|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Supplementary Table 3. Genome-wide significant loci associated with risk-taking in UK Biobank: basic and conditional analyses** | | | | | | | | | | | | | | |
|  |  |  |  |  | Basic analysis (N =115 770) | | | | | Conditional analysis (n=115 770) | | | | |
| SNP | CHR | BP | A1 | MAF | BETA | SE | L95 | U95 | P | BETA | SE | L95 | U95 | P |
| rs10511087 | 3 | 85439136 | A | 0.379 | 0.055 | 0.010 | 0.036 | 0.075 | 3.44E-08 | 0.032 | 0.014 | 0.004 | 0.060 | 2.48E-02 |
| rs1368742 | 3 | 85442208 | A | 0.380 | 0.055 | 0.010 | 0.036 | 0.075 | 3.44E-08 | 0.032 | 0.014 | 0.004 | 0.060 | 2.63E-02 |
| rs1991872 | 3 | 85443793 | G | 0.379 | 0.055 | 0.010 | 0.036 | 0.075 | 3.51E-08 | 0.032 | 0.014 | 0.004 | 0.060 | 2.51E-02 |
| rs12637798 | 3 | 85446776 | A | 0.380 | 0.055 | 0.010 | 0.036 | 0.075 | 2.97E-08 | 0.032 | 0.014 | 0.004 | 0.061 | 2.37E-02 |
| rs4308294 | 3 | 85447830 | A | 0.379 | 0.055 | 0.010 | 0.036 | 0.075 | 3.18E-08 | 0.032 | 0.014 | 0.004 | 0.060 | 2.46E-02 |
| rs12638482 | 3 | 85454815 | C | 0.380 | 0.055 | 0.010 | 0.035 | 0.074 | 4.66E-08 | 0.031 | 0.014 | 0.003 | 0.059 | 3.15E-02 |
| rs11918899 | 3 | 85458577 | A | 0.381 | 0.055 | 0.010 | 0.035 | 0.074 | 4.52E-08 | 0.031 | 0.014 | 0.003 | 0.059 | 3.15E-02 |
| rs4856569 | 3 | 85464125 | A | 0.380 | 0.055 | 0.010 | 0.036 | 0.075 | 3.42E-08 | 0.030 | 0.014 | 0.002 | 0.058 | 3.39E-02 |
| rs80285517 | 3 | 85467372 | C | 0.378 | 0.056 | 0.010 | 0.037 | 0.076 | 1.87E-08 | 0.030 | 0.014 | 0.002 | 0.058 | 3.49E-02 |
| rs2053108 | 3 | 85467972 | C | 0.380 | 0.055 | 0.010 | 0.035 | 0.074 | 3.61E-08 | 0.029 | 0.014 | 0.001 | 0.057 | 4.40E-02 |
| rs6808400 | 3 | 85468059 | T | 0.380 | 0.055 | 0.010 | 0.035 | 0.074 | 3.61E-08 | 0.029 | 0.014 | 0.001 | 0.057 | 4.40E-02 |
| rs62250686 | 3 | 85468446 | T | 0.379 | 0.055 | 0.010 | 0.036 | 0.075 | 2.81E-08 | 0.029 | 0.014 | 0.000 | 0.057 | 4.65E-02 |
| rs6780968 | 3 | 85469041 | C | 0.380 | 0.055 | 0.010 | 0.035 | 0.074 | 3.51E-08 | 0.028 | 0.014 | 0.000 | 0.057 | 4.68E-02 |
| rs62250687 | 3 | 85469353 | T | 0.380 | 0.055 | 0.010 | 0.035 | 0.074 | 4.11E-08 | 0.028 | 0.014 | 0.000 | 0.056 | 4.87E-02 |
| rs60311538 | 3 | 85470687 | T | 0.380 | 0.055 | 0.010 | 0.035 | 0.074 | 3.90E-08 | 0.028 | 0.014 | 0.000 | 0.056 | 5.02E-02 |
| rs144059553 | 3 | 85471325 | AAC | 0.380 | 0.055 | 0.010 | 0.035 | 0.074 | 4.43E-08 | 0.028 | 0.014 | 0.000 | 0.056 | 4.91E-02 |
| rs7636243 | 3 | 85472033 | C | 0.380 | 0.055 | 0.010 | 0.035 | 0.074 | 3.68E-08 | 0.028 | 0.014 | 0.000 | 0.057 | 4.73E-02 |
| rs7650284 | 3 | 85472227 | T | 0.380 | 0.055 | 0.010 | 0.035 | 0.074 | 3.92E-08 | 0.028 | 0.014 | 0.000 | 0.056 | 4.76E-02 |
| rs7638953 | 3 | 85472462 | G | 0.380 | 0.055 | 0.010 | 0.035 | 0.074 | 4.36E-08 | 0.028 | 0.014 | 0.000 | 0.056 | 4.74E-02 |
| rs4856571 | 3 | 85474868 | G | 0.381 | 0.055 | 0.010 | 0.035 | 0.074 | 4.19E-08 | 0.027 | 0.014 | -0.001 | 0.055 | 6.24E-02 |
| rs35894540 | 3 | 85475647 | T | 0.380 | 0.055 | 0.010 | 0.035 | 0.074 | 3.71E-08 | 0.027 | 0.014 | -0.001 | 0.055 | 5.81E-02 |
| rs11716233 | 3 | 85481659 | T | 0.225 | 0.064 | 0.012 | 0.041 | 0.087 | 3.01E-08 | -0.008 | 0.102 | -0.207 | 0.191 | 9.37E-01 |
| rs35827242 | 3 | 85482661 | G | 0.380 | 0.055 | 0.010 | 0.035 | 0.075 | 3.59E-08 | 0.028 | 0.014 | 0.000 | 0.056 | 5.07E-02 |
| rs35489310 | 3 | 85486209 | G | 0.225 | 0.064 | 0.012 | 0.042 | 0.087 | 2.59E-08 | -0.012 | 0.102 | -0.211 | 0.187 | 9.08E-01 |
| rs12629036 | 3 | 85488299 | T | 0.380 | 0.054 | 0.010 | 0.035 | 0.074 | 4.77E-08 | 0.026 | 0.014 | -0.002 | 0.055 | 6.52E-02 |
| rs9874491 | 3 | 85489907 | T | 0.225 | 0.064 | 0.012 | 0.042 | 0.087 | 2.62E-08 | -0.008 | 0.102 | -0.207 | 0.192 | 9.40E-01 |
| rs2082556 | 3 | 85490947 | G | 0.381 | 0.054 | 0.010 | 0.035 | 0.074 | 4.97E-08 | 0.026 | 0.014 | -0.002 | 0.054 | 6.78E-02 |
| rs9820228 | 3 | 85493753 | T | 0.225 | 0.063 | 0.012 | 0.041 | 0.086 | 3.90E-08 | -0.074 | 0.104 | -0.279 | 0.130 | 4.76E-01 |
| rs2033526 | 3 | 85496758 | A | 0.384 | 0.057 | 0.010 | 0.037 | 0.077 | 1.34E-08 | 0.030 | 0.014 | 0.002 | 0.059 | 3.62E-02 |
| rs9828679 | 3 | 85497198 | C | 0.225 | 0.064 | 0.012 | 0.041 | 0.086 | 3.10E-08 | -0.068 | 0.104 | -0.273 | 0.137 | 5.16E-01 |
| rs145394945 | 3 | 85503999 | C | 0.379 | 0.055 | 0.010 | 0.035 | 0.074 | 4.74E-08 | 0.027 | 0.014 | -0.002 | 0.055 | 6.44E-02 |
| rs2196098 | 3 | 85505246 | G | 0.225 | 0.064 | 0.012 | 0.041 | 0.086 | 3.65E-08 | -0.095 | 0.106 | -0.302 | 0.113 | 3.71E-01 |
| rs13068434 | 3 | 85508814 | G | 0.225 | 0.064 | 0.012 | 0.041 | 0.086 | 3.42E-08 | -0.095 | 0.106 | -0.302 | 0.113 | 3.71E-01 |
| rs78867021 | 3 | 85510809 | TATG | 0.379 | 0.055 | 0.010 | 0.036 | 0.075 | 3.68E-08 | 0.027 | 0.014 | -0.001 | 0.055 | 6.27E-02 |
| rs6762267 | 3 | 85513115 | C | 0.381 | 0.055 | 0.010 | 0.035 | 0.074 | 4.37E-08 | 0.026 | 0.014 | -0.002 | 0.054 | 7.33E-02 |
| rs62250712 | 3 | 85513716 | C | 0.381 | 0.055 | 0.010 | 0.035 | 0.074 | 4.67E-08 | 0.026 | 0.014 | -0.003 | 0.054 | 7.45E-02 |
| rs62250713 | 3 | 85513793 | A | 0.363 | 0.056 | 0.010 | 0.037 | 0.076 | 2.13E-08 | 0.027 | 0.015 | -0.003 | 0.057 | 7.30E-02 |
| rs112911909 | 3 | 85517112 | A | 0.364 | -0.057 | 0.010 | -0.077 | -0.037 | 1.66E-08 | **-0.044** | **0.012** | **-0.067** | **-0.022** | **1.26E-04** |
| rs13070166 | 3 | 85517507 | A | 0.229 | 0.065 | 0.012 | 0.042 | 0.088 | 1.71E-08 | -0.013 | 0.156 | -0.319 | 0.292 | 9.32E-01 |
| rs34133544 | 3 | 85517748 | G | 0.352 | 0.056 | 0.010 | 0.036 | 0.076 | 4.02E-08 | 0.025 | 0.016 | -0.006 | 0.055 | 1.16E-01 |
| rs62250716 | 3 | 85517752 | G | 0.366 | -0.058 | 0.010 | -0.078 | -0.038 | 1.24E-08 | **-0.045** | **0.012** | **-0.068** | **-0.022** | **1.02E-04** |
| rs2875907 | 3 | 85518580 | A | 0.352 | 0.056 | 0.010 | 0.036 | 0.076 | 3.16E-08 | 0.025 | 0.016 | -0.006 | 0.055 | 1.16E-01 |
| rs960986 | 3 | 85519305 | T | 0.364 | -0.056 | 0.010 | -0.076 | -0.036 | 2.87E-08 | **-0.043** | **0.012** | **-0.066** | **-0.020** | **1.91E-04** |
| rs144888873 | 3 | 85520967 | T | 0.226 | 0.065 | 0.012 | 0.043 | 0.088 | 1.44E-08 | -0.357 | 0.516 | -1.368 | 0.653 | 4.88E-01 |
| rs62250717 | 3 | 85521990 | G | 0.369 | -0.055 | 0.010 | -0.075 | -0.035 | 4.82E-08 | **-0.041** | **0.011** | **-0.064** | **-0.019** | **3.19E-04** |
| rs9841144 | 3 | 85531199 | T | 0.227 | 0.064 | 0.011 | 0.042 | 0.087 | 2.46E-08 | 0.146 | 0.333 | -0.507 | 0.798 | 6.62E-01 |
| rs1379778 | 3 | 85536091 | AT | 0.355 | -0.058 | 0.010 | -0.078 | -0.037 | 2.77E-08 | **-0.043** | **0.012** | **-0.066** | **-0.020** | **2.25E-04** |
| rs9849399 | 3 | 85537665 | C | 0.227 | 0.064 | 0.011 | 0.041 | 0.086 | 2.76E-08 | 0.026 | 0.343 | -0.646 | 0.698 | 9.41E-01 |
| rs56088977 | 3 | 85538811 | G | 0.218 | 0.064 | 0.012 | 0.041 | 0.088 | 4.55E-08 | 0.259 | 0.187 | -0.108 | 0.625 | 1.66E-01 |
| rs34418561 | 3 | 85538846 | C | 0.227 | 0.064 | 0.011 | 0.041 | 0.086 | 2.63E-08 | 0.026 | 0.343 | -0.646 | 0.697 | 9.41E-01 |
| rs138246680 | 3 | 85539217 | C | 0.354 | 0.056 | 0.010 | 0.036 | 0.076 | 4.86E-08 | 0.027 | 0.016 | -0.003 | 0.058 | 8.04E-02 |
| rs9844512 | 3 | 85544070 | A | 0.227 | 0.064 | 0.011 | 0.041 | 0.087 | 2.59E-08 | -0.662 | 0.663 | -1.961 | 0.638 | 3.19E-01 |
| rs76395182 | 3 | 85547337 | G | 0.341 | -0.061 | 0.011 | -0.082 | -0.040 | 1.06E-08 | **-0.046** | **0.012** | **-0.070** | **-0.023** | **1.12E-04** |
| rs4637303 | 3 | 85552787 | C | 0.351 | 0.056 | 0.010 | 0.036 | 0.075 | 4.42E-08 | 0.026 | 0.016 | -0.005 | 0.057 | 9.77E-02 |
| rs6809805 | 3 | 85553096 | A | 0.227 | 0.064 | 0.012 | 0.042 | 0.087 | 2.13E-08 | 0.440 | 0.495 | -0.530 | 1.411 | 3.74E-01 |
| rs13084531 | 3 | 85553994 | G | 0.225 | 0.067 | 0.012 | 0.044 | 0.089 | 8.75E-09 |  |  |  |  |  |
| rs12495758 | 3 | 85554262 | G | 0.351 | 0.055 | 0.010 | 0.036 | 0.075 | 4.62E-08 | 0.024 | 0.016 | -0.006 | 0.055 | 1.20E-01 |
| rs62250759 | 3 | 85569026 | G | 0.368 | -0.055 | 0.010 | -0.075 | -0.035 | 4.90E-08 | **-0.041** | **0.011** | **-0.064** | **-0.019** | **3.11E-04** |
| rs9841829 | 3 | 85569361 | G | 0.227 | 0.064 | 0.012 | 0.041 | 0.086 | 3.34E-08 | 0.080 | 0.302 | -0.512 | 0.672 | 7.92E-01 |
| rs9851444 | 3 | 85576706 | C | 0.229 | 0.065 | 0.012 | 0.042 | 0.087 | 2.06E-08 | 0.018 | 0.167 | -0.310 | 0.346 | 9.14E-01 |
| rs9873400 | 3 | 85590097 | A | 0.227 | 0.063 | 0.012 | 0.040 | 0.085 | 4.61E-08 | -0.232 | 0.213 | -0.649 | 0.186 | 2.77E-01 |
| rs12492753 | 3 | 85601440 | T | 0.351 | 0.056 | 0.010 | 0.036 | 0.076 | 3.73E-08 | 0.023 | 0.016 | -0.007 | 0.054 | 1.33E-01 |
| rs72585634 | 3 | 85602434 | ATC | 0.354 | 0.057 | 0.010 | 0.037 | 0.077 | 2.28E-08 | 0.025 | 0.016 | -0.005 | 0.056 | 1.05E-01 |
| rs7652808 | 3 | 85603643 | T | 0.351 | 0.055 | 0.010 | 0.035 | 0.075 | 4.90E-08 | 0.024 | 0.016 | -0.007 | 0.054 | 1.29E-01 |
| rs11713902 | 3 | 85604425 | T | 0.225 | 0.063 | 0.012 | 0.041 | 0.086 | 4.00E-08 | 0.032 | 0.171 | -0.303 | 0.367 | 8.50E-01 |
| rs13077660 | 3 | 85616260 | C | 0.226 | 0.063 | 0.012 | 0.040 | 0.086 | 4.73E-08 | 0.011 | 0.173 | -0.327 | 0.350 | 9.47E-01 |
| rs13353478 | 3 | 85621395 | T | 0.226 | 0.064 | 0.012 | 0.041 | 0.086 | 3.68E-08 | -0.045 | 0.186 | -0.410 | 0.319 | 8.07E-01 |
| rs6790699 | 3 | 85624189 | A | 0.372 | 0.055 | 0.010 | 0.035 | 0.074 | 4.91E-08 | 0.026 | 0.015 | -0.002 | 0.055 | 7.33E-02 |
| rs9379971 | 6 | 27259308 | A | 0.349 | -0.063 | 0.011 | -0.084 | -0.042 | 2.31E-09 |  |  |  |  |  |
| rs7746841 | 6 | 27261700 | G | 0.451 | -0.054 | 0.010 | -0.073 | -0.035 | 3.94E-08 | -0.018 | 0.019 | -0.055 | 0.019 | 3.44E-01 |
| rs35316606 | 6 | 27267230 | CA | 0.451 | -0.054 | 0.010 | -0.073 | -0.035 | 3.32E-08 | -0.020 | 0.019 | -0.056 | 0.017 | 2.91E-01 |
| rs2393923 | 6 | 27270261 | C | 0.321 | -0.059 | 0.010 | -0.079 | -0.038 | 1.73E-08 | -0.028 | 0.016 | -0.060 | 0.003 | 7.42E-02 |
| rs7771953 | 6 | 27271343 | A | 0.437 | -0.055 | 0.010 | -0.074 | -0.036 | 1.88E-08 | -0.018 | 0.020 | -0.057 | 0.020 | 3.45E-01 |
| rs6456772 | 6 | 27273365 | A | 0.451 | -0.054 | 0.010 | -0.073 | -0.035 | 2.69E-08 | -0.021 | 0.019 | -0.058 | 0.015 | 2.49E-01 |
| rs3800319 | 6 | 27280407 | G | 0.435 | -0.055 | 0.010 | -0.074 | -0.036 | 2.38E-08 | -0.015 | 0.020 | -0.053 | 0.024 | 4.59E-01 |
| rs2893911 | 6 | 27283303 | A | 0.436 | -0.054 | 0.010 | -0.074 | -0.035 | 3.25E-08 | -0.017 | 0.020 | -0.056 | 0.022 | 4.02E-01 |
| rs9379973 | 6 | 27288419 | C | 0.453 | -0.055 | 0.010 | -0.074 | -0.036 | 2.11E-08 | -0.022 | 0.018 | -0.058 | 0.014 | 2.28E-01 |
| rs112356720 | 6 | 27289497 | ACTTTT | 0.453 | -0.055 | 0.010 | -0.074 | -0.036 | 1.63E-08 | -0.023 | 0.018 | -0.059 | 0.013 | 2.12E-01 |
| rs6923811 | 6 | 27289776 | C | 0.320 | -0.059 | 0.010 | -0.079 | -0.038 | 1.92E-08 | -0.025 | 0.016 | -0.056 | 0.006 | 1.18E-01 |
| rs2092114 | 6 | 27290082 | C | 0.459 | -0.055 | 0.010 | -0.074 | -0.036 | 2.04E-08 | -0.025 | 0.018 | -0.060 | 0.010 | 1.55E-01 |
| rs9368501 | 6 | 27295082 | G | 0.453 | -0.055 | 0.010 | -0.074 | -0.036 | 2.16E-08 | -0.021 | 0.018 | -0.057 | 0.015 | 2.51E-01 |
| Where: Basic analysis included age, sex, 8 principle components and array; Conditional analysis included age, sex, 8 principle components and array and the index SNP for each locus. The index SNP in each locus is highlihgted in grey. SNPs in the suggestive secondary signal in chr 3 are in bold. | | | | | | | | | | | | | | |