SARS-CoV-2 infection GWAS
n SNPs = 7,090,494
n cases = 38,984
n controls = 1,644,784
COVID-19 hospitalization GWAS (ver. population)
n SNPs = 6,591,679
n cases = 9,986
n controls = 1,877,672
COVID-19 hospitalization GWAS (ver nonhospitalized)
n SNPs = 6,782,715
n cases = 4,829
n controls = 11,816
very severe COVID-19 GWAS
n SNPs = 8,045,256
n cases = 5,101
n controls = 1,383,241
zinc GWAS
n SNPs = 2,557,381
n samples = 2,603
Main analysis:
2 independent SNPs at
p-value < 5x10-8
selenium GWAS
n SNPs = 2,557,388
n samples = 9,639
Main analysis:
12 independent SNPs at
p-value < 5x10-8
copper GWAS
n SNPs = 2,557,417
n samples = 2,603
Main analysis:
2 independent SNPs at
p-value < 5x10-8
phylloquinone GWAS
n SNPs = ~ 2,500,000
n samples = 2,138
Main analysis:
11 independent SNPs at
p-value < 5x10-5
clump and merge
clump and merge
clump and merge
clump, merge and remove pleiotropic SNPs
2 SNPs with R2 = 4.6%
2 SNPs with R2 = 2.25%
2 SNPs with R2 = 4.6%
3 SNPs with R2 = 3.06%
Inverse variance weighted method
Median method
Mode method
MR-Egger
Two Sample Mendelian Randomization analysis
Two Sample Mendelian Randomization analysis
Two Sample Mendelian Randomization analysis
Two Sample Mendelian Randomization analysis