**Supplementary Table S1.** Basic information of the GWAS data[*]

| Phenotype | Cases | | Control | |
|---|---|---|---|---|
| | *n* | Definition | *n* | Definition |
| UKB-COVID-19 | 6,696 | Individuals with laboratory confirmation of SARS-CoV-2 infection (RNA and/or serology based) OR EHR/ICD coding/Physician Confirmed COVID-19 OR self-reported COVID-19 positive (e.g. by questionnaire) | 1,073,072 | Everybody who is not a case, e.g. population |
| UKB-COVID-19 negative[&] | 3,523 | Individuals with laboratory confirmation of SARS-CoV-2 infection (RNA and/or serology based) OR EHR/ICD coding/Physician Confirmed COVID-19 OR self-reported COVID-19 positive (e.g. by questionnaire) | 36,634 | [Laboratory tested for SARS-CoV-2 infection (RNA and/or serology based) AND all tests (if multiple tests) negative[*]] OR self-reported tested negative for SARS-CoV-2 infection (e.g. by questionnaire) |
| Severe UKB-COVID-19 | 536 | Hospitalized laboratory confirmed SARS-CoV-2 infection (RNA and/or serology based), AND (death OR respiratory support (intubation, CPAP, BiPAP, CNP (continue external negative pressure), Optiflow/very high flow Positive End Expiratory Pressure Oxygen[*] - AND hospitalization with COVID19 as primary reason for admission | 329,391 | Everybody who is not a case, e.g. population |
| Severe COVID-19[#] | 1,610 | Hospitalization with respiratory failure and a confirmed SARS-CoV-2 viral RNA polymerase-chain-reaction (PCR) test from nasopharyngeal swabs or other relevant biologic fluids | 2,205 | Everybody who is not a case, e.g. population |

*Note.* [*]Summarized data were provided by the COVID-19 *host genetics* initiative (https://www.covid19hg.org/results/) unless otherwise noted. [#]The GWAS summarized data were provided by the Severe Covid-19 GWAS Group (https://ikmb.shinyapps.io/COVID-19_GWAS_Browser/). [&]The control is the non-predicted COVID-19 and non-self-reported COVID-19. COVID-19, corona virus disease 2019; UKB, UK Biobank.
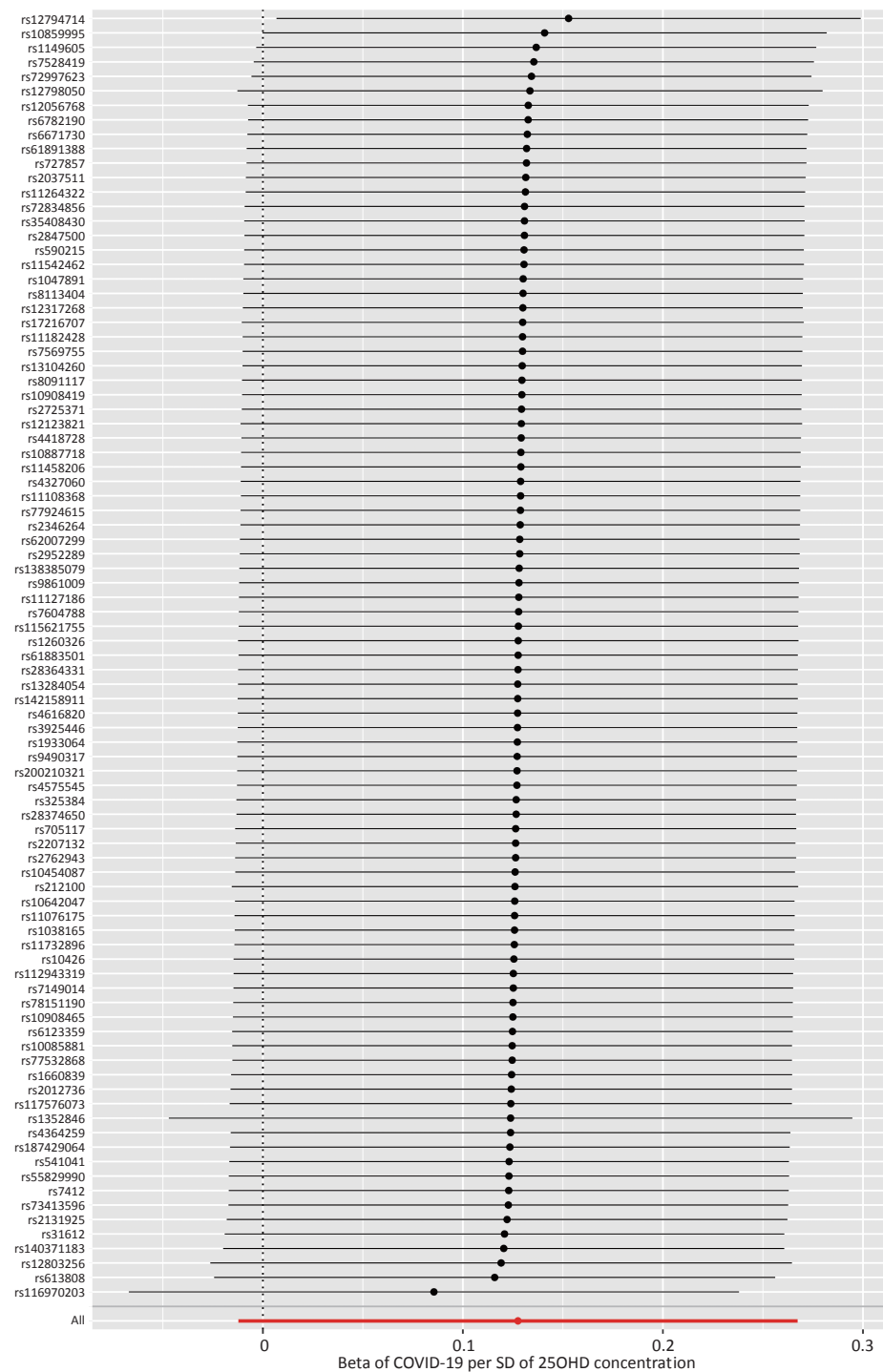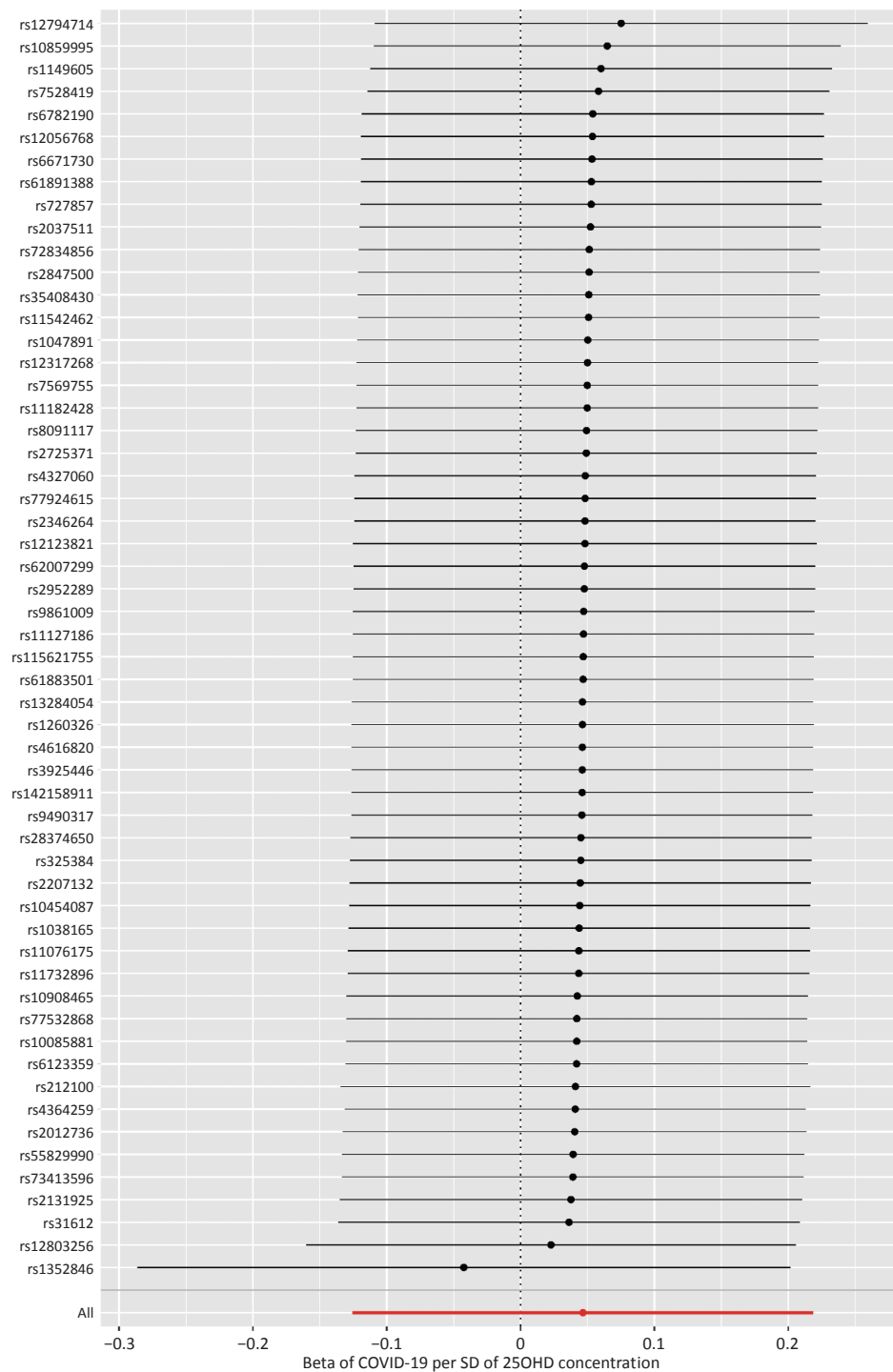
**Supplementary Figure S1.** MR leave-one-out sensitivity analysis for '25OHD concentration' on 'COVID-19' in the population of UKB-COVID-19 based on 89 SNPs. Leave-one-out analysis: each row represents a MR analysis of 25OHD concentration on COVID-19 using all instruments expect for the SNP listed on the y-axis. The point represents the beta with that SNP removed and the line represents 95% confidence interval. The summary data are reported by the COVID-19 host genetics initiative. COVID-19, coronavirus disease 2019; MR, mendelian randomization; SNP, single-nucleotide polymorphism; 25OHD, 25-hydroxyitamin D; SD, standard deviation; UKB, UK biobank.
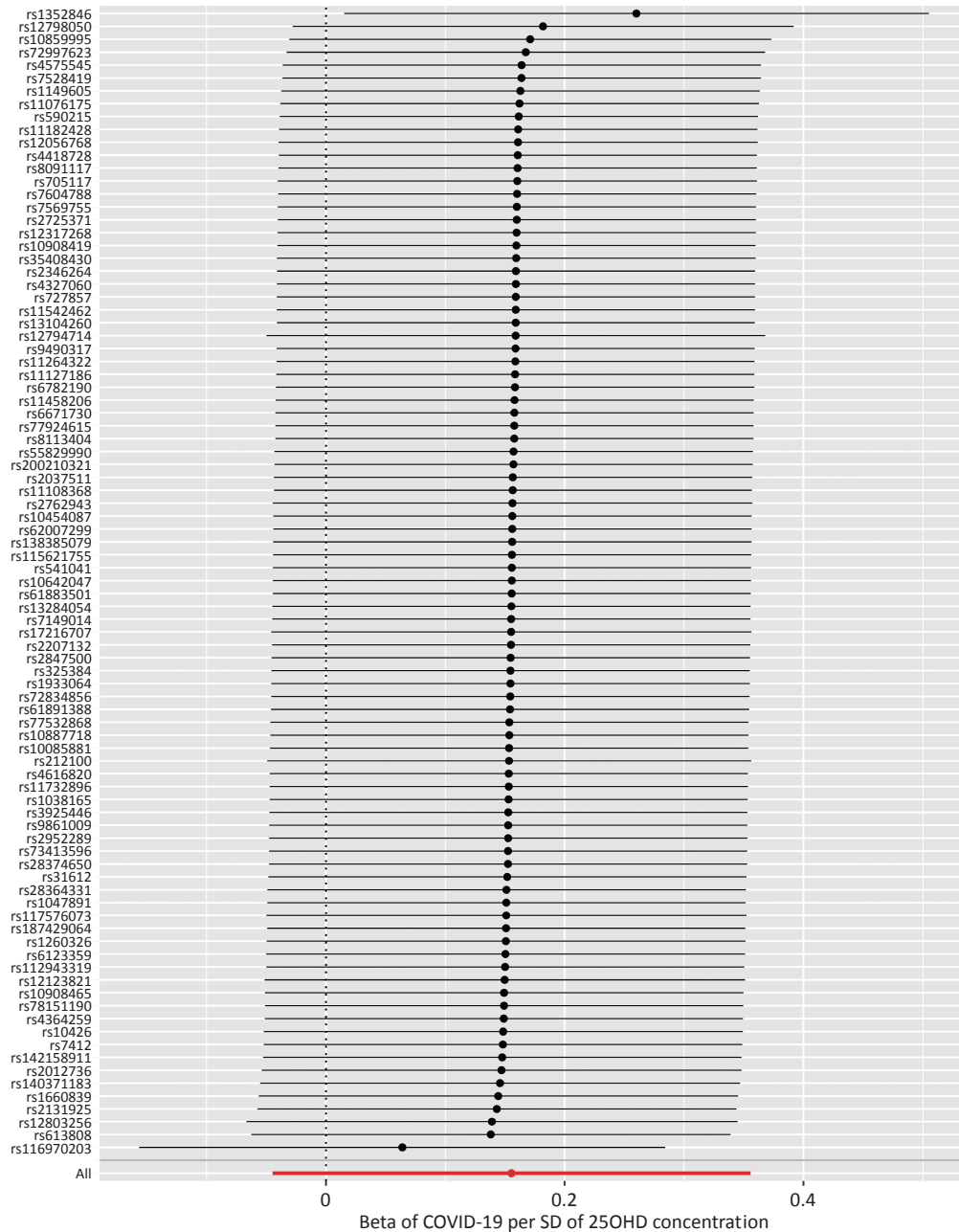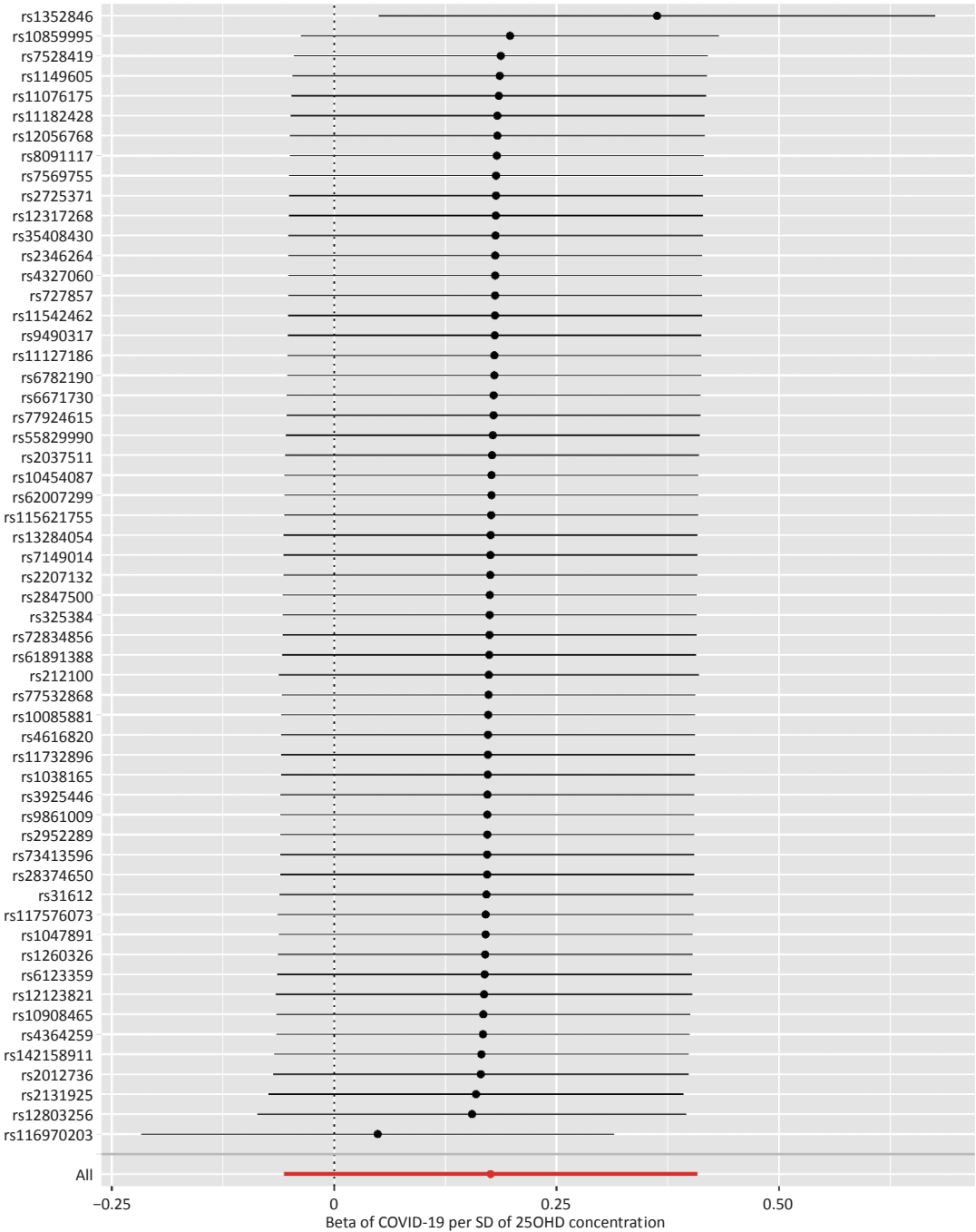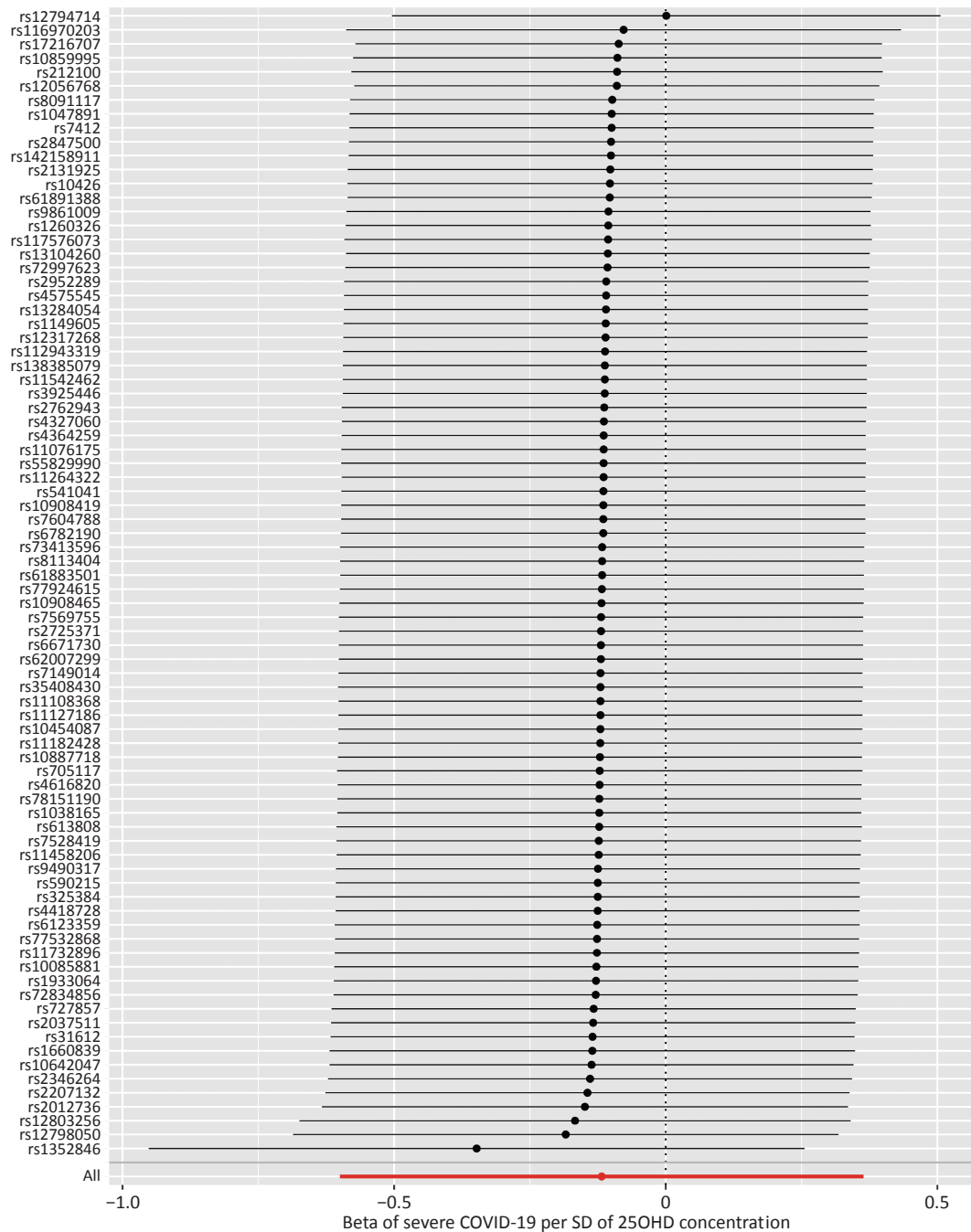
**Supplementary Figure S2.** MR leave-one-out sensitivity analysis for '25OHD concentration' on 'COVID-19' in the population of UKB-COVID-19 negative based on 89 SNPs. Leave-one-out analysis: each row represents a MR analysis of 25OHD concentration on COVID-19 using all instruments expect for the SNP listed on the y-axis. The point represents the beta with that SNP removed and the line represents 95% confidence interval. The summary data are reported by the COVID-19 host genetics initiative. COVID-19, coronavirus disease 2019; MR, mendelian randomization; SNP, single-nucleotide polymorphism; 25OHD, 25-hydroxyitamin D; SD, standard deviation; UKB, UK biobank.

**Supplementary Figure S3.** MR leave-one-out sensitivity analysis for '25OHD concentration' on 'COVID-19' in the population of UKB-COVID-19 based on 56 SNPs. Leave-one-out analysis: each row represents a MR analysis of 25OHD concentration on COVID-19 using all instruments expect for the SNP listed on the y-axis. The point represents the beta with that SNP removed and the line represents 95% confidence interval. The summary data are reported by the COVID-19 host genetics initiative. COVID-19, coronavirus disease 2019; MR, mendelian randomization; SNP, single-nucleotide polymorphism; 25OHD, 25-hydroxyitamin D; SD, standard deviation; UKB, UK biobank.
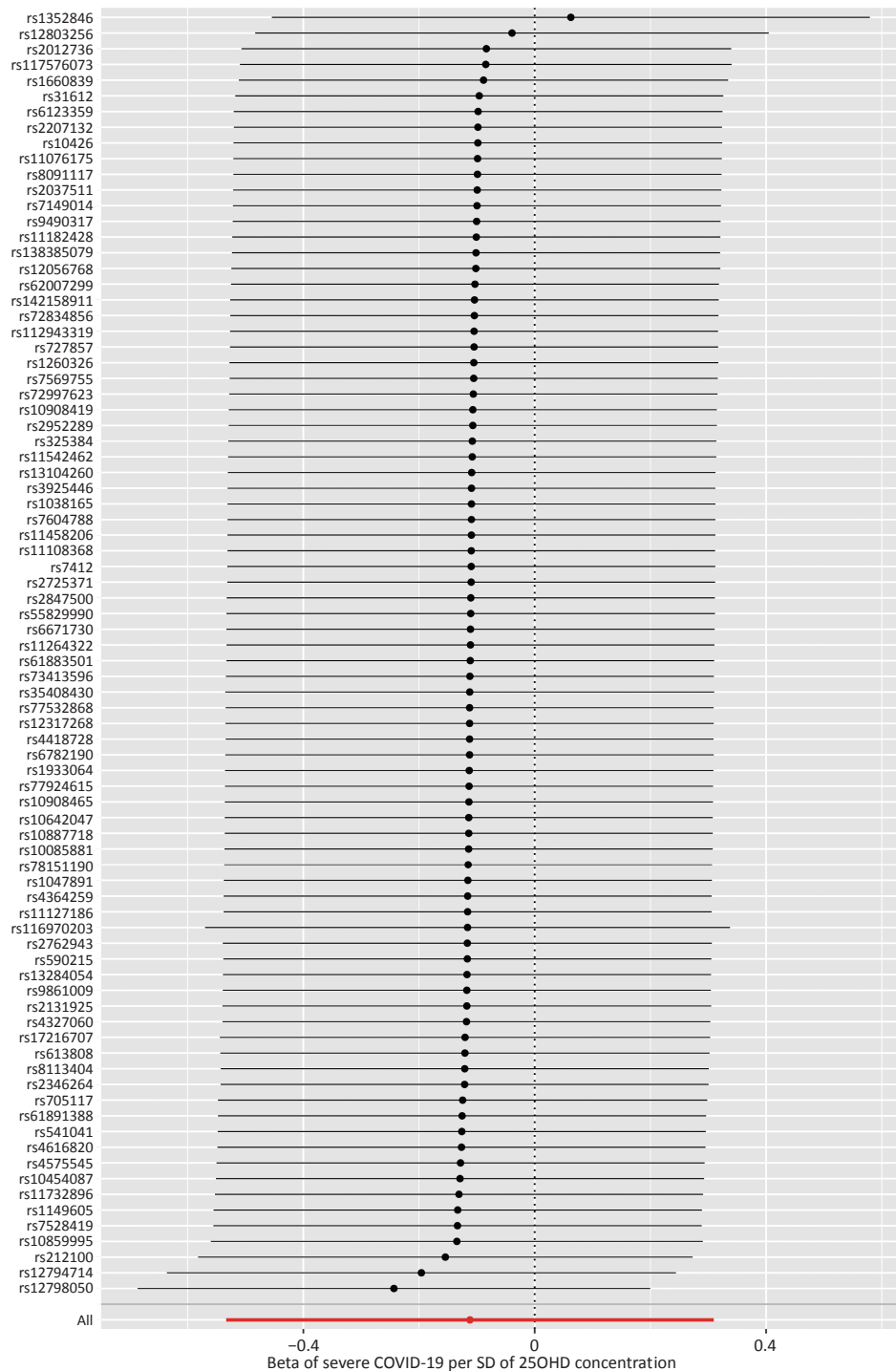
**Supplementary Figure S4.** MR leave-one-out sensitivity analysis for '25OHD concentration' on 'COVID-19' in the population of UKB-COVID-19 negative based on 57 SNPs. Leave-one-out analysis: each row represents a MR analysis of 25OHD concentration on COVID-19 using all instruments expect for the SNP listed on the y-axis. The point represents the beta with that SNP removed and the line represents 95% confidence interval. The summary data are reported by the COVID-19 host genetics initiative. COVID-19, coronavirus disease 2019; MR, mendelian randomization; SNP, single-nucleotide polymorphism; 25OHD, 25-hydroxyitamin D; SD, standard deviation; UKB, UK biobank.
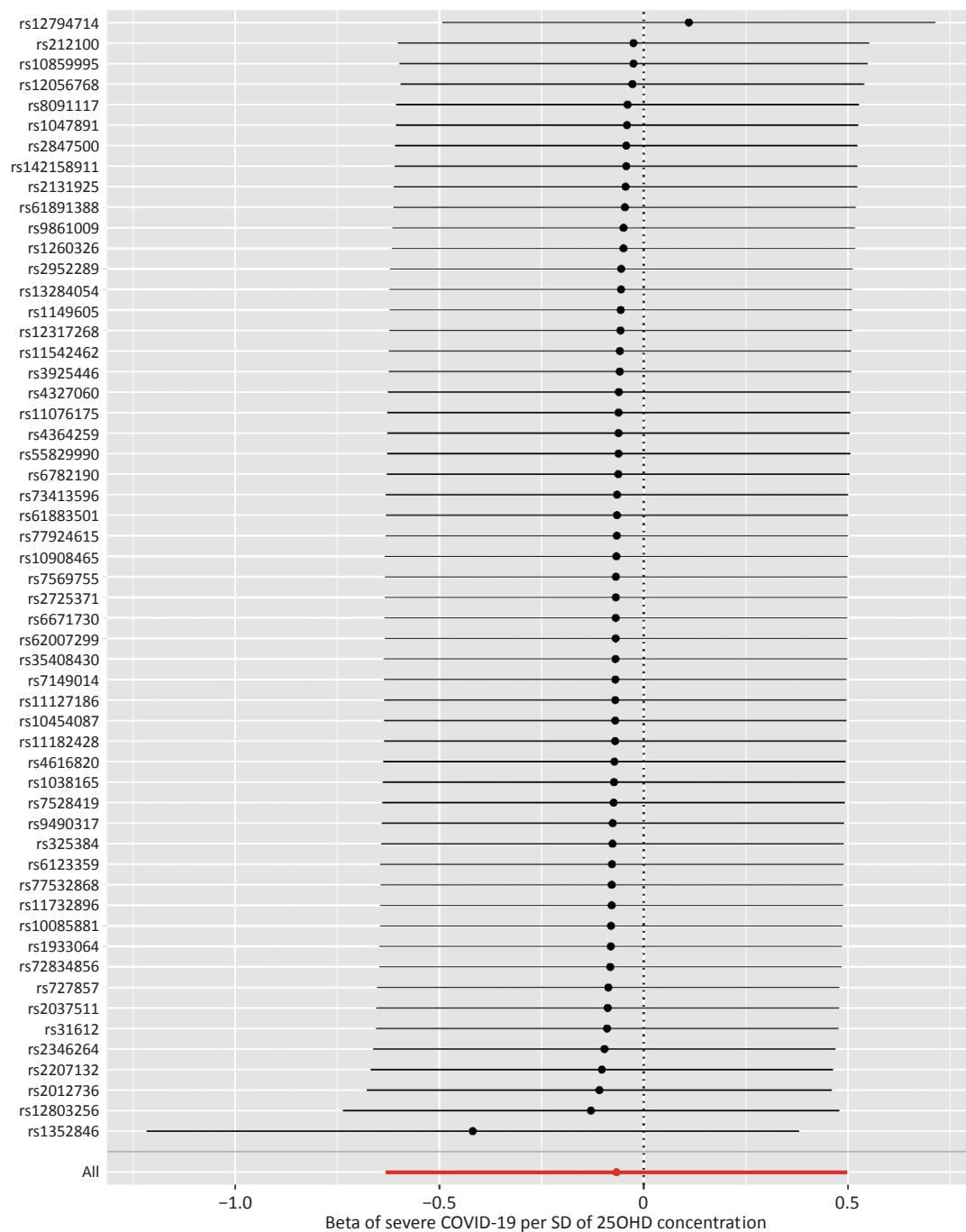
**Supplementary Figure S5.** MR leave-one-out sensitivity analysis for '25OHD concentration' on 'severe COVID-19' in the population of severe UKB-COVID-19 based on 82 SNPs. Leave-one-out analysis: each row represents a MR analysis of 25OHD concentration on severe COVID-19 using all instruments expect for the SNP listed on the y-axis. The point represents the beta with that SNP removed and the line represents 95% confidence interval. The summary data are reported by the COVID-19 host genetics initiative. COVID-19, coronavirus disease 2019; MR, mendelian randomization; SNP, single-nucleotide polymorphism; 25OHD, 25-hydroxyitamin D; SD, standard deviation; UKB, UK biobank.
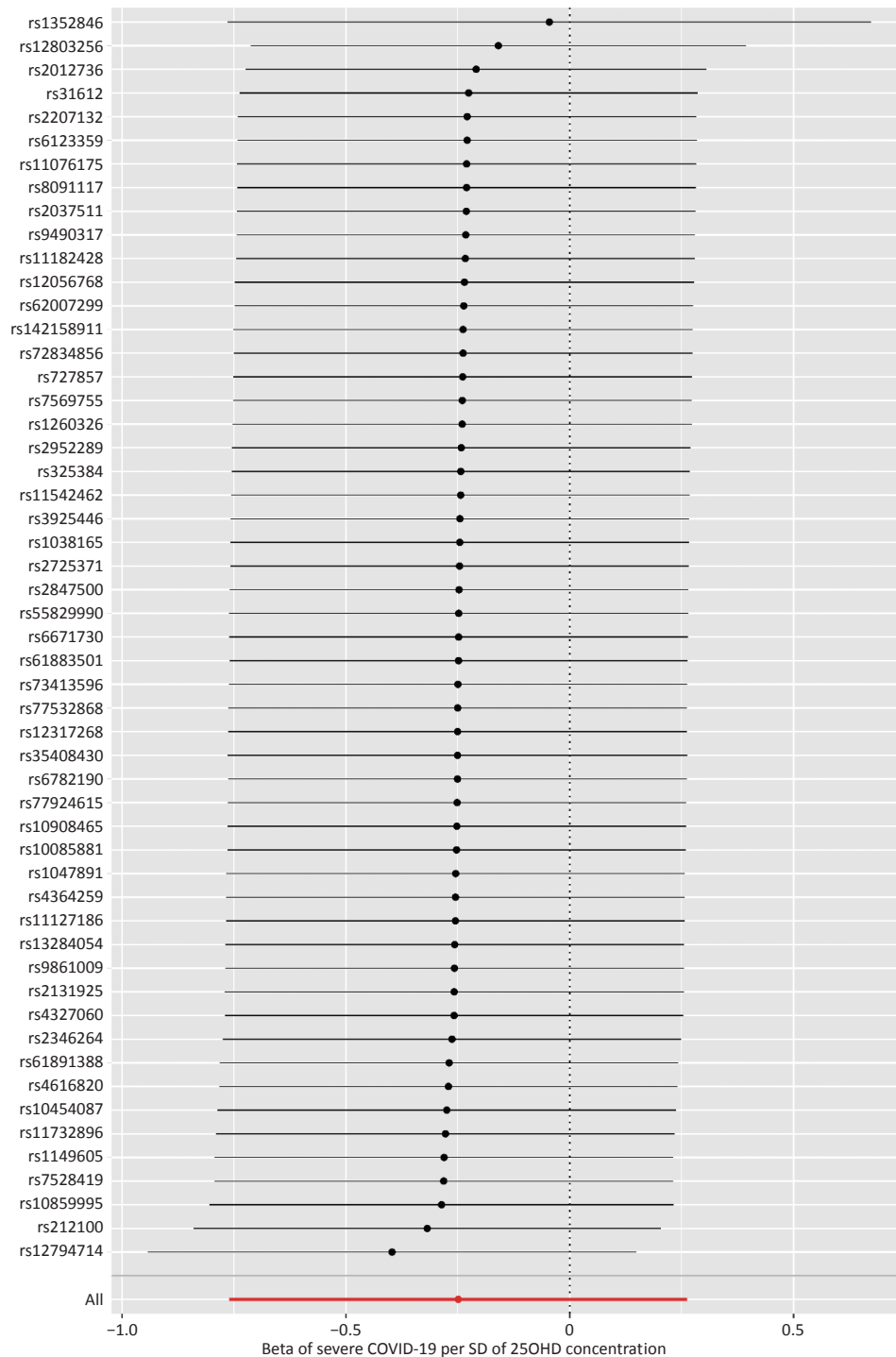
**Supplementary Figure S6.** MR leave-one-out sensitivity analysis for '25OHD concentration' on 'severe COVID-19' in the population of severe COVID-19 based on 82 SNPs. Leave-one-out analysis: each row represents a MR analysis of 25OHD concentration on severe COVID-19 using all instruments expect for the SNP listed on the y-axis. The point represents the beta with that SNP removed and the line represents 95% confidence interval. The summary data are reported by the severe COVID-19 GWAS Group. COVID-19, coronavirus disease 2019; MR, mendelian randomization; SNP, single-nucleotide polymorphism; 25OHD, 25-hydroxyitamin D; SD, standard deviation; GWAS, genome wide association study.

**Supplementary Figure S7.** MR leave-one-out sensitivity analysis for '25OHD concentration' on 'severe COVID-19' in the population of severe UKB-COVID-19 based on 55 SNPs. Leave-one-out analysis: each row represents a MR analysis of 25OHD concentration on severe COVID-19 using all instruments expect for the SNP listed on the y-axis. The point represents the beta with that SNP removed and the line represents 95% confidence interval. The summary data are reported by the COVID-19 host genetics initiative. COVID-19, coronavirus disease 2019; MR, mendelian randomization; SNP, single-nucleotide polymorphism; 25OHD, 25-hydroxyitamin D; SD, standard deviation; UKB, UK biobank.

**Supplementary Figure S8.** MR leave-one-out sensitivity analysis for '25OHD concentration' on 'severe COVID-19' in the population of severe COVID-19 based on 53 SNPs. Leave-one-out analysis: each row represents a MR analysis of 25OHD concentration on severe COVID-19 using all instruments expect for the SNP listed on the y-axis. The point represents the beta with that SNP removed and the line represents 95% confidence interval. The summary data are reported by the severe COVID-19 GWAS Group. COVID-19, coronavirus disease 2019; MR, mendelian randomization; SNP, single-nucleotide polymorphism; 25OHD, 25-hydroxyitamin D; SD, standard deviation; GWAS, genome wide association study.