***Twin Research and Human Genetics***

**Genome-wide association study of post-traumatic stress disorder in two**

**high-risk populations**

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**Supplementary Information**

**Supplementary Table S1.** Top 50 hits for PTSD in the Mexican American sample.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| CHR | End BP (hg19) | dbSNP 138 | Minor allele | Major allele | BETAa | STAT | *P* | EMP1b | # Permu-tations | MAFc | Gene.refGene | Refd | Alte | X1000g2014oct\_allf | X1000g2014oct\_eurg |
| 1 | 248004296 | rs6681483 | G | A | 4.183 | 4.898 | 1.83E-06 | 3.00E-06 | 1000000 | 0.084 | *OR11L1* | A | G | 0.149 | 0.101 |
| 1 | 248004614 | rs6667389 | G | A | 4.183 | 4.898 | 1.83E-06 | 3.00E-06 | 1000000 | 0.084 | *OR11L1* | G | A | 0.847 | 0.899 |
| 1 | 248004687 | rs10888255 | C | G | 4.183 | 4.898 | 1.83E-06 | 3.00E-06 | 1000000 | 0.084 | *OR11L1* | C | G | 0.870 | 0.899 |
| 1 | 248004877 | rs10888257 | C | T | 4.183 | 4.898 | 1.83E-06 | 3.00E-06 | 1000000 | 0.084 | *OR11L1* | C | T | 0.871 | 0.899 |
| 1 | 248004775 | rs10888256 | C | T | 4.147 | 4.872 | 2.05E-06 | 3.00E-06 | 1000000 | 0.080 | *OR11L1* | C | T | 0.891 | 0.899 |
| 1 | 248004848 | rs4607924 | G | C | 4.147 | 4.872 | 2.05E-06 | 3.00E-06 | 1000000 | 0.080 | *OR11L1* | G | C | 0.890 | 0.899 |
| 3 | 176592050 | rs1601949 | C | T | -2.551 | -4.278 | 2.77E-05 | 2.80E-05 | 1000000 | 0.267 | *LINC01209; TBL1XR1* | C | T | 0.640 | 0.831 |
| 4 | 21476630 | rs146145060 | C | - | 2.013 | 4.065 | 6.60E-05 | 7.57E-05 | 528203 | 0.346 | *KCNIP4* | C | - | 0.689 | 0.660 |
| 4 | 21476830 | rs358593 | A | T | 2.013 | 4.065 | 6.60E-05 | 7.57E-05 | 528203 | 0.346 | *KCNIP4* | A | T | 0.697 | 0.661 |
| 4 | 21476990 | rs358592 | C | T | 2.013 | 4.065 | 6.60E-05 | 7.57E-05 | 528203 | 0.346 | *KCNIP4* | C | T | 0.690 | 0.661 |
| 4 | 21481537 | rs358588 | G | A | 2.013 | 4.065 | 6.60E-05 | 7.57E-05 | 528203 | 0.346 | *KCNIP4* | G | A | 0.690 | 0.661 |
| 3 | 56665355 | rs75058227 | C | T | 2.744 | 4.022 | 7.81E-05 | 7.49E-05 | 534047 | 0.181 | *FAM208A* | T | C | 0.200 | 0.101 |
| 14 | 104394850 | rs9324066 | C | T | -1.974 | -4.01 | 8.21E-05 | 9.64E-05 | 415029 | 0.468 | *TDRD9* | C | T | 0.461 | 0.402 |
| 17 | 39025633 | rs4890136 | A | G | 2.996 | 3.869 | 1.43E-04 | 1.48E-04 | 270941 | 0.104 | *KRT12;*  *KRT20* | G | A | 0.093 | 0.101 |
| 22 | 36123313 | rs2073198 | A | G | 2.471 | 3.848 | 1.54E-04 | 1.87E-04 | 214119 | 0.214 | *APOL5* | G | A | 0.315 | 0.289 |
| 3 | 56627048 | rs1388256 | A | G | 2.47 | 3.802 | 1.84E-04 | 1.99E-04 | 200619 | 0.193 | *CCDC66* | A | G | 0.736 | 0.896 |
| 3 | 56630653 | rs282525 | A | C | 2.47 | 3.802 | 1.84E-04 | 1.99E-04 | 200619 | 0.193 | *CCDC66* | A | C | 0.735 | 0.896 |
| 3 | 56635313 | rs282542 | G | A | 2.47 | 3.802 | 1.84E-04 | 1.99E-04 | 200619 | 0.193 | *CCDC66* | G | A | 0.742 | 0.896 |
| 3 | 56639458 | rs9841851 | C | G | 2.47 | 3.802 | 1.84E-04 | 1.99E-04 | 200619 | 0.193 | *CCDC66* | C | G | 0.723 | 0.896 |
| 3 | 56642618 | rs59331585 | - | TTTTGTATTTCTTT | 2.47 | 3.802 | 1.84E-04 | 1.99E-04 | 200619 | 0.193 | *CCDC66* | - | TTTTGTATTTCTTT | 0.728 | 0.891 |
| 3 | 56644358 | rs282530 | A | G | 2.47 | 3.802 | 1.84E-04 | 1.99E-04 | 200619 | 0.193 | *CCDC66* | A | G | 0.736 | 0.896 |
| 3 | 56644680 | rs282531 | A | G | 2.47 | 3.802 | 1.84E-04 | 1.99E-04 | 200619 | 0.193 | *CCDC66* | A | G | 0.736 | 0.896 |
| 3 | 56658314 | rs2291500 | A | G | 2.45 | 3.761 | 2.15E-04 | 2.08E-04 | 192735 | 0.195 | *FAM208A* | G | A | 0.265 | 0.105 |
| 3 | 56658871 | rs2291498 | C | T | 2.45 | 3.761 | 2.15E-04 | 2.08E-04 | 192735 | 0.195 | *FAM208A* | T | C | 0.292 | 0.105 |
| 3 | 56660896 | NA | CTGCTT | - | 2.45 | 3.761 | 2.15E-04 | 2.08E-04 | 192735 | 0.195 | *FAM208A* | - | CTGCTT | 0.288 | 0.105 |
| 3 | 56662727 | rs10222629 | T | A | 2.45 | 3.761 | 2.15E-04 | 2.08E-04 | 192735 | 0.195 | *FAM208A* | A | T | 0.265 | 0.105 |
| 3 | 56663552 | rs4681937 | G | A | 2.45 | 3.761 | 2.15E-04 | 2.08E-04 | 192735 | 0.195 | *FAM208A* | A | G | 0.292 | 0.105 |
| 3 | 56664048 | rs11712664 | T | C | 2.45 | 3.761 | 2.15E-04 | 2.08E-04 | 192735 | 0.195 | *FAM208A* | C | T | 0.265 | 0.105 |
| 3 | 56664184 | rs11712799 | A | G | 2.45 | 3.761 | 2.15E-04 | 2.08E-04 | 192735 | 0.195 | *FAM208A* | G | A | 0.288 | 0.105 |
| 3 | 56665231 | rs9868059 | C | T | 2.45 | 3.761 | 2.15E-04 | 2.08E-04 | 192735 | 0.195 | *FAM208A* | T | C | 0.281 | 0.105 |
| 3 | 56665673 | rs139834324 | A | G | 2.45 | 3.761 | 2.15E-04 | 2.08E-04 | 192735 | 0.195 | *FAM208A* | G | A | 0.292 | 0.105 |
| 3 | 56669010 | rs75830054 | C | T | 2.45 | 3.761 | 2.15E-04 | 2.08E-04 | 192735 | 0.195 | *FAM208A* | T | C | 0.292 | 0.105 |
| 3 | 56670651 | rs78522019 | A | G | 2.45 | 3.761 | 2.15E-04 | 2.08E-04 | 192735 | 0.195 | *FAM208A* | G | A | 0.292 | 0.105 |
| 3 | 56671593 | rs55742226 | G | A | 2.45 | 3.761 | 2.15E-04 | 2.08E-04 | 192735 | 0.195 | *FAM208A* | A | G | 0.293 | 0.105 |
| 3 | 56671733 | rs11719726 | G | T | 2.45 | 3.761 | 2.15E-04 | 2.08E-04 | 192735 | 0.195 | *FAM208A* | T | G | 0.292 | 0.105 |
| 3 | 56675215 | rs3215018 | - | TTGTAAC | 2.45 | 3.761 | 2.15E-04 | 2.08E-04 | 192735 | 0.195 | *FAM208A* | TTGTAAC | - | 0.292 | 0.105 |
| 3 | 56677182 | rs9883842 | T | C | 2.45 | 3.761 | 2.15E-04 | 2.08E-04 | 192735 | 0.195 | *FAM208A* | C | T | 0.265 | 0.105 |
| 3 | 56677762 | rs9834239 | A | G | 2.45 | 3.761 | 2.15E-04 | 2.08E-04 | 192735 | 0.195 | *FAM208A* | G | A | 0.277 | 0.105 |
| 3 | 56678364 | rs55646706 | T | - | 2.45 | 3.761 | 2.15E-04 | 2.08E-04 | 192735 | 0.195 | *FAM208A* | - | T | 0.292 | 0.105 |
| 3 | 56681406 | rs4681955 | A | G | 2.45 | 3.761 | 2.15E-04 | 2.08E-04 | 192735 | 0.195 | *FAM208A* | G | A | 0.293 | 0.105 |
| 3 | 56681653 | rs9311609 | G | A | 2.45 | 3.761 | 2.15E-04 | 2.08E-04 | 192735 | 0.195 | *FAM208A* | A | G | 0.293 | 0.105 |
| 3 | 56682414 | rs7649872 | A | G | 2.45 | 3.761 | 2.15E-04 | 2.08E-04 | 192735 | 0.195 | *FAM208A* | G | A | 0.292 | 0.105 |
| 3 | 56684648 | rs9867302 | T | C | 2.45 | 3.761 | 2.15E-04 | 2.08E-04 | 192735 | 0.195 | *FAM208A* | C | T | 0.292 | 0.105 |
| 3 | 56684873 | rs9816100 | C | T | 2.45 | 3.761 | 2.15E-04 | 2.08E-04 | 192735 | 0.195 | *FAM208A* | T | C | 0.292 | 0.105 |
| 11 | 2810731 | rs2237886 | T | C | -2.911 | -3.745 | 2.28E-04 | 2.70E-04 | 147918 | 0.116 | *KCNQ1* | C | T | 0.113 | 0.095 |
| 11 | 36004699 | rs7952702 | C | T | 3.968 | 3.733 | 2.38E-04 | 1.82E-04 | 219330 | 0.048 | *LDLRAD3* | T | C | 0.206 | 0.019 |
| 11 | 36005241 | rs7927809 | C | T | 3.968 | 3.733 | 2.38E-04 | 1.82E-04 | 219330 | 0.048 | *LDLRAD3* | T | C | 0.209 | 0.019 |
| 17 | 80900645 | rs2292965 | A | G | 2.125 | 3.731 | 2.40E-04 | 2.03E-04 | 202031 | 0.250 | *TBCD* | G | A | 0.296 | 0.298 |
| 17 | 80901020 | rs1044661 | A | G | 2.125 | 3.731 | 2.40E-04 | 2.03E-04 | 202031 | 0.250 | *TBCD* | G | A | 0.295 | 0.294 |
| 1 | 53580449 | rs150708334 | T | C | 7.029 | 3.729 | 2.42E-04 | 2.28E-04 | 175759 | 0.012 | *SLC1A7* | C | T | 0.001 | NA |

aThe direction of the regression coefficient represents the effect of each extra minor allele whereby a positive regression coefficient means that the minor allele increases risk

bDerived from phenotype permutations

cMinor allele frequency

dReference allele

eAlternate allele

fAlternate allele frequency for all populations from the 1000G data

gAlternate allele frequency for the European population from the 1000G data

**Supplementary Table S2.** Top 50 hits for PTSD in the American Indian sample.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| CHR | BP (hg19) | dbSNP 138 | Tested Allele | Other Allele | Freqa | beta | seb | *p* | Gene.refGene | Refc | Altd | X1000g2014\_\_oct\_alle | X1000g2014oct\_eurf |
| 17 | 48072225 | rs33937843 | A | G | 0.200 | 2.862 | 0.685 | 2.96E-05 | *DLX3* | G | A | 0.154 | 0.039 |
| 12 | 96153846 | rs7134025 | C | T | 0.399 | -2.245 | 0.563 | 6.72E-05 | *NTN4* | C | T | 0.774 | 0.843 |
| 12 | 96154298 | rs6538671 | G | A | 0.399 | -2.245 | 0.563 | 6.72E-05 | *NTN4* | G | A | 0.774 | 0.843 |
| 17 | 80804371 | rs7208121 | A | G | 0.463 | 2.210 | 0.573 | 1.13E-04 | *TBCD* | A | G | 0.478 | 0.411 |
| 12 | 96148540 | rs7294430 | C | T | 0.401 | -2.172 | 0.563 | 1.14E-04 | *NTN4* | C | T | 0.773 | 0.842 |
| 12 | 96149288 | rs4341610 | A | C | 0.401 | -2.172 | 0.563 | 1.14E-04 | *NTN4* | A | C | 0.775 | 0.843 |
| 12 | 96150420 | rs11108235 | G | A | 0.401 | -2.172 | 0.563 | 1.14E-04 | *NTN4* | G | A | 0.774 | 0.843 |
| 12 | 96153658 | rs7316122 | C | T | 0.401 | -2.172 | 0.563 | 1.14E-04 | *NTN4* | C | T | 0.775 | 0.847 |
| 17 | 80793900 | rs9903208 | A | C | 0.463 | 2.229 | 0.583 | 1.31E-04 | *TBCD; ZNF750* | A | C | 0.464 | 0.420 |
| 17 | 80790611 | rs11077947 | A | G | 0.465 | 2.207 | 0.579 | 1.38E-04 | *TBCD; ZNF750* | A | G | 0.474 | 0.420 |
| 12 | 40594722 | rs2638233 | C | A | 0.287 | -2.143 | 0.578 | 2.10E-04 | *SLC2A13; LRRK2* | C | A | 0.649 | 0.617 |
| 17 | 80796671 | rs8069699 | C | T | 0.467 | 2.122 | 0.576 | 2.32E-04 | *TBCD; ZNF750* | C | T | 0.471 | 0.413 |
| 17 | 80793850 | rs9897676 | A | G | 0.465 | 2.104 | 0.573 | 2.42E-04 | *TBCD; ZNF750* | A | G | 0.464 | 0.420 |
| 17 | 80793833 | rs9903483 | T | G | 0.469 | 2.140 | 0.584 | 2.49E-04 | *TBCD; ZNF750* | T | G | 0.434 | 0.420 |
| 17 | 80792728 | rs11654320 | C | T | 0.475 | 2.160 | 0.591 | 2.60E-04 | *TBCD; ZNF750* | C | T | 0.433 | 0.420 |
| 12 | 40592388 | rs2708419 | C | T | 0.289 | -2.089 | 0.574 | 2.70E-04 | *SLC2A13; LRRK2* | C | T | 0.634 | 0.610 |
| 17 | 80799248 | rs1317387 | C | T | 0.477 | 2.125 | 0.588 | 3.00E-04 | *TBCD* | C | T | 0.430 | 0.411 |
| 17 | 80795625 | rs28706217 | G | A | 0.469 | 2.086 | 0.579 | 3.12E-04 | *TBCD; ZNF750* | G | A | 0.470 | 0.411 |
| 17 | 80801904 | rs11655723 | G | A | 0.469 | 2.086 | 0.579 | 3.12E-04 | *TBCD* | A | G | 0.523 | 0.591 |
| 17 | 80802353 | rs9897808 | A | C | 0.469 | 2.086 | 0.579 | 3.12E-04 | *TBCD* | A | C | 0.472 | 0.412 |
| 8 | 3253768 | rs3802303 | T | C | 0.310 | 2.194 | 0.609 | 3.19E-04 | *CSMD1* | C | T | 0.300 | 0.424 |
| 8 | 3255336 | rs7833969 | T | C | 0.310 | 2.194 | 0.609 | 3.19E-04 | *CSMD1* | C | T | 0.294 | 0.425 |
| 17 | 80801745 | rs7219521 | G | A | 0.473 | 2.094 | 0.583 | 3.29E-04 | *TBCD* | G | A | 0.430 | 0.410 |
| 2 | 160600789 | rs62173031 | A | G | 0.043 | 4.557 | 1.269 | 3.30E-04 | *MARCH7* | G | A | 0.048 | 0.071 |
| 17 | 17292491 | rs7223406 | G | A | 0.200 | 2.444 | 0.684 | 3.53E-04 | *NT5M; MED9* | A | G | 0.427 | 0.187 |
| 17 | 80792802 | rs11654361 | C | T | 0.471 | 2.110 | 0.592 | 3.65E-04 | *TBCD; ZNF750* | C | T | 0.433 | 0.419 |
| 3 | 44635461 | rs13319803 | A | G | 0.585 | -1.965 | 0.553 | 3.79E-04 | *ZNF660* | G | A | 0.531 | 0.425 |
| 4 | 16770235 | rs189988 | T | A | 0.308 | 2.095 | 0.590 | 3.86E-04 | *LDB2* | T | A | 0.784 | 0.931 |
| 12 | 40600696 | rs2723259 | G | A | 0.289 | -2.031 | 0.573 | 3.91E-04 | *SLC2A13; LRRK2* | G | A | 0.649 | 0.618 |
| 12 | 40602224 | rs1491932 | T | G | 0.289 | -2.031 | 0.573 | 3.91E-04 | *SLC2A13; LRRK2* | T | G | 0.649 | 0.618 |
| 12 | 40604075 | rs2638230 | T | G | 0.289 | -2.031 | 0.573 | 3.91E-04 | *SLC2A13; LRRK2* | T | G | 0.654 | 0.618 |
| 12 | 40605916 | rs2263419 | G | A | 0.289 | -2.031 | 0.573 | 3.91E-04 | *SLC2A13; LRRK2* | G | A | 0.649 | 0.618 |
| 12 | 40606007 | rs2263420 | C | T | 0.289 | -2.031 | 0.573 | 3.91E-04 | *SLC2A13; LRRK2* | C | T | 0.649 | 0.618 |
| 6 | 31332527 | rs2523548 | G | A | 0.428 | 1.959 | 0.555 | 4.15E-04 | *HLA-B; MICA* | G | A | 0.453 | 0.437 |
| 4 | 16772305 | rs207683 | G | A | 0.314 | 2.053 | 0.582 | 4.16E-04 | *LDB2* | G | A | 0.760 | 0.931 |
| 4 | 16773219 | rs207684 | A | G | 0.314 | 2.053 | 0.582 | 4.16E-04 | *LDB2* | A | G | 0.715 | 0.932 |
| 1 | 13802325 | rs3013105 | C | T | 0.341 | 1.899 | 0.539 | 4.26E-04 | *LRRC38* | T | C | 0.462 | 0.384 |
| 12 | 40592501 | rs2708420 | G | T | 0.287 | -2.010 | 0.573 | 4.50E-04 | *SLC2A13; LRRK2* | G | T | 0.648 | 0.617 |
| 12 | 40593676 | rs2708422 | T | C | 0.287 | -2.010 | 0.573 | 4.50E-04 | *SLC2A13; LRRK2* | T | C | 0.648 | 0.617 |
| 12 | 40594173 | rs2708423 | G | A | 0.287 | -2.010 | 0.573 | 4.50E-04 | *SLC2A13; LRRK2* | G | A | 0.648 | 0.617 |
| 17 | 80790772 | rs12603419 | T | C | 0.477 | 2.059 | 0.593 | 5.21E-04 | *TBCD; ZNF750* | T | C | 0.426 | 0.420 |
| 21 | 48017197 | rs2839349 | G | A | 0.545 | -1.878 | 0.543 | 5.40E-04 | *DIP2A; S100B* | G | A | 0.463 | 0.385 |
| 3 | 168162869 | rs6802578 | T | C | 0.401 | -1.855 | 0.540 | 5.96E-04 | *EGFEM1P* | C | T | 0.232 | 0.109 |
| 17 | 80800818 | rs12942471 | G | A | 0.477 | 2.017 | 0.588 | 5.99E-04 | *TBCD* | G | A | 0.431 | 0.412 |
| 17 | 80803648 | rs11652203 | G | A | 0.477 | 2.017 | 0.588 | 5.99E-04 | *TBCD* | G | A | 0.431 | 0.410 |
| 3 | 168157367 | rs9852456 | A | G | 0.403 | -1.840 | 0.537 | 6.08E-04 | *EGFEM1P* | G | A | 0.232 | 0.112 |
| 3 | 44599103 | rs2293600 | G | T | 0.587 | -1.880 | 0.550 | 6.37E-04 | *ZKSCAN7* | T | G | 0.530 | 0.419 |
| 2 | 179484054 | rs1864243 | T | C | 0.161 | -2.516 | 0.737 | 6.41E-04 | *MIR548N;*  *TTN-AS1* | C | T | 0.076 | 0.033 |
| 2 | 179487683 | rs2366752 | G | T | 0.161 | -2.516 | 0.737 | 6.41E-04 | *MIR548N* | T | G | 0.078 | 0.034 |
| 2 | 179528335 | rs10204913 | C | T | 0.161 | -2.516 | 0.737 | 6.41E-04 | *MIR548N* | T | C | 0.070 | 0.033 |

aFrequency of the tested allele

bStandard error

cReference allele

dAlternate allele

eAlternate allele frequency for all populations from the 1000G data

fAlternate allele frequency for the European population from the 1000G data

**Supplementary Table S3.** Top 50 hits from the meta-analysis on PTSD in the Mexican American and American Indian cohorts.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| CHR | BP (hg19) | dbSNP 138 | A1a | *P*b | *P*(R)c | BETAd | BETA  (R)e | Qf | Ig | Refh | Alti | Gene.refGene | X1000g2014oct\_allj | X1000g2014oct\_eurk |
| 8 | 104420200 | rs3134255 | A | 3.20E-05 | 3.20E-05 | 1.692 | 1.692 | 0.909 | 0 | T | A | *SLC25A32* | 0.255 | 0.232 |
| 8 | 104440751 | rs3098227 | T | 3.75E-05 | 3.75E-05 | 1.686 | 1.686 | 0.923 | 0 | C | T | *DCAF13* | 0.246 | 0.231 |
| 8 | 104430225 | rs3134250 | A | 3.94E-05 | 3.94E-05 | 1.673 | 1.673 | 0.950 | 0 | G | A | *DCAF13* | 0.248 | 0.231 |
| 8 | 104410420 | rs3098259 | A | 4.16E-05 | 4.16E-05 | 1.668 | 1.668 | 0.963 | 0 | G | A | *SLC25A32* | 0.250 | 0.232 |
| 8 | 104426045 | rs3134292 | A | 4.59E-05 | 4.59E-05 | 1.667 | 1.667 | 0.964 | 0 | C | A | *SLC25A32* | 0.248 | 0.231 |
| 8 | 104441923 | rs3134265 | A | 4.89E-05 | 4.89E-05 | 1.652 | 1.652 | 0.997 | 0 | G | A | *DCAF13* | 0.252 | 0.231 |
| 5 | 60233836 | rs2694518 | G | 4.91E-05 | 4.91E-05 | -1.635 | -1.635 | 0.990 | 0 | G | A | *ERCC8* | 0.693 | 0.570 |
| 8 | 104426245 | rs3133817 | G | 4.94E-05 | 4.94E-05 | 1.660 | 1.660 | 0.981 | 0 | A | G | *SLC25A32* | 0.248 | 0.230 |
| 8 | 104438653 | rs3134261 | T | 4.97E-05 | 4.97E-05 | 1.653 | 1.653 | 0.996 | 0 | C | T | *DCAF13* | 0.253 | 0.231 |
| 8 | 104435734 | rs3134258 | G | 5.05E-05 | 5.05E-05 | 1.657 | 1.657 | 0.987 | 0 | T | G | *DCAF13* | 0.248 | 0.232 |
| 8 | 104416693 | rs1865853 | T | 5.41E-05 | 5.41E-05 | 1.635 | 1.635 | 0.965 | 0 | C | T | *SLC25A32* | 0.255 | 0.232 |
| 8 | 104421720 | rs3133814 | G | 5.41E-05 | 5.41E-05 | 1.635 | 1.635 | 0.965 | 0 | A | G | *SLC25A32* | 0.250 | 0.232 |
| 8 | 104419442 | rs3133813 | C | 5.47E-05 | 5.47E-05 | 1.642 | 1.642 | 0.980 | 0 | T | C | *SLC25A32* | 0.250 | 0.232 |
| 5 | 60237984 | rs158935 | C | 5.73E-05 | 5.73E-05 | -1.614 | -1.614 | 0.966 | 0 | C | T | *ERCC8* | 0.693 | 0.570 |
| 5 | 60238696 | rs158932 | C | 5.73E-05 | 5.73E-05 | -1.614 | -1.614 | 0.966 | 0 | C | G | *ERCC8* | 0.693 | 0.570 |
| 5 | 60239443 | rs158572 | G | 5.73E-05 | 5.73E-05 | -1.614 | -1.614 | 0.966 | 0 | G | A | *ERCC8* | 0.694 | 0.570 |
| 5 | 60239698 | rs158931 | C | 5.73E-05 | 5.73E-05 | -1.614 | -1.614 | 0.966 | 0 | C | G | *ERCC8* | 0.693 | 0.570 |
| 8 | 104427578 | rs3134297 | C | 6.41E-05 | 6.41E-05 | 1.626 | 1.626 | 0.946 | 0 | T | C | *DCAF13* | 0.254 | 0.231 |
| 8 | 104432545 | rs3134253 | G | 6.41E-05 | 6.41E-05 | 1.626 | 1.626 | 0.946 | 0 | A | G | *DCAF13* | 0.253 | 0.232 |
| 8 | 104435022 | rs3098236 | C | 6.41E-05 | 6.41E-05 | 1.626 | 1.626 | 0.946 | 0 | A | C | *DCAF13* | 0.254 | 0.232 |
| 5 | 60241946 | rs158919 | T | 6.58E-05 | 6.58E-05 | -1.614 | -1.614 | 0.965 | 0 | T | G | *NDUFAF2* | 0.693 | 0.570 |
| 5 | 60245533 | rs158915 | G | 6.58E-05 | 6.58E-05 | -1.614 | -1.614 | 0.965 | 0 | G | A | *NDUFAF2* | 0.693 | 0.570 |
| 5 | 60251851 | rs158924 | C | 6.58E-05 | 6.58E-05 | -1.614 | -1.614 | 0.965 | 0 | C | A | *NDUFAF2* | 0.694 | 0.570 |
| 5 | 60234329 | rs290516 | T | 6.70E-05 | 6.70E-05 | -1.606 | -1.606 | 0.947 | 0 | T | C | *ERCC8* | 0.693 | 0.570 |
| 8 | 104411282 | rs1061195 | C | 7.06E-05 | 7.06E-05 | 1.609 | 1.609 | 0.909 | 0 | T | C | *SLC25A32* | 0.256 | 0.232 |
| 8 | 104417350 | rs3133811 | G | 7.06E-05 | 7.06E-05 | 1.609 | 1.609 | 0.909 | 0 | A | G | *SLC25A32* | 0.255 | 0.232 |
| 8 | 104422854 | rs3133815 | G | 7.06E-05 | 7.06E-05 | 1.609 | 1.609 | 0.909 | 0 | A | G | *SLC25A32* | 0.255 | 0.231 |
| 8 | 104424337 | rs3133816 | G | 7.80E-05 | 7.80E-05 | 1.608 | 1.608 | 0.905 | 0 | C | G | *SLC25A32* | 0.251 | 0.231 |
| 8 | 104416785 | rs1865854 | T | 8.25E-05 | 8.25E-05 | 1.594 | 1.594 | 0.876 | 0 | C | T | *SLC25A32* | 0.255 | 0.234 |
| 8 | 104431198 | rs3134251 | G | 8.84E-05 | 8.84E-05 | 1.603 | 1.603 | 0.893 | 0 | A | G | *DCAF13* | 0.253 | 0.231 |
| 5 | 60241142 | rs158921 | G | 9.28E-05 | 9.28E-05 | -1.561 | -1.561 | 0.854 | 0 | G | A | *NDUFAF2* | 0.693 | 0.570 |
| 11 | 16007446 | rs66830472 | A | 1.23E-04 | 1.23E-04 | 1.427 | 1.427 | 0.946 | 0 | A | G | *SOX6* | 0.478 | 0.402 |
| 6 | 32674318 | rs12192620 | A | 1.26E-04 | 1.26E-04 | 1.429 | 1.429 | 0.782 | 0 | G | A | *HLA-DQB1;*  *HLA-DQA2* | 0.506 | 0.418 |
| 2 | 219007060 | rs11677534 | C | 1.47E-04 | 1.47E-04 | 1.329 | 1.329 | 0.452 | 0 | T | C | *CXCR2;*  *CXCR1* | 0.563 | 0.504 |
| 2 | 219007752 | rs13009946 | G | 1.47E-04 | 1.47E-04 | 1.329 | 1.329 | 0.452 | 0 | T | G | *CXCR2;*  *CXCR1* | 0.563 | 0.504 |
| 5 | 94261260 | rs13171147 | T | 1.49E-04 | 1.49E-04 | -3.381 | -3.381 | 0.697 | 0 | C | T | *MCTP1* | 0.022 | 0.052 |
| 17 | 40086986 | rs34516580 | T | 1.63E-04 | 2.77E-03 | -4.042 | -4.042 | 0.208 | 37.01 | C | T | *TTC25* | 0.016 | 0.043 |
| 2 | 219008000 | rs7594532 | C | 1.70E-04 | 1.70E-04 | 1.320 | 1.320 | 0.436 | 0 | T | C | *CXCR2;*  *CXCR1* | 0.583 | 0.504 |
| 6 | 29565287 | rs9468559 | C | 1.76E-04 | 1.76E-04 | 4.744 | 4.744 | 0.535 | 0 | A | C | *OR2H2;*  *GABBR1* | 0.066 | 0.016 |
| 4 | 21476990 | rs358592 | C | 1.94E-04 | 6.57E-02 | 1.354 | 1.313 | 0.050 | 73.95 | C | T | *KCNIP4* | 0.690 | 0.661 |
| 4 | 21481537 | rs358588 | G | 1.94E-04 | 6.57E-02 | 1.354 | 1.313 | 0.050 | 73.95 | G | A | *KCNIP4* | 0.690 | 0.661 |
| 5 | 94264884 | rs34619416 | G | 2.08E-04 | 2.08E-04 | -3.339 | -3.339 | 0.733 | 0 | A | G | *MCTP1* | 0.022 | 0.052 |
| 5 | 94269748 | rs35329539 | G | 2.08E-04 | 2.08E-04 | -3.339 | -3.339 | 0.733 | 0 | A | G | *MCTP1* | 0.022 | 0.052 |
| 5 | 94269898 | rs34846897 | G | 2.08E-04 | 2.08E-04 | -3.339 | -3.339 | 0.733 | 0 | A | G | *MCTP1* | 0.022 | 0.052 |
| 14 | 64988830 | rs45512391 | A | 2.26E-04 | 2.26E-04 | 1.563 | 1.563 | 0.685 | 0 | C | A | *ZBTB1* | 0.055 | 0.075 |
| 6 | 32674343 | rs28371271 | A | 2.32E-04 | 2.32E-04 | 1.373 | 1.373 | 0.910 | 0 | G | A | *HLA-DQB1;*  *HLA-DQA2* | 0.506 | 0.418 |
| 5 | 60235240 | rs158938 | G | 2.41E-04 | 2.41E-04 | -1.504 | -1.504 | 0.894 | 0 | G | A | *ERCC8* | 0.710 | 0.617 |
| 1 | 245245378 | rs10927386 | C | 2.55E-04 | 2.55E-04 | 1.444 | 1.444 | 0.850 | 0 | T | C | *EFCAB2* | 0.302 | 0.446 |
| 2 | 71052940 | rs67290967 | G | 2.63E-04 | 1.09E-02 | 1.321 | 1.276 | 0.172 | 46.32 | A | G | *CLEC4F;*  *CD207* | 0.396 | 0.369 |
| 6 | 32652687 | rs9275162 | T | 2.72E-04 | 2.72E-04 | -1.440 | -1.440 | 0.873 | 0 | T | C | *HLA-DQB1;*  *HLA-DQA2* | 0.592 | 0.502 |

aMinor allele

bFixed-effects meta-analysis *p*-value

cRandom-effects meta-analysis *p*-value

dFixed-effects beta estimate (relative to A1; if positive, A1 is interpreted as the risk allele)

eRandom-effects beta estimate

f*P*-value for Cochrane's Q statistic

gI2 heterogeneity index (0-100)

hReference allele

iAlternate allele

jAlternate allele frequency for all populations from the 1000G data

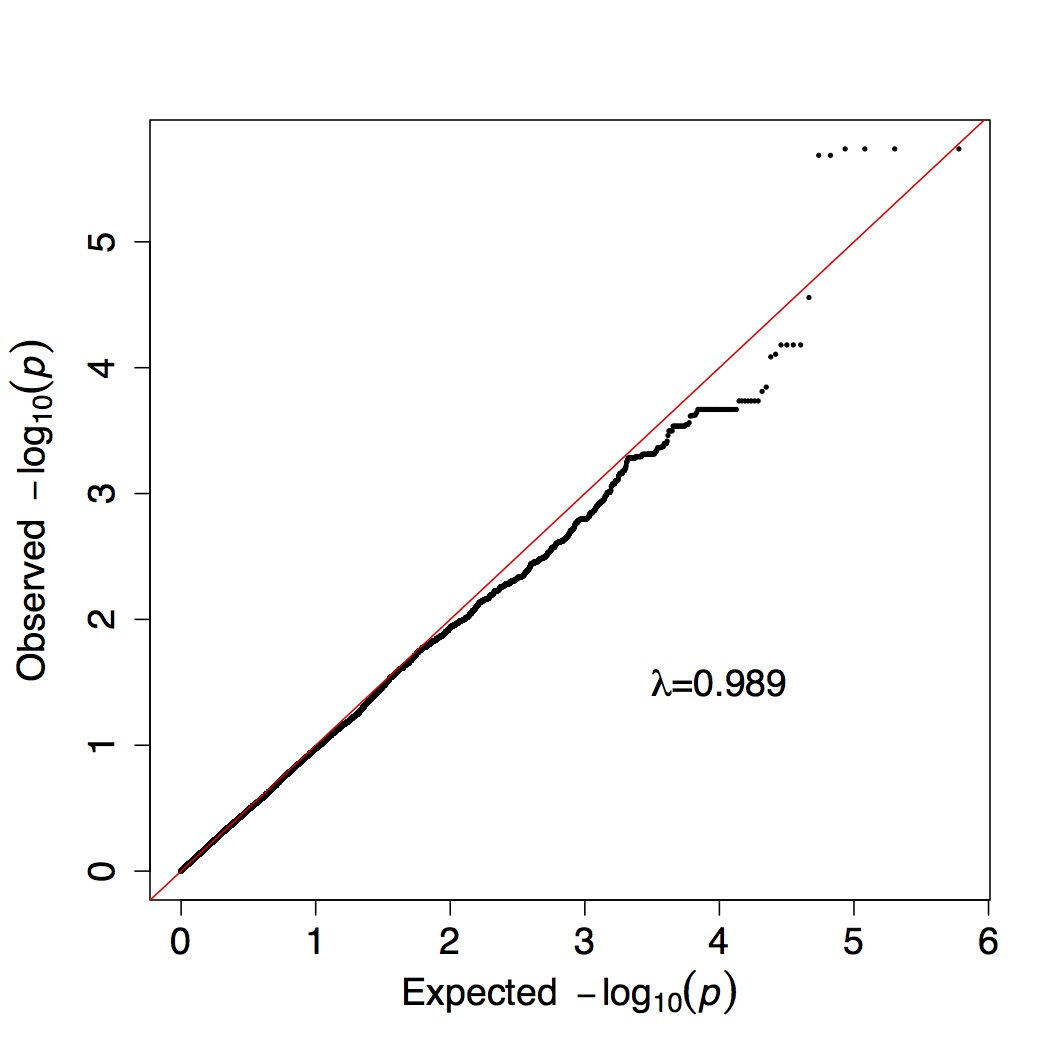
kAlternate allele frequency for the European population from the 1000G data

**Supplementary Table S4**. Remaining clusters with enrichment score > 1.3 from the functional annotation clustering tool in DAVID v6.8.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Annotation cluster 2: enrichment score 2.60 | | | | | | |
| Category | **Term** | **Counta** | | **%b** | **Modified Fisher Exact *p*-value** | **Benjamini corrected *p*-value** |
| UP\_SEQ\_FEATURE | glycosylation site:N-linked (GlcNAc...) | 50 | | 31.25 | 5.28E-05 | 0.0343 |
| UP\_KEYWORDS | Glycoprotein | 52 | | 32.50 | 1.24E-04 | 0.0137 |
| UP\_SEQ\_FEATURE | topological domain:Cytoplasmic | 41 | | 25.62 | 3.55E-04 | 0.0753 |
| UP\_SEQ\_FEATURE | topological domain:Extracellular | 35 | | 21.88 | 4.42E-04 | 0.0704 |
| UP\_KEYWORDS | Transmembrane helix | 58 | | 36.25 | 6.17E-04 | 0.0270 |
| UP\_KEYWORDS | Transmembrane | 58 | | 36.25 | 6.72E-04 | 0.0246 |
| GOTERM\_CC\_DIRECT | GO:0016021~integral component of membrane | 55 | | 34.38 | 7.42E-04 | 0.1322 |
| UP\_SEQ\_FEATURE | transmembrane region | 52 | | 32.50 | 1.18E-03 | 0.1448 |
| UP\_SEQ\_FEATURE | disulfide bond | 34 | | 21.25 | 2.02E-03 | 0.1993 |
| UP\_KEYWORDS | Receptor | 23 | | 14.37 | 2.17E-03 | 0.0521 |
| UP\_KEYWORDS | Disulfide bond | 37 | | 23.13 | 4.56E-03 | 0.0965 |
| UP\_KEYWORDS | Membrane | 65 | | 40.63 | 1.67E-02 | 0.2670 |
| GOTERM\_CC\_DIRECT | GO:0005886~plasma membrane | 39 | | 24.38 | 3.94E-02 | 0.6169 |
| UP\_KEYWORDS | Cell membrane | 30 | | 18.75 | 5.37E-02 | 0.5585 |
| UP\_SEQ\_FEATURE | signal peptide | 30 | | 18.75 | 9.93E-02 | 0.9829 |
| UP\_KEYWORDS | Signal | 36 | | 22.50 | 1.11E-01 | 0.7116 |
| Annotation cluster 3: enrichment score 1.78 | | | | | | |
| Category | **Term** | | **Counta** | **%b** | **Modified Fisher Exact *p*-value** | **Benjamini corrected *p*-value** |
| INTERPRO | IPR002035:von Willebrand factor, type A | | 5 | 3.13 | 5.19E-03 | 0.2583 |
| UP\_SEQ\_FEATURE | domain:VWFA | | 4 | 2.50 | 1.04E-02 | 0.6281 |
| SMART | SM00327:VWA | | 3 | 1.88 | 8.28E-02 | 0.8441 |
| Annotation cluster 4: enrichment score 1.73 | | | | | | |
| Category | **Term** | | **Counta** | **%b** | **Modified Fisher Exact *p*-value** | **Benjamini corrected *p*-value** |
| KEGG\_PATHWAY | hsa04612:Antigen processing and presentation | | 6 | 3.75 | 2.93E-04 | 0.0342 |
| KEGG\_PATHWAY | hsa04915:Estrogen signaling pathway | | 6 | 3.75 | 9.89E-04 | 0.0385 |
| KEGG\_PATHWAY | hsa05145:Toxoplasmosis | | 6 | 3.75 | 2.16E-03 | 0.0624 |
| KEGG\_PATHWAY | hsa04144:Endocytosis | | 8 | 5.00 | 3.68E-03 | 0.0840 |
| GOTERM\_CC\_DIRECT | GO:0072562~blood microparticle | | 6 | 3.75 | 3.74E-03 | 0.3007 |
| GOTERM\_BP\_DIRECT | GO:0042026~protein refolding | | 3 | 1.88 | 5.01E-03 | 0.6280 |
| INTERPRO | IPR013126:Heat shock protein 70 family | | 3 | 1.88 | 5.02E-03 | 0.3029 |
| INTERPRO | IPR018181:Heat shock protein 70, conserved site | | 3 | 1.88 | 5.02E-03 | 0.3029 |
| GOTERM\_MF\_DIRECT | GO:0001664~G-protein coupled receptor binding | | 4 | 2.50 | 7.54E-03 | 0.4111 |
| KEGG\_PATHWAY | hsa05164:Influenza A | | 6 | 3.75 | 1.12E-02 | 0.1737 |
| KEGG\_PATHWAY | hsa05162:Measles | | 5 | 3.13 | 1.98E-02 | 0.2568 |
| GOTERM\_MF\_DIRECT | GO:0031072~heat shock protein binding | | 3 | 1.88 | 3.60E-02 | 0.8538 |
| KEGG\_PATHWAY | hsa04141:Protein processing in endoplasmic reticulum | | 5 | 3.13 | 4.24E-02 | 0.3492 |
| KEGG\_PATHWAY | hsa05169:Epstein-Barr virus infection | | 5 | 3.13 | 6.04E-02 | 0.4111 |
| KEGG\_PATHWAY | hsa05134:Legionellosis | | 3 | 1.88 | 6.63E-02 | 0.3995 |
| KEGG\_PATHWAY | hsa03040:Spliceosome | | 4 | 2.50 | 8.52E-02 | 0.4448 |
| GOTERM\_BP\_DIRECT | GO:1900034~regulation of cellular response to heat | | 3 | 1.88 | 1.00E-01 | 0.9946 |
| UP\_KEYWORDS | Stress response | | 3 | 1.88 | 1.49E-01 | 0.7624 |
| GOTERM\_MF\_DIRECT | GO:0051082~unfolded protein binding | | 3 | 1.88 | 1.81E-01 | 0.9905 |
| KEGG\_PATHWAY | hsa04010:MAPK signaling pathway | | 4 | 2.50 | 3.21E-01 | 0.8653 |
| GOTERM\_MF\_DIRECT | GO:0031625~ubiquitin protein ligase binding | | 3 | 1.88 | 6.17E-01 | 0.9998 |
| Annotation cluster 5: enrichment score 1.32 | | | | | | |
| Category | **Term** | | **Counta** | **%b** | **Modified Fisher Exact *p*-value** | **Benjamini corrected *p*-value** |
| UP\_SEQ\_FEATURE | domain:Sushi 1 | | 3 | 1.88 | 3.79E-02 | 0.8806 |
| UP\_SEQ\_FEATURE | domain:Sushi 2 | | 3 | 1.88 | 3.79E-02 | 0.8806 |
| SMART | SM00032:CCP | | 3 | 1.88 | 5.00E-02 | 0.8898 |
| UP\_KEYWORDS | Sushi | | 3 | 1.88 | 5.72E-02 | 0.5585 |
| INTERPRO | IPR000436:Sushi/SCR/CCP | | 3 | 1.88 | 6.28E-02 | 0.9024 |

aNumber of genes involved in the term from the imported gene list

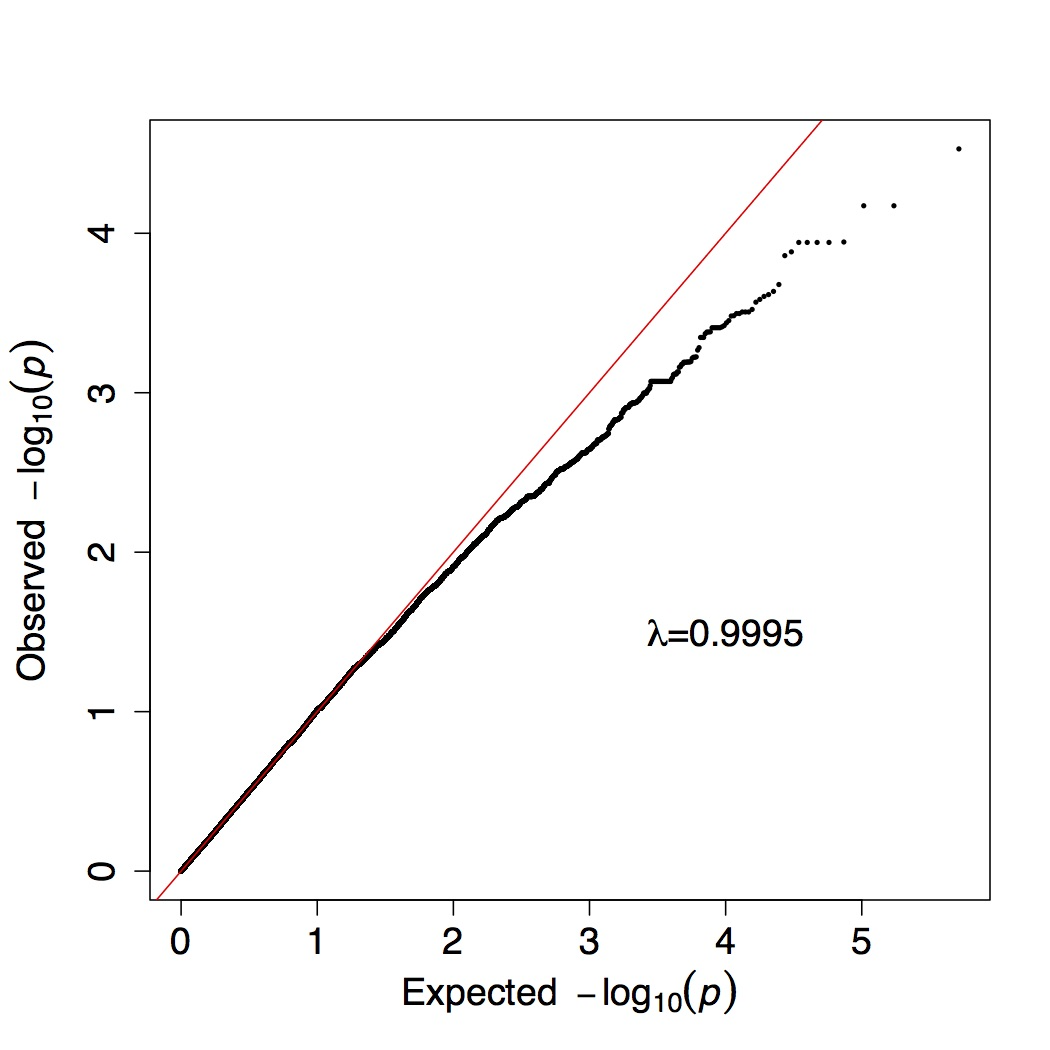
bPercentage of genes involved in the term from the list

****

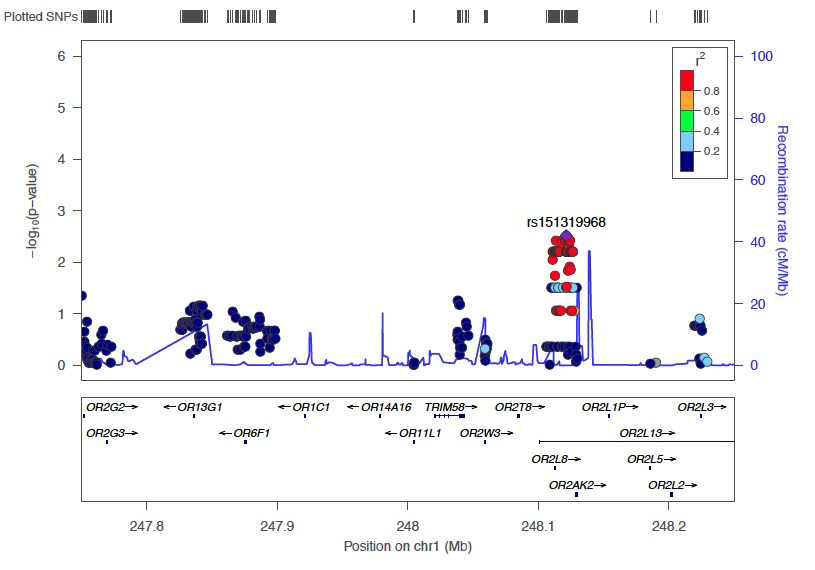
**Supplementary Figure S1.** Quantile-Quantile (QQ) plot for the GWAS on PTSD in the Mexican American cohort.

****

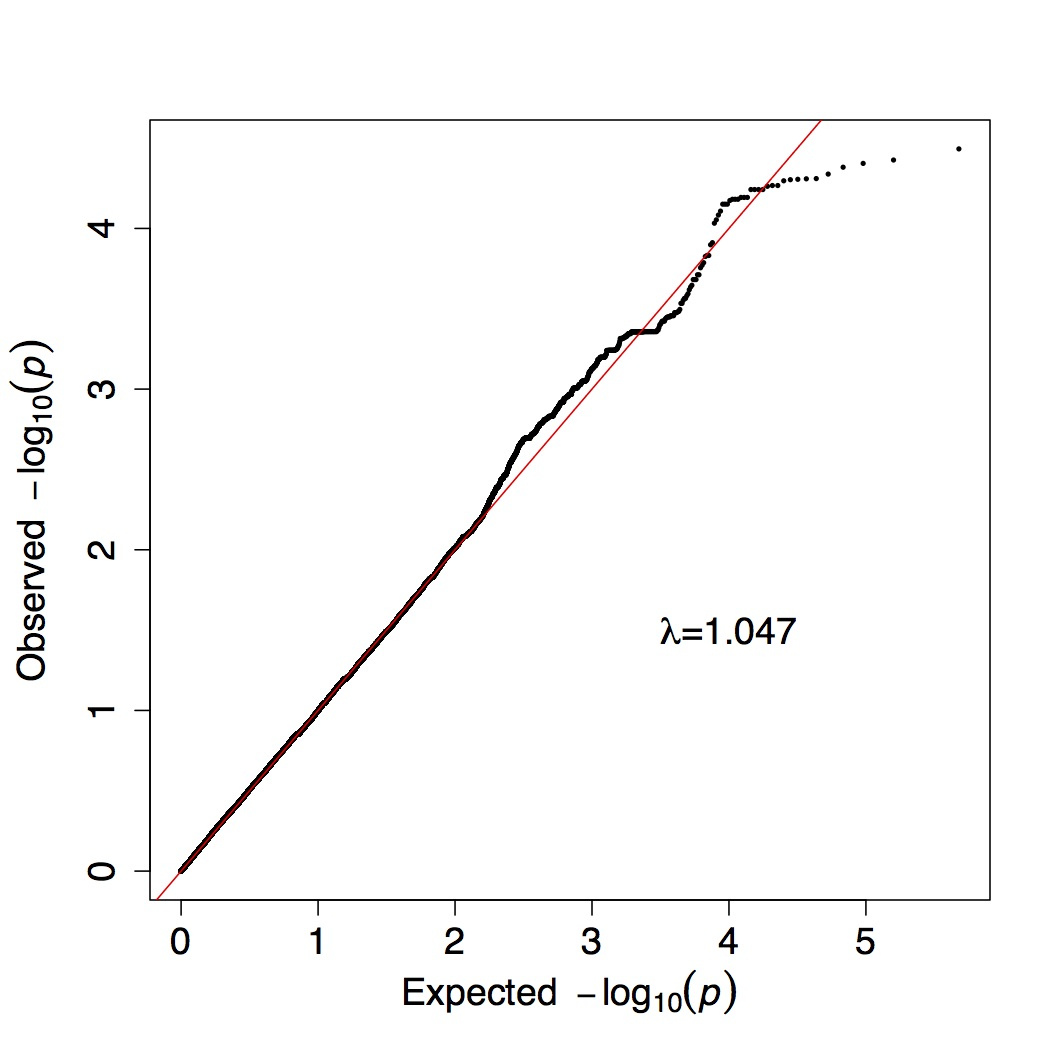
**Supplementary Figure S2.** Locus zoom plot of the *OR11L1* region in the Mexican American sample. The plot was generated using the 1000G American (AMR) population as a reference population and the hg19 build.



**Supplementary Figure S3.** QQ plot from the mixed linear model association (MLMA) in GCTA on PTSD in the American Indian sample.



**Supplementary Figure S4.** Locus zoom plot of the *OR11L1* region in the American Indian sample. The plot was generated using the 1000G American (AMR) population as a reference population and the hg19 build.



**Supplementary Figure S5.** QQ plot from the fixed effects meta-analysis of the Mexican American and American Indian cohorts.