Phenotype description: A direct measure of non-suicidal self-injury is not provided by the UK Biobank; however, we derived this phenotype using information from the UK Biobank's on-line "Thoughts and Feelings" mental health questionnaire. The questionnaire asked individuals "*Have you deliberately harmed yourself, whether or not you meant to end your life?*" (Data-Field 20480, N = 137,969), and those who answered "Yes" (N = 5,924) were then asked in a follow-up question, "*Have you harmed yourself with the intention to end your life?*" (Data-Field 20483). Individuals who answered yes to both questions (N = 3,056), indicating self-harm with suicidal intent, were excluded from our analyses. After quality control (see below), we were left with a remaining sample size of 133,620 individuals (N cases = 2,846). GWAS was only performed in individuals with European genetic ancestry using the genetic ancestry assignments returned by Pan-UK Biobank.

Citation for studies using this data: to be posted as soon as a pre-print is made available

File description: * Please note that association results are with regard to Allele2.
CHR: chromosome
POS: genome position
rsID: rs ID for variant
SNPID: variant ID
Allele1: allele 1
Allele2: allele 2
AC_Allele2: allele count of allele 2
AF_Allele2: allele frequency of allele 2
imputationInfo: imputation info. If not in dosage/genotype input file, will output 1
N: sample size
BETA: effect size of allele 2
SE: standard error of BETA
Tstat: score statistic of allele 2
p.value: p value (with SPA applied for binary traits)
p.value.NA: p value when SPA is not applied (only for binary traits)
Is.SPA.converge: whether SPA is converged or not (only for binary traits)
varT: estimated variance of score statistic with sample relatedness incorporated
varTstar: variance of score statistic without sample relatedness incorporated
AF.Cases: allele frequency of allele 2 in cases (only for binary traits and if --IsOutputAFinCaseCtrl=TRUE)
AF.Controls: allele frequency of allele 2 in controls (only for binary traits and if --IsOutputAFinCaseCtrl=TRUE)