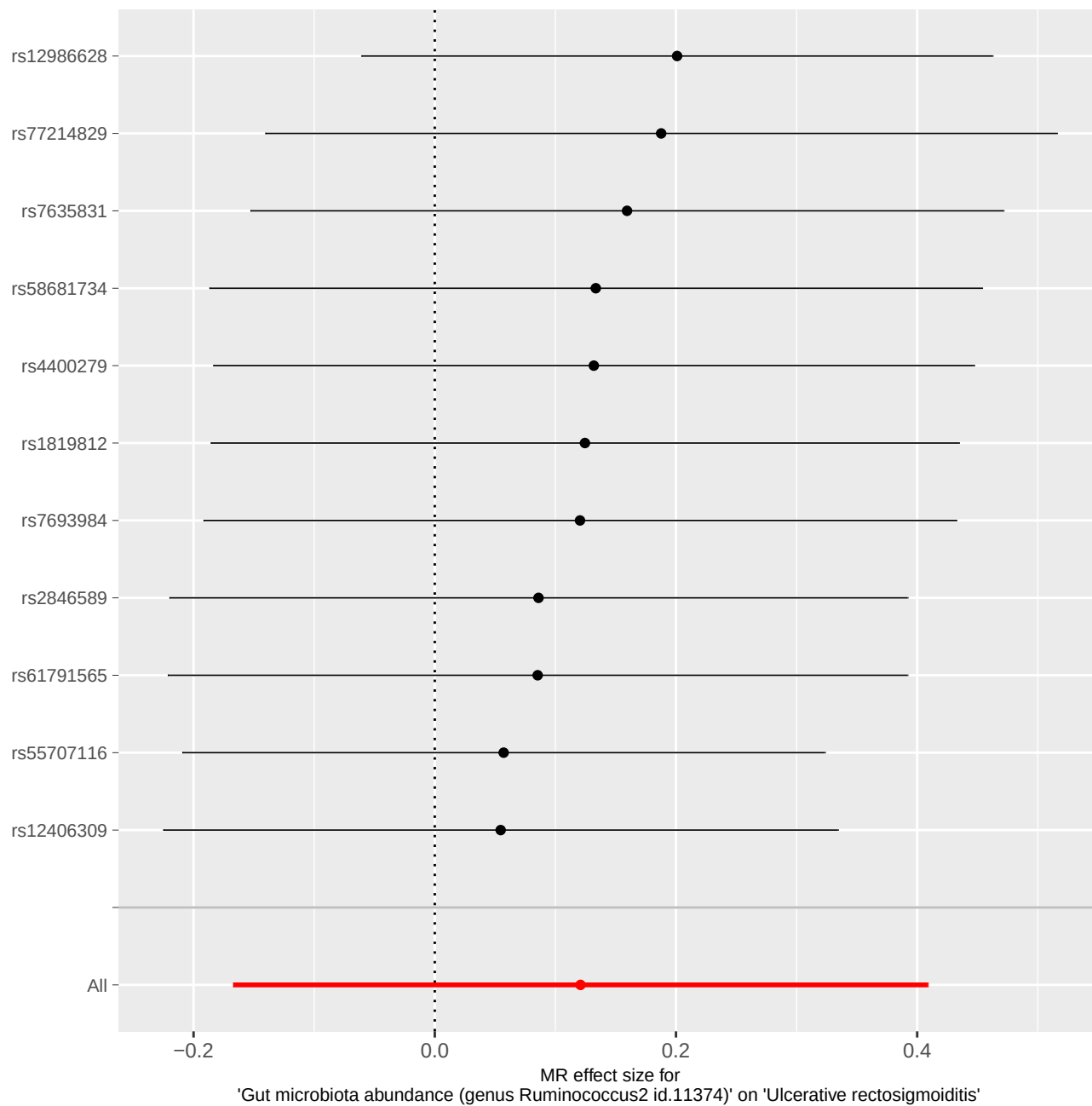


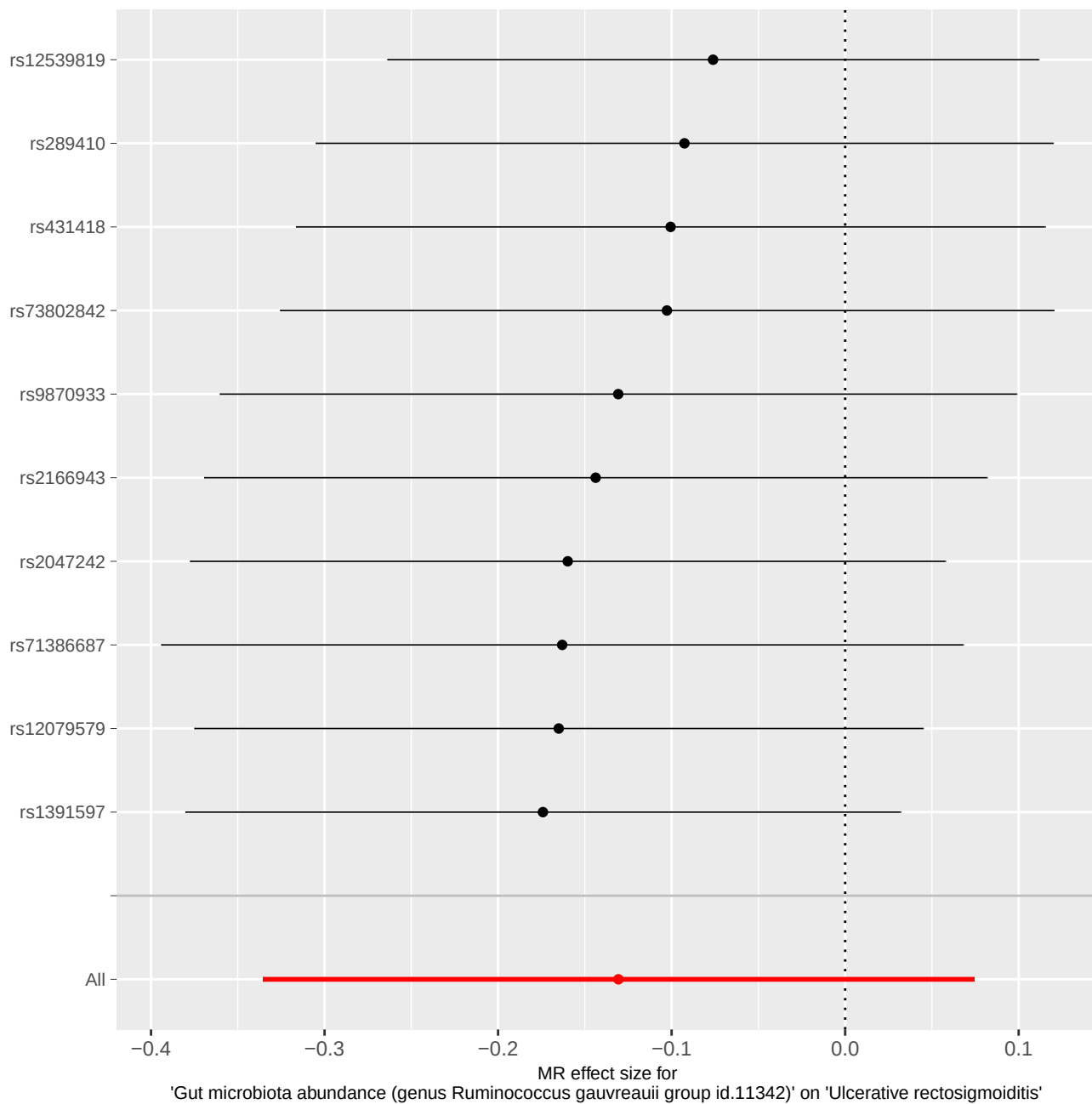










MR effect size for
'Gut microbiota abundance (genus Ruminococcus gauvreauii group id.11342)' on 'Ulcerative rectosigmoiditis'

