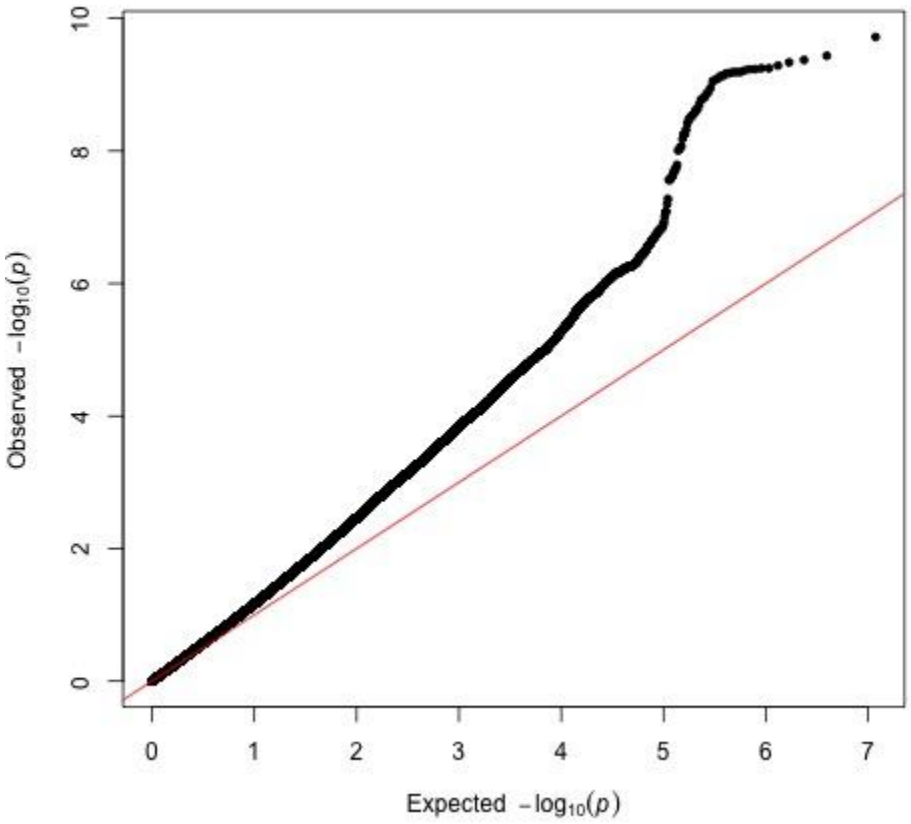
Dissecting the Shared Genetic Architecture of Suicide Attempt, Psychiatric Disorders and Known Risk Factors

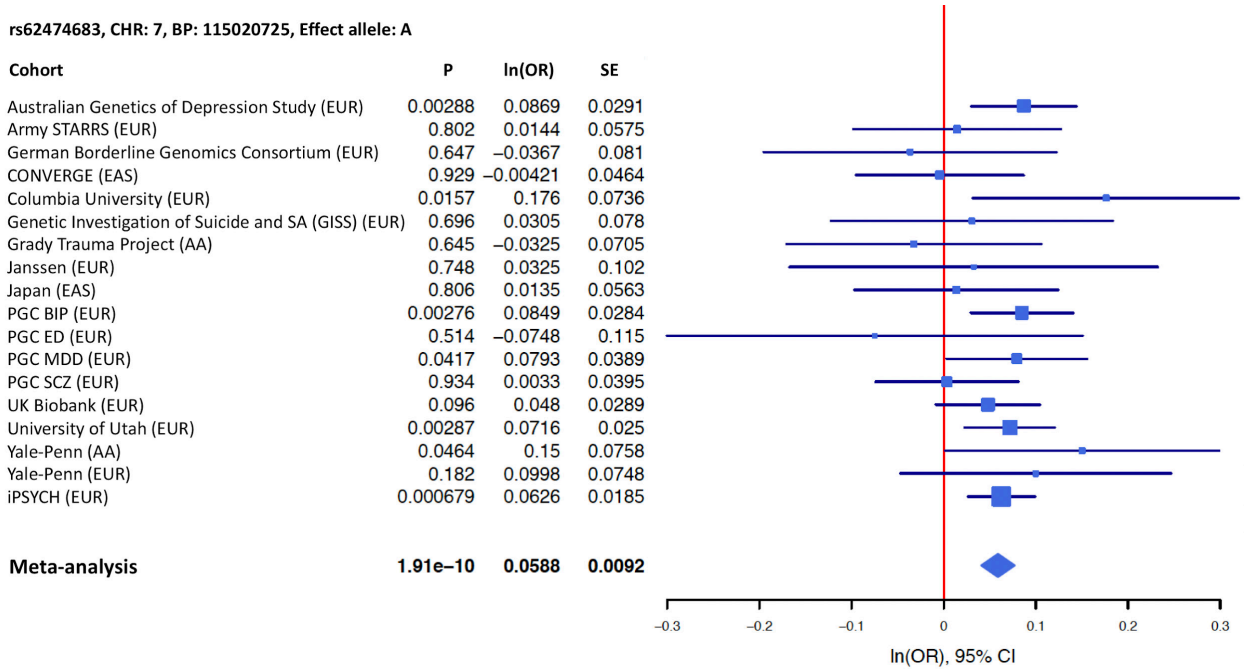
Supplement 1

CONTENTS

Supplementary Figures

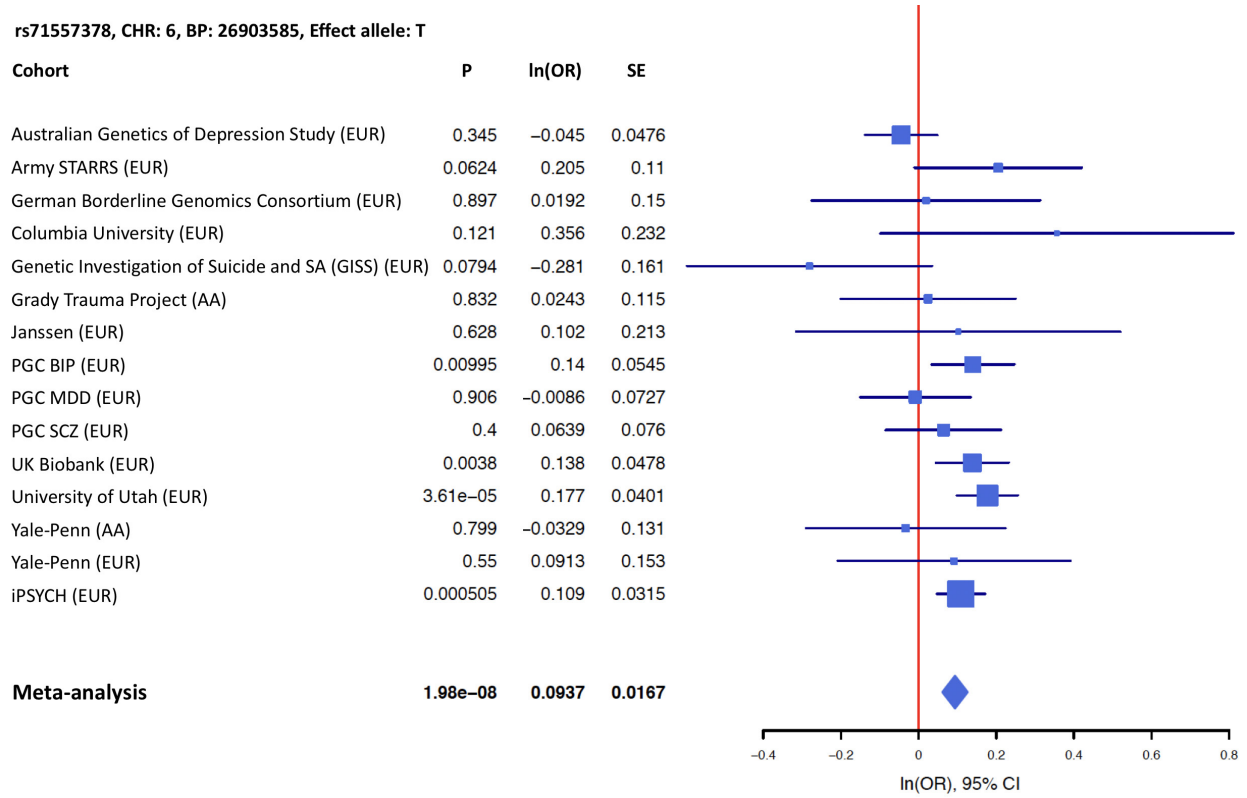


Supplementary Figure S1: Quantile-quantile plot of association test results from primary suicide attempt meta-analysis (trans-ancestry).
The 5902088 SNPs plotted have a minor allele frequency >= 1%, were present in >= 80% of total effective sample size and have an imputation INFO score (weighted by effective N across cohorts) >= 0.6. The lambda genomic control was 1.209.



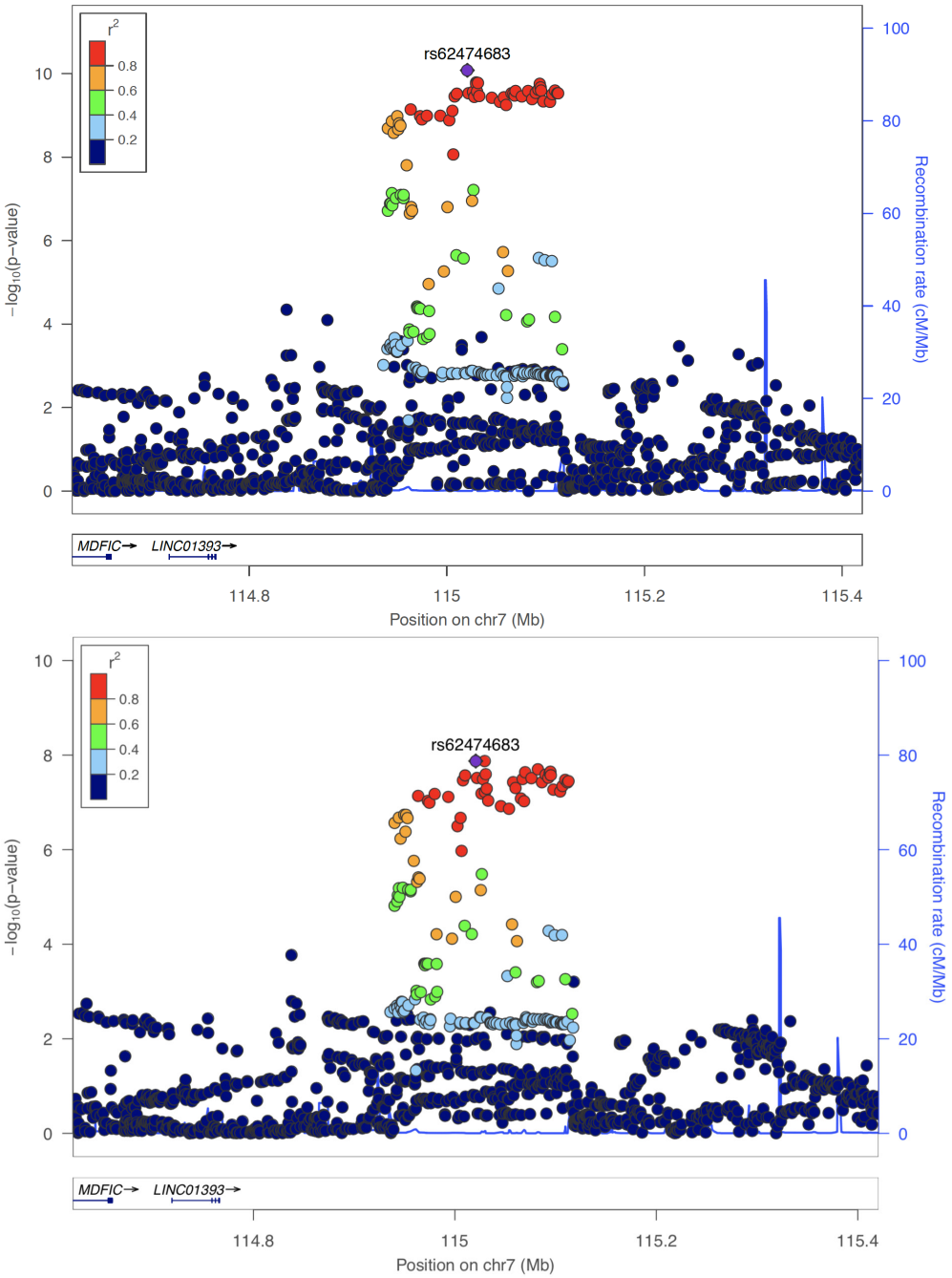
Supplementary Figure S2: Forest plot for index SNP (rs62474683) at genome-wide significant locus for suicide attempt on chromosome 7

Results shown are from the primary suicide attempt meta-analysis (trans-ancestry). CHR- chromosome, BP - base pair position based on hg19, EUR - European ancestry, EAS - East Asian ancestry, AA - admixed African American ancestry, PGC - Psychiatric Genomics Consortium, MDD - major depressive disorder, BIP - Bipolar disorder, SCZ - schizophrenia, ED - eating disorder, ln(OR) - log of the odds ratio of the effect allele on suicide attempt, CI - confidence interval



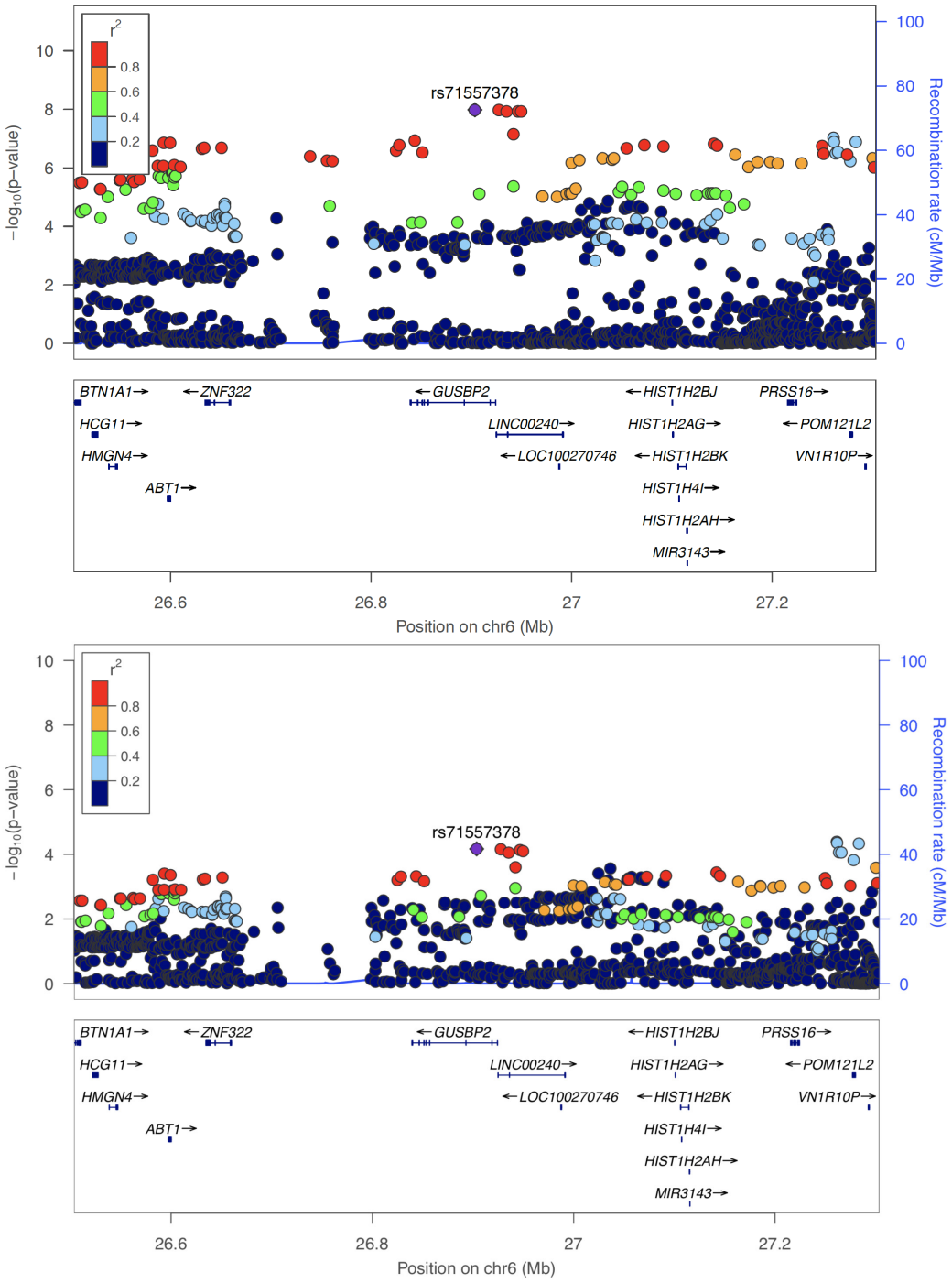
Supplementary Figure S3: Forest plot for index SNP (rs71557378) at genome-wide significant locus for suicide attempt in the major histocompatibility complex

Results shown are from the primary suicide attempt meta-analysis (trans-ancestry). CHR- chromosome, BP - base pair position based on hg19, EUR - European ancestry, EAS - East Asian ancestry, AA - admixed African American ancestry, PGC - Psychiatric Genomics Consortium, MDD - major depressive disorder, BIP - Bipolar disorder, SCZ - schizophrenia, ln(OR) - log of the odds ratio of the effect allele on suicide attempt, CI - confidence interval



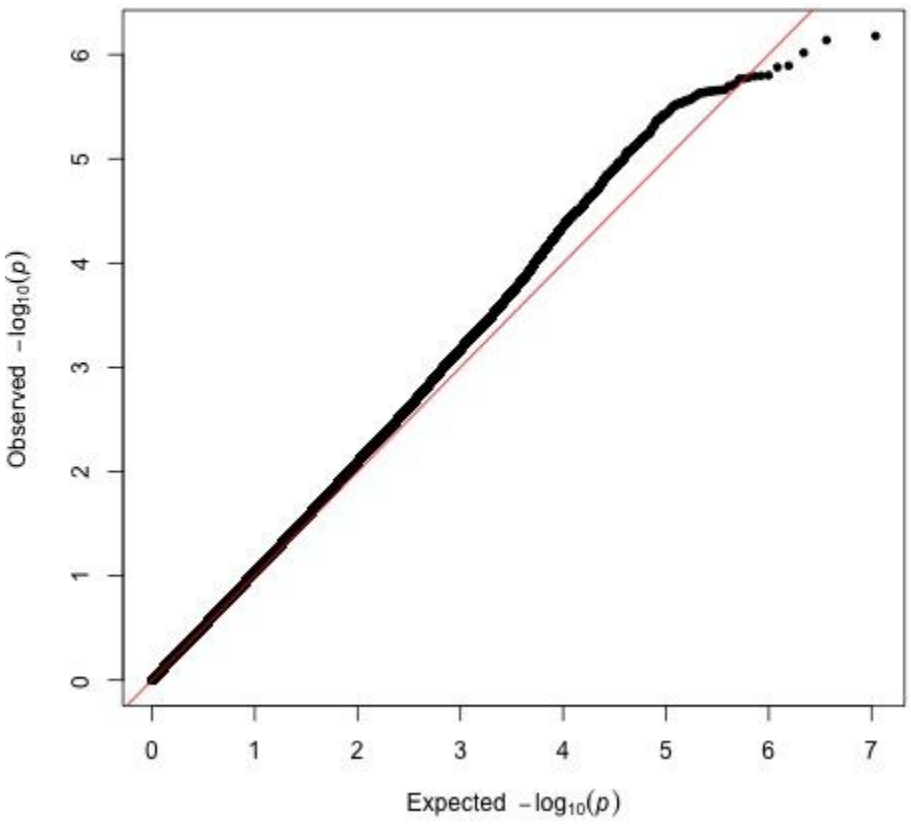
Supplementary Figure S4: Regional plot of suicide attempt association statistics at chromosome 7 genome-wide significant locus before and after conditioning on major depressive disorder.

The *x* axis shows genomic position and the *y* axis shows statistical significance as $-\log_{10}(P \text{ value})$. SNPs are colored by linkage disequilibrium (r^2) to the top lead SNP rs62474683, which is shown as a purple diamond. The upper panel shows the results from the European-only suicide attempt meta-analysis (SA-EUR) and the lower panel shows these results after conditioning on major depressive disorder (SA-EUR|MDD).



Supplementary Figure S5: Regional plot of suicide attempt association statistics at genome-wide significant locus in the major histocompatibility complex before and after conditioning on major depressive disorder.

The *x* axis shows genomic position and the *y* axis shows statistical significance as $-\log_{10}(P \text{ value})$. SNPs are colored by linkage disequilibrium (r^2) to the top lead SNP rs71557378, which is shown as a purple diamond. The upper panel shows the results before conditioning and the lower panel shows the results from the European-only suicide attempt meta-analysis (SA-EUR) and the lower panel shows these results after conditioning on major depressive disorder (SA-EUR|MDD).



Supplementary Figure S6: Quantile-quantile plot of association test results from genome-wide association meta-analysis of suicide attempt within psychiatric diagnosis.

The 5467827 SNPs plotted have a minor allele frequency >= 1%, were present in >= 80% of total effective sample size and have an imputation INFO score (weighted by effective N across cohorts) >= 0.6. The lambda genomic control was 1.043.

Replication in Million Veteran Program

The genome-wide significant loci for SA on chromosomes 6 and 7 were tested for replication in a sample of 14,089 SA cases versus 395,359 controls from Million Veteran Program (MVP). SA assignment was based on ICD-9 and ICD-10 codes, mental health surveys (e.g., the PHQ-9) and data from the Suicide Prevention Application Network (SPAN), a database maintained by suicide prevention coordinators. Veteran participants with no documented lifetime history of suicide attempts or suicidal ideation based on qualifying ICD codes, suicide behavior reports, or mental health survey responses were classified as controls. Veterans with a history of suicidal ideation in the absence of suicide attempts were excluded from analysis. Genotyping methods and quality control (QC) for the MVP genotype data have been described in detail previously[1]. Imputation of the genotype data was performed by phasing the chromosomes with EAGLE v2.4 and performing imputation with minimac v4 using the 1000 Genomes p3v5 reference haplotypes as the global reference panel. Markers with a minor allele frequency (MAF) < 0.01 in the entire data set were excluded from analysis.

The frequency of SA was statistically different among the four most prevalent ancestry groups in MVP (African American: 4.5%, Asian American: 2.7%, European: 3.1% and Latino: 4.2%; P<0.0001). Thus, the association of the index SNPs at both loci (rs62474683 on chromosome 7 and rs71557378 on chromosome 6) with SA were tested separately by ancestry, followed by trans-ancestry meta-analysis. Substructure within each ancestral group was assessed using principal component analysis. Association tests were performed using logistic/firth regression model in Plink2.0, controlling for sex, age and up to 10 principal components within each ancestral group. Meta-analyses were conducted using R package metafor 2.4-0.

Pairwise GWAS

Pairwise GWAS[2,3] was used to investigate genome-wide significant loci for SA and overlapping putative causal variants with propensity towards risk-taking behavior[4] and lifetime smoking index[5]. These phenotypes were chosen because they share genome-wide significant loci in the same region as a genome-wide significant locus for SA identified on chromosome 7. The genome-wide significant locus for SA on chromosome 6 is in the major histocompatibility complex (MHC), and due to the complex long-range LD of this region, it was not included for this analysis. Pairwise GWAS uses association statistics from two GWAS to estimate the probability that a genomic region contains 1) a variant influencing trait 1 only, 2) a variant influencing trait 2 only, 3) a pleiotropic variant influencing both traits, and 4) two separate variants, one influencing trait 1 and the other influencing trait 2. The SA-EUR GWAS results were used, since Pairwise GWAS requires an ancestry-matched LD reference panel. The genome was divided into approximately independent LD blocks (mean block size of 10,000 SNPs) based on the LD structure of the 1000 Genomes Phase 1 EUR reference panel[2,3]. We divided the 3 Mb-wide genome block containing the chromosome 7 genome-wide significant locus for SA into two blocks, to separate the two independent variants for risk-taking behavior in that region (rs8180817 and rs4275159, LD r^2=0.001)[4]. The fgwas package[6] was used to determine the baseline correlation between the two GWAS by extracting all genomic regions with a posterior probability <0.2 of containing an association and calculating the correlation in Z-scores between the two GWAS. This summary statistic-level correlation was used as a correction factor to each Pairwise GWAS analysis.

Gene-based, gene-set and tissue-set enrichment

The primary SA GWAS results were tested for signal enrichment in genes, gene-sets and tissue-sets using MAGMA (v1.08), implemented in FUMA (v1.3.6a)[7,8]. Gene-based tests were performed for 18,517 genes (Bonferroni-corrected significance threshold $P<2.70x10^{-6}$), and 11,638 curated gene sets from MSigDB V7.0 were also tested for enrichment (Bonferroni-corrected significance threshold $P<4.30x10^{-6}$). Gene-set tests were competitive, corrected for gene size, variant density and LD within and between genes. Gene-sets including <10 genes were excluded. Finally, tissue-set enrichment analyses were performed to test for signal enrichment in genes expressed in 54 tissues from the Genotype-Tissue Expression (GTEx) project V8[9] (Bonferroni-corrected significance threshold $P<9.26x10^{-4}$).

Integrative eQTL analysis

A transcriptome-wide association study (TWAS) was conducted using FUSION software[10] and precomputed expression reference weights from PsychENCODE data[11]. The PsychENCODE Consortium has conducted a genome-wide eQTL analysis using 1,321 brain samples, predominantly from the dorsolateral prefrontal cortex[11]. For genes with significant *cis*-SNP heritability (13,435 genes), a TWAS was performed to test whether SNPs influencing brain gene expression are also associated with SA, using the primary SA GWAS summary statistics (TWAS Bonferroni-corrected significance threshold $P<4.28x10^{-6}$ adjusting for 11,683 genes tested).

GWAS of suicide attempt within psychiatric diagnosis

A genome-wide association study (GWAS) meta-analysis of "suicide attempt (SA) within psychiatric diagnosis" was conducted as an alternative means of controlling for the genetic effects of psychiatric disorders. These results were compared against the results of conditioning the primary SA GWAS on psychiatric disorders, using GWAS summary statistics via the mtCOJO method, in order to assess the validity of the statistical conditioning approach. The GWAS of SA within psychiatric diagnosis included 14,847 cases and 69,951 controls from 13 cohorts (Table S1). SA cases in each cohort were compared against a control group of individuals with the same psychiatric disorder, all of whom were screened for the absence of SA. This GWAS meta-analysis included 8 cohorts of European (EUR) ancestry, 1 of admixed African American (AA) ancestry, and 4 of East Asian (EAS) ancestry. All cases in the GWAS of SA within psychiatric diagnosis were of non-fatal SA. Cohorts were included in the primary SA GWAS and/or the GWAS of SA within psychiatric diagnosis, depending on the type of controls available, and therefore there is overlap of cohorts and individuals between these GWAS (Table S1).

Genotyping, quality control, imputation and GWAS of SA within psychiatric diagnosis were conducted in each cohort by the collaborating research teams (full details for each cohort are described below). GWAS summary statistics were shared with the International Suicide Genetics Consortium (ISGC) and a meta-analysis was conducted across cohorts, in the same manner as described for the primary SA GWAS (Main Text). The LDSC intercept was 1.01 (SE=0.007, $P=1.77x10^{-2}$) and the lambda genomic control was 1.04, indicating that the majority of inflation of the GWAS test statistics was due to polygenicity (Figure S6). No SNPs reached genome-wide significance in the GWAS of SA within psychiatric diagnosis. The index SNP at the chromosome 7 locus, which reached genome-wide significance for SA in the primary GWAS, had the same direction of effect on SA within psychiatric diagnosis, but with a slightly smaller effect size (index SNP = rs62474683, OR A allele = 1.04 [1.01-1.07], P=0.007) (Table S4). The index SNP in the major histocompatibility complex, which reached genome-wide significance for SA in the primary GWAS, was not associated with SA within psychiatric diagnosis (Table S4).

The SNP-heritability (h^2_{SNP}) of SA within psychiatric diagnosis, ranged from 3.7% to 4.6% on the liability scale, using a prevalence of SA in psychiatric populations from 10-20% ($P<1.35x10^{-3}$)(Table S12). These estimates were on par with the $h^2_{SNP}$of SA conditioned on major depressive disorder (SA-EUR|MDD), which was 4.1% (SE=0.005, $P=1.20x10^{-16}$) on the liability scale (Table S12). The genetic correlation between the primary SA GWAS and the GWAS of SA within psychiatric diagnosis was 0.93 (SE=0.09, $P=5.35x10^{-24}$)(Table S12). Polygenic risk scores (PRS) derived from the primary SA GWAS were significantly associated with SA within psychiatric diagnosis in the Psychiatric Genomics Consortium (PGC) cohorts, with an R^2 of 0.43% ($P=5.83x10^{-6}$), 0.81% ($P=2.33x10^{-11}$) and 0.71% ($P=5.78x10^{-6}$) on the liability scale, for SA within MDD, bipolar disorder (BIP) and schizophrenia (SCZ) respectively (Table S2). (For conversion to the liability scale, the lifetime prevalence of SA in MDD, BIP, and SCZ was 16%, 37% and 36% respectively. These numbers represent the observed prevalence of SA in these disorders in the PGC cohorts.) The genetic correlation between SA-EUR|MDD and the GWAS of SA within psychiatric diagnosis was not significantly different from 1 (rg=1.13, SE=0.13) (Table S12). PRS for SA-EUR|MDD remained significantly associated with SA within psychiatric diagnosis in the PGC cohorts, with slightly lower phenotypic variance explained (0.32%, 0.67% and 0.46% for SA within MDD, BIP and SCZ respectively) (Table S2).

Examining the genetic correlations between SA within psychiatric diagnosis and psychiatric disorders, most genetic correlations were comparable to those observed with SA-EUR|MDD (Table S13). As exceptions, BIP and SCZ had non-significant genetic correlations with SA within psychiatric diagnosis (SCZ: rg=-0.07, SE=0.075, $P=3.24x10^{-1}$, BIP: rg=-0.08, SE=0.10, $P=4.38x10^{-1}$). This is consistent with a previous report that BIP and SCZ cases who had attempted suicide did not have higher BIP or SCZ PRS, compared with cases who did not attempt suicide[12].

Overall, the results of these genetic correlation and PRS analyses, demonstrate the comparability of the GWAS of SA within psychiatric diagnosis with SA-EUR|MDD, confirming the validity of the statistical conditioning approach to control for the genetic effects of psychiatric disorders. Statistical conditioning using mtCOJO only requires GWAS summary statistics, is readily applicable to different types of cohort and circumvents the need for samples with specific psychiatric diagnoses, detailed phenotypic information or individual-level genotype data available.

Cohort ascertainment, case and control definitions

Psychiatric Genomics Consortium Major Depressive Disorder

Subjects were drawn from 14 major depressive disorder (MDD) case-control cohorts in the Psychiatric Genomics Consortium (PGC), where information on suicide attempt (SA) had been collected[12]. MDD was diagnosed using structured psychiatric interviews according to international consensus criteria (DSM-IV, ICD-9, or ICD-10). Items from these interviews provided information on self-harm, suicidal ideation, plans and SA for patients with MDD. Patients with MDD endorsing SA were included as cases in this study. The controls for the primary genome-wide association study (GWAS) of SA included patients with MDD who did not endorse SA as well as healthy controls. MDD cases who were missing information on SA were excluded from the study. The healthy controls from PGC MDD cohorts were largely screened for the absence of depression and other psychiatric disorders (12/14 cohorts), however information on SA was not available for these individuals. All subjects were of European ancestry and gave written informed

consent to participate in the source studies. The source, inclusion and exclusion criteria for each individual PGC MDD cohort have been reported in detail previously[13], as well as the specific items used to ascertain information on SA from psychiatric interviews[12].

Psychiatric Genomics Consortium Bipolar Disorder

Subjects were drawn from 22 bipolar disorder (BIP) case-control cohorts in the PGC, where information on SA had been collected[12]. As described for the PGC MDD cohorts, structured psychiatric interviews were used to diagnose BIP and ascertain information on SA. Cases and controls were defined in the same way as for the PGC MDD sample. The healthy controls from most PGC BIP cohorts were screened for the absence of lifetime psychiatric disorders. The source, inclusion and exclusion criteria for each individual PGC BIP cohort have been reported in detail previously[14], as well as the specific items used to ascertain information on SA from psychiatric interviews[12] .

Psychiatric Genomics Consortium Schizophrenia

Subjects were drawn from 9 schizophrenia (SCZ) case-control cohorts in the PGC, where information on SA had been collected[12]. The same procedures were used to make psychiatric diagnoses, ascertain information on SA and define cases and controls, as described previously for PGC MDD and BIP studies. The source, inclusion and exclusion criteria for each individual PGC SCZ cohort have been reported in detail previously[15], as well as the specific items used to ascertain information on SA from psychiatric interviews[12].

Psychiatric Genomics Consortium Eating Disorders

Subjects originated from 4 anorexia nervosa (AN) case-control cohorts in PGC, where information on SA had been collected. The ascertainment, phenotype measurement, and inclusion and exclusion criteria have been described previously for these cohorts[16,17]. The cohorts were the Children's Hospital of Philadelphia/Price Foundation Collaborative Group (CHOP/PFCG) case-control cohort, and the France, Spain, and USA/Canada case cohorts from the Genetic Consortium for Anorexia Nervosa/Wellcome Trust Case Control Consortium-3 (GCAN/WTCCC-3) with controls sourced as described in Duncan et al[17]. Control cohorts from a similar geographic location and genotyping platform were preferentially sought. PGC AN cases had DSM-III-R or DSM-IV diagnoses of AN or EDNOS-AN (i.e., without the requirement of amenorrhea) based on structured diagnostic interviews. Controls had not been screened for AN but prevalence of lifetime AN is rare (~1%), nor had they been screened for SA. The same procedures described for the PGC MDD cohorts were used to define cases and controls.

CONVERGE

MDD cases were recruited from 58 provincial mental health centers and psychiatric departments within general hospitals, from 23 provinces in China[18]. Controls were recruited from patients undergoing minor surgery at general hospitals or local community centers. All subjects were Han Chinese women with four Han Chinese grandparents. Cases were excluded if they had a history of bipolar disorder, psychosis, or mental retardation. Cases were between ages 30-60 and had at least two episodes of MDD based on DSM-IV criteria, and with the first episode occurring between ages 14-50. They could not have abused drugs or alcohol prior to their first depressive episode. All subjects were interviewed using a computerized assessment program. The MDD diagnosis was determined using the Composite International Diagnostic Interview (WHO lifetime version 2.1; Chinese version). Cases were asked whether they had contemplated suicide during their worst depressive episode, and if so, whether they made a plan. Those who endorsed making a plan were asked whether they had attempted suicide. Controls were asked whether they had thought a lot about death or harming themselves and excluded if they responded in the affirmative.

Army STARRS

Subjects come from several components of the Army Study To Assess Risk and Resilience in Servicemembers (STARRS): New Soldier Study (NSS), Pre/Post Deployment Study (PPDS), and Soldier Health Outcomes Study A (SHOS-A). Detailed information about the design and conduct of STARRS is available in a separate report[19]. Soldiers from the respective studies are unique and independent as confirmed by analysis of genetic relatedness. Suicidal behaviors were assessed using a version of the Columbia Suicidal Severity Rating Scale (C-SSRS)[20] assessing lifetime occurrence of suicidal ideation ("Did you ever in your life have thoughts of killing yourself" or "Did you ever wish you were dead or would go to sleep and never wake up?") and, among respondents who reported lifetime suicidal ideation, suicide plans ("Did you ever have any intention to act [on these thoughts/on that wish]?" and, if so, "Did you ever think about how you might kill yourself [e.g., taking pills, shooting yourself] or work out a plan of how to kill yourself?") and suicide attempts ("Did you ever make a suicide attempt [i.e., purposefully hurt yourself with at least some intention to die]?"). For the primary GWAS of SA (n=670 cases), controls (n=10637) included individuals with no lifetime history of SA (who may or may not have a lifetime history of suicidal ideation). The GWAS of SA within psychiatric diagnosis included 376 cases of SA with MDD and 3447 individuals with MDD and no history of SA as controls.

German Borderline Genomics Consortium

Subjects were drawn from a GWAS sample on Borderline Personality Disorder[21]. The selected subjects consist of cases recruited in Berlin and Mannheim, and controls recruited in Mainz and from a sample of blood donors recruited in Mannheim, Germany. The diagnosis of Borderline Personality Disorder was assigned according to DSM-IV criteria on the basis of structured clinical interviews (either IPDE or SCID-II). Life-time attempt of suicide and, in the case of a positive answer, the number of attempts were documented. Diagnostic interviews were conducted by trained and experienced raters. Controls from Mainz were screened for a list of psychiatric disorders (panic disorder, agoraphobia, social phobia, specific phobia, generalized anxiety disorder, PTSD, obsessive-compulsive disorder, major depression, dysthymia, mania, hypochondriacal disorder, somatoform disorder, pain, conversion disorders, anorexia nervosa, bulimia nervosa, harmful alcohol use, alcoholism, harmful drug use, drug addiction, schizophrenia, schizotypal disorders). Controls from Mannheim were blood donors who filled out a questionnaire including questions on mental and somatic health. For the current study the following information was used: self-report of psychiatric disorders, self-report of diagnosis of psychiatric disorder by a healthcare professional, and a questionnaire version of the SCID items for depression criteria A1–A9. The subgroup of subjects affirming at least one of the two SCID depression screening items were asked for their lifetime history of suicide attempts. Control subjects with a history of suicide attempt were excluded.

Grady Trauma Project (GTP)

The subjects for this study were part of a larger investigation of genetic and environmental factors that predict the response to stressful life events in a predominantly African American, urban population of low socioeconomic status. Participants were approached while in the waiting rooms of primary care, diabetes, or obstetrical-gynecological clinics of Grady Memorial Hospital in Atlanta, Georgia. Screen interviews, including participants' demographic information (e.g., self-identified race, sex, and age), prior hospitalization for psychiatric diseases, and psychiatric symptoms including Posttraumatic Stress Disorder (PTSD), depression, schizophrenia, and bipolar disorder, were completed on site. Suicide attempt history was assessed based on self-report (yes/no) when obtaining demographic information. Further details regarding the GTP dataset can be found in Gillespie et al[22]. Written and verbal informed consent was obtained for all participants and all procedures in this study were approved by the institutional review boards of Emory University School of Medicine and Grady Memorial Hospital, Atlanta, Georgia. The

primary GWAS of SA included 669 cases and 4473 controls and the GWAS of SA within psychiatric diagnosis included 355 cases and 1116 controls, all with PTSD.

UK Biobank

The UK Biobank is a prospective cohort study of 501,726 individuals, recruited at 23 centres across the United Kingdom[23]. Extensive phenotypic data are available for UK Biobank participants from health records and questionnaires, including an online follow-up questionnaire focussing on mental health (Mental Health Questionnaire, MHQ [Resource 22 on http://biobank.ctsu.ox.ac.uk]). A total of 157,366 participants provided responses to an online mental health questionnaire (MHQ) as a follow up to initial phenotyping in the UK Biobank sample. Of these, 6,872 were asked this question from Data-Field 20483, Category: Self-harm behaviors, "Have you harmed yourself with the intention of ending your life?" Most participants were not asked this question as it required a positive response to a previous self-harm question. In total, 3,563 of 6,872 respondents indicated "yes", 3,089 responded "no" and 220 preferred not to answer. In an effort to maximize power and because the phenotype is rare, we included all UK Biobank participants as controls in the primary GWAS of SA except for those responding yes to attempting suicide; this includes those that did not take the mental health assessment at all and those who preferred not to answer. After reducing our sample to a set of homogenous individuals with white British ancestry, we retained case-control data of 2,433 individuals having attempted suicide and 334,766 controls.

For the GWAS of SA within psychiatric diagnosis, cases were individuals with a mood disorder who reported a lifetime suicide attempt and controls were individuals with a mood disorder who reported no lifetime deliberate self-harm. Participants were classified as having a mood disorder if they either self-reported a professional diagnosis of depression or bipolar disorder as part of the MHQ [UK Biobank field 20544, responses 10 or 11] or if they met criteria for depression on MHQ questions derived from the Composite International Diagnostic Interview (CIDI). To meet these latter criteria, participants must have reported ever feeling depressed [UK Biobank field 20446] or anhedonic [UK Biobank field 20441] for two weeks in a row, for at least most of the day [UK Biobank field 20436] almost every day [UK Biobank field 20439] with more than a little interference with daily activities [UK Biobank field 20440]. In addition, they must have reported experiencing at least five of the following symptoms in this period of depression or anhedonia: depression [UK Biobank field 20446], anhedonia [UK Biobank field 20441], tiredness [UK Biobank field 20449], weight change [UK Biobank field 20536], sleep change [UK Biobank field 20532], loss of concentration [UK Biobank field 20435], worthlessness [UK Biobank field 20450] and thoughts of death [UK Biobank field 20437]. The MHQ additionally contained screening questions for bipolar disorder[24]. However, for the purpose of defining potential bipolar disorder, all individuals scoring positively on these screening questions were also required to meet the CIDI depression criteria defined above, and as such participants with potential bipolar disorder were a subset of those meeting criteria for depression. Individuals who self-reported a professional diagnosis of psychosis on the MHQ [UK Biobank field 20544, responses 2 or 3] were excluded. Cases of suicide attempt with mood disorders (n=2149) were defined as those who answered yes to the question "Have you ever harmed yourself with the intention to end your life?" [UK Biobank field f20483]. Controls with mood disorders were defined as those who reported no self-harm on the MHQ (n=35912).

Taiwan Major Depressive Disorder

MDD patients were drawn from a family study of mood disorders in Taiwan. Patients aged between 18 to 70 years, who met diagnostic criteria of MDD using the Diagnostic and Statistical Manual of Mental Disorders, fourth edition (DSM-IV) were consecutively referred by psychiatrists in clinical settings. Exclusion criteria include patients diagnosed with schizophrenia, schizoaffective or substance-induced mood disorders. SA was measured based on the Chinese version of the Composite International

Diagnostic Interview (CIDI), the modified Schedule of Affective Disorder and Schizophrenia-Lifetime (SADS-L), or Hamilton Depression Rating Scale (HAM-D). SA cases were identified with the answer of "Yes" in item "Have you ever attempted suicide?" in CIDI, or "Yes" in item "Have you ever had suicide attempt and really wanted to die?" in SADS-L, or the score of suicide item equal or greater than 3 in HAM-D. Each participant was interviewed with either of the aforementioned instruments. The Taiwan MDD cohort was included in the GWAS of SA within psychiatric diagnosis only and 222 MDD cases with a history of SA were compared with 318 MDD cases without a history of SA as controls. More details regarding sample recruitment were described elsewhere[25].

Taiwan Bipolar Disorder

The inclusion and exclusion criteria of Taiwan BIP cohort is the same as those of Taiwan MDD. Patients who met bipolar disorder subtype I or bipolar disorder subtype II using the DSM-IV were referred by psychiatrists in clinical settings. CIDI or SADS-L were used to collect SA information through interviews as the same in Taiwan MDD data. SA cases were defined as subjects who answered "Yes" for the SA item (n=235) and controls were individuals with BIP who answered "No" to the SA item (n=397). Details of sample recruitment and assessment please refer to Tsai et a [26].

Taiwan Schizophrenia

Schizophrenia patients were recruited from two study projects: Schizophrenia Trio Genomic Research in Taiwan (S-TOGET) and Taiwan Schizophrenia Linkage Study (TSLS). Participants enrolled from the S-TOGET project were parent-proband trio samples. There were in total 3008 families with probands diagnosed as schizophrenia or schizoaffective disorder based on DSM-IV in psychiatric hospitals or community care centers nation-wide in Taiwan. After excluding patients without suicide information, there were in total 1119 probands retained. Details about the ascertainment of the S-TOGET sample can be found elsewhere[27].

Samples from TSLS were probands with clinical record of schizophrenia or depressive type of schizoaffective disorder from hospitals or psychiatric service stations. According to the inclusion criteria of TSLS, proband had to have at least one other sibling affected with similar diagnosis. In the present study, only 94 probands but not family members were included in analysis. More detailed information of TSLS is included in a previous report[28].

SA information for SCZ patients in both S-TOGET and TSLS were measured using the Diagnostic Interview for Genetic Studies (DIGS), a semi-structured psychiatric interview. The item related to suicide in this instrument was: "Have you ever attempted suicide (YES/NO)?". SA cases were defined as those who answered "YES".

iPSYCH

All individuals included in this study were a part of the Danish iPSYCH 2012 population-based case-control cohort[29]. SA cases were identified according to information available from the Danish Psychiatric Central Research Register and the National Registry of Patients both complete until December 31, 2016. SA cases were identified as individuals with ICD-10 diagnoses of SA (ICD-10: X60-X84, equivalent to intentional self-harm), with SA indicated as 'reason for contact' in the registers, and with a main diagnosis of poisoning (ICD-10: T39, T42, T43, and T58). The SA case group also included individuals with a diagnosis in the ICD-10: F chapter as main diagnosis and report of poisoning by drugs or other substances (ICD-10: T36–T50, T52–T60) or injuries to hand, wrist, and forearm (ICD-10: S51, S55, S59, S61, S65, S69). Individuals who died by suicide according to Cause of Death Register available until December 31, 2015 were also classified as SA cases. Only contacts starting at age 10 years old or older were considered to be reliably reported SA

cases. Individuals not fulfilling any of the above SA case criteria were considered to be controls for the primary GWAS of SA. The study was approved by the regional Danish ethics committee and the Danish Data Protection Agency.

Janssen

The Janssen lifetime suicide attempt cohort consisted of subjects of European ancestry and was drawn from multiple clinical trial samples (NCT00044681, NCT00397033, NCT00412373, NCT00334126, NCT01193153, NCT00094926) conducted by Janssen Research & Development, LLC as well healthy control samples from NINDS Human Genetics Repository (neurologically normal Caucasian control panel NDPT020, NDPT079, NDPT084, NDPT090, NDPT093, NDPT094, NDPT095, NDPT096, NDPT098, and NDPT099) managed by Coriell Institute for Medical Research (Camden, NJ) and from BioIVT (Westbury, NY). A subset of clinical trial samples (NCT00334126, NCT00397033, NCT00412373, and NCT00044681) was described previously[13,15,30,31,21,32] . The clinical diagnosis of MDD, schizophrenia, schizoaffective disorder, and bipolar disorder in Janssen clinical studies were based on expert clinician interviews conducted using DSM-IV-TR criteria. In two studies (NCT00397033 and NCT00412373), the diagnosis of schizoaffective disorder was confirmed using an interview based SCID (Structured Clinical Interview for DSM-IV-TR). The lifetime suicide attempt history was based on detailed clinical interview and medical records. The disease diagnosis for Coriell cohort was based on medical history including bipolar/manic depressive disorder, depression, schizophrenia, and suicide attempt. All patients who provided genetic samples gave written informed consent to the genetic testing. The primary GWAS included 255 cases and 1684 controls.

Genetic Investigation of Suicide and SA (GISS)

Sample recruitment, selection criteria, demographics, ancestry and psychiatric diagnoses have been described previously[33,34,35,36]. Briefly, lifetime SA was the main outcome ascertained in the offspring of nuclear family trios (all complete with both biological parents and one SA offspring per trio; n = 660). Trios were collected in Ukraine by first recruiting offspring from emergency care due to a severe SA, defined as a score of = 2 on the Medical Damage Rating Scale (MDS),[37] which represented the primary ascertainment criteria for inclusion. Persons who have engaged in suicidal thoughts without actual behavior would not be included. Other exclusion criteria were subject adopted, mental retardation, organic mental disorder, or other chronic medical illness involving the central nervous system. The SA were verified independently by both parents, the suicide attempter and by examining medical records. The suicidal intent of the SA was assessed by using both objective (levels of precaution) and subjective (intent to die) aspects.[38] Previous life-time SA was documented, as well as the history of suicides in family and relatives. Secondary outcomes included ICD-10 diagnoses according to the Composite International Diagnostic Interview (CIDI), personality traits according to the NEO personality inventory (NEO-PI-R), levels of anger, Beck's depression inventory, the WHO well-being index and the Global assessment of functioning (GAF) scale. Exposures to lifetime stressful and traumatic life-events (SLEs) were also assessed. Overall, the SA offspring included 51.1% males (n=337)/48.9% females (n=323), with mean ages of 24.6 (S.D. ± 7.3)/23.8 (S.D. ± 7.1) years, and 94.4% (n=318)/93.2% (n=301) of the SA subjects had = 3 Ukrainian or Russian grandparents, respectively. Overall, n=498 SA subjects did not have any of the major psychiatric diagnoses, e.g. schizophrenia (ICD-10 code F20), schizoaffective disorder (F25) or moderate / severe depression diagnoses (F32-33). The collection of research subjects followed the code of ethics of the World Medical Association (Declaration of Helsinki), and written consent was obtained. The study was approved by the Research Ethics Committee at the Karolinska Institute (Dnr 97–188) and by the Ministry of Health in Ukraine.

Australian Genetics of Depression Study and QSkin

Sample recruitment has been described in detail elsewhere[39]. In brief, two separate approaches were used. First, a nationwide recruitment based on antidepressant prescription history was possible through the Australian Government Department of Human Services (DHS; now known as *Services Australia*) which keeps the pharmaceutical benefits scheme national database. After obtaining the relevant ethics approvals by both the DHS and QIMR Berghofer, the researchers engaged the DHS to send ~110,000 invitations, in two waves, to participants with a prescription history of antidepressants. The second strategy consisted of a media publicity campaign launched on April 4, 2017. Under both strategies, participants were directed to a website which provided information on the study and collected informed consent for participation, including donation of a saliva sample for genotyping. Consenting participants were then referred to a modular online questionnaire consisting of a *core module*, which assessed essential clinical information on mental health diagnoses, treatment history, effectiveness and side effects, and multiple satellite modules. As of the 3 September 2018, 20,689 (75% female, mean age 43 years) participants had completed the online core module and provided consent to donate a saliva sample. Most of them (19,803) reported being diagnosed with depression and 17,698 met the DSM-5 criteria for a major depressive episode. SA was assessed using the suicidal ideation attributes scale (SIDAS)[40] and defined as an episode of self-harm with some intent to die. Healthy controls were ascertained from the QSkin Sun & Health Study (QSkin). QSkin consists of a randomly sampled cohort of individuals between 40 and 69 years from the state of Queensland[41]. A genetic study within QSkin has been initiated following a similar protocol for DNA collection by mail. During saliva donation participants were directed to fill in a short questionnaire on previous diagnoses of physician and psychiatric disorders[39]. Due to a lack of suicide attempt assessment in QSKIN, participants with a history of any psychiatric disorder were excluded. The final samples (unrelated individuals with genotype data passing quality control filters) comprised 2,792 SA cases and 20,193 controls for the primary GWAS of SA and 2,792 SA cases and 8,718 individuals with depression without a history of SA, for the GWAS of SA within psychiatric diagnosis.

Yale-Penn (European and African American cohorts)

Participants in this study were recruited from five sites in the eastern United States, for studies of the genetics of drug or alcohol dependence - the Yale-Penn study[42,43]. All participants were interviewed using the Semi-Structured Assessment for Drug Dependence and Alcoholism (SSADDA)[44], which contains several items relevant to suicidal behavior. Specifically, if a participant responded “Yes” to the item “Have you ever tried to kill yourself?” they were considered as a case. If they responded “No” to both this question and also “Have you ever thought about killing yourself?” they were treated as a control. Participants provided written informed consent and the study was approved by the institutional review board at each participating site (Yale Human Research Protection Program, University of Pennsylvania Institutional Review Board, University of Connecticut Human Subjects Protection Program, Medical University of South Carolina Institutional Review Board for Human Research, and the McLean Hospital Institutional Review Board).

Columbia University

Sample selection and diagnoses have been described previously[45]. Briefly, 2,382 unrelated individuals of Caucasian ancestry from three sites (New York, USA; Montreal, Canada, Munich, Germany) were recruited between 1991 and 2011. and gave written informed consent to participate as required by the relevant Institutional Review Boards. In total, 1,765 live subjects and 617 postmortem subjects were genotyped using the Illumina Omni1-Quad Beadchip (1,014,770 SNPs). Subjects with SA were defined as individuals who died by suicide or attempted suicide and in 64 percent of cases were known to have had a DSM-IV defined MDD, diagnosed by a SCID I structured clinical interview. SA was defined as a self-injurious act

that has at least partial intent to end one's life. A group of subjects with MDD and without a history of a suicide attempt provided a psychiatric control group. Additionally, unrelated healthy volunteers of German descent were randomly selected from the general population of Munich, Germany, and contacted by mail. In New York and Montreal healthy volunteers were solicited through advertising. The Montreal sample was confined to French Canadians, whereas the New York sample included Europeans of any origin. Healthy volunteers were assessed by psychiatrists or clinical psychologists and evaluated using the SCID-NP version and were free of axis I diagnoses, cluster B personality disorder, substance use disorder and lifetime history of a suicide attempt. One thousand nine hundred and forty-two of the genotyped samples passed QC procedures. After filtering of ethnic outliers, 1,810 subjects remained: 925 males and 885 females, 577 cases with suicidal behavior (260 suicide attempters and 317 suicides), and 1,233 subjects without SB (1,096 live subjects without a history of attempt and 137 sudden death victims). A breakdown of subjects by diagnosis and site has been summarized in a table previously published[45].

Japan

For the Japanese cohort, we used data from 746 suicide decedents (386 suicides who died between June 1996 and July 2012 in the 1st set and 360 suicides who died between August 2012 and February 2017 in the 2nd set)[46]. Autopsies on suicides were performed and the decision of assigning the status "suicide" was made through discussion with the Medical Examiner's Office of the Hyogo Prefecture and the Division of Legal Medicine in the Kobe University Graduate School of Medicine. For non-suicide controls, we used genome-wide genotype data from 14,049 subjects (7,458 controls in the 1st set and 6,591 controls in the 2nd set) in the Biobank Japan project who had been genotyped as case subjects for non-psychiatric disorders and healthy volunteers.

University of Utah

The Utah GWAS samples included 4380 persons who died by suicide and 20,702 ancestry matched controls, genotyped on the PsychChip by the Psychiatric Genomics Consortium. Suicide cause-of-death determination results from a detailed investigation, done by the centralized Utah State Office of the Medical Examiner, of the scene of the death and circumstances of death, determination of medical conditions by full autopsy, review of medical and other public records concerning the case, interviews with survivors, in addition to standard toxicology workups. Suicide determination is traditionally made quite conservatively due to its impact on surviving relatives. DNA from suicide deaths was extracted from whole blood using the Qiagen Autopure LS automated DNA extractor (www.qiagen.com).

Controls for the University of Utah sample were drawn from the following cohorts which had been genotyped on the PsychChip by the Psychiatric Genomics Consortium. The boldfaced first line for each sample is study PI, PubMed ID if published, study name, PGC internal tag or study identifier and number of controls.

Braff D | PMID: 17035358 | Consortium on the Genetics of Schizophrenia (COGS-1) | cogs1 (n=416)

Participants were recruited from seven sites in the United States, as part of the Consortium on the Genetics of Schizophrenia (COGS-1) family study: University of California at San Diego (UCSD) and Los Angeles (UCLA), University of Colorado (CUHSC), Mount Sinai School of Medicine (MSSM), University of Pennsylvania (PENN), Harvard Medical School (HMS) and University of Washington (UW). Participants provided written informed consent and the study was approved by the institutional review board at each participating site. Unrelated community comparison subjects without personal or family history of psychosis were recruited. To parallel psychiatric comorbidity in relatives of probands, nonpsychotic axis I

psychopathology was accepted in approximately 30% of the community comparison subjects but clinical stability and/or remission was required. Subjects were excluded if they had ECT in the last 6 months, substance abuse or dependence, head injury with loss of consciousness >15 minutes, and for any neurological or severe systemic illness. All subjects underwent a standardized clinical assessment using the Diagnostic Interview for Genetic Studies (DIGS) Details of the ascertainment, diagnostic, and screening procedures are provided elsewhere[47]. Written informed consent was obtained for each subject per local IRB protocols.

Sonuga-Barke E | Not published | South Hampshire ADHD Register - University of Southampton (SHaRE)| barke (n=65)

SHaRE was a clinical database including child and adolescent patients from CAMHS clinics across the south coast in the UK. Controls were ascertained from local schools of a similar age and sex to patients. All undertook a detailed clinical and psychometric assessment. DNA was extracted from cheek cells and genotyped on the PsychChip by the Psychiatric Genetics Consortium.

Baune, BT, Dannlowski, U | Not published | [PGC Psychchip] | bdtrs (n=722)

The Bipolar Disorder treatment response Study (BP-TRS) comprises BD inpatient cases and screened controls of Caucasian background. Psychiatric diagnosis of Bipolar Disorders was ascertained using SCID or MINI 6.0 using DSM-IV criteria in a face-to-face interview by a trained psychologist / psychiatrist for both cases and controls. Healthy controls were included if no current or lifetime psychiatric diagnosis was identified.

Bau C | Not published | [PGC Psychchip] |clait (n=272)

The Brazilian ADHD Porto Alegre Cohort is part of the International Multi-centre persistent ADHD CollaboraTion (IMpACT). It comprises adult patients and controls ascertained in the Hospital de Clínicas de Porto Alegre. Individuals from the control group were recruited in the blood donation centre. The inclusion criteria were (A) being Brazilian of European descent and (B) aged 18 years or older. The exclusion criteria were: (A) positive screening in the 6-item Adult ADHD Self-Rated Scale Screener (ASRS), (B) evidence of a clinically significant neurological disease that might affect cognition (e.g., delirium, dementia, epilepsy, head trauma, and multiple sclerosis), and (C) current or past history of psychosis. The control group also underwent a broad sociodemographic assessment and a screening for comorbidities with the SCID epidemiologic screener. The study was carried out in accordance with the Declaration of Helsinki, and all participants signed an informed consent form previously approved by the institutional review board of the hospital (No. 00000921).

Ophoff R, Posthuma D, Lochner C, Franke B | Not published | [PGC Psychchip] | dutch (n=1111)

Ophoff R: Controls were collected at different sites in the Netherlands and were volunteers with no psychiatric history after screening with the (MINI[48]). Ethical approval was provided by UCLA and local ethics committees and all participants gave written informed consent.

Lochner C: Controls include population based-controls ascertained from blood banks and controls recruited through university campuses and newspaper advertisements, who underwent a psychiatric interview and had no current or lifetime psychiatric disorder[49,50].

Franke B: The controls included are healthy individuals from the Dutch part of the International Multicenter ADHD Genetics (IMAGE) project[51,52].
Posthuma D: Data were provided for 960 unscreened Dutch population controls from the Netherlands Study of Cognition, Environment and Genes (NESCOG)[53]. The study was approved by the institutional review board of Vrije Universiteit Amsterdam and participants provided informed consent.

Gawlik M | Not published | [PGC Psychchip] | gawli (n=572)
Patients were recruited at the Department of Psychiatry, Psychosomatics and Psychotherapy, University of Würzburg, Germany. Diagnosis according to DSM-IV (Diagnostic and Statistical Manual of Mental Disorders-fourth edition) was made by the best estimate lifetime diagnosis method, based on all available information, including medical records, and the family history method. Healthy control subjects were recruited from the blood donor centre at the University of Würzburg.

Reif, A | Not published | [PGC Psychchip] | germ1 (n=1072)
Control subjects were healthy participants who were recruited from the community of the same region as cases for a genetic study of bipolar disorder. They were of Caucasian descent and fluent in German. Exclusion criteria were manifest or lifetime DSM-IV axis I disorder, severe medical conditions, intake of psychoactive medication as well as alcohol abuse or abuse of illicit drugs. Absence of DSM-IV axis I disorder was ascertained using the German versions of the Mini International Psychiatric Interview. IQ was above 85 as ascertained by the German version of the Culture Fair Intelligence Test 2[54]. Study protocols were reviewed and approved by the ethical committee of the Medical Faculty of the University of Frankfurt. All subjects provided written informed consent.

Pato, C | Not published | [PGC Psychchip] | gpcw1 (n=1858)
Genomic Psychiatry Consortium (GPC) cases and controls were collected via the University of Southern California healthcare system, as previously described[55]. Using a combination of focused, direct interviews and data extraction from medical records, diagnoses were established using the OPCRIT and were based on DSM-IV-TR criteria. Age and gender-matched controls were ascertained from the University of Southern California health system and assessed using a validated screening instrument and medical records.

Spalletta G | Not published | [PGC Psychchip] | spal1 (n=40)
The IRCCS Santa Lucia Foundation of Rome, Italy, sample of healthy people was recruited from the hospital personnel and using local advertisement and was screened for a current or lifetime history of psychiatric and personality disorders according to the DSM-IV-TR, using the SCID_non patient edition. Exclusion criteria are as follows: history of alcohol or drug abuse in the last 2 years before the assessment, lifetime drug dependence, traumatic head injury with loss of consciousness, past or present major medical illnesses or neurological disorders, any psychiatric disorders or mental retardation, dementia or cognitive deterioration according to DSM-IV-TR criteria and Mini-Mental State Examination (MMSE) normative data within the Italian population, any potential brain abnormalities and vascular lesions as apparent on conventional T1 and T2 weighted and FLAIR magnetic resonance imaging scans. All included subjects signed an informed consent approved by the local ethic committee.

Serretti A | Not published | [PGC Psychchip] | serr1 (n=147)

The sample has been described previously (Mapping genomic loci prioritises genes and implicates synaptic biology in schizophrenia. The Schizophrenia Working Group of the Psychiatric Genomics Consortium - manuscript submitted). Briefly, healthy controls were recruited and included in the context of a medical screening, no formal psychiatric interview was administered but the absence of major and invalidating psychiatric disorder was recorded. The study was approved by the San Raffaele Pisana and by ASL RME Ethics Committees, and all participants provided written informed consent.

Nurnberger JI, Edenberg HJ, McInnis M, Wilcox HC, Glowinski AL, Fullerton JM | PMID: 29173741| [PGC Psychchip] | iupui (n=65)

Young people with familial risk of bipolar disorder and healthy controls (aged 12 to 21 years) were ascertained from 4 independent sites in the United States: Johns Hopkins University, University of Michigan, Washington University in St. Louis, and Indiana University[56,57]. Recruitment procedures and clinical batteries were aligned with those also employed by the Australian Bipolar High Risk Study site (represented in the *neura* cohort). Control parents were recruited through general medicine clinics, motor vehicle records, and campus advertising. Exclusion criteria for control parents included BPI, BPII, recurrent major depression, schizoaffective disorder, or schizophrenia in either parent; we also excluded parents with a first-degree relative with a psychiatric hospitalization.[56,57]

Rivera M, Cervilla J.A | Not published | [PGC Psychchip] | marg1 (n=1354)

All control participants were part of the PISMA study, the first epidemiological study focussed on mental health disorders, and their associated factors, ever undertaken in a representative sample of the entire Andalusian population (Spain)[58]. This was a cross-sectional study targeting a large representative stratified sample of community-dwelling Andalusian adults between 18 and 75 years of age. All provinces in the Andalusian community were included. A comprehensive account of risk, neuropsychological, personality and psychiatric assessments were undergone in the PISMA sample (4507 participants) and have been reported elsewhere[58]. Interviews were undertaken by psychologists specially trained by the PI of the study (J.A.Cervilla). Interviewers demonstrated sufficient knowledge on both interviewing techniques on all protocol scales and inventories, most of which had been originally designed for administration by lay-interviewers. Teaching techniques used included lectures, role playing between interviewers and scoring of videoed interviews held by experts on volunteers. All instruments used had, nonetheless, previously been validated and demonstrated sufficient inter and intra-rater reliabilities along with most other psychometric properties. Specific inter-rater reliabilities between interviewers on such instruments after training sessions were high [58]. The psychiatric interview to identify mental disorder (MDs) diagnoses was performed using the MINI, which generates diagnoses compatible with both Axis I DSM-4 and ICD-10 criteria for 16 common MDs, two additional diagnoses of major depression with melancholia and mood disorder with psychotic symptoms, one Axis II diagnosis (antisocial personality disorder), as well as a suicidal risk estimate. A biological sample was obtained from each participant using the Oragene DNA saliva collection kit (OG-500; DNA Genotek Inc.). DNA extraction was performed using Oragene saliva Kit protocol as per manufacturer's instructions. Samples were genotyped on the PsychChip array at the Stanley Centre. Participants in the PISMA study gave their informed consent. The study had ethics approval granted by “Comité de Ética en Investigación, Universidad de Granada” which permits inclusion

of the data in meta-analyses. Genotype data can be accessed for secondary analysis after explicit PI approval. This study was funded by Consejería de Innovación, Proyecto de Excelencia CTS-2010-6682.

Liberzon, I., King, A.P., Galea, S., Calabrese, J. | PMID 25162199 | Ohio Army National Guard (OHARNG) | mich1 (n=111)

The Ohio Army National Guard (OHARNG) study[59] was a prospective, longitudinal study of Ohio Army National Guard soldiers who were initially recruited and had a comprehensive intake psychiatric assessment (CATI telephone interview with standardized instruments) after their unit was activated and before their unit was deployed to Iraq or Afghanistan. Saliva samples for DNA (Oragene tube) were obtained at follow-up assessment Waves 2-4 by return mail to our lab, and DNA for GWAS analysis was isolated and stored. The control subjects included in this sample were healthy European-American male soldiers who did not meet criteria for PTSD, MDD, or any other psychiatric diagnosis at intake or any follow-up assessment Wave. Controls (N=125) were matched by age and lifetime "trauma load" to N=125 PTSD cases within the same cohort. A total of 37 potentially traumatic events were identified using the Clinician-Administered PTSD Scale (CAPS-IV)[60] and the 1996 Detroit Area Survey of Trauma[60] PTSD symptoms were assessed using a 17-item structured interview scale derived from the PTSD Checklist (PCL) for DSM-IV performed by trained lay telephone interviewers using epidemiological methods (forced choice symptom severity range, 1-5). Reliability of the telephone interview was validated against the criterion standard (in-person CAPS interview by mental health professional) in a clinical subsample (n = 500), demonstrating high specificity (0.92)[61]. Respondents were considered to have a diagnosis (cases) if lifetime DSM-IV PTSD criteria were met. Respondents were considered to have a current diagnosis if past month DSM-IV criteria were met. The PCL calculates PTSD symptom severity, which ranged from 17 to 85, by sum of scores of items endorsed. For this cohort (125 cases, 125 controls), the mean severity was 38.4 and the standard deviation 17.6.

Fullerton JM, Mitchell PB, Schofield PR, Green MJ, Weickert CS, Weickert TW | Not published | [PGC Psychchip] | neura (n=161)

The NeuRA collection comprised psychiatrically screened healthy control subjects from three cohort studies ascertained in Australia: the Bipolar High Risk "kids and sibs" study[57,62], the Imaging Genetics in Psychosis Study (IGP)[63] and the Cognitive and Affective Symptoms of Schizophrenia Intervention (CASSI) trial[64]. The Bipolar High Risk study is a collaborative study with 4 US sites (represented in the *iupui* cohort), and young Australian participants aged 12-30[56]. Healthy controls from each study were recruited from the community, had no personal lifetime history of a DSM-IV Axis-I diagnosis as determined by psychiatric interview, and no history of psychotic disorders among first-degree biological relatives.

Koenen K | Not published | Nurses' Health Study II| nhsii (n=739)

In 2008 the Trauma and PTSD Screening Questionnaire was mailed to 60,804 Nurses' Health Study II (NHSII) participants who had completed recent questionnaires. The response rate was 84% (N = 50,953). We identified 17,666 women for diagnostic interviews who reported exposure to at least one traumatic event on the modified Brief Trauma Questionnaire and agreed to be interviewed[65,66]. We then identified probable PTSD cases and probable controls using Breslau's lifetime PTSD screen[67], which classifies PTSD cases with 80% sensitivity, 97% specificity, 71% positive predictive value, and 98% negative predictive value. We randomly selected 2,112 probable PTSD cases and 2,001 probable controls for diagnostic interviews. The Partners Human Research Committee approved this study; the protocol has been published[68].

PTSD was then assessed using the PTSD Checklist (PCL-C), a 17-item self-report measure of DSM-IV PTSD symptoms[69,70]. Participants rated each of the 17 symptoms on a scale indicating how much they had been

bothered by a particular symptom as a result of the event, from “not at all” to “extremely.” The Checklist assesses re-experiencing symptoms (Criterion B), avoidance/numbing symptoms (Criterion C), and arousal symptoms (Criterion D). To be a PTSD case, respondents must have reported experiencing one or more of the 5 re-experiencing symptoms, 3 or more of the 7 avoidance/numbing symptoms, and 2 or more of the 5 arousal symptoms at least “moderately.” Additional questions assessed the other three DSM-IV criteria: intense fear, horror, or helplessness in response to the event (Criterion A2), symptom duration of at least one month (Criterion E), and clinically significant impairment in functioning due to symptoms (Criterion F). The PCL-C had excellent internal consistency (Cronbach’s α=0.87). Respondents were considered affected by lifetime PTSD if all six DSM-IV criteria were met in reference to the worst event.

Krebs M-O | Not published | [PGC Psychchip] | paris n=420

Controls from the Psydev Paris cohort were healthy unrelated French adults (both genders) recruited from among staff members at the GHU Paris or from physiotherapist schools as part of a study PsyDev (Promotor Inserm RBM03-021). They gave their written consent after receiving a full descrip-tion of the study and study procedures were approved by the French ethics committees CPP Paris Ile de France 4 and were in accordance with the Declaration of Helsinki. They were screened for medical and psychiatric history either using the Diagnosis Interview for Genetic Studies (DIGS version 3.0) conducted by trained psychiatrists and psycholo-gists and/or self-rated questionnaires followed by face-to- face interviews. Exclusion criteria included personal or in first degree relatives with psychiatric history, personal history of neurologic signs, unstable medical condition, pregnancy and substance dependence. All controls were of European ancestry ("Caucasian") and were born in France.

Campion D, Laurent C, Levinson D | Not published | [PGC Psychchip] | rouen (n=190)

Controls from the Rouen cohort were recruited from among staff members and blood donors at the Centre Hospitalier Universitaire Rouen (France) as part of a study on hyperprolactinemia in schizophrenia[71]. All controls were of European ancestry (“Caucasian”) and were born in France. All controls denied (by self-report in response to direct questions) any history of psychiatric disorder in themselves or in first-degree relatives or current use of medications or drugs other than oral contraceptives in women. The protocol was approved by the appropriate regional ethics committee. All participants gave written informed consent.

Gareeva, A; Khusnutdinova, E; Escott-Price, V | Not published | [PGC Psychchip] | russ1 n=344

All controls have a negative family history for neuro-psychiatric disorders. For all individuals key phenotypic information has been collected, including information about sex, age, ethnicity, age at onset and family history of psychiatric disorders. All subjects have provided written and informed consent. This study has been approved by the local bioethical committee of the Institute of Biochemistry and Genetics of Ufa Federal Research Center of the Russian Academy of Sciences (IBG UFRC RAS). Peripheral blood was taken from all participants of the study. DNA was extracted from peripheral blood by the phenol and chloroform method.

Perlis, R; Sklar, P; Smoller, J| Not published | [PGC Psychchip] | smol0 (n=1052), smol2 (n=493), smol3 (n=555)

Perlis, R; Sklar, P; Smoller, J: EHR data were obtained from a health care system of more than 4.6 million patients[72] spanning more than 20 years. Experienced clinicians reviewed charts to identify text features and coded data consistent or inconsistent with a diagnosis of bipolar disorder. Natural language processing was used to train a diagnostic algorithm with 95% specificity for classifying bipolar disorder. Filtered coded data were used to derive three additional classification rules for case subjects and one for control subjects. No EHR-classified control subject received a diagnosis of bipolar disorder on the basis of direct interview (positive predictive value (PPV)=1.0). For most subphenotypes, PPV exceeded 0.80. The

EHR-based classifications were used to accrue bipolar disorder cases and controls for genetic analyses. Samples were genotyped on the Psychchip array.

Ribases M | PMID 32279069 | [PGC Psychchip] | span1 (n=2054), span2 (n=430)
The Spanish controls were part of the Mental-Cat clinical sample or the INSchool population-based cohort. A total of 1,774 controls from the Mental-Cat cohort (60.5% males) were evaluated and recruited prospectively from a restricted geographic area at the Hospital Universitari Vall d'Hebron of Barcelona (Spain) and consisted of unrelated healthy blood donors[73]. The INSchool sample consisting of 771 children (76.2% males) from schools in Catalonia were involved for screening using the Achenbach System of Empirically Based Assessment (ASEBA) with the Child Behavior Checklist CBCL/4-18 (completed by parents or surrogates), the Teacher Report Form TRF/5-18 (completed by teachers and other school staff) and the Youth Self-Report YSR/11-18 (completed by youths); the Strengths and Difficulties Questionnaire (SDQ) and the Conner's ADHD Rating Scales (Parents and Teachers). Genomic DNA samples were obtained either from peripheral blood lymphocytes by the salting out procedure or from saliva using the Oragene DNA Self-Collection Kit (DNA Genotek, Kanata, Ontario Canada). DNA concentrations were determined using the Pico- Green dsDNA Quantitation Kit (Molecular Probes, Eugene, OR) and genotyped with the Illumina Infinium PsychArray-24 v1.1 at the Genomics Platform of the Broad Institute. The study was approved by the Clinical Research Ethics Committee (CREC) of Hospital Universitari Vall d'Hebron, all methods were performed in accordance with the relevant guidelines and regulations and written informed consent was obtained from participant parents before inclusion into the study. Detailed information has been published previously[73].

Landen M, Hillert J, Alfredsson L | Not published | [PGC Psychchip] | swed1 (n=2886)
Population-based controls, randomly selected from the Swedish national population register, were collected as part of two case-control studies of multiple sclerosis: GEMS (Genes and Environment in Multiple Sclerosis) and EIMS (Epidemiological Investigation of Multiple Sclerosis)[74].

Di Florio A, McQuillin A, McIntosh A, Breen G | Not published | [PGC Psychchip] | ukwa1 (n=2527)
McQuillin A: A subset of the UCL control subjects (n=814) were recruited from London branches of the National Blood Service, from local NHS family doctor clinics and from university student volunteers. All control subjects were interviewed with the SADS-L to exclude all psychiatric disorders. All volunteers read an information sheet approved by the Metropolitan Medical Research Ethics Committee who also approved the project for all NHS hospitals. Written informed consent was obtained from each volunteer. A subset (n=448) of the control subjects were random UK blood donors obtained from the ECACC DNA Panels (https://www.phe-culturecollections.org.uk/products/dna/hrcdna/hrcdna.jsp).
McIntosh AM: Cases with bipolar disorder were recruited from the clinical case loads of treating psychiatrists from Edinburgh and across the central belt of Scotland. Controls were identified from non-genetic family members and from the extended networks of the participants themselves. All participants were of European ancestry and diagnosis was confirmed using an established battery developed for ICCCBD.
Breen G: Controls were drawn from blood donors to the UK Motor Neuron Disease Association DNA Biobank.[75]

Gatt JM, Williams LM, Bryant R, Fullerton JM, Schofield PR | PMID: 32785990| [PGC Psychchip] | unsw1 (n= 641)

This sample is drawn from the TWIN-E study, an ongoing longitudinal prospective study of 1,660 individuals (aged 18–62 years) sourced from Twins Research Australia. The baseline study was originally conducted at the University of Sydney, under approval from the Human Research Ethics Committee (03-2009/11430). Participants were community dwelling, healthy, same-sex, adult twin-pairs with English as their primary language. Participants did not complete formal psychiatric assessments, but provided questionnaire, neurocognitive, electrophysiological, neuroimaging and saliva samples for genetic material[76]. The genotyped sample comprised 1,333 DNA samples comprising ~710 unrelated individuals (pi_hat<0.2) plus co-twins, as previously described[77].

Mathews CA| Not published | [PGC Psychchip] | matt1 (n=20)

Control samples were ascertained as part of ongoing genetic and neurophysiological studies of hoarding, obsessive compulsive and tic disorders. Controls reported no current or lifetime history of mania or hypomania at the time of ascertainment. Sixty-two of the 104 controls were screened for psychiatric illness using the Structured Clinical Interview for DSM-IV TR diagnoses and diagnoses of bipolar disorder, lifetime or current, were ruled out through a best estimate consensus diagnosis. Other psychiatric diagnoses were not excluded. The remaining 42 participants were not formally screened, but reported no lifetime or current history of bipolar disorder, obsessive compulsive, hoarding, or tic disorders. Samples were genotyped on the Psychchip array. Ethical approvals were obtained from the University of Florida Human Subjects Review Board.

Medland SE, Martin NG | Not published | [PGC Psychchip] | usadd-mart1 (n=395)

Control samples were ascertained as part of a study on ADHD traits and inattention more broadly. Controls were screened for ADHD using the SWAN questionnaire[78] and did not meet criteria for ADHD at the time of recruitment. Samples were genotyped on the Psychchip array. Ethical approvals were obtained from the QIMR Berghofer Medical Research Institute Human Research Ethics Committee.

Waldman I | Not published | [PGC Psychchip] | wald1 (n=55), wald2 (n=110)

Control samples were ascertained as part of an ongoing genetic study of ADHD and other Externalizing disorders (I.e., Oppositional Defiant Disorder and Conduct Disorder). Controls reported no current diagnoses of Externalizing or Internalizing disorders at the time of ascertainment. Controls were assessed for psychiatric conditions using the Emory Diagnostic Rating Scale (EDRS)[79], a questionnaire that assessed parent ratings of symptoms of common DSM-IV Externalizing and Internalizing disorders (e.g., Major Depressive Disorder and various anxiety disorders). Samples were genotyped on the Psychchip array. Ethical approvals were obtained from the Emory University and University of Arizona Human Subjects Review Boards.

<u>Cohort genotyping, QC, imputation and analysis</u>

Psychiatric Genomics Consortium Major Depressive Disorder

Cohorts were genotyped following their local protocols, after which standardized quality control and imputation and analyses were performed centrally using RICOPILI (Rapid Imputation for COnsortias PIpeLIne), for each cohort separately[80]. These procedures have been described in detail previously[13]. Briefly, the quality control parameters for retaining SNPs and subjects were: SNP missingness < 0.05 (before sample removal), subject missingness < 0.02, autosomal heterozygosity deviation (F_{het} < 0.2), SNP missingness < 0.02 (after sample removal), difference in SNP missingness between psychiatric cases and

healthy controls < 0.02 and SNP Hardy-Weinberg equilibrium ($P > 10^{-10}$ in psychiatric cases, $P > 10^{-6}$ in healthy controls). Genotype imputation was performed using the pre-phasing/ imputation stepwise approach implemented in IMPUTE2/ SHAPEIT (chunk size of 3 Mb and default parameters) to the 1000 Genomes Project reference panel[81,82,83]. Relatedness between subjects was calculated using identity by descent and one of each pair of related individuals (pi_hat > 0.2) was excluded. Relatedness with subjects in the PGC BIP and PGC SCZ samples was also calculated and one of each pair of relatives (pi_hat > 0.2) was excluded across all three of the samples. Overlapping individuals between PGC MDD and the UK Biobank sample were determined using genotype-based checksums (https://personal.broadinstitute.org/sripke/share_links/zpXkV8INxUg9bayDpLToG4g58TMtjN_PGC_SCZ_w3.0718d.76), and excluded from the PGC MDD study. One of the PGC MDD cohorts (BACCs) was excluded from the primary GWAS of SA due to overlapping controls with one of the PGC BIP cohorts (BOMA-Germany).

GWAS were performed using PLINK 1.9 by comparing imputed marker dosages under an additive logistic regression model between cases and controls in each of the 14 cohorts separately[84]. Principal components (PCs) generated using EIGENSTRAT were used as covariates in all GWAS as required, to control for population stratification[85]. SNPs were filtered from the GWAS summary statistics from each cohort using sample minor allele frequency (MAF) >= 1% and sample MAF corresponding to a minor allele count of 10 in cases or controls (whichever had smaller N), in order to control test statistic inflation at low MAFs from small cohorts. Meta-analyses were then performed across cohorts using an inverse variance-weighted fixed effects model in METAL, to obtain results for the primary GWAS of SA and the GWAS of SA within psychiatric diagnosis[86].

Psychiatric Genomics Consortium Bipolar Disorder
Genotyping, QC imputation and analyses were conducted in the same manner as described for the PGC MDD sample and have been described in full previously[12,14].

Psychiatric Genomics Consortium Schizophrenia
Genotyping, QC imputation and analyses were conducted in the same manner as described for the PGC MDD sample and have been described in full previously[12,15]. The Danish PGC SCZ cohort was excluded from the primary GWAS of SA, to ensure no overlap with the Danish iPSYCH cohort.

Psychiatric Genomics Consortium Eating Disorders
Genotyping has been described previously for these cohorts[16,17]. Quality control, principal components analysis to identify and remove ancestry outliers and generate covariates, and imputation to the 1000 Genomes Phase 3 reference panel were performed within PGC's GWAS pipeline RICOPILI [16,80] as described in full previously[16]. The first 5 PCs were included as covariates and GWASs were performed within RICOPILI using imputed variant dosages and an additive model. Identical individuals between PGC ED cohorts and PGC MDD, BIP and SCZ cohorts were detected using genotype-based checksums (https://personal.broadinstitute.org/sripke/share_links/zpXkV8INxUg9bayDpLToG4g58TMtjN_PGC_SCZ_w3.0718d.76). The USA/Canada GCAN/WTCCC-3 cohort was excluded from the primary GWAS of SA due to overlap of controls with one of the PGC BIP cohorts.

CONVERGE
DNA sequencing, variant calling, and imputation have been previously described[18]. Briefly, sequencing reads were aligned to GRCh37.p5 with Stampy (c.10.17)[87] using default parameters after filtering out reads of poor quality. Variant discovery and genotyping at all SNPs in the 1000 Genomes Phase 1 East Asian (ASN) [88] was performed using the GATK's UnifiedGenotyper (version 2.7-2-g6bda569). Imputation

was performed using BEAGLE (version 3.3.2)[89]. GWAS were performed using PLINK 1.9 by comparing imputed marker dosages under an additive logistic regression model between cases and controls. Based on prior studies, the first two principal components were included as covariates; these were derived from an eigen-decomposition of the genetic relatedness matrix. Variants were excluded from analysis if they had an INFO score <0.3, minor allele frequency <0.001, or HWE p<1e-7.

Army STARRS

Samples were genotyped using the Illumina OmniExpress + Exome array with additional custom content (N SNP = 967,537) or the Illumina PsychChip (N SNP = 571,054; 477,757 SNPs overlap with OmniExpress + Exome array). Relatedness testing was carried out with PLINK v1.90 and pairs of subjects with π of >0.2 were identified, randomly retaining one member of each related pair. We used a two-step pre-phasing/imputation approach for genotype imputation, with reference to the 1000 Genomes Project multi-ethnic panel (August 2012 phase 1 integrated release; 2,186 phased haplotypes with 40,318,245 variants). We removed SNPs that were not present in the 1000 Genomes Project reference panel, had non-matching alleles to 1000 Genome Project reference, or had ambiguous, unresolvable alleles (AT/GC SNPs with minor allele frequency [MAF] > 0.1). For the Illumina OmniExpress array 664,457 SNPs and for the Illumina PsychChip 360,704 SNPs entered the imputation procedure. For quality control (QC) purposes we kept autosomal SNPs with missing rate < 0.05; kept samples with individual-wise missing rate < 0.02; and kept SNPs with missing rate < 0.02. After QC, we merged our study samples with HapMap3 samples. We kept SNPs with minor allele frequency (MAF) > 0.05 and LD pruned at $R^2 > 0.05$. In order to avoid long range LD structure from interfering with the PCA analysis, we excluded SNPs in the MHC region (Chr 6:25-35Mb) and Chr 8 inversion (Chr 8:7-13Mb). We used PLINK v1.90 to conduct genome-wide association tests for each model on imputed SNP dosage with logistic regression adjusted for age, sex, and the top 10 within-population principal components (PCs).

German Borderline Genomics Consortium

Genotyping was performed using the Infinium PsychArray-24 Bead Chip as previously described[21]. Updated quality control and imputation were carried out using the RICOPILI GWAS pipeline[80] for the present manuscript. Briefly, the exclusion criteria for SNPs and subjects in the first round of quality control were: genotyping call rate for given SNPs or individuals <98%, difference in SNP genotyping call rate between cases and controls >2%, deviation of autosomal heterozygosity from the mean (|Fhet|>0.2), or a deviation from Hardy-Weinberg equilibrium (p<1x10−10 in cases; p<1x10−6 in controls). Imputation was conducted using a publicly available reference panel consisting of 54,330 phased haplotypes with 36,678,882 variants from the haplotype reference consortium (EGAD00001002729) and the prephasing/imputation stepwise approach in EAGLE/MINIMAC3 (default parameters and a variable chunk size of 132 genomic chunks)[90,91]. Relatedness testing and population structure analysis were performed using a subset of 65,408 SNPs that fulfilled strict quality criteria after imputation (INFO >0.8, missingness <1%, minor allele frequency >0.05), and which had been subjected to LD pruning (r2>0.02) in the second round of quality control. In the case of cryptically related subjects with pi-hat >0.2, one member of each pair was removed at random following the preferential retention of cases over controls. Principal components (PCs) were estimated from the quality-controlled genotypic data, and phenotype association was tested using logistic regression. The effect of individual PCs on genome-wide test statistics was assessed using λ. The GWAS was performed using an additive logistic regression model including the PCs associated with Borderline Borderline Personality Disorder case-control status (1-4; 7) as covariates to test single-marker associations in PLINK 1.9.

Grady Trauma Project (GTP)

Genotyping for the Grady Trauma Project was performed using the Omni-Quad 1M Bead Chip. Quality control and imputation (1000 Genomes Phase 3-hg19) were performed by using the Psychiatric Genomics Consortium PTSD Workgroup guidelines[92]. Only individuals with African American ancestry based on SNPweights software17 were included in the models. Principal components for ancestry were calculated according to the PGC guidelines in each separate ancestry group[92]. For each model, GWAS was performed using an additive logistic regression adjusting for 5 ancestry principal components (PLINK 1.9).

UK Biobank

Genotypic data were available for 488,380 individuals and were imputed to the Haplotype Reference Consortium (HRC), UK10K and 1,000 Genomes Phase 3 reference panels using IMPUTE4 to identify ≈ 93M variants for 487,409 individuals[93]. Variants for analysis were limited to those with minor allele frequency >= 0.01, imputation INFO-score >= 0.4, and which were either genotyped or imputed to the HRC reference panel, leaving a total of 7794483 SNPs for analysis. Using the genotyped SNPs, individuals were removed if: recommended by the UK Biobank core analysis team for unusual levels of missingness or heterozygosity; SNP genotype call rate < 98%; related to another individual in the dataset (KING r < 0.044, equivalent to removing up to third-degree relatives inclusive); phenotypic and genotypic gender information was discordant (X-chromosome homozygosity (FX) < 0.9 for phenotypic males, FX > 0.5 for phenotypic females). Removal of relatives was performed using a greedy algorithm, which minimises exclusions (for example, by excluding the child in a mother-father-child trio). All analyses were limited to individuals of White Western European ancestry, as defined by 4-means clustering on the first two genetic principal components provided by the UK Biobank[93]. Principal component analysis was also performed on the European-only subset of the data using the software flashpca2[94]. The GWAS of SA within psychiatric diagnosis was performed using BGenie v.1.2[93], covarying for 6 PCs, and factors capturing site of recruitment and genotyping batch. QC, imputation and analysis for the primary GWAS of SA followed similar procedures and has been described previously[95].

Taiwan MDD

Genotyping for MDD cases was obtained using Affymetrix CHB Array with 642,832 markers, Affymetrix TWB Array with 642,545 markers, and Illumina Human Omni Express Exome Beadchips with 949,974 markers. Samples with a completion call rate below 95 % were repeatedly assayed on a new aliquot DNA. Imputation was conducted by Michigan Imputation Server (https://imputationserver.sph.umich.edu/index.html#!) using 1000G phase 3 v5 as a reference panel, Eagle v2.3 for phasing, and EAS population for QC. We imputed ~46 million variants for both MDD and based on 1000 genome data of the East Asian panel. Samples that did not meet the 95% threshold of call rate were removed. We also removed kinship-pairs and outliers in population stratification. Markers with call rate <95%, minor allele frequency <0.01, p-value of Hardy-Weinberg equilibrium <1E-6, or imputation INFO score <0.7 were excluded. GWAS were performed using PLINK 1.9 and adjusted for 5 ancestry principal components.

Taiwan BIP

Genotyping for BIP cases was obtained using Affymetrix CHB Array with 642,832 markers, Affymetrix 6.0 Human Omni Express with 730,525 markers, and Affymetrix TWB Array with 642,545 markers. Samples with a completion call rate below 95 % were repeatedly assayed on a new aliquot DNA. The imputation processes, QC criteria and GWAS analysis were all the same as those in Taiwan MDD.

Taiwan SCZ

Genotyping for SCZ cases was obtained using the Axiom Genome-wide CHB 1 Array Plate in TSLS participants [96]. Samples with a completion call rate below 95 % were dropped from analysis. The imputation processes, QC criteria and GWAS analysis were all the same as those in Taiwan MDD and BIP.

iPSYCH

Genotyping, QC and imputation procedures for iPSYCH 2012 cohort were conducted in the same manner as described for the previous GWAS of SA[12,97,98]. Genotyping waves with less than 50 SA cases were removed from the analysis followed by removal of related individuals, duplicated samples, and restricting individuals to European population and Danish origin only. After the filtering of genotyping data 7,003 SA cases and 52,227 non-SA controls were identified. The GWAS analysis was adjusted for sex, the first 10 principal components of genetic ancestry and genotyping batch. Association analyses were performed and are reported only for variants for which P-value was calculated and for variants with MAF ≥ 1% or ≤ 99% in the control group.

Janssen

Clinical samples from NCT00334126, NCT00397033, and NCT00412373 were genotyped using Illumina Human1M-DuoV3, while samples from NCT00044681 were genotyped using HumanOmni5Exome-4v1. The rest of the samples were genotyped using PsychArray. Standard QC were applied. Genotype data were imputed using Impute2 against 1000 Genome reference panel (integrated_phase1_v3). The imputed genotype dosages were assessed for association in a logistic regression model, correcting for four principal components to account for population substructure.

Genetic Investigation of Suicide and SA (GISS)

SNP genotyping was done using the HumanOmni1-Quad_v1 chip (Illumina Inc.) at the SNP&SEQ Technology Platform facility (snpseq.medsci.uu.se), assaying ~1 million SNPs with each trio plated consecutively. For the raw data, 96.7% of SNPs had call rate >99%, >99.99% of calls were reproducible, >99.99% of family-wize calls had no mendelian errors, and duplicated individuals could be ruled out. SNPs were filtered to obtain call rates >= 95%, hardy weinberg equilibrium (HWE) exakt P = 10^{-6}, minor allele frequency (MAF) = 0.01 and no mendelian errors, whereby 739,780 autosomal- and 17,501 X-chromosomal SNPs remained. Phased reference panels (1000 genomes, phase 1; filtered for 1.00<MAF<0.005), BEAGLE v.3.3.2 and utils were downloaded (faculty.washington.edu/browning) [99]. SNPs were checked against the phased EUR individuals in the 1000 genomes reference-panel, for inconsistencies in SNP-strands, -positions, -names, MAFs, linkage disequilibrium (LD) and number of alleles, using the available check_strands python routines. 729,956 autosomal SNPs remained for imputation using ~9 million reference panel SNPs (1.00 > MAF > 0.005). The X-chromosome was not imputed. Phasing (nsamples=2) and imputation (nsamples=1) were executed separately, running one chromosome at a time in low-memory mode on a desktop PC. Only SNPs imputed with Beagle allelic R^2 = 0.7 were retained. ~5.5% of SNPs had a rare frequency (MAF < 0.01). The net imputation SNP gain after accounting for LD with r^2-threshold < 0.8 pruning and MAF > 0.01, was from 450,348 autosomal SNPs pre-imputation to 1,035,345 autosomal SNPs post-imputation, i.e. ~2.3 fold. Quantiles vs quantiles (QQ) plots showed that observed SNP P-values followed the uniform null (genomic inflation = 1.002), as previously described.[34] For this analysis, the ~6.8 million post-imputation SNP data was converted into a case-control sample by use of --tucc command in plink v.1.07 (660 cases and 660 controls; each control is a non-SA pseudo-sib, matched to a case on all other features), followed by analysis with --assoc --ci 0.95 in plink v.1.9.

Australian Genetics of Depression Study and QSkin

Samples from the AGDS were genotyped on three different genotyping centers using the same array (GSAMD-24v1-0_20011747). Healthy controls (QSkin cohort) were also genotyped using the GSA array. Quality control procedures that follow were applied to both AGDS and QSKIN genotypes. A common set of high QC markers between the different genotyping batches was obtained prior to joint imputation. Marker exclusion criteria (prior to imputation) included: unknown or ambiguous map position and strand alignment in a BLAST search, missingness >5%, p(HWE test)< 10^-6), MAF<1%, GenTrain score <0.6. The Michigan imputation server was used to impute the genotypes using the HRCr1.1 as a reference panel. Individuals were excluded based on a high missingness (missing rate > 3%), inconsistent (and unresolvable) sex, or if deemed ancestry outliers from the European population (6 sd deviations from the first two genetic principal components). The GWAS was done employing a logistic regression using PLINK 1.9 and imputed dosage genotypes while correcting for the genotyping center and the first five ancestry principal components as covariates.

Yale-Penn (European and African American cohorts)

We included two different sets of identically ascertained subjects who were genotyped on different platforms. Yale-Penn 1, collected earlier, was genotyped using the HumanOmni-Quad v1.0 array (Illumina) containing 988,306 autosomal single nucleotide polymorphism (SNP) markers. Yale-Penn 2 was genotyped on the HumanCore Exome array (Illumina) containing 550,601 SNPs. Individuals and SNPs with call rates <98% were removed. Only imputed SNPs with an accuracy greater than 0.8 were retained, and all SNPs with a Hardy-Weinberg equilibrium P < 10−5 were removed. SNPs with MAF < 1% were removed. Subject population was defined based on two ancestry groups, European American (EA) and African American (AA), assigned using 1000 genome phase 3 for EUR and AFR as reference.

Columbia University

QC procedures were performed using PLINK. Markers were retained if they had a minor allele frequency (MAF) of 1% or more, a call rate 95%, and no significant departures from Hardy–Weinberg Equilibrium (HWE P>0.0001). Samples with ambiguous sex, genotyping call completeness <95%, and duplicated individuals were excluded. Multidimensional Scaling Analysis (MDS) in PLINK, and comparison to HapMap Phase 3 populations were used to exclude individuals of non-European ancestry. The majority of samples from all three sites were found to be superimposed on the CEU population, outliers more than 3 trimmed standard deviations away from the sample average (using 5% trimming) were deleted,and, after rerunning the MDS analysis, the first five components were retained. For the purposes of the present analysis, genotypes were imputed using the following Imputation reference panel**:** 1000 Genomes Phase 3 (Version 5) and genome build**:** 37. Logistic regression was run on the imputed data, using the "dosage" statement in PLINK, adjusted for the following covariates: sex, age and first 5 MDS components. MDS components were calculated on the unimputed data. In the logistic regression, cases were all subjects with suicidal behavior, regardless of whether they were cases of SA or suicide, while controls were live subjects or sudden death victims. without a history of attempt but with or without a psychiatric diagnosis.

Japan

The details of genotyping, QC and imputation are reported in our previous GWAS paper[46]. Briefly, samples were genotyped using Illumina HumanOmniExpress and HumanOmniExpressExome BeadChips for the 1st and 2nd set of samples ascertained, respectively. We performed QC using PLINK 1.9. Firstly, for each set, we excluded SNPs with a call rate < 0.98 and MAF < 0.01, and those with $p < 1.0 \times 10^{-6}$ for HWE in controls. Related individuals were excluded (PI_HAT ≥ 0.175). We performed PCA, and confirmed all of the above subjects were in the Japanese cluster. After estimating haplotypes using SHAPEIT2 (v2.r778), we performed genotype imputation by Minimac3 (1.0.13) using ALL samples in the 1000 Genomes Project

phase 3v5 as a reference. In order to finalize the summary statistics of imputed data which consist of 746 suicide decedents and 14,049 controls, we combined the summary statistics of imputed variants of the 1st and 2nd control sets as implemented in Rvtests software, performing meta-analysis with METAL software using a fixed effects model with inverse-variance weighted approach, with adjustment for 10 PCs.

University of Utah

Suicide cases were genotyped using Illumina Infinium PsychArray platform measuring 593,260 single nucleotide polymorphisms (SNPs). Genotypes were subsequently imputed in all cases and controls jointly. Cases resulted from population-based ascertainment and cryptic relatedness was modeled via the derivation of genomic relatedness matrices. Genotyping quality control was performed using SNP clustering in Illumina Genome Studio. SNPs were retained if the GenTrain score was > 0.5 and the Cluster separation score was > 0.4. SNPs were converted to HG19 plus strand, and SNPs with >5% missing genotypes were removed. Samples with a call rate < 95% were removed. The ancestry PCA was performed using RaMWAS[100]. Approximately 20% of the population-based suicide cases had a significant degree of non-Northwestern European ancestry (chiefly of admixed ancestry) and were excluded from GWAS analyses. To exclude ancestrally heterogeneous samples, the top principal components (defined as those components which accounted for > 0.1% of the genotype variance, n_{pc} = 4) were used to establish PC centroid limits centered around 1000 Genomes CEU data, such that 99% of the CEU data fell within the limits. Only suicide and control samples also falling within these limits were considered ancestrally homogenous and thus were included in the GWAS. PCA was performed on control, suicide, and 1000 Genomes cohorts after LD pruning at a 0.2 threshold. European ancestry cases and controls were well-matched to 1000 Genomes CEPH. The Haplotype Reference Consortium is comprised in part by UK controls used in the GWAS, so we imputed genotypes based on the 1000 Genomes reference panel using minimac3[90] and Eagle[90,101] . SNPs with ambiguous strand orientation, >5% missing calls, or Hardy-Weinberg equilibrium p < 0.001 were excluded. SNPs with minor allele frequency below 0.01 or imputation R^2 < 0.5 were also excluded. Genomic data were handled using PLINK 1.9[84]. Final GWAS analysis was performed on 7,519,308 variants passing quality control. GWAS were performed by comparing imputed marker dosages under an additive logistic regression model between cases and controls.

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Psychiatric Genomics Consortium Major Depressive Disorder Cohorts

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RADIANT	C Lewis, G Breen	G0701420	MRC	UK
RADIANT	G Breen	G0901245	MRC	UK
RADIANT	G Breen	U01 MH109528	NIMH	UK
BoMa	M Rietschel	RI 908/11-1	Deutsche Forschungsgemeinschaft	Germany
BoMa	MM Nöthen	NO246/10-1	Deutsche Forschungsgemeinschaft	Germany
BoMa	MM Nöthen	Excellence Cluster ImmunoSensation	Deutsche Forschungsgemeinschaft	Germany
BoMa	MM Nöthen, M Rietschel, S Cichon	01ZX1314A/01ZX1614A, 01ZX1314G/01ZX1614G,	BMBF Integrament	Germany
BoMa	MM Nöthen, M Rietschel, S Cichon	01GS08144, 01GS08147	BMBF NGFNplus MooDS	Germany
CoFaMS - Adelaide	BT Baune	APP1060524	NHMRC	Australia
NESDA	BWJH Penninx	ZonMW Geestkracht grant	N.W.O.	Netherlands
NTR	DI Boomsma	480-15-001/674	N.W.O.	Netherlands
SHIP-LEGEND/TREND	HJ Grabe	DFG: GR 1912/5-1	German Research Foundation	Germany
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Psychiatric Genomics Consortium Bipolar Disorder Cohorts

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PGC	D Posthuma	Netherlands, Scientific Organization Netherlands, 480-05-003
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BiGS, Uchicago	ES Gershon	R01 MH103368
BiGS, GAIN	FJ McMahon	US, NIMH, R01 MH061613, ZIA MH002843
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BOMA-Germany I, II, III	S Cichon	Switzerland, SNSF, 156791
BOMA-Germany I, II, III	MM Nöthen	Germany, BMBF Integrament, 01ZX1314A/01ZX1614A
BOMA-Germany I, II, III	MM Nöthen	Germany, BMBF NGFNplus MooDS, 01GS08144
BOMA-Germany I, II, III	MM Nöthen	Germany, Deutsche Forschungsgemeinschaft, Excellence Cluster ImmunoSensation
BOMA-Germany I, II, III	MM Nöthen	Germany, Deutsche Forschungsgemeinschaft, NO246/10-1
BOMA-Germany I, II, III	SH Witt	Germany, Deutsche Forschungsgemeinschaft, WI 3429/3-1
BOMA-Germany I, II, III, BOMA-Spain	M Rietschel	Germany, BMBF Integrament, 01ZX1314G/01ZX1614G
BOMA-Germany I, II, III, BOMA-Spain	M Rietschel	Germany, BMBF NGFNplus MooDS, 01GS08147

BOMA-Germany I, II, III, BOMA-Spain	M Rietschel	Germany, Deutsche Forschungsgemeinschaft, RI 908/11-1
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BOMA-Germany I, II, III, PsyCourse, BiGS	TG Schulze	Germany, DFG, SCHU 1603/4-1, SCHU 1603/5-1, SCHU 1603/7-1
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Psychiatric Genomics Consortium Schizophrenia Cohorts

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Psychiatric Genomics Consortium PsychChip controls

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