**Table S1. Association of Serum HDL cholesterol, ApoA1, Triglyceride Levels with Risk of Severe SARS-CoV-2 Infection After Exclusion of Subjects who Died from COVID-19.**

IQR=interquartile range.

Sample sizes (n) indicate number of cases/controls. Data are shown as odds ratios (OR) and 95% confidence intervals (CI).

[a]Logistic regression analysis: Model 1 was adjusted for age, sex, PC1-10, obesity, hypertension, type 2 diabetes, and CAD. Model 2 included the same covariates as model 1 with additional adjustment for BMI, education, and smoking.

[b]Conditional logistic regression analysis: Model 1 was only adjusted for PC1-10 and did not include any of the matching variables (age, sex, obesity, hypertension, type 2 diabetes, and CAD). Model 2 was adjusted for PC1-10, BMI, education, and smoking.

| | [a]Cases vs. Unmatched Hospital-based Controls | | | | [b]Cases vs. Matched Hospital-based Controls | | | |
|---|---|---|---|---|---|---|---|---|
| **Trait** | | **Per 10mg/dL** | **Per IQR** | | | **Per 10mg/dL** | **Per IQR** | |
| **HDL cholesterol** | **n** | **OR (95% CI)** | **OR (95% CI)** | **P-value** | **n** | **OR (95% CI)** | **OR (95% CI)** | **P-value** |
| Model 1 | 502/3087 | 0.88 (0.82 - 0.96) | 0.79 (0.68 - 0.92) | 2.0E-04 | 345/690 | 0.84 (0.75 - 0.95) | 0.73 (0.60 - 0.90) | 3.4E-03 |
| Model 2 | 502/3087 | 0.90 (0.83 - 0.98) | 0.82 (0.71 - 0.96) | 0.01 | 345/690 | 0.86 (0.76 - 0.96) | 0.75 (0.60 - 0.94) | 0.01 |
| **ApoA1** | | | | | | | | |
| Model 1 | 502/3069 | 0.95 (0.91 - 0.99) | 0.82 (0.71 - 0.95) | 8.0E-03 | 346/692 | 0.93 (0.88 - 0.98) | 0.78 (0.64 - 0.94) | 0.01 |
| Model 2 | 502/3069 | 0.96 (0.92 - 0.99) | 0.85 (0.74 - 0.99) | 0.03 | 346/692 | 0.93 (0.88 - 0.99) | 0.79 (0.64 - 0.97) | 0.02 |
| **Triglycerides** | | | | | | | | |
| Model 1 | 545/3365 | 1.01 (1.00 - 1.02) | 1.11 (1.00 - 1.23) | 0.04 | 373/745 | 1.02 (1.01 - 1.04) | 1.25 (1.07 - 1.44) | 3.7E-03 |
| Model 2 | 545/3365 | 1.01 (1.00 - 1.02) | 1.09 (0.98 - 1.21) | 0.10 | 373/745 | 1.02 (1.01 - 1.04) | 1.23 (1.06 - 1.42) | 7.5E-03 |

**Table S2. Association of 155 Previously Reported HDL Cholesterol SNPs with Lipid Levels in the UK Biobank.**

EA, effect (HDL cholesterol raising) allele; NEA, non-effect allele.

Linear regression analyses were carried out in subjects of self-reported white European ancestry for whom each lipid trait was available, with adjustment for age, sex, PC1-10, and genotyping array.

[a]Based on log-transformed values.

[b]Proxy for previously reported variant.

[c]Excluded from tier 1 in MR analyses due to being either palindromic (rs4655268 and rs4766578) or missing association results for SARS-CoV-2 infection (rs77375493, rs138326449, rs139271800).

[d]Considered as tier 2 SNP in MR analyses (see Table S6).

| | | | | | | HDL cholesterol (mg/dL) | | | | Triglycerides (mg/dL) | | | | LDL cholesterol (mg/dL) | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **SNP** | **CHR** | **BP (hg19)** | **EA** | **NEA** | **EAF** | **N** | **BETA** | **SE** | **P-value** | **N** | **[a]BETA** | **[a]SE** | **[a]P-Value** | **N** | **BETA** | **SE** | **P-value** |
| rs79598313 | 1 | 27,284,913 | C | T | 0.98 | 400,515 | 1.055 | 0.099 | 2.8E-26 | 437,275 | -0.042 | 0.004 | 6.6E-32 | 436,811 | -1.835 | 0.237 | 8.9E-15 |
| rs3768321 | 1 | 40,035,928 | G | T | 0.81 | 399,400 | 0.682 | 0.038 | 1.9E-72 | 436,051 | -0.014 | 0.001 | 6.8E-25 | 435,587 | 0.116 | 0.090 | 2.0E-01 |
| [b]rs11207977 | 1 | 62,977,307 | C | T | 0.65 | 400,620 | 0.193 | 0.032 | 9.8E-10 | 437,382 | 0.041 | 0.001 | 2.1E-292 | 436,919 | 1.340 | 0.075 | 1.7E-71 |
| [d]rs10874777 | 1 | 93,862,020 | T | C | 0.37 | 397,552 | 0.307 | 0.031 | 8.3E-23 | 434,036 | -0.006 | 0.001 | 1.9E-08 | 433,575 | 0.202 | 0.074 | 6.5E-03 |
| rs2878349 | 1 | 107,549,245 | G | A | 0.67 | 400,068 | 0.056 | 0.032 | 0.08 | 436,803 | 0.001 | 0.001 | 0.60 | 436,342 | -0.424 | 0.076 | 2.4E-08 |
| rs3832016 | 1 | 109,818,158 | C | CT | 0.22 | 400,524 | 0.426 | 0.037 | 2.5E-31 | 437,281 | -0.005 | 0.001 | 8.7E-05 | 436,818 | -3.948 | 0.087 | 7.9E-450 |
| rs10494363 | 1 | 149,909,495 | A | G | 0.08 | 400,323 | 0.364 | 0.056 | 7.9E-11 | 437,066 | -0.014 | 0.002 | 7.9E-12 | 436,603 | -0.081 | 0.133 | 5.4E-01 |
| [d]rs267738 | 1 | 150,940,625 | G | T | 0.22 | 400,718 | 0.309 | 0.036 | 1.7E-17 | 437,493 | 0.000 | 0.001 | 0.88 | 437,029 | -0.283 | 0.086 | 1.0E-03 |
| [d]rs4077194 | 1 | 178,533,832 | G | T | 0.47 | 400,074 | 0.256 | 0.030 | 2.0E-17 | 436,795 | -0.005 | 0.001 | 1.0E-06 | 436,333 | 0.157 | 0.072 | 2.8E-02 |
| [d]rs61805076 | 1 | 182,154,990 | T | C | 0.67 | 398,982 | 0.391 | 0.032 | 1.6E-34 | 435,594 | -0.002 | 0.001 | 0.08 | 435,134 | -0.369 | 0.076 | 1.2E-06 |
| rs10911505 | 1 | 184,049,978 | T | C | 0.64 | 397,843 | 0.086 | 0.031 | 6.1E-03 | 434,334 | -0.002 | 0.001 | 0.04 | 433,873 | 0.167 | 0.075 | 2.5E-02 |
| [d]rs823114 | 1 | 205,719,532 | A | G | 0.54 | 400,104 | 0.183 | 0.030 | 1.3E-09 | 436,816 | -0.002 | 0.001 | 0.049 | 436,353 | 0.061 | 0.072 | 4.0E-01 |
| [c]rs4655268 | 1 | 214,992,980 | C | G | 0.45 | 382,884 | 0.063 | 0.031 | 0.04 | 418,057 | -0.001 | 0.001 | 0.43 | 417,618 | 0.156 | 0.073 | 3.4E-02 |
| rs2066152 | 1 | 219,664,030 | A | G | 0.39 | 394,334 | 0.208 | 0.031 | 1.8E-11 | 430,489 | -0.011 | 0.001 | 3.6E-22 | 430,034 | -0.155 | 0.074 | 0.04 |
| rs2642438 | 1 | 220,970,028 | G | A | 0.71 | 400,718 | 0.379 | 0.033 | 8.6E-31 | 437,493 | -0.006 | 0.001 | 3.2E-08 | 437,029 | 0.845 | 0.078 | 3.2E-27 |
| rs4846914 | 1 | 230,295,691 | A | G | 0.60 | 400,718 | 0.866 | 0.031 | 1.6E-174 | 437,493 | -0.025 | 0.001 | 3.0E-113 | 437,029 | -0.221 | 0.073 | 2.6E-03 |
| [d]rs6710091 | 2 | 239,597 | G | C | 0.35 | 400,262 | 0.200 | 0.032 | 2.3E-10 | 436,991 | -0.005 | 0.001 | 3.1E-05 | 436,527 | 0.137 | 0.075 | 6.9E-02 |
| [d]rs4850047 | 2 | 3,634,753 | T | C | 0.13 | 400,718 | 0.359 | 0.044 | 6.0E-16 | 437,493 | -0.009 | 0.002 | 2.0E-08 | 437,029 | 0.645 | 0.106 | 1.0E-09 |
| rs676210 | 2 | 21,231,524 | A | G | 0.21 | 400,718 | 0.904 | 0.037 | 1.4E-130 | 437,493 | -0.038 | 0.001 | 4.2E-185 | 437,029 | -1.655 | 0.088 | 4.0E-78 |
| rs17615494 | 2 | 58,950,363 | G | T | 0.71 | 393,111 | 0.179 | 0.034 | 9.2E-08 | 429,146 | -0.005 | 0.001 | 1.3E-04 | 428,697 | 0.104 | 0.080 | 1.9E-01 |
| rs6728523 | 2 | 65,282,708 | C | G | 0.24 | 399,599 | 0.169 | 0.035 | 1.5E-06 | 436,276 | -0.008 | 0.001 | 2.0E-11 | 435,814 | 0.085 | 0.084 | 3.1E-01 |
| rs2280334 | 2 | 66,665,146 | C | T | 0.68 | 400,718 | 0.187 | 0.032 | 5.6E-09 | 437,493 | -0.004 | 0.001 | 3.3E-04 | 437,029 | 0.031 | 0.076 | 6.9E-01 |
| rs6720034 | 2 | 111,664,756 | A | G | 0.64 | 399,659 | 0.149 | 0.031 | 1.9E-06 | 436,345 | 0.001 | 0.001 | 0.26 | 435,882 | 0.101 | 0.074 | 1.7E-01 |
| rs13396091 | 2 | 146,371,961 | G | A | 0.56 | 399,835 | 0.100 | 0.030 | 9.2E-04 | 436,524 | -0.005 | 0.001 | 4.9E-06 | 436,061 | -0.172 | 0.072 | 1.7E-02 |
| rs5835988 | 2 | 165,501,927 | TG | T | 0.41 | 398,899 | 0.424 | 0.031 | 2.1E-43 | 435,476 | -0.019 | 0.001 | 1.7E-69 | 435,010 | -0.402 | 0.073 | 3.5E-08 |
| rs72926946 | 2 | 203,477,868 | C | A | 0.71 | 399,648 | 0.273 | 0.033 | 1.1E-16 | 436,327 | 0.005 | 0.001 | 2.3E-05 | 435,866 | 0.544 | 0.078 | 3.7E-12 |
| [b]rs78058190 | 2 | 219,699,999 | G | A | 0.97 | 369,221 | 1.080 | 0.088 | 8.3E-35 | 403,163 | -0.042 | 0.003 | 3.8E-42 | 402,738 | 0.168 | 0.208 | 4.2E-01 |
| rs2203452 | 2 | 227,094,758 | A | G | 0.35 | 400,602 | 0.626 | 0.031 | 2.1E-88 | 437,364 | -0.021 | 0.001 | 1.6E-81 | 436,900 | -0.025 | 0.075 | 7.4E-01 |
| rs35240997 | 3 | 12,379,351 | G | A | 0.21 | 398,434 | 0.252 | 0.037 | 7.3E-12 | 434,999 | -0.011 | 0.001 | 1.4E-16 | 434,540 | 0.235 | 0.087 | 7.1E-03 |
| rs2044753 | 3 | 24,293,001 | T | C | 0.89 | 399,072 | 0.210 | 0.048 | 1.3E-05 | 435,688 | -0.007 | 0.002 | 1.2E-05 | 435,226 | -0.087 | 0.115 | 4.5E-01 |
| rs6777217 | 3 | 36,979,042 | G | A | 0.56 | 399,114 | 0.148 | 0.030 | 1.1E-06 | 435,766 | -0.005 | 0.001 | 7.8E-07 | 435,305 | -0.135 | 0.072 | 6.2E-02 |
| rs62246406 | 3 | 47,097,985 | G | A | 0.83 | 400,521 | 0.213 | 0.040 | 7.5E-08 | 437,274 | -0.001 | 0.001 | 0.29 | 436,810 | -0.159 | 0.094 | 9.1E-02 |

| | | | | | | HDL cholesterol (mg/dL) | | | | Triglycerides (mg/dL) | | | | LDL cholesterol (mg/dL) | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **SNP** | **CHR** | **BP (hg19)** | **EA** | **NEA** | **EAF** | **N** | **BETA** | **SE** | **P-value** | **N** | **[a]BETA** | **[a]SE** | **[a]P-Value** | **N** | **BETA** | **SE** | **P-value** |
| rs6808104 | 3 | 48,767,877 | A | G | 0.50 | 391,840 | 0.046 | 0.030 | 0.13 | 427,742 | -0.001 | 0.001 | 0.21 | 427,284 | 0.086 | 0.072 | 2.4E-01 |
| [d]rs111439884 | 3 | 50,024,038 | A | C | 0.50 | 364,876 | 0.327 | 0.032 | 2.7E-25 | 398,339 | -0.004 | 0.001 | 1.7E-03 | 397,925 | 0.175 | 0.075 | 2.0E-02 |
| rs11706108 | 3 | 52,372,366 | C | T | 0.19 | 400,080 | 0.336 | 0.038 | 1.4E-18 | 436,790 | -0.015 | 0.001 | 7.6E-27 | 436,326 | -0.119 | 0.091 | 1.9E-01 |
| rs151105710 | 3 | 136,125,678 | TTAAA | G | 0.20 | 392,874 | 0.302 | 0.038 | 1.5E-15 | 428,937 | -0.012 | 0.001 | 3.1E-20 | 428,486 | -0.338 | 0.090 | 1.7E-04 |
| rs3773910 | 3 | 152,171,870 | G | C | 0.26 | 396,945 | 0.135 | 0.034 | 8.9E-05 | 433,350 | 0.000 | 0.001 | 0.97 | 432,890 | 0.279 | 0.082 | 6.4E-04 |
| rs9817452 | 3 | 156,795,414 | T | G | 0.38 | 398,010 | 0.258 | 0.031 | 1.0E-16 | 434,529 | -0.010 | 0.001 | 5.8E-18 | 434,072 | 0.043 | 0.074 | 5.6E-01 |
| [d]rs2268840 | 3 | 185,931,174 | C | T | 0.23 | 400,718 | 0.250 | 0.036 | 2.6E-12 | 437,493 | -0.001 | 0.001 | 0.30 | 437,029 | 0.037 | 0.085 | 6.6E-01 |
| rs11248051 | 4 | 858,332 | C | T | 0.91 | 400,718 | 0.214 | 0.052 | 4.0E-05 | 437,493 | -0.007 | 0.002 | 1.0E-04 | 437,029 | 0.009 | 0.124 | 9.4E-01 |
| [b]rs73243877 | 4 | 26,047,616 | A | G | 0.84 | 400,718 | 0.395 | 0.040 | 8.7E-23 | 437,493 | -0.015 | 0.001 | 1.2E-24 | 437,029 | -0.282 | 0.096 | 3.2E-03 |
| rs1117816 | 4 | 69,349,018 | C | A | 0.24 | 400,178 | 0.238 | 0.035 | 1.0E-11 | 436,903 | 0.008 | 0.001 | 9.0E-10 | 436,439 | 0.750 | 0.083 | 1.9E-19 |
| rs13133548 | 4 | 89,740,128 | G | A | 0.55 | 400,718 | 0.285 | 0.030 | 3.4E-21 | 437,493 | -0.008 | 0.001 | 2.9E-14 | 437,029 | -0.119 | 0.072 | 9.7E-02 |
| rs12509976 | 4 | 100,517,324 | T | C | 0.04 | 400,672 | 0.380 | 0.077 | 8.4E-07 | 437,441 | 0.010 | 0.003 | 1.7E-04 | 436,977 | 0.570 | 0.184 | 1.9E-03 |
| rs13107325 | 4 | 103,188,709 | C | T | 0.93 | 400,718 | 1.150 | 0.057 | 4.4E-90 | 437,493 | -0.016 | 0.002 | 4.3E-15 | 437,029 | 0.812 | 0.136 | 2.4E-09 |
| rs41278045 | 4 | 110,638,764 | A | G | 1.00 | 399,435 | 2.017 | 0.498 | 5.2E-05 | 436,097 | -0.076 | 0.018 | 2.1E-05 | 435,634 | -1.591 | 1.196 | 1.8E-01 |
| rs17369400 | 4 | 154,224,048 | A | G | 0.90 | 400,718 | 0.133 | 0.049 | 6.7E-03 | 437,493 | 0.008 | 0.002 | 2.7E-06 | 437,029 | 0.544 | 0.117 | 3.4E-06 |
| rs4691380 | 4 | 157,720,124 | T | C | 0.33 | 400,718 | 0.149 | 0.032 | 3.5E-06 | 437,493 | -0.007 | 0.001 | 3.3E-10 | 437,029 | 0.015 | 0.076 | 8.4E-01 |
| rs28499105 | 5 | 53,274,467 | G | A | 0.30 | 394,897 | 0.180 | 0.033 | 4.5E-08 | 431,170 | -0.008 | 0.001 | 1.3E-11 | 430,723 | 0.163 | 0.078 | 3.7E-02 |
| rs459193 | 5 | 55,806,751 | A | G | 0.26 | 400,718 | 0.380 | 0.035 | 3.0E-28 | 437,493 | -0.017 | 0.001 | 2.2E-44 | 437,029 | 0.128 | 0.082 | 1.2E-01 |
| rs6881956 | 5 | 72,926,514 | G | A | 0.71 | 398,091 | 0.119 | 0.033 | 3.6E-04 | 434,639 | 0.002 | 0.001 | 0.16 | 434,174 | -0.067 | 0.079 | 4.0E-01 |
| rs2307111 | 5 | 75,003,678 | C | T | 0.40 | 400,718 | 0.293 | 0.031 | 1.8E-21 | 437,493 | -0.003 | 0.001 | 0.01 | 437,029 | 1.354 | 0.073 | 2.4E-76 |
| rs1045241 | 5 | 118,729,286 | T | C | 0.27 | 394,973 | 0.231 | 0.034 | 1.4E-11 | 431,225 | -0.011 | 0.001 | 4.4E-19 | 430,764 | -0.057 | 0.081 | 4.8E-01 |
| rs2434612 | 5 | 158,022,041 | A | G | 0.79 | 390,224 | 0.255 | 0.038 | 1.1E-11 | 426,032 | -0.011 | 0.001 | 1.0E-16 | 425,585 | -0.046 | 0.089 | 6.0E-01 |
| rs7730898 | 5 | 170,459,675 | G | A | 0.27 | 400,088 | 0.147 | 0.034 | 1.5E-05 | 436,799 | -0.003 | 0.001 | 0.04 | 436,336 | 0.027 | 0.080 | 7.3E-01 |
| [d]rs9368830 | 6 | 34,668,635 | T | C | 0.66 | 400,276 | 0.350 | 0.032 | 5.7E-28 | 437,007 | 0.000 | 0.001 | 0.88 | 436,544 | 0.109 | 0.076 | 1.5E-01 |
| [d]rs4130023 | 6 | 41,934,514 | C | T | 0.79 | 396,687 | 0.264 | 0.037 | 6.1E-13 | 433,086 | -0.004 | 0.001 | 1.3E-03 | 432,621 | -0.136 | 0.087 | 1.2E-01 |
| rs998584 | 6 | 43,757,896 | C | A | 0.52 | 396,507 | 0.462 | 0.030 | 7.5E-53 | 432,896 | -0.021 | 0.001 | 1.0E-85 | 432,437 | -0.290 | 0.072 | 5.5E-05 |
| rs2489629 | 6 | 127,476,717 | C | T | 0.45 | 400,630 | 0.267 | 0.030 | 1.0E-18 | 437,396 | -0.012 | 0.001 | 4.5E-30 | 436,932 | -0.490 | 0.072 | 9.4E-12 |
| rs6925103 | 6 | 137,076,010 | C | T | 0.48 | 398,587 | 0.151 | 0.030 | 5.6E-07 | 435,173 | -0.001 | 0.001 | 0.61 | 434,715 | 0.192 | 0.072 | 7.5E-03 |
| rs199607859 | 6 | 139,835,418 | T | G | 0.59 | 396,110 | 0.304 | 0.031 | 5.2E-23 | 432,473 | -0.015 | 0.001 | 6.5E-45 | 432,011 | -0.270 | 0.073 | 2.2E-04 |
| rs11751347 | 6 | 161,092,438 | C | T | 0.90 | 397,247 | 0.830 | 0.050 | 4.3E-61 | 433,697 | -0.021 | 0.002 | 5.4E-31 | 433,234 | 0.662 | 0.120 | 3.3E-08 |
| [d]rs79949326 | 7 | 6,461,310 | T | C | 0.26 | 399,140 | 0.383 | 0.034 | 9.8E-29 | 435,762 | 0.001 | 0.001 | 0.62 | 435,302 | 0.331 | 0.082 | 5.3E-05 |
| rs3173615 | 7 | 12,269,417 | C | G | 0.58 | 400,718 | 0.161 | 0.030 | 1.2E-07 | 437,493 | -0.005 | 0.001 | 4.1E-06 | 437,029 | -0.104 | 0.072 | 1.5E-01 |
| rs1917368 | 7 | 17,911,752 | G | T | 0.60 | 399,475 | 0.388 | 0.031 | 1.9E-36 | 436,140 | -0.008 | 0.001 | 5.4E-14 | 435,681 | 0.172 | 0.073 | 1.8E-02 |
| rs4722593 | 7 | 26,370,190 | A | G | 0.36 | 384,681 | 0.149 | 0.032 | 2.7E-06 | 419,944 | -0.009 | 0.001 | 5.4E-14 | 419,493 | -0.104 | 0.076 | 1.7E-01 |
| rs55747707 | 7 | 73,037,366 | A | G | 0.20 | 398,723 | 0.551 | 0.038 | 1.1E-48 | 435,304 | -0.055 | 0.001 | 1.5E-374 | 434,845 | -0.110 | 0.089 | 2.2E-01 |
| rs3211938 | 7 | 80,300,449 | G | T | 0.001 | 400,674 | 2.049 | 2.254 | 0.36 | 437,440 | -0.008 | 0.082 | 0.92 | 436,976 | -5.021 | 5.446 | 3.6E-01 |
| rs6971365 | 7 | 130,432,481 | T | C | 0.71 | 398,643 | 0.465 | 0.033 | 7.9E-45 | 435,241 | -0.017 | 0.001 | 7.6E-46 | 434,780 | -0.318 | 0.079 | 5.3E-05 |
| rs17173637 | 7 | 150,529,449 | T | C | 0.92 | 400,718 | 0.300 | 0.054 | 2.7E-08 | 437,493 | -0.009 | 0.002 | 9.0E-07 | 437,029 | -0.245 | 0.129 | 5.7E-02 |
| rs2936512 | 8 | 6,599,005 | C | T | 0.68 | 394,755 | 0.159 | 0.032 | 8.3E-07 | 430,957 | -0.003 | 0.001 | 0.02 | 430,500 | 0.369 | 0.077 | 1.5E-06 |
| rs4841132 | 8 | 9,183,596 | G | A | 0.91 | 400,718 | 1.215 | 0.052 | 2.6E-119 | 437,493 | 0.003 | 0.002 | 0.08 | 437,029 | 1.518 | 0.125 | 3.8E-34 |
| rs79407615 | 8 | 19,850,099 | G | T | 0.10 | 400,614 | 2.369 | 0.051 | 1.1E-478 | 437,377 | -0.100 | 0.002 | 1.4E-674 | 436,912 | -0.522 | 0.121 | 1.5E-05 |

| | | | | | | HDL cholesterol (mg/dL) | | | | Triglycerides (mg/dL) | | | | LDL cholesterol (mg/dL) | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **SNP** | **CHR** | **BP (hg19)** | **EA** | **NEA** | **EAF** | **N** | **BETA** | **SE** | **P-value** | **N** | **[a]BETA** | **[a]SE** | **[a]P-Value** | **N** | **BETA** | **SE** | **P-value** |
| rs10504474 | 8 | 71,260,460 | G | A | 0.90 | 400,557 | 0.312 | 0.050 | 5.2E-10 | 437,317 | -0.004 | 0.002 | 0.05 | 436,852 | -0.058 | 0.120 | 6.3E-01 |
| [d]rs2721954 | 8 | 116,603,103 | T | C | 0.57 | 398,504 | 0.478 | 0.030 | 1.4E-55 | 435,109 | -0.003 | 0.001 | 6.4E-03 | 434,648 | -0.205 | 0.072 | 4.6E-03 |
| rs2954038 | 8 | 126,507,389 | A | C | 0.70 | 400,718 | 0.556 | 0.033 | 1.3E-64 | 437,493 | -0.045 | 0.001 | 7.1E-333 | 437,029 | -1.530 | 0.078 | 7.9E-86 |
| rs78123380 | 8 | 144,297,020 | A | G | 0.002 | 400,715 | 0.202 | 0.639 | 0.75 | 437,490 | 0.016 | 0.023 | 0.48 | 437,026 | 1.612 | 1.528 | 2.9E-01 |
| [c]rs77375493 | 9 | 5,073,770 | T | G | 0.0001 | 400,233 | 0.572 | 1.765 | 0.75 | 436,967 | -0.069 | 0.065 | 0.29 | 436,503 | -4.189 | 4.313 | 3.3E-01 |
| rs686030 | 9 | 15,304,782 | A | C | 0.86 | 399,977 | 0.786 | 0.043 | 4.8E-74 | 436,692 | 0.009 | 0.002 | 8.8E-09 | 436,229 | 0.356 | 0.103 | 5.4E-04 |
| rs10963012 | 9 | 17,295,541 | G | C | 0.26 | 356,125 | 0.041 | 0.037 | 0.26 | 388,690 | -0.002 | 0.001 | 0.10 | 388,266 | -0.187 | 0.087 | 3.2E-02 |
| rs4149307 | 9 | 107,589,744 | T | C | 0.16 | 400,278 | 0.957 | 0.042 | 3.6E-117 | 437,014 | 0.002 | 0.001 | 0.22 | 436,551 | 0.722 | 0.099 | 2.9E-13 |
| rs4749779 | 10 | 8,576,206 | G | A | 0.27 | 399,266 | 0.074 | 0.034 | 0.03 | 435,908 | -0.001 | 0.001 | 0.34 | 435,445 | -0.057 | 0.080 | 0.47 |
| [d]rs71515364 | 10 | 46,060,433 | T | TAA | 0.22 | 385,164 | 0.415 | 0.037 | 6.5E-29 | 420,418 | 0.000 | 0.001 | 0.82 | 419,968 | 0.161 | 0.088 | 6.9E-02 |
| [d]rs1408579 | 10 | 101,912,194 | T | C | 0.49 | 400,631 | 0.198 | 0.030 | 4.7E-11 | 437,395 | 0.006 | 0.001 | 1.1E-08 | 436,931 | 0.365 | 0.072 | 3.3E-07 |
| rs2792735 | 10 | 113,921,825 | G | A | 0.28 | 400,414 | 0.535 | 0.034 | 2.2E-57 | 437,168 | -0.010 | 0.001 | 1.2E-15 | 436,705 | 0.594 | 0.080 | 9.7E-14 |
| [d]rs72823013 | 10 | 115,786,233 | A | G | 0.12 | 398,711 | 0.443 | 0.045 | 1.9E-22 | 435,288 | -0.007 | 0.002 | 4.1E-05 | 434,822 | -0.731 | 0.108 | 1.4E-11 |
| rs2901286 | 10 | 122,900,623 | A | C | 0.01 | 400,718 | 0.387 | 0.136 | 4.3E-03 | 437,493 | -0.012 | 0.005 | 0.01 | 437,029 | 0.203 | 0.323 | 5.3E-01 |
| rs6486121 | 11 | 13,355,770 | C | T | 0.37 | 399,727 | 0.071 | 0.031 | 0.02 | 436,433 | -0.010 | 0.001 | 8.5E-18 | 435,968 | -0.086 | 0.074 | 2.5E-01 |
| rs150090666 | 11 | 14,865,399 | T | C | 0.001 | 400,274 | 5.449 | 0.566 | 6.7E-22 | 437,014 | -0.204 | 0.020 | 7.0E-24 | 436,551 | -3.920 | 1.354 | 3.8E-03 |
| rs11434755 | 11 | 18,067,020 | C | CA | 0.58 | 394,345 | 0.050 | 0.031 | 0.10 | 430,542 | -0.002 | 0.001 | 0.07 | 430,085 | 0.065 | 0.073 | 3.8E-01 |
| rs1519480 | 11 | 27,675,712 | T | C | 0.67 | 398,567 | 0.212 | 0.032 | 4.5E-11 | 435,135 | -0.007 | 0.001 | 1.7E-09 | 434,673 | 0.052 | 0.077 | 5.0E-01 |
| rs75393320 | 11 | 47,266,471 | C | G | 0.15 | 399,646 | 0.763 | 0.042 | 5.3E-74 | 436,336 | -0.014 | 0.001 | 1.9E-20 | 435,874 | 0.056 | 0.100 | 5.8E-01 |
| rs174537 | 11 | 61,552,680 | G | T | 0.66 | 400,356 | 0.844 | 0.032 | 5.4E-157 | 437,096 | -0.026 | 0.001 | 6.0E-118 | 436,633 | 1.104 | 0.075 | 1.0E-48 |
| rs71468663 | 11 | 64,018,104 | A | AC | 0.96 | 399,677 | 0.747 | 0.072 | 3.6E-25 | 436,349 | -0.035 | 0.003 | 1.7E-41 | 435,888 | -0.453 | 0.171 | 8.2E-03 |
| rs2306363 | 11 | 65,405,600 | T | G | 0.20 | 398,970 | 0.293 | 0.037 | 3.7E-15 | 435,586 | -0.010 | 0.001 | 4.6E-15 | 435,125 | 0.558 | 0.089 | 2.9E-10 |
| [b,d]rs11236564 | 11 | 75,567,227 | G | A | 0.92 | 398,426 | 0.544 | 0.054 | 1.5E-23 | 435,002 | 0.006 | 0.002 | 1.6E-03 | 434,543 | 0.218 | 0.129 | 9.3E-02 |
| [d]rs689183 | 11 | 110,012,143 | G | T | 0.25 | 396,273 | 0.241 | 0.035 | 5.5E-12 | 432,665 | -0.004 | 0.001 | 1.9E-03 | 432,211 | 0.009 | 0.083 | 9.1E-01 |
| [c]rs138326449 | 11 | 116,701,354 | A | G | 0.001 | 399,975 | 12.781 | 0.451 | 8.3E-177 | 436,674 | -0.553 | 0.016 | 1.1E-258 | 436,211 | -4.632 | 1.077 | 1.7E-05 |
| rs1945391 | 11 | 122,520,291 | T | A | 0.39 | 399,380 | 0.361 | 0.031 | 1.2E-31 | 436,040 | 0.002 | 0.001 | 0.08 | 435,578 | 0.427 | 0.073 | 6.3E-09 |
| rs11054527 | 12 | 7,725,583 | G | A | 0.05 | 400,029 | 0.286 | 0.073 | 8.3E-05 | 436,735 | -0.004 | 0.003 | 0.11 | 436,273 | -0.292 | 0.173 | 9.2E-02 |
| rs11045171 | 12 | 20,470,199 | G | A | 0.19 | 396,003 | 0.431 | 0.038 | 1.3E-29 | 432,364 | -0.013 | 0.001 | 1.2E-21 | 431,904 | -0.096 | 0.091 | 2.9E-01 |
| rs10842708 | 12 | 26,474,867 | A | G | 0.75 | 398,510 | 0.217 | 0.035 | 6.2E-10 | 435,094 | -0.008 | 0.001 | 5.8E-10 | 434,627 | 0.109 | 0.083 | 1.9E-01 |
| rs4551851 | 12 | 33,459,554 | G | A | 0.49 | 396,646 | 0.079 | 0.030 | 9.2E-03 | 433,048 | 0.000 | 0.001 | 0.83 | 432,591 | 0.134 | 0.072 | 6.2E-02 |
| rs1126930 | 12 | 49,399,132 | G | C | 0.96 | 400,718 | 0.260 | 0.081 | 1.4E-03 | 437,493 | -0.012 | 0.003 | 3.7E-05 | 437,029 | -0.158 | 0.194 | 4.1E-01 |
| rs3809114 | 12 | 57,848,639 | A | G | 0.56 | 376,925 | 0.397 | 0.031 | 4.9E-37 | 411,597 | -0.010 | 0.001 | 2.6E-18 | 411,155 | -0.218 | 0.074 | 3.4E-03 |
| rs2373459 | 12 | 101,873,956 | T | C | 0.67 | 398,470 | 0.148 | 0.032 | 3.8E-06 | 435,043 | -0.002 | 0.001 | 0.06 | 434,578 | 0.001 | 0.076 | 9.9E-01 |
| [d]rs7954144 | 12 | 110,015,893 | G | A | 0.52 | 400,611 | 0.344 | 0.030 | 2.5E-30 | 437,376 | 0.002 | 0.001 | 0.08 | 436,912 | 0.159 | 0.072 | 0.03 |
| [c]rs4766578 | 12 | 111,904,371 | A | T | 0.51 | 400,556 | 0.351 | 0.030 | 1.6E-31 | 437,310 | -0.004 | 0.001 | 3.5E-05 | 436,846 | 0.810 | 0.072 | 1.1E-29 |
| rs10507274 | 12 | 117,160,976 | C | T | 0.06 | 400,718 | 0.320 | 0.061 | 1.8E-07 | 437,493 | -0.003 | 0.002 | 0.13 | 437,029 | -0.294 | 0.146 | 4.4E-02 |
| [d]rs4759375 | 12 | 123,796,238 | T | C | 0.08 | 387,582 | 0.611 | 0.058 | 5.7E-26 | 423,139 | 0.001 | 0.002 | 0.54 | 422,698 | 0.392 | 0.138 | 4.5E-03 |
| [d]rs10773112 | 12 | 125,338,529 | T | C | 0.72 | 400,718 | 0.513 | 0.033 | 5.4E-53 | 437,493 | -0.001 | 0.001 | 0.45 | 437,029 | 0.149 | 0.080 | 6.2E-02 |
| [d]rs13379043 | 14 | 74,250,126 | C | T | 0.28 | 376,410 | 0.296 | 0.035 | 1.7E-17 | 410,904 | -0.003 | 0.001 | 0.02 | 410,476 | -0.378 | 0.083 | 4.8E-06 |
| [d]rs2494748 | 14 | 105,258,892 | C | T | 0.39 | 397,116 | 0.418 | 0.031 | 2.4E-41 | 433,550 | -0.003 | 0.001 | 0.01 | 433,091 | 0.048 | 0.074 | 5.1E-01 |
| [b]rs150844304 | 15 | 43,726,625 | A | C | 0.98 | 400,599 | 1.309 | 0.095 | 2.6E-43 | 437,367 | -0.073 | 0.003 | 9.7E-103 | 436,903 | -0.101 | 0.226 | 6.5E-01 |

| | | | | | | HDL cholesterol (mg/dL) | | | | Triglycerides (mg/dL) | | | | LDL cholesterol (mg/dL) | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **SNP** | **CHR** | **BP (hg19)** | **EA** | **NEA** | **EAF** | **N** | **BETA** | **SE** | **P-value** | **N** | **[a]BETA** | **[a]SE** | **[a]P-Value** | **N** | **BETA** | **SE** | **P-value** |
| rs139097404 | 15 | 43,933,941 | T | C | 0.98 | 398,986 | 1.281 | 0.101 | 8.2E-37 | 435,610 | -0.074 | 0.004 | 3.6E-93 | 435,151 | -0.005 | 0.241 | 9.8E-01 |
| [b]rs2043082 | 15 | 58,674,308 | A | G | 0.35 | 399,253 | 1.464 | 0.031 | 5.1E-474 | 435,903 | 0.013 | 0.001 | 3.3E-33 | 435,441 | 0.542 | 0.075 | 4.3E-13 |
| rs2245477 | 15 | 61,948,435 | C | A | 0.63 | 398,377 | 0.165 | 0.031 | 1.2E-07 | 434,918 | -0.007 | 0.001 | 8.3E-10 | 434,459 | -0.046 | 0.074 | 5.3E-01 |
| [d]rs55703462 | 15 | 63,395,428 | G | A | 0.53 | 391,627 | 0.213 | 0.030 | 2.9E-12 | 427,560 | -0.005 | 0.001 | 5.6E-07 | 427,104 | 0.168 | 0.072 | 2.1E-02 |
| [c]rs139271800 | 15 | 90,214,777 | G | A | 0.001 | 400,192 | 1.681 | 0.618 | 6.5E-03 | 436,912 | -0.078 | 0.022 | 3.8E-04 | 436,450 | -1.169 | 1.458 | 4.2E-01 |
| rs3751812 | 16 | 53,818,460 | G | T | 0.61 | 400,718 | 0.176 | 0.031 | 1.2E-08 | 437,493 | -0.001 | 0.001 | 0.48 | 437,029 | 0.463 | 0.073 | 2.5E-10 |
| rs821840 | 16 | 56,993,886 | G | A | 0.32 | 400,011 | 3.441 | 0.032 | 6.7E-2527 | 436,716 | -0.017 | 0.001 | 1.6E-50 | 436,253 | -1.109 | 0.076 | 1.2E-47 |
| [d]rs56070533 | 16 | 67,942,320 | A | G | 0.12 | 400,596 | 0.891 | 0.047 | 6.2E-79 | 437,355 | -0.007 | 0.002 | 2.9E-05 | 436,891 | 0.070 | 0.113 | 5.4E-01 |
| [d]rs16958751 | 16 | 69,357,406 | A | G | 0.04 | 400,718 | 0.368 | 0.076 | 1.3E-06 | 437,493 | -0.002 | 0.003 | 0.46 | 437,029 | 0.143 | 0.181 | 4.3E-01 |
| rs5471 | 16 | 72,088,461 | C | A | 0.001 | 400,648 | 1.659 | 1.916 | 0.39 | 437,419 | -0.204 | 0.069 | 3.0E-03 | 436,955 | 3.344 | 4.590 | 4.7E-01 |
| rs2925979 | 16 | 81,534,790 | C | T | 0.70 | 400,718 | 0.549 | 0.033 | 5.4E-63 | 437,493 | -0.017 | 0.001 | 1.3E-47 | 437,029 | -0.135 | 0.078 | 8.4E-02 |
| [d]rs12938449 | 17 | 486,821 | C | A | 0.81 | 399,930 | 0.247 | 0.038 | 8.4E-11 | 436,613 | -0.007 | 0.001 | 6.3E-08 | 436,152 | 0.009 | 0.090 | 9.2E-01 |
| [d]rs34879232 | 17 | 26,722,039 | G | GA | 0.45 | 393,083 | 0.201 | 0.030 | 4.8E-11 | 429,182 | 0.005 | 0.001 | 7.4E-07 | 428,721 | -0.401 | 0.073 | 3.2E-08 |
| [d]rs11078917 | 17 | 37,746,359 | C | A | 0.72 | 393,423 | 0.406 | 0.034 | 7.0E-33 | 429,565 | -0.002 | 0.001 | 0.07 | 429,110 | 0.147 | 0.081 | 6.9E-02 |
| rs72836561 | 17 | 41,926,126 | C | T | 0.97 | 400,718 | 2.261 | 0.086 | 1.1E-151 | 437,493 | -0.072 | 0.003 | 1.2E-121 | 437,029 | 0.637 | 0.205 | 1.9E-03 |
| rs56325564 | 17 | 45,766,771 | A | G | 0.48 | 390,132 | 0.109 | 0.031 | 3.6E-04 | 425,955 | -0.002 | 0.001 | 0.12 | 425,496 | 0.887 | 0.073 | 2.2E-34 |
| rs61676547 | 17 | 65,892,507 | G | C | 0.81 | 395,045 | 0.175 | 0.039 | 6.1E-06 | 431,267 | -0.012 | 0.001 | 6.4E-18 | 430,808 | -0.285 | 0.092 | 2.0E-03 |
| rs12601079 | 17 | 76,400,329 | A | G | 0.60 | 389,598 | 0.437 | 0.031 | 1.0E-44 | 425,356 | -0.010 | 0.001 | 2.7E-19 | 424,901 | 0.486 | 0.074 | 5.3E-11 |
| rs1788783 | 18 | 21,161,134 | T | C | 0.50 | 397,378 | 0.217 | 0.030 | 7.0E-13 | 433,847 | -0.008 | 0.001 | 1.6E-12 | 433,385 | -0.193 | 0.072 | 7.4E-03 |
| rs77960347 | 18 | 47,109,955 | G | A | 0.01 | 400,718 | 4.408 | 0.131 | 4.0E-249 | 437,493 | 0.018 | 0.005 | 1.5E-04 | 437,029 | 2.526 | 0.311 | 4.8E-16 |
| rs12975319 | 19 | 3,414,088 | G | A | 0.70 | 392,249 | 0.185 | 0.033 | 2.5E-08 | 428,270 | -0.002 | 0.001 | 0.049 | 427,815 | -0.111 | 0.079 | 1.6E-01 |
| rs56149994 | 19 | 7,242,261 | C | T | 0.79 | 394,895 | 0.210 | 0.038 | 2.4E-08 | 431,119 | -0.009 | 0.001 | 6.5E-12 | 430,663 | 0.091 | 0.090 | 3.1E-01 |
| rs116843064 | 19 | 8,429,323 | A | G | 0.02 | 400,718 | 3.020 | 0.109 | 2.4E-169 | 437,493 | -0.117 | 0.004 | 1.1E-198 | 437,029 | -0.081 | 0.259 | 7.6E-01 |
| rs2278426 | 19 | 11,350,488 | C | T | 0.96 | 400,718 | 1.231 | 0.082 | 4.1E-51 | 437,493 | 0.022 | 0.003 | 6.8E-14 | 437,029 | 1.448 | 0.195 | 1.0E-13 |
| [d]rs56121005 | 19 | 11,414,706 | C | T | 0.98 | 395,755 | 0.998 | 0.110 | 1.4E-19 | 432,066 | 0.016 | 0.004 | 4.6E-05 | 431,605 | 1.162 | 0.262 | 9.3E-06 |
| rs748891192 | 19 | 33,940,662 | G | :GGTG | 0.52 | 399,670 | 0.197 | 0.030 | 5.7E-11 | 436359 | -0.005 | 0.001 | 8.3E-07 | 435896 | 0.136 | 0.072 | 0.06 |
| rs429358 | 19 | 45,411,941 | T | C | 0.85 | 400,718 | 1.055 | 0.042 | 6.9E-142 | 437,493 | -0.031 | 0.001 | 2.6E-99 | 437,029 | -6.420 | 0.098 | 2.9E-921 |
| rs61743199 | 19 | 50,161,091 | A | G | 0.93 | 400,718 | 0.315 | 0.058 | 5.9E-08 | 437,493 | -0.003 | 0.002 | 0.13 | 437,029 | 0.349 | 0.138 | 0.01 |
| [d]rs74256604 | 19 | 52,304,069 | G | A | 0.88 | 395,517 | 0.274 | 0.046 | 2.6E-09 | 431,783 | -0.002 | 0.002 | 0.25 | 431,321 | -0.044 | 0.110 | 6.9E-01 |
| [d]rs380267 | 19 | 54,799,083 | G | A | 0.22 | 400,346 | 0.609 | 0.036 | 8.6E-64 | 437,081 | -0.005 | 0.001 | 8.0E-05 | 436,617 | 0.313 | 0.086 | 2.8E-04 |
| rs6120815 | 20 | 30,184,866 | C | T | 0.16 | 400,705 | 0.201 | 0.041 | 9.5E-07 | 437,479 | -0.007 | 0.001 | 5.5E-06 | 437,015 | 0.057 | 0.098 | 5.6E-01 |
| rs3746428 | 20 | 33,719,183 | G | A | 0.84 | 398,223 | 0.197 | 0.041 | 1.3E-06 | 434,778 | -0.001 | 0.001 | 0.61 | 434,317 | 0.169 | 0.097 | 8.1E-02 |
| rs1800961 | 20 | 43,042,364 | C | T | 0.97 | 400,718 | 1.956 | 0.086 | 3.5E-113 | 437,493 | -0.006 | 0.003 | 0.04 | 437,029 | 2.019 | 0.206 | 1.2E-22 |
| [d]rs2281279 | 20 | 46,290,250 | C | T | 0.30 | 400,718 | 0.215 | 0.033 | 5.0E-11 | 437,493 | 0.000 | 0.001 | 0.78 | 437,029 | 0.040 | 0.078 | 6.0E-01 |
| rs856404 | 20 | 51,263,786 | G | A | 0.34 | 398,089 | 0.186 | 0.032 | 5.4E-09 | 434,622 | -0.007 | 0.001 | 4.3E-09 | 434,159 | -0.015 | 0.076 | 8.4E-01 |
| rs2834707 | 21 | 36,343,552 | C | T | 0.64 | 398,680 | 0.149 | 0.031 | 1.7E-06 | 435,258 | -0.002 | 0.001 | 0.07 | 434,793 | 0.026 | 0.074 | 7.3E-01 |
| [d]rs235314 | 21 | 46,271,452 | C | T | 0.47 | 399,699 | 0.250 | 0.030 | 1.0E-16 | 436,366 | 0.002 | 0.001 | 0.02 | 435,903 | -0.062 | 0.072 | 3.8E-01 |
| [d]rs7444 | 22 | 21,976,934 | T | C | 0.80 | 400,427 | 0.445 | 0.038 | 1.7E-31 | 437,169 | 0.006 | 0.001 | 4.8E-06 | 436,705 | 0.369 | 0.091 | 4.6E-05 |
| rs8142788 | 22 | 29,400,515 | G | A | 0.85 | 388,011 | 0.125 | 0.042 | 3.0E-03 | 423,622 | -0.002 | 0.002 | 0.13 | 423,175 | -0.040 | 0.100 | 6.9E-01 |
| rs2899297 | 22 | 38,594,668 | G | A | 0.40 | 399,670 | 0.278 | 0.031 | 1.2E-19 | 436,353 | -0.011 | 0.001 | 2.7E-25 | 435,895 | -0.136 | 0.073 | 6.2E-02 |
| rs2294915 | 22 | 44,340,904 | C | T | 0.77 | 398,589 | 0.185 | 0.036 | 2.2E-07 | 435,191 | 0.005 | 0.001 | 1.3E-04 | 434,728 | 0.242 | 0.085 | 4.4E-03 |

**Table S3. Associations of 155 Previously Reported HDL Cholesterol SNPs with Risk of SARS-Cov-2 Infection.**

EA, effect (HDL cholesterol raising) allele; NEA, non-effect allele.

Logistic regression analyses for risk of SARS-CoV-2 infection using unmatched hospital-based controls were adjusted for age, sex, PC1-10, and genotyping array.

Conditional logistic regression analyses for risk of SARS-CoV-2 infection using matched hospital-based controls were adjusted for PC1-10 and genotyping array.

[a]Excluded from tier 1 in MR analyses due to being either palindromic (rs4655268 and rs4766578) or missing association results for SARS-CoV-2 infection (rs77375493, rs138326449, rs139271800).

[b]Considered as tier 2 SNP in MR analyses (see Table S6).

| | | | | | Cases vs. Unmatched Hospital-based Controls | | | | | Cases vs. Matched Hospital-based Controls | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **SNP** | **CHR** | **BP (hg19)** | **EA** | **NEA** | **N** | **OR** | **L95** | **U95** | **P-value** | **N** | **OR** | **L95** | **U95** | **P-value** |
| rs79598313 | 1 | 27,284,913 | C | T | 4,127 | 0.88 | 0.63 | 1.22 | 0.43 | 2156 | 0.90 | 0.60 | 1.37 | 0.63 |
| rs3768321 | 1 | 40,035,928 | G | T | 4,112 | 1.08 | 0.95 | 1.22 | 0.26 | 2142 | 0.98 | 0.84 | 1.15 | 0.81 |
| rs11207977 | 1 | 62,977,307 | C | T | 4,127 | 0.99 | 0.89 | 1.10 | 0.88 | 2157 | 1.12 | 0.97 | 1.28 | 0.12 |
| [b]rs10874777 | 1 | 93,862,020 | T | C | 4,090 | 0.96 | 0.87 | 1.07 | 0.48 | 2123 | 0.97 | 0.85 | 1.11 | 0.68 |
| rs2878349 | 1 | 107,549,245 | G | A | 4,125 | 1.04 | 0.93 | 1.16 | 0.50 | 2154 | 1.10 | 0.96 | 1.27 | 0.17 |
| rs3832016 | 1 | 109,818,158 | C | CT | 4,124 | 1.06 | 0.93 | 1.20 | 0.39 | 2156 | 1.01 | 0.86 | 1.18 | 0.92 |
| rs10494363 | 1 | 149,909,495 | A | G | 4,125 | 1.16 | 0.96 | 1.39 | 0.12 | 2157 | 1.21 | 0.97 | 1.51 | 0.10 |
| [b]rs267738 | 1 | 150,940,625 | G | T | 4,127 | 0.99 | 0.87 | 1.11 | 0.81 | 2157 | 0.95 | 0.82 | 1.11 | 0.55 |
| [b]rs4077194 | 1 | 178,533,832 | G | T | 4,120 | 0.96 | 0.87 | 1.06 | 0.41 | 2155 | 0.98 | 0.86 | 1.11 | 0.70 |
| [b]rs61805076 | 1 | 182,154,990 | T | C | 4,109 | 1.03 | 0.93 | 1.15 | 0.57 | 2147 | 1.14 | 0.99 | 1.31 | 0.06 |
| rs10911505 | 1 | 184,049,978 | T | C | 4,099 | 1.08 | 0.97 | 1.20 | 0.15 | 2140 | 1.02 | 0.89 | 1.17 | 0.76 |
| [b]rs823114 | 1 | 205,719,532 | A | G | 4,119 | 1.11 | 1.00 | 1.23 | 0.04 | 2149 | 1.16 | 1.02 | 1.32 | 0.03 |
| [a]rs4655268 | 1 | 214,992,980 | C | G | 3,955 | 0.99 | 0.89 | 1.09 | 0.79 | 2013 | 0.90 | 0.79 | 1.02 | 0.09 |
| rs2066152 | 1 | 219,664,030 | A | G | 4,067 | 1.02 | 0.92 | 1.13 | 0.73 | 2112 | 0.98 | 0.86 | 1.12 | 0.75 |
| rs2642438 | 1 | 220,970,028 | G | A | 4,127 | 1.07 | 0.96 | 1.20 | 0.23 | 2157 | 1.12 | 0.98 | 1.29 | 0.09 |
| rs4846914 | 1 | 230,295,691 | A | G | 4,127 | 1.02 | 0.92 | 1.14 | 0.69 | 2157 | 1.09 | 0.95 | 1.24 | 0.22 |
| [b]rs6710091 | 2 | 239,597 | G | C | 4,125 | 0.99 | 0.89 | 1.10 | 0.87 | 2156 | 0.96 | 0.84 | 1.09 | 0.54 |
| [b]rs4850047 | 2 | 3,634,753 | T | C | 4,127 | 1.09 | 0.94 | 1.27 | 0.23 | 2157 | 0.89 | 0.73 | 1.08 | 0.23 |
| rs676210 | 2 | 21,231,524 | A | G | 4,127 | 1.04 | 0.91 | 1.18 | 0.58 | 2157 | 0.95 | 0.81 | 1.11 | 0.50 |
| rs17615494 | 2 | 58,950,363 | G | T | 4,045 | 0.97 | 0.87 | 1.09 | 0.61 | 2089 | 1.10 | 0.95 | 1.27 | 0.20 |
| rs6728523 | 2 | 65,282,708 | C | G | 4,113 | 1.06 | 0.94 | 1.20 | 0.32 | 2144 | 1.04 | 0.89 | 1.20 | 0.63 |
| rs2280334 | 2 | 66,665,146 | C | T | 4,127 | 1.00 | 0.89 | 1.11 | 0.96 | 2157 | 0.97 | 0.85 | 1.11 | 0.70 |
| rs6720034 | 2 | 111,664,756 | A | G | 4,115 | 0.97 | 0.87 | 1.08 | 0.54 | 2155 | 1.09 | 0.95 | 1.25 | 0.22 |
| rs13396091 | 2 | 146,371,961 | G | A | 4,117 | 1.04 | 0.94 | 1.16 | 0.44 | 2145 | 0.98 | 0.86 | 1.11 | 0.74 |
| rs5835988 | 2 | 165,501,927 | TG | T | 4,111 | 1.05 | 0.94 | 1.16 | 0.38 | 2144 | 1.03 | 0.91 | 1.18 | 0.63 |
| rs72926946 | 2 | 203,477,868 | C | A | 4,113 | 1.05 | 0.94 | 1.17 | 0.40 | 2147 | 0.94 | 0.82 | 1.08 | 0.39 |
| rs78058190 | 2 | 219,699,999 | G | A | 3,847 | 1.03 | 0.77 | 1.38 | 0.82 | 1883 | 1.12 | 0.77 | 1.62 | 0.57 |
| rs2203452 | 2 | 227,094,758 | A | G | 4,127 | 1.03 | 0.92 | 1.15 | 0.61 | 2157 | 1.01 | 0.88 | 1.16 | 0.88 |
| rs35240997 | 3 | 12,379,351 | G | A | 4,110 | 1.11 | 0.98 | 1.26 | 0.09 | 2143 | 1.16 | 0.99 | 1.35 | 0.07 |

| | | | | | Cases vs. Unmatched Hospital-based Controls | | | | | Cases vs. Matched Hospital-based Controls | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **SNP** | **CHR** | **BP (hg19)** | **EA** | **NEA** | **N** | **OR** | **L95** | **U95** | **P-value** | **N** | **OR** | **L95** | **U95** | **P-value** |
| rs2044753 | 3 | 24,293,001 | T | C | 4,105 | 1.01 | 0.86 | 1.18 | 0.92 | 2145 | 0.98 | 0.81 | 1.20 | 0.86 |
| rs6777217 | 3 | 36,979,042 | G | A | 4,103 | 0.96 | 0.86 | 1.06 | 0.40 | 2134 | 0.91 | 0.80 | 1.04 | 0.16 |
| rs62246406 | 3 | 47,097,985 | G | A | 4,122 | 0.91 | 0.79 | 1.04 | 0.17 | 2154 | 0.90 | 0.76 | 1.06 | 0.21 |
| rs6808104 | 3 | 48,767,877 | A | G | 4,043 | 1.03 | 0.93 | 1.14 | 0.55 | 2075 | 1.10 | 0.97 | 1.24 | 0.16 |
| [b]rs111439884 | 3 | 50,024,038 | A | C | 3,747 | 0.90 | 0.81 | 1.01 | 0.07 | 1848 | 0.90 | 0.78 | 1.03 | 0.12 |
| rs11706108 | 3 | 52,372,366 | C | T | 4,123 | 0.89 | 0.78 | 1.02 | 0.09 | 2154 | 0.94 | 0.79 | 1.11 | 0.45 |
| rs151105710 | 3 | 136,125,678 | TTAA/ | G | 4,034 | 1.01 | 0.89 | 1.14 | 0.92 | 2068 | 0.91 | 0.78 | 1.07 | 0.27 |
| rs3773910 | 3 | 152,171,870 | G | C | 4,092 | 1.12 | 1.00 | 1.26 | 0.05 | 2127 | 1.17 | 1.01 | 1.35 | 0.04 |
| rs9817452 | 3 | 156,795,414 | T | G | 4,097 | 1.05 | 0.94 | 1.16 | 0.40 | 2125 | 0.94 | 0.83 | 1.08 | 0.40 |
| [b]rs2268840 | 3 | 185,931,174 | C | T | 4,127 | 1.04 | 0.92 | 1.17 | 0.57 | 2157 | 1.05 | 0.91 | 1.22 | 0.52 |
| rs11248051 | 4 | 858,332 | C | T | 4,127 | 1.25 | 1.03 | 1.51 | 0.02 | 2157 | 1.25 | 1.00 | 1.56 | 0.05 |
| rs73243877 | 4 | 26,047,616 | A | G | 4,127 | 1.02 | 0.89 | 1.17 | 0.79 | 2157 | 1.00 | 0.84 | 1.19 | 1.00 |
| rs1117816 | 4 | 69,349,018 | C | A | 4,121 | 0.95 | 0.85 | 1.07 | 0.43 | 2156 | 1.02 | 0.88 | 1.17 | 0.80 |
| rs13133548 | 4 | 89,740,128 | G | A | 4,127 | 1.02 | 0.92 | 1.13 | 0.76 | 2157 | 0.89 | 0.79 | 1.01 | 0.08 |
| rs12509976 | 4 | 100,517,324 | T | C | 4,127 | 0.79 | 0.60 | 1.04 | 0.10 | 2157 | 0.87 | 0.62 | 1.21 | 0.40 |
| rs13107325 | 4 | 103,188,709 | C | T | 4,127 | 0.89 | 0.74 | 1.07 | 0.21 | 2157 | 0.73 | 0.58 | 0.93 | 0.01 |
| rs41278045 | 4 | 110,638,764 | A | G | 4,112 | 3.26 | 0.41 | 25.70 | 0.26 | 2144 | NA | NA | NA | NA |
| rs17369400 | 4 | 154,224,048 | A | G | 4,127 | 0.94 | 0.80 | 1.11 | 0.46 | 2157 | 0.85 | 0.70 | 1.04 | 0.12 |
| rs4691380 | 4 | 157,720,124 | T | C | 4,127 | 0.95 | 0.85 | 1.06 | 0.38 | 2157 | 0.95 | 0.83 | 1.09 | 0.49 |
| rs28499105 | 5 | 53,274,467 | G | A | 4,068 | 1.15 | 1.03 | 1.28 | 0.01 | 2098 | 1.05 | 0.91 | 1.20 | 0.52 |
| rs459193 | 5 | 55,806,751 | A | G | 4,127 | 1.00 | 0.88 | 1.12 | 0.95 | 2157 | 0.97 | 0.84 | 1.13 | 0.73 |
| rs6881956 | 5 | 72,926,514 | G | A | 4,092 | 1.01 | 0.90 | 1.13 | 0.90 | 2125 | 0.98 | 0.85 | 1.13 | 0.73 |
| rs2307111 | 5 | 75,003,678 | C | T | 4,127 | 1.14 | 1.03 | 1.27 | 0.01 | 2157 | 1.09 | 0.96 | 1.24 | 0.20 |
| rs1045241 | 5 | 118,729,286 | T | C | 4,072 | 1.11 | 0.99 | 1.25 | 0.07 | 2111 | 1.12 | 0.97 | 1.29 | 0.13 |
| rs2434612 | 5 | 158,022,041 | A | G | 4,021 | 1.11 | 0.97 | 1.26 | 0.12 | 2057 | 1.04 | 0.88 | 1.22 | 0.69 |
| rs7730898 | 5 | 170,459,675 | G | A | 4,119 | 1.01 | 0.90 | 1.14 | 0.86 | 2148 | 1.06 | 0.91 | 1.22 | 0.47 |
| [b]rs9368830 | 6 | 34,668,635 | T | C | 4,125 | 0.97 | 0.87 | 1.09 | 0.64 | 2156 | 0.99 | 0.86 | 1.14 | 0.87 |
| [b]rs4130023 | 6 | 41,934,514 | C | T | 4,090 | 0.88 | 0.78 | 1.00 | 0.05 | 2118 | 0.89 | 0.76 | 1.03 | 0.12 |
| rs998584 | 6 | 43,757,896 | C | A | 4,090 | 1.06 | 0.96 | 1.18 | 0.23 | 2118 | 1.03 | 0.91 | 1.18 | 0.62 |
| rs2489629 | 6 | 127,476,717 | C | T | 4,126 | 0.98 | 0.88 | 1.08 | 0.64 | 2156 | 0.97 | 0.86 | 1.10 | 0.67 |
| rs6925103 | 6 | 137,076,010 | C | T | 4,110 | 0.95 | 0.86 | 1.05 | 0.31 | 2135 | 0.90 | 0.79 | 1.02 | 0.08 |
| rs199607859 | 6 | 139,835,418 | T | G | 4,088 | 1.07 | 0.96 | 1.18 | 0.23 | 2130 | 1.03 | 0.91 | 1.17 | 0.65 |
| rs11751347 | 6 | 161,092,438 | C | T | 4,094 | 1.03 | 0.87 | 1.22 | 0.75 | 2122 | 1.10 | 0.89 | 1.35 | 0.39 |
| [b]rs79949326 | 7 | 6,461,310 | T | C | 4,113 | 0.93 | 0.83 | 1.05 | 0.24 | 2145 | 0.93 | 0.80 | 1.08 | 0.35 |
| rs3173615 | 7 | 12,269,417 | C | G | 4,127 | 1.01 | 0.91 | 1.12 | 0.82 | 2157 | 1.02 | 0.90 | 1.16 | 0.76 |
| rs1917368 | 7 | 17,911,752 | G | T | 4,120 | 0.98 | 0.89 | 1.09 | 0.78 | 2145 | 1.00 | 0.88 | 1.14 | 0.98 |
| rs4722593 | 7 | 26,370,190 | A | G | 3,969 | 0.96 | 0.86 | 1.07 | 0.50 | 2027 | 0.97 | 0.84 | 1.12 | 0.68 |
| rs55747707 | 7 | 73,037,366 | A | G | 4,104 | 0.91 | 0.80 | 1.03 | 0.15 | 2138 | 1.03 | 0.88 | 1.20 | 0.75 |

| | | | | | Cases vs. Unmatched Hospital-based Controls | | | | | Cases vs. Matched Hospital-based Controls | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **SNP** | **CHR** | **BP (hg19)** | **EA** | **NEA** | **N** | **OR** | **L95** | **U95** | **P-value** | **N** | **OR** | **L95** | **U95** | **P-value** |
| rs3211938 | 7 | 80,300,449 | G | T | 4,126 | NA | NA | NA | NA | 2157 | NA | NA | NA | NA |
| rs6971365 | 7 | 130,432,481 | T | C | 4,110 | 1.00 | 0.89 | 1.12 | 0.99 | 2150 | 1.04 | 0.91 | 1.19 | 0.57 |
| rs17173637 | 7 | 150,529,449 | T | C | 4,127 | 1.02 | 0.84 | 1.22 | 0.87 | 2157 | 0.95 | 0.76 | 1.19 | 0.66 |
| rs2936512 | 8 | 6,599,005 | C | T | 4,062 | 1.04 | 0.94 | 1.16 | 0.44 | 2110 | 0.95 | 0.83 | 1.09 | 0.48 |
| rs4841132 | 8 | 9,183,596 | G | A | 4,127 | 1.09 | 0.91 | 1.30 | 0.36 | 2157 | 1.19 | 0.95 | 1.50 | 0.13 |
| rs79407615 | 8 | 19,850,099 | G | T | 4,126 | 1.20 | 1.03 | 1.42 | 0.02 | 2154 | 1.11 | 0.90 | 1.37 | 0.34 |
| rs10504474 | 8 | 71,260,460 | G | A | 4,125 | 0.94 | 0.79 | 1.12 | 0.49 | 2157 | 1.03 | 0.83 | 1.27 | 0.80 |
| [b]rs2721954 | 8 | 116,603,103 | T | C | 4,112 | 1.04 | 0.94 | 1.15 | 0.47 | 2143 | 1.07 | 0.94 | 1.22 | 0.32 |
| rs2954038 | 8 | 126,507,389 | A | C | 4,127 | 0.93 | 0.83 | 1.04 | 0.19 | 2157 | 0.90 | 0.79 | 1.04 | 0.15 |
| rs78123380 | 8 | 144,297,020 | A | G | 4,127 | NA | NA | NA | NA | 2157 | NA | NA | NA | NA |
| [a]rs77375493 | 9 | 5,073,770 | T | G | 4,121 | NA | NA | NA | NA | 2154 | NA | NA | NA | NA |
| rs686030 | 9 | 15,304,782 | A | C | 4,122 | 1.04 | 0.90 | 1.21 | 0.58 | 2150 | 1.20 | 1.00 | 1.45 | 0.06 |
| rs10963012 | 9 | 17,295,541 | G | C | 3,671 | 0.98 | 0.86 | 1.11 | 0.73 | 1769 | 0.95 | 0.81 | 1.12 | 0.55 |
| rs4149307 | 9 | 107,589,744 | T | C | 4,122 | 1.06 | 0.92 | 1.22 | 0.42 | 2155 | 1.12 | 0.94 | 1.33 | 0.21 |
| rs4749779 | 10 | 8,576,206 | G | A | 4,112 | 0.96 | 0.86 | 1.08 | 0.53 | 2145 | 1.03 | 0.90 | 1.18 | 0.70 |
| [b]rs71515364 | 10 | 46,060,433 | T | TAA | 3,981 | 0.97 | 0.86 | 1.11 | 0.68 | 2008 | 0.95 | 0.81 | 1.12 | 0.55 |
| [b]rs1408579 | 10 | 101,912,194 | T | C | 4,123 | 0.98 | 0.89 | 1.09 | 0.76 | 2151 | 1.05 | 0.92 | 1.19 | 0.46 |
| rs2792735 | 10 | 113,921,825 | G | A | 4,127 | 0.99 | 0.88 | 1.11 | 0.87 | 2157 | 0.93 | 0.81 | 1.08 | 0.34 |
| [b]rs72823013 | 10 | 115,786,233 | A | G | 4,110 | 0.99 | 0.85 | 1.16 | 0.89 | 2143 | 0.91 | 0.76 | 1.10 | 0.34 |
| rs2901286 | 10 | 122,900,623 | A | C | 4,127 | 1.08 | 0.72 | 1.63 | 0.70 | 2157 | 1.38 | 0.82 | 2.33 | 0.23 |
| rs6486121 | 11 | 13,355,770 | C | T | 4,118 | 1.08 | 0.97 | 1.20 | 0.16 | 2153 | 1.07 | 0.94 | 1.23 | 0.32 |
| rs150090666 | 11 | 14,865,399 | T | C | 4,123 | 0.48 | 0.06 | 3.90 | 0.49 | 2156 | 1.00 | 0.09 | 10.99 | 1.00 |
| rs11434755 | 11 | 18,067,020 | C | CA | 4,067 | 1.03 | 0.93 | 1.15 | 0.54 | 2106 | 1.14 | 1.00 | 1.30 | 0.05 |
| rs1519480 | 11 | 27,675,712 | T | C | 4,100 | 1.01 | 0.90 | 1.12 | 0.89 | 2131 | 1.04 | 0.91 | 1.19 | 0.59 |
| rs75393320 | 11 | 47,266,471 | C | G | 4,115 | 0.94 | 0.82 | 1.09 | 0.42 | 2145 | 0.95 | 0.80 | 1.14 | 0.60 |
| rs174537 | 11 | 61,552,680 | G | T | 4,121 | 0.97 | 0.87 | 1.08 | 0.57 | 2154 | 0.93 | 0.81 | 1.06 | 0.29 |
| rs71468663 | 11 | 64,018,104 | A | AC | 4,117 | 0.96 | 0.75 | 1.22 | 0.72 | 2155 | 0.95 | 0.71 | 1.28 | 0.75 |
| rs2306363 | 11 | 65,405,600 | T | G | 4,114 | 0.89 | 0.78 | 1.01 | 0.08 | 2149 | 0.97 | 0.83 | 1.14 | 0.72 |
| [b]rs11236564 | 11 | 75,567,227 | G | A | 4,108 | 1.00 | 0.83 | 1.21 | 1.00 | 2138 | 1.25 | 0.97 | 1.61 | 0.08 |
| [b]rs689183 | 11 | 110,012,143 | G | T | 4,077 | 0.94 | 0.84 | 1.07 | 0.36 | 2110 | 1.08 | 0.93 | 1.25 | 0.32 |
| [a]rs138326449 | 11 | 116,701,354 | A | G | 4,119 | NA | NA | NA | NA | 2148 | NA | NA | NA | NA |
| rs1945391 | 11 | 122,520,291 | T | A | 4,115 | 0.97 | 0.88 | 1.08 | 0.62 | 2147 | 0.92 | 0.81 | 1.05 | 0.23 |
| rs11054527 | 12 | 7,725,583 | G | A | 4,124 | 1.10 | 0.86 | 1.39 | 0.45 | 2152 | 1.20 | 0.89 | 1.62 | 0.23 |
| rs11045171 | 12 | 20,470,199 | G | A | 4,076 | 1.05 | 0.93 | 1.20 | 0.42 | 2120 | 1.15 | 0.98 | 1.35 | 0.09 |
| rs10842708 | 12 | 26,474,867 | A | G | 4,105 | 0.93 | 0.83 | 1.05 | 0.25 | 2131 | 0.95 | 0.82 | 1.10 | 0.47 |
| rs4551851 | 12 | 33,459,554 | G | A | 4,088 | 1.00 | 0.90 | 1.11 | 0.97 | 2126 | 1.06 | 0.93 | 1.20 | 0.40 |
| rs1126930 | 12 | 49,399,132 | G | C | 4,127 | 1.08 | 0.82 | 1.43 | 0.57 | 2157 | 1.32 | 0.92 | 1.89 | 0.13 |
| rs3809114 | 12 | 57,848,639 | A | G | 3,888 | 0.91 | 0.81 | 1.01 | 0.07 | 1,922 | 1.04 | 0.91 | 1.19 | 0.58 |

| | | | | | Cases vs. Unmatched Hospital-based Controls | | | | | Cases vs. Matched Hospital-based Controls | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **SNP** | **CHR** | **BP (hg19)** | **EA** | **NEA** | **N** | **OR** | **L95** | **U95** | **P-value** | **N** | **OR** | **L95** | **U95** | **P-value** |
| rs2373459 | 12 | 101,873,956 | T | C | 4,104 | 1.01 | 0.91 | 1.13 | 0.85 | 2,140 | 0.89 | 0.78 | 1.02 | 0.11 |
| [b]rs7954144 | 12 | 110,015,893 | G | A | 4,125 | 1.03 | 0.93 | 1.14 | 0.53 | 2,156 | 0.96 | 0.85 | 1.09 | 0.53 |
| [a]rs4766578 | 12 | 111,904,371 | A | T | 4,127 | 1.09 | 0.98 | 1.20 | 0.10 | 2,156 | 1.04 | 0.91 | 1.18 | 0.59 |
| rs10507274 | 12 | 117,160,976 | C | T | 4,127 | 0.99 | 0.80 | 1.22 | 0.94 | 2,157 | 1.12 | 0.86 | 1.44 | 0.40 |
| [b]rs4759375 | 12 | 123,796,238 | T | C | 3,995 | 0.93 | 0.76 | 1.14 | 0.46 | 2,037 | 0.97 | 0.77 | 1.24 | 0.83 |
| [b]rs10773112 | 12 | 125,338,529 | T | C | 4,127 | 1.03 | 0.91 | 1.15 | 0.67 | 2,157 | 1.06 | 0.92 | 1.22 | 0.44 |
| [b]rs13379043 | 14 | 74,250,126 | C | T | 3,866 | 0.89 | 0.79 | 1.01 | 0.07 | 1,931 | 0.91 | 0.78 | 1.06 | 0.20 |
| [b]rs2494748 | 14 | 105,258,892 | C | T | 4,088 | 0.94 | 0.85 | 1.05 | 0.25 | 2,125 | 0.90 | 0.80 | 1.02 | 0.11 |
| rs150844304 | 15 | 43,726,625 | A | C | 4,126 | 1.11 | 0.80 | 1.56 | 0.52 | 2,157 | 1.05 | 0.72 | 1.52 | 0.81 |
| rs139097404 | 15 | 43,933,941 | T | C | 4,105 | 0.96 | 0.68 | 1.34 | 0.81 | 2,145 | 0.90 | 0.61 | 1.32 | 0.59 |
| rs2043082 | 15 | 58,674,308 | A | G | 4,111 | 1.01 | 0.91 | 1.12 | 0.85 | 2,139 | 0.97 | 0.85 | 1.10 | 0.62 |
| rs2245477 | 15 | 61,948,435 | C | A | 4,108 | 0.95 | 0.86 | 1.06 | 0.36 | 2,137 | 0.84 | 0.73 | 0.96 | 0.01 |
| [b]rs55703462 | 15 | 63,395,428 | G | A | 4,060 | 1.01 | 0.91 | 1.12 | 0.92 | 2,089 | 0.99 | 0.87 | 1.12 | 0.84 |
| [a]rs139271800 | 15 | 90,214,777 | G | A | 4,122 | NA | NA | NA | NA | 2,152 | NA | NA | NA | NA |
| rs3751812 | 16 | 53,818,460 | G | T | 4,127 | 0.99 | 0.89 | 1.10 | 0.87 | 2,157 | 0.94 | 0.83 | 1.07 | 0.38 |
| rs821840 | 16 | 56,993,886 | G | A | 4,119 | 1.00 | 0.90 | 1.11 | 0.99 | 2,146 | 1.01 | 0.88 | 1.15 | 0.93 |
| [b]rs56070533 | 16 | 67,942,320 | A | G | 4,125 | 1.11 | 0.95 | 1.29 | 0.20 | 2,157 | 1.07 | 0.88 | 1.29 | 0.53 |
| [b]rs16958751 | 16 | 69,357,406 | A | G | 4,127 | 0.74 | 0.56 | 0.97 | 0.03 | 2,157 | 0.60 | 0.42 | 0.85 | 3.7E-03 |
| rs5471 | 16 | 72,088,461 | C | A | 4,127 | NA | NA | NA | NA | 2,155 | NA | NA | NA | NA |
| rs2925979 | 16 | 81,534,790 | C | T | 4,127 | 1.05 | 0.94 | 1.18 | 0.36 | 2,157 | 0.99 | 0.86 | 1.14 | 0.92 |
| [b]rs12938449 | 17 | 486,821 | C | A | 4,117 | 1.08 | 0.95 | 1.24 | 0.22 | 2,152 | 1.01 | 0.86 | 1.19 | 0.89 |
| [b]rs34879232 | 17 | 26,722,039 | G | GA | 4,044 | 0.90 | 0.81 | 1.00 | 0.04 | 2,079 | 0.93 | 0.81 | 1.06 | 0.25 |
| [b]rs11078917 | 17 | 37,746,359 | C | A | 4,058 | 1.01 | 0.90 | 1.14 | 0.81 | 2,105 | 1.04 | 0.90 | 1.20 | 0.58 |
| rs72836561 | 17 | 41,926,126 | C | T | 4,127 | 0.90 | 0.67 | 1.21 | 0.49 | 2,157 | 0.74 | 0.52 | 1.05 | 0.09 |
| rs56325564 | 17 | 45,766,771 | A | G | 4,015 | 0.99 | 0.89 | 1.10 | 0.88 | 2,061 | 0.99 | 0.87 | 1.13 | 0.91 |
| rs61676547 | 17 | 65,892,507 | G | C | 4,079 | 1.09 | 0.96 | 1.25 | 0.18 | 2,119 | 1.05 | 0.89 | 1.23 | 0.57 |
| rs12601079 | 17 | 76,400,329 | A | G | 4,002 | 1.08 | 0.97 | 1.21 | 0.15 | 2,061 | 1.06 | 0.93 | 1.21 | 0.39 |
| rs1788783 | 18 | 21,161,134 | T | C | 4,092 | 0.93 | 0.84 | 1.03 | 0.18 | 2,129 | 0.91 | 0.80 | 1.03 | 0.13 |
| rs77960347 | 18 | 47,109,955 | G | A | 4,127 | 1.13 | 0.73 | 1.74 | 0.59 | 2,157 | 1.07 | 0.63 | 1.81 | 0.81 |
| rs12975319 | 19 | 3,414,088 | G | A | 4,037 | 0.98 | 0.88 | 1.10 | 0.72 | 2,077 | 1.00 | 0.87 | 1.15 | 0.98 |
| rs56149994 | 19 | 7,242,261 | C | T | 4,077 | 1.03 | 0.91 | 1.17 | 0.67 | 2,112 | 1.14 | 0.97 | 1.34 | 0.11 |
| rs116843064 | 19 | 8,429,323 | A | G | 4,127 | 1.23 | 0.87 | 1.73 | 0.24 | 2,157 | 1.06 | 0.70 | 1.62 | 0.78 |
| rs2278426 | 19 | 11,350,488 | C | T | 4,127 | 1.14 | 0.86 | 1.49 | 0.37 | 2,157 | 1.05 | 0.75 | 1.45 | 0.79 |
| [b]rs56121005 | 19 | 11,414,706 | C | T | 4,078 | 1.34 | 0.92 | 1.96 | 0.13 | 2,114 | 1.21 | 0.78 | 1.88 | 0.39 |
| rs748891192 | 19 | 33,940,662 | G | GGTGTC | 4,121 | 1.03 | 0.87 | 1.21 | 0.76 | 2,145 | 0.97 | 0.85 | 1.10 | 0.63 |
| rs429358 | 19 | 45,411,941 | T | C | 4,127 | 0.79 | 0.69 | 0.90 | 4.6E-04 | 2,157 | 0.84 | 0.71 | 0.99 | 0.03 |
| rs61743199 | 19 | 50,161,091 | A | G | 4,127 | 1.12 | 0.92 | 1.37 | 0.26 | 2,157 | 1.10 | 0.86 | 1.41 | 0.45 |
| [b]rs74256604 | 19 | 52,304,069 | G | A | 4,081 | 1.01 | 0.86 | 1.19 | 0.90 | 2,109 | 1.01 | 0.83 | 1.23 | 0.94 |

| | | | | | Cases vs. Unmatched Hospital-based Controls | | | | | Cases vs. Matched Hospital-based Controls | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **SNP** | **CHR** | **BP (hg19)** | **EA** | **NEA** | **N** | **OR** | **L95** | **U95** | **P-value** | **N** | **OR** | **L95** | **U95** | **P-value** |
| [b]rs380267 | 19 | 54,799,083 | G | A | 4,120 | 0.93 | 0.83 | 1.06 | 0.28 | 2,150 | 0.92 | 0.78 | 1.07 | 0.28 |
| rs6120815 | 20 | 30,184,866 | C | T | 4,127 | 0.93 | 0.81 | 1.07 | 0.33 | 2,157 | 0.93 | 0.78 | 1.11 | 0.43 |
| rs3746428 | 20 | 33,719,183 | G | A | 4,099 | 1.03 | 0.89 | 1.19 | 0.69 | 2,134 | 1.05 | 0.88 | 1.26 | 0.57 |
| rs1800961 | 20 | 43,042,364 | C | T | 4,127 | 1.12 | 0.82 | 1.53 | 0.46 | 2,157 | 1.15 | 0.80 | 1.66 | 0.45 |
| [b]rs2281279 | 20 | 46,290,250 | C | T | 4,127 | 1.06 | 0.95 | 1.18 | 0.31 | 2,157 | 1.00 | 0.87 | 1.14 | 0.96 |
| rs856404 | 20 | 51,263,786 | G | A | 4,107 | 1.06 | 0.95 | 1.18 | 0.31 | 2,135 | 0.98 | 0.85 | 1.12 | 0.75 |
| rs2834707 | 21 | 36,343,552 | C | T | 4,111 | 1.02 | 0.91 | 1.13 | 0.78 | 2,134 | 1.05 | 0.92 | 1.20 | 0.48 |
| [b]rs235314 | 21 | 46,271,452 | C | T | 4,119 | 1.01 | 0.91 | 1.12 | 0.86 | 2,150 | 0.96 | 0.84 | 1.09 | 0.53 |
| [b]rs7444 | 22 | 21,976,934 | T | C | 4,122 | 1.05 | 0.92 | 1.19 | 0.50 | 2,147 | 0.99 | 0.84 | 1.16 | 0.86 |
| rs8142788 | 22 | 29,400,515 | G | A | 3,989 | 0.93 | 0.81 | 1.07 | 0.34 | 2,035 | 0.90 | 0.75 | 1.07 | 0.24 |
| rs2899297 | 22 | 38,594,668 | G | A | 4,115 | 0.97 | 0.87 | 1.08 | 0.56 | 2,142 | 0.98 | 0.86 | 1.11 | 0.77 |
| rs2294915 | 22 | 44,340,904 | C | T | 4,109 | 1.06 | 0.94 | 1.20 | 0.34 | 2,136 | 1.04 | 0.90 | 1.21 | 0.60 |

**Table S4. Association of ApoE4 Alleles with Severe SARS-Cov-2 Infection and Mortality from COVID-19 After Removal of Patients Diagnosed with Dementia or Alzheimer's Disease Prior to January 2020.**

Data are shown as odds ratios (OR) and 95% confidence intervals (CI).

*Only includes subjects with complete data on HDL cholesterol levels.

[a]Logistic regression analysis: Model 1 was adjusted for age, sex, obesity, hypertension, type 2 diabetes, CAD, BMI, education, smoking, PC1-10, and genotyping array. Model 2 was adjusted for the same variables as model 1 with additional adjustment for HDL cholesterol levels.

[b]Conditional logistic regression analysis: Model 1 was adjusted for BMI, education, smoking, PC1-10, and genotyping array. Model 2 was adjusted for the same variables as model 1 with additional adjustment for serum HDL cholesterol levels.

[c]P-values are for comparisons between E4/E4 vs. E3/E3 groups.

| | ApoE Genotypes | | | |
|---|---|---|---|---|
| **Comparison Groups*** | **E3/E3** | **E3/E4** | **E4/E4** | **[c]P-value** |
| **[a]Cases vs. Unmatched Hospital-based Controls (n)** | 492/1,719 | 197/696 | 34/68 | |
| Model 1 | 1 | 1.04 (0.86 - 1.26) | 1.86 (1.21 - 2.86) | 4.9E-03 |
| Model 2 | 1 | 1.03 (0.85 - 1.25) | 1.83 (1.19 - 2.83) | 5.7E-03 |
| **[b]Cases vs. Matched Hospital-based Controls (n)** | 324/625 | 118/236 | 20/21 | |
| Model 1 | 1 | 1.09 (0.82 - 1.46) | 2.15 (1.04 - 4.41) | 0.04 |
| Model 2 | 1 | 1.10 (0.83 - 1.48) | 2.13 (1.04 - 4.37) | 0.04 |
| **[a]Mortality among Cases (Yes/No)** | 209/283 | 87/110 | 19/15 | |
| Model 1 | 1 | 1.17 (0.79 - 1.75) | 2.52 (1.12 - 5.69) | 0.03 |
| Model 2 | 1 | 1.16 (0.78 - 1.73) | 2.52 (1.12 - 5.70) | 0.03 |

**Table S5. Cumulative Genetic Association of HDL Cholesterol-Raising Alleles with Risk of Severe SARS-Cov-2 Infection.**

Number of cases and controls for each comparison group are shown in parentheses.

Data are shown as odds ratios (OR) and 95% confidence intervals (CI) for a 1-unit increase in genetic risk scores (GRS) constructed for HDL cholesterol levels with 155 previously reported SNPs.

Unweighted GRS were based on summing the number of HDL cholesterol-raising alleles for each subject used from the UK Biobank.

Weighted GRS were constructed by multiplying the number of HDL cholesterol-raising alleles carried by each subject from the UK Biobank by the respective weight (beta) for each variant as shown in Table S2 or the weight taken from a previously reported GWAS for HDL levels (Klarin et al. 2018; PMID 30275531).

[a]Logistic regression adjusted for age, sex, obesity, hypertension, type 2 diabetes, CAD, BMI, education, smoking, PC1-10, and genotyping array.

[b]Conditional logistic regression adjusted for BMI, education, smoking, PC1-10, and genotyping array.

| | | GRS for HDL cholesterol (range) | | | | | |
|---|---|---|---|---|---|---|---|
| | | Unweighted (128-183) | | Weighted (61.8-95.8) | | Klarin et al. Weighted (5.28-8.23) | |
| **Comparison Groups** | **n** | **OR (95% CI)** | **P-value** | **OR (95% CI)** | **P-value** | **OR (95% CI)** | **P-value** |
| **[a]Cases vs. Unmatched Hospital-based Controls** | 1,117/3,544 | 1.00 (0.99 - 1.01) | 0.47 | 1.01 (0.99 - 1.02) | 0.50 | 1.10 (0.87 - 1.38) | 0.44 |
| **[b]Cases vs. Matched Hospital-based Controls** | 719/1,438 | 1.00 (0.99 - 1.01) | 0.82 | 1.00 (0.97 - 1.02) | 0.69 | 0.95 (0.70 - 1.29) | 0.75 |
| **[a]Mortality Among Cases (Yes/No)** | 526/591 | 1.00 (0.98 - 1.02) | 0.73 | 0.99 (0.96 - 1.02) | 0.54 | 0.84 (0.53 - 1.33) | 0.45 |

**Table S6. Mendelian Randomization Analyses with HDL Cholesterol-raising Alleles and Risk of Severe SARS-Cov-2 Infection.**

Data are shown as odds ratios (OR) and 95% confidence intervals (CI) for various combinations of HDL cholesterol-associated SNPs used as instrumental variables with HDL cholesterol as the exposures.

[a]Betas for HDL cholesterol levels and SARS-CoV-2 infection based on white European ancestry subjects and cases vs. unmatched hospital-based controls in the UK Biobank, respectively.

[b]Betas for HDL cholesterol levels and SARS-CoV-2 infection based on white European ancestry subjects and cases vs. matched hospital-based controls in the UK Biobank, respectively.

[c]Betas for HDL cholesterol levels and SARS-CoV-2 infection taken from Klarin et al. 2018 (PMID: 30275531) and Ellinghaus et al. 2020 (PMID: 32558485), respectively.

[d]Tier 1 did not include palindromic variants where both alleles had similar frequencies or SNPs with missing association results for HDL cholesterol levels or risk of SARS-CoV-2 infection.

[d]Tier 2: Only included variants associated with HDL cholesterol, but not LDL cholesterol or triglyceride, levels at the genome-wide significance threshold ($P=5.0x10^{-8}$) .

[e]Exposure variables in multivariate MR (MVMR) analyses were HDL cholesterol, LDL cholesterol, and triglyceride levels but only results for HDL cholesterol are shown.

| | | [a]Analysis I | | | [b]Analysis II | | | [c]Analysis III | | |
|---|---|---|---|---|---|---|---|---|---|---|
| **MR Method** | **[d]Tier** | **# of SNPs** | **OR (95% CI)** | **P-value** | **# of SNPs** | **OR (95% CI)** | **P-value** | **# of SNPs** | **OR (95% CI)** | **P-value** |
| MR Egger | 1 | 147 | 1.00 (0.97 - 1.03) | 0.95 | 146 | 0.99 (0.96 - 1.02) | 0.61 | 144 | 0.91 (0.57 - 1.47) | 0.71 |
| Weighted median | | 147 | 1.00 (0.97 - 1.03) | 0.99 | 146 | 1.00 (0.96 - 1.04) | 0.95 | 144 | 0.87 (0.63 - 1.21) | 0.42 |
| Inverse variance weighted | | 147 | 1.00 (0.98 - 1.01) | 0.64 | 146 | 0.98 (0.95 - 1.00) | 0.09 | 144 | 0.96 (0.56 - 1.64) | 0.88 |
| [e]Inverse variance weighted - MVMR | | 147 | 1.00 (0.97 - 1.02) | 0.79 | 146 | 0.99 (0.96 - 1.02) | 0.52 | 144 | N/A | N/A |
| MR Egger | 2 | 35 | 1.06 (0.89 - 1.26) | 0.53 | 35 | 1.02 (0.80 - 1.29) | 0.89 | 35 | 1.60 (0.20 - 13.1) | 0.66 |
| Weighted median | | 35 | 0.97 (0.90 - 1.06) | 0.54 | 35 | 0.92 (0.83 - 1.02) | 0.13 | 35 | 1.07 (0.44 - 2.62) | 0.88 |
| Inverse variance weighted | | 35 | 0.96 (0.90 - 1.02) | 0.19 | 35 | 0.93 (0.86 - 1.02) | 0.11 | 35 | 1.06 (0.29 - 3.84) | 0.93 |
| [e]Inverse variance weighted - MVMR | | 33 | 0.95 (0.88 - 1.02) | 0.17 | 33 | 0.95 (0.86 - 1.05) | 0.33 | 35 | N/A | N/A |