**Methods**

**Genotyping.** DNA was isolated on a Qiagen AutoPure instrument with Qiagen reagents; concentrations were normalized using the Quant-iT™ PicoGreen dsDNA fluorescent assay (Invitrogen). DNA quality and quantity was ascertained by the TaqMan® RNase P Detection assay (Applied Biosystems Assay, Life Technologies, Carlsbad, CA) with fluorescence detection on a 7900 Fast Real Time PCR System (Applied Biosystems, Life Technologies, Carlsbad, CA) according to the manufacturer's protocol. DNA samples were whole-genome amplified, fragmented, precipitated and resuspended prior to hybridization on Illumina HumanOmni2.5-8 beadchips for 20 hours at 48⁰C according to the manufacturer’s protocol (Illumina, San Diego, CA). After hybridization, a single-base extension followed by a multi-layered staining process was performed. Beadchips were imaged using the Illumina iScan System (Illumina, San Diego, CA, USA) and analyzed with Illumina GenomeStudio v2011.1 software containing Genotyping v1.9.4 module. A GenomeStudio project was created with a custom genotyping cluster file, and call rates were > 0.994 for all samples. Technical replicates had genotyping reproducibility error rates < 0.0005 prior to SNP data cleaning.

SNP data cleaning and manipulation was performed using PLINK (Purcell et al., 2007). X-chromosome genotypes were concordant with self-reported sex in all cases. IBD analysis was used to check for cryptic relatedness in the sample. Concordance between self-reported and genetic ancestry was investigated using principal components analysis as implemented in EIGENSTRAT (Price et al., 2006), based on the genotypes of 100,000 common SNPs.

Modules, or sets of regions having more within- than between-module coupling, were computed on the mean (across sample) network using the Louvain algorithm followed by the Kernighan-Lin fine-tuning algorithm (10,000 repetitions, modularization with highest modularity chosen). **Graph Property Computation.** Module membership (bilateral unless noted) was as follows: Module 1 (red nodes in Figure 1) = caudate, putamen, pallidum, thalamus. Module 2 (cyan nodes) = amygdala, hippocampus, nucleus accumbens, medial orbitofrontal cortex, lateral orbitofrontal cortex, rostral anterior cingulate cortex, isthmus of the cingulate, entorhinal cortex, parahippocampal cortex, fusiform gyrus, inferior temporal gyrus. Module 3 (green nodes) = superior frontal gyrus, rostral middle frontal gyrus, caudal middle frontal gyrus, left inferior frontal gyrus pars opercularis, inferior frontal gyrus pars orbitalis, inferior frontal gyrus pars triangularis, middle temporal gyrus, banks of the superior temporal sulcus, inferior parietal lobule. Module 4 = right inferior frontal gyrus pars opercularis, caudal anterior cingulate cortex, posterior cingulate cortex, insula, precentral gyrus, postcentral gyrus, paracentral lobule, superior temporal gyrus, transverse temporal gyrus, supramarginal gyrus, superior parietal lobule.

**Results**

**Supplemental Figure 1.**

Bivariate association between externalizing polygenic score and mean connectivity in the resting-state neural network.

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**Effects of Comorbid Disorders.** To ensure that results could not be accounted for by comorbidity with lifetime mood and anxiety disorders, PTSD, or mild TBI, we first examined associations between these disorders and the main study variables (see Supplementary Table 1 below). For disorders with significant associations with the main study variables, specifically unipolar mood disorders and PTSD, we re-conducted analyses with these disorders entered as covariates. This analysis demonstrated that all significant findings reported in the Results section of the main text remained significant and no new significant results emerged.

**Supplemental Table 1.**

*Correlations between Study Variables, Clinical Characteristics, and Covariates (N = 155)*

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Externalizing Polygenic Score | Neural Network Connectivity | L Amygdala Participation Coefficient | L rACC Participation Coefficient | Inhibitory Control | Lifetime Alcohol/ Substance Use Diagnosis |
| Comorbid Diagnoses |  |  |  |  |  |  |
| Lifetime Unipolar Mood Disorder | .05 | -.16\* | -.10 | -.07 | -.03 | .10 |
| Lifetime Anxiety Disorder | .04 | .04 | .00 | .01 | .09 | .03 |
| Lifetime Posttraumatic Stress Disorder | .00 | -.12 | -.04 | -.14 | -.01 | .22\* |
| Lifetime Mild Traumatic Brain Injury | .03 | .04 | -.02 | -.01 | -.02 | .09 |
| Covariates |  |  |  |  |  |  |
| Age | .03 | -.06 | -.01 | .17\* | .05 | -.16\* |
| Male | .14 | -.06 | .06 | -.08 | .06 | -.04 |
| Currently Employed | -.09 | .02 | -.15 | .09 | .15 | -.27\* |
| Military Blast Exposure | -.03 | .09 | .05 | .03 | -.01 | .08 |
| Total Cholesterol | .08 | -.04 | .01 | .09 | .00 | -.16\* |
| Handedness | .03 | .15 | .14 | -.09 | -.06 | -.12 |

*Note.* L = left hemisphere. rACC = Rostral anterior cingulate cortex. For clinical diagnoses: 0 = No diagnosis, 1 = Diagnosis present. \* *p* < .05