***Twin Research and Human Genetics***

**Genetic influences on evening preference overlap with those for bipolar disorder in a sample of Mexican Americans and American Indians**

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**Supplementary Information**

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**Supplementary Table S1.** Top 50 hits from the mixed linear model association in GCTA on the “owl” phenotype in the combined American Indian and Mexican American samples.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Chra | dbSNP 138 | BP (hg19) | A1b | A2c | Freqd | Effect | see | *p* | Gene (refGene) | Function (refGene) | Reff | Altg | 1000G (all)h | 1000G (eur)i |
| 11 | rs10768009 | 33632390 | A | C | 0.4227 | -0.1104 | 0.0238 | 3.53E-06 | *KIAA1549L* | intronic | C | A | 0.3466 | 0.3817 |
| 11 | rs7115532 | 33633523 | T | A | 0.4239 | -0.1103 | 0.0238 | 3.77E-06 | *KIAA1549L* | intronic | A | T | 0.3908 | 0.3807 |
| 11 | rs2073174 | 33630891 | T | A | 0.4233 | -0.1095 | 0.0238 | 4.04E-06 | *KIAA1549L* | intronic | A | T | 0.3397 | 0.3807 |
| 11 | rs2076622 | 33631423 | A | G | 0.4305 | -0.1078 | 0.0238 | 6.11E-06 | *KIAA1549L* | exonic (synon) | G | A | 0.4517 | 0.3857 |
| 9 | rs6477769 | 113193574 | T | C | 0.1817 | -0.1274 | 0.0300 | 2.23E-05 | *SVEP1* | intronic | C | T | 0.2999 | 0.1451 |
| 9 | rs7031072 | 113185801 | G | A | 0.1769 | -0.1269 | 0.0303 | 2.84E-05 | *SVEP1* | intronic | A | G | 0.2987 | 0.1412 |
| 9 | rs7042836 | 113191819 | G | T | 0.1984 | -0.1182 | 0.0290 | 4.54E-05 | *SVEP1* | intronic | T | G | 0.3147 | 0.1521 |
| 9 | rs7865430 | 113199768 | T | C | 0.1990 | -0.1178 | 0.0290 | 4.74E-05 | *SVEP1* | intronic | C | T | 0.3097 | 0.1511 |
| 9 | rs7855991 | 113200806 | C | T | 0.1990 | -0.1178 | 0.0290 | 4.74E-05 | *SVEP1* | intronic | T | C | 0.3097 | 0.1511 |
| 17 | rs904381 | 71390366 | A | C | 0.4814 | -0.0914 | 0.0226 | 5.44E-05 | *SDK2* | exonic (synon) | C | A | 0.2073 | 0.4354 |
| 17 | rs12949882 | 71392512 | A | G | 0.4808 | -0.0902 | 0.0227 | 6.97E-05 | *SDK2* | intronic | G | A | 0.2081 | 0.4364 |
| 7 | rs13241786 | 100486656 | T | G | 0.2932 | -0.0978 | 0.0252 | 1.04E-04 | *UFSP1* | exonic (synon) | T | G | 0.6518 | 0.5427 |
| 1 | rs2070803 | 155157715 | A | G | 0.4155 | 0.0921 | 0.0245 | 1.68E-04 | *MUC1; TRIM46* | down-stream | A | G | 0.5070 | 0.4145 |
| 10 | rs1888922 | 91070701 | C | T | 0.1193 | -0.1365 | 0.0366 | 1.89E-04 | *IFIT2; IFIT3* | inter-genic | T | C | 0.0693 | 0.1650 |
| 9 | rs7038903 | 113221247 | C | T | 0.1613 | -0.1142 | 0.0313 | 2.62E-04 | *SVEP1* | exonic (non-synon) | T | C | 0.1755 | 0.1421 |
| 10 | rs61151381 | 105370496 | G | C | 0.1595 | 0.1171 | 0.0321 | 2.68E-04 | *SH3PXD2A* | intronic | C | G | 0.1356 | 0.1988 |
| 10 | rs1888921 | 91070699 | C | T | 0.1205 | -0.1319 | 0.0365 | 2.98E-04 | *IFIT2; IFIT3* | inter-genic | T | C | 0.0741 | 0.1650 |
| 7 | rs1799806 | 100488658 | C | G | 0.2620 | -0.0936 | 0.0260 | 3.17E-04 | *ACHE* | exonic (non-synon) | G | C | 0.2694 | 0.4533 |
| 9 | rs7852962 | 113196733 | C | A | 0.1625 | -0.1121 | 0.0312 | 3.33E-04 | *SVEP1* | exonic (non-synon) | A | C | 0.1789 | 0.1421 |
| 9 | rs7863519 | 113208250 | G | T | 0.2086 | -0.1014 | 0.0283 | 3.43E-04 | *SVEP1* | exonic (non-synon) | T | G | 0.3397 | 0.1918 |
| 7 | rs2720392 | 100486035 | A | C | 0.2746 | -0.0923 | 0.0258 | 3.44E-04 | *SRRT* | intronic | C | A | 0.2766 | 0.4811 |
| 7 | rs12666785 | 100476229 | C | T | 0.3195 | -0.0877 | 0.0245 | 3.48E-04 | *SRRT* | intronic | C | T | 0.5567 | 0.5149 |
| 10 | rs3740471 | 105363289 | C | T | 0.1577 | 0.1151 | 0.0322 | 3.52E-04 | *SH3PXD2A* | exonic (synon) | T | C | 0.1356 | 0.1998 |
| 2 | rs2361502 | 234698790 | C | T | 0.2974 | -0.0880 | 0.0247 | 3.60E-04 | *MROH2A* | intronic | T | C | 0.2817 | 0.2485 |
| 10 | rs17468739 | 91065949 | C | A | 0.1169 | -0.1309 | 0.0368 | 3.73E-04 | *IFIT2* | exonic (non-synon) | A | C | 0.0517 | 0.1531 |
| 11 | rs7949404 | 33583840 | G | A | 0.3729 | -0.0867 | 0.0245 | 4.07E-04 | *KIAA1549L* | intronic | A | G | 0.3896 | 0.3867 |
| 2 | rs1431087 | 226483833 | A | G | 0.3082 | 0.0899 | 0.0256 | 4.39E-04 | *NYAP2* | intronic | A | G | 0.5435 | 0.5825 |
| 14 | rs382179 | 69179829 | T | C | 0.3555 | 0.0846 | 0.0242 | 4.85E-04 | *RAD51B; ZFP36L1* | inter-genic | T | C | 0.5697 | 0.6491 |
| 1 | rs423144 | 155169355 | G | T | 0.4209 | 0.0842 | 0.0241 | 4.88E-04 | *THBS3* | intronic | G | T | 0.4567 | 0.4155 |
| 1 | rs7366775 | 155168930 | G | A | 0.4227 | 0.0843 | 0.0242 | 4.99E-04 | *THBS3* | intronic | G | A | 0.4571 | 0.4155 |
| 20 | rs62208003 | 62043227 | G | A | 0.0126 | -0.3638 | 0.1047 | 5.10E-04 | *KCNQ2* | intronic | A | G | 0.0060 | 0.0209 |
| 2 | rs12615891 | 226476675 | A | G | 0.3076 | 0.0885 | 0.0256 | 5.33E-04 | *NYAP2* | intronic | A | G | 0.5435 | 0.5825 |
| 2 | rs13421400 | 226481145 | C | T | 0.3076 | 0.0885 | 0.0256 | 5.33E-04 | *NYAP2* | intronic | C | T | 0.5439 | 0.5825 |
| 1 | rs4971100 | 155155731 | G | A | 0.4221 | 0.0839 | 0.0242 | 5.41E-04 | *TRIM46* | intronic | G | A | 0.4565 | 0.4135 |
| 9 | rs59712735 | 113209482 | C | T | 0.1625 | -0.1079 | 0.0312 | 5.53E-04 | *SVEP1* | intronic | T | C | 0.1763 | 0.1421 |
| 9 | rs3739450 | 113192427 | C | T | 0.2512 | -0.0931 | 0.0270 | 5.56E-04 | *SVEP1* | intronic | T | C | 0.3550 | 0.2515 |
| 7 | rs314375 | 100457344 | G | A | 0.3177 | -0.0845 | 0.0245 | 5.57E-04 | *SLC12A9* | intronic | G | A | 0.5745 | 0.5159 |
| 7 | rs314377 | 100458049 | A | G | 0.3177 | -0.0845 | 0.0245 | 5.57E-04 | *SLC12A9* | intronic | A | G | 0.5745 | 0.5149 |
| 7 | rs314378 | 100458795 | T | C | 0.3177 | -0.0845 | 0.0245 | 5.57E-04 | *SLC12A9* | exonic (synon) | T | C | 0.5785 | 0.5159 |
| 7 | rs4729615 | 100462332 | A | G | 0.3177 | -0.0845 | 0.0245 | 5.57E-04 | *SLC12A9* | intronic | A | G | 0.5787 | 0.5159 |
| 7 | rs4729616 | 100462565 | G | T | 0.3177 | -0.0845 | 0.0245 | 5.57E-04 | *SLC12A9* | intronic | G | T | 0.5739 | 0.5149 |
| 2 | rs12468481 | 226485264 | T | A | 0.3064 | 0.0881 | 0.0256 | 5.68E-04 | *NYAP2* | intronic | T | A | 0.5421 | 0.5825 |
| 1 | rs4971101 | 155157635 | G | A | 0.4221 | 0.0833 | 0.0242 | 5.78E-04 | *MUC1; TRIM46* | down-stream | G | A | 0.4573 | 0.4145 |
| 17 | rs1554227 | 40818451 | A | G | 0.4856 | -0.0795 | 0.0232 | 6.09E-04 | *TUBG2* | exonic (synon) | G | A | 0.5038 | 0.5189 |
| 20 | rs6011891 | 62173279 | G | C | 0.0186 | -0.2951 | 0.0864 | 6.41E-04 | *SRMS* | Intronic | C | G | 0.0319 | 0.0348 |
| 20 | rs34969822 | 62173817 | T | C | 0.0186 | -0.2951 | 0.0864 | 6.41E-04 | *SRMS* | exonic (non-synon) | C | T | 0.0421 | 0.0348 |
| 1 | rs9426886 | 155151754 | A | T | 0.4209 | 0.0827 | 0.0243 | 6.61E-04 | *TRIM46* | intronic | A | T | 0.4651 | 0.4145 |
| 2 | rs6711137 | 226444996 | T | G | 0.2734 | 0.0905 | 0.0266 | 6.64E-04 | *NYAP2* | intronic | T | G | 0.5351 | 0.6928 |
| 1 | rs6426254 | 247697624 | T | C | 0.4371 | -0.0789 | 0.0232 | 6.67E-04 | *GCSAML* | intronic | C | T | 0.4876 | 0.6630 |
| 1 | rs2075571 | 155174106 | C | T | 0.4191 | 0.0822 | 0.0242 | 6.70E-04 | *THBS3* | intronic | C | T | 0.4573 | 0.4175 |

aChromosome

bEffect allele

cOther allele

dFrequency of the effect allele

eStandard error

fReference allele

gAlternate allele

hAlternate allele frequency from the 1000 Genomes Project (Oct. 2014; all populations)

iAlternate allele frequency from the 1000 Genomes Project (Oct. 2014; European ancestry)

**Supplementary Table S2.** Single variant association statistics from the mixed linear model association for genes previously reported to be associated with chronotype from large-scale GWAS in the combined American Indian and Mexican American sample.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Chra | BP (hg19) | snp138 | A1b | A2c | Freqd | Effect | see | *p* | Gene (refGene) | Function (refGene) | Reff | Altg | 1000G (all)h | 1000G (eur)i |
| 1 | 182569626 | rs1144566 | T | C | 0.0132 | -0.0229 | 0.0983 | 0.8157 | *RGS16* | exonic (nonsynon) | T | C | 0.9860 | 0.9781 |
| 1 | 77690858 | rs1253226j | G | A | 0.1805 | 0.0154 | 0.0306 | 0.6159 | *PIGK; AK5* | intergenic | A | G | 0.1915 | 0.0706 |
| 1 | 77966756 | rs2803152j | C | T | 0.3939 | 0.0421 | 0.0248 | 0.0898 | *AK5* | intronic | T | C | 0.4956 | 0.3439 |
| 6 | 55142337 | rs2653349k | A | G | 0.1097 | 0.0083 | 0.0375 | 0.8245 | *HCRTR2* | exonic (nonsynon) | A | G | 0.8788 | 0.8161 |
| 6 | 55144956 | rs2292040l | T | C | 0.2380 | -0.0165 | 0.0273 | 0.5459 | *HCRTR2* | intronic | C | T | 0.0980 | 0.0030 |
| 6 | 55148103 | rs9367630l | A | G | 0.2380 | -0.0165 | 0.0273 | 0.5459 | *HCRTR2* | downstream | G | A | 0.0988 | 0.0030 |
| 6 | 55149379 | rs12665239l | A | G | 0.2380 | -0.0165 | 0.0273 | 0.5459 | *HCRTR2; GFRAL* | intergenic | G | A | 0.0988 | 0.0030 |
| 6 | 55149734 | rs61216006l | C | T | 0.2380 | -0.0165 | 0.0273 | 0.5459 | *HCRTR2; GFRAL* | intergenic | T | C | 0.1136 | 0.0030 |
| 6 | 55154930 | rs9382475l | G | A | 0.2374 | -0.0166 | 0.0273 | 0.5427 | *HCRTR2; GFRAL* | intergenic | A | G | 0.1136 | 0.0030 |
| 6 | 55159736 | rs9357856l | G | A | 0.2374 | -0.0166 | 0.0273 | 0.5427 | *HCRTR2; GFRAL* | intergenic | A | G | 0.0992 | 0.0030 |
| 6 | 55161314 | rs9382478l | C | T | 0.2374 | -0.0166 | 0.0273 | 0.5427 | *HCRTR2; GFRAL* | intergenic | T | C | 0.0992 | 0.0030 |
| 7 | 102553603 | rs17135923 | G | C | 0.0354 | -0.0957 | 0.0622 | 0.1240 | *FBXL13m* | exonic (nonsynon) | C | G | 0.1022 | 0.0378 |
| 7 | 102568624 | rs12056296 | C | T | 0.1847 | -0.0283 | 0.0299 | 0.3452 | *FBXL13; LRRC17* | intronic | T | C | 0.2654 | 0.1382 |
| 7 | 102571960 | rs73408250 | T | C | 0.1847 | -0.0283 | 0.0299 | 0.3452 | *FBXL13; LRRC17* | intronic | C | T | 0.2638 | 0.1382 |
| 7 | 102572121 | rs12673840 | T | C | 0.0270 | 0.0392 | 0.0728 | 0.5902 | *FBXL13; LRRC17* | intronic | C | T | 0.0679 | 0.0368 |
| 7 | 102575952 | rs6942688 | A | G | 0.0276 | 0.0248 | 0.0721 | 0.7303 | *FBXL13; LRRC17* | intronic | G | A | 0.0707 | 0.0368 |
| 7 | 102577176 | rs6465884 | A | G | 0.0270 | 0.0392 | 0.0728 | 0.5902 | *FBXL13; LRRC17* | intronic | G | A | 0.0677 | 0.0368 |
| 7 | 102577433 | rs6465885 | T | C | 0.1847 | -0.0283 | 0.0299 | 0.3452 | *FBXL13; LRRC17* | intronic | C | T | 0.2650 | 0.1382 |
| 7 | 102580738 | rs12532495 | A | G | 0.1847 | -0.0283 | 0.0299 | 0.3452 | *FBXL13; LRRC17* | intronic | G | A | 0.2628 | 0.1382 |
| 7 | 102624227 | rs7789252 | A | C | 0.3375 | 0.0104 | 0.0242 | 0.6665 | *FBXL13* | intronic | C | A | 0.4407 | 0.3082 |
| 7 | 102632247 | rs869332 | G | A | 0.3369 | 0.0093 | 0.0242 | 0.7021 | *FBXL13* | intronic | A | G | 0.4407 | 0.3082 |
| 7 | 102650631 | rs117374106 | C | T | 0.0288 | 0.0495 | 0.0706 | 0.4830 | *FBXL13* | intronic | T | C | 0.0735 | 0.0427 |
| 7 | 102660284 | rs117313790 | C | T | 0.0342 | 0.0585 | 0.0653 | 0.3701 | *FBXL13* | intronic | T | C | 0.1064 | 0.0437 |
| 7 | 102665620 | rs61749912 | G | C | 0.0342 | 0.0585 | 0.0653 | 0.3701 | *FBXL13* | exonic (nonsynon) | C | G | 0.1060 | 0.0437 |
| 7 | 102670933 | rs11543780 | T | C | 0.0336 | 0.0471 | 0.0659 | 0.4747 | *FBXL13* | intronic | C | T | 0.1026 | 0.0437 |
| 7 | 102674811 | rs79049204 | A | G | 0.0336 | 0.0471 | 0.0659 | 0.4747 | *FBXL13* | intronic | G | A | 0.1026 | 0.0437 |
| 7 | 102701632 | rs59099783 | G | T | 0.0294 | 0.0577 | 0.0699 | 0.4085 | *FBXL13* | intronic | T | G | 0.0739 | 0.0427 |

aChromosome

bEffect allele

cOther allele

dFrequency of the effect allele

eStandard error

fReference allele

gAlternate allele

hAlternate allele frequency from the 1000 Genomes Project (Oct. 2014; all populations)

iAlternate allele frequency from the 1000 Genomes Project (Oct. 2014; European ancestry)

jNot in linkage disquilibrium (LD) at r2>0.5 in subjects of Northern and Western European ancestry (CEU) from the 1000 Genomes Pilot 1 data with rs11162296 (Jones et al., 2016), rs76681500 (Lane et al., 2016), or rs10493596 (Hu et al., 2016), as assessed by SNAP (Johnson et al., 2008)

kNot in LD at r2>0.5 in CEU panel from the 1000 Genomes Pilot 1 data with rs35833281 (Hu et al., 2016), as assessed by SNAP

lNo matching proxy SNPs found in 1000 Genomes Pilot 1 data

mSNPs in *FBXL13* associated with chronotype from previous work, rs372229746 (Jones et al., 2016; Lane et al., 2016) and rs3972456 (Hu et al., 2016), were not in the 1000 Genomes Pilot 1 data and thus we were unable to assess LD between those SNPs and the ones included in this study

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**Supplementary Figure S1.** Quantile-Quantile (QQ) plot for the GWAS on the owl phenotype in the combined American Indian and Mexican American cohorts.

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**Supplementary Figure S2.** Locus zoom plot of the *KIAA1549L* region. The plot was generated using the 1000G American (AMR) population as a reference population and the hg19 build.

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**Supplementary Figure S3.** Plots showing the number of SNPs used in generating each genetic risk score given the p-value threshold for bipolar disorder (BP; top left), depressive symptoms (DS; top right), schizophrenia (SZ; bottom left) and body mass index (BMI; bottom right).

**References**

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