README (Contact: Vivek Appadurai | vivek.appadurai@regionh.dk)

Summary statistics from the publication "Genetic of suicide attempts in individuals with and without mental disorders: a population-based genome-wide association study" by Erlangsen et. al in Molecular Psychiatry, June 2018. (https://doi.org/10.1038/s41380-018-0218-y)

Three summary statistics files:

1. Model1.txt: Corresponds to model 1 from the publication where cases (N = 6024) were individuals over the age of 15 as of December 2012 with at least one incidence of self-harm as per the Danish national health registers, controls (N = 44240) were individuals over the age of 15 as of December 2012 with no incidence of self-harm. Covariates included in the model were gender, age and first ten principal components of genetic ancestry.

2. Model2.txt: Corresponds to model 2 from the publication where cases (N = 6024) were individuals over the age of 15 as of December 2012 with at least one incidence of self-harm as recorded in the Danish national health registers, controls (N = 44240) were individuals over the age of 15 as of December 2012 with no incidence of self-harm. Covariates included in the model were gender, age, first ten principal components of genetic ancestry, a binary covariate indicating diagnostic status for the six major iPSYCH disorders (Schizophrenia, Bipolar disorder, Autism, ADHD, Anorexia and Affective Disorder) and an additional covariate indicating diagnosis for any psychiatric disorder.

3. Model3.txt: Corresponds to model 3 from the publication where cases (N = 4302) were individuals over the age of 15 as of December 2012, who were diagnosed with affective disorder and at least one incidence of self-harm as per the Danish national health registers, controls (N = 13294) were individuals over the age of 15 as of December 2012 with no psychiatric diagnosis. Covariates included in the model were gender, age and first ten principal components of genetic ancestry.

All association analyses were conducted using PLINK.

Columns:

1. SNP: rsId or unique identifier for each genetic marker tested
2. CHR: chromosome
3. POS: Genomic position as per hg19
4. A1: Effect Allele
5. A2: Alternate Allele
6. FRQ: Allele frequency of A1 as calculated by PLINK
7. INFO: Imputation info score as calculated by PLINK
8. BETA: Effect size
9. OR: Odds ratio
10. SE: Standard Error of the Effect
11. P: p-value