

HERMES 2.0 GWAS meta-analysis summary statistics

Last updated: 2024-03-27

The zipped file `HERMES2_GWAS_DCM_EUR.zip` contains bundled summary statistics from the case-control GWAS meta-analysis of dilated cardiomyopathy (DCM) phenotypes in up to 1.1 million individuals of European ancestry by the HERMES Consortium.

File structure

Each `{phenotype}_{ancestry}` directory in the zipped file contains a set of 3 files with the following naming convention:

File	Description
<code>FORMAT-METAL_{phenotype}_{ancestry}.tsv.gz</code>	GWAS summary statistics
<code>FORMAT-METAL_{phenotype}_{ancestry}.tsv.gz.tbi</code>	Tabix index file
<code>FORMAT-METAL_{phenotype}_{ancestry}.tsv.gz.md5</code>	MD5 checksum file

Phenotype

Phenotype code	Description	N sample (ALL ancestry)
Pheno5	Dilated cardiomyopathy (broad definition, including hypokinetic non-dilated cardiomyopathy)	14,256
Pheno5-MTAG	multi-trait analysis of GWAS (MTAG) of dilated cardiomyopathy (broad definition) with LVESV, LVEF, and global circumferential strain	14,256
Pheno5-DCM	Dilated cardiomyopathy (strict definition)	6,001

GWAS = genome-wide association study, MTAG = multi-trait analysis of GWAS, LVEF = left ventricular ejection fraction, LVESV = left ventricular end systolic volume, DCM = dilated cardiomyopathy

Ancestry

Ancestry code	Description
EUR	European

Column headers

The summary statistics file contains the following columns:

Column	Description
#key	Unique variant ID in <chr>:<pos_b37>:<A1>_<A2> format
rsID	dbSNP rsID
chr	chromosome
pos_b37	base pair coordinate (genome build b37 / hg19)
A1	effect allele (first allele in alphabetical order)
A2	non-effect allele (second allele in alphabetical order)
A1_beta	log odds ratio estimated from fixed-effect meta-analysis implemented in METAL per one allele increase of A1
A1_freq	effect allele frequency
se	standard error of A1_beta
pval	P-value for association with phenotype
logP	-log10 P-value for association with phenotype
N_case	variant-specific number of cases contributed to the meta-analysis
N_total	variant-specific total number of sample (case + control) contributed to the meta-analysis
isq_het	I squared statistic for heterogeneity estimated using METAL
p_het	P-value for heterogeneity estimated using METAL

Reference

For more details, please refer to the following preprint (manuscript to follow):

- [Genome-wide association analysis reveals insights into the molecular etiology underlying dilated cardiomyopathy](#)

Authorship & Acknowledgements

Journal publications using shared GWAS summary statistics must not precede publication of the main results manuscript. Please include ‘HERMES consortium’ banner authorship in future publication using the shared GWAS summary statistics. Please consider including named HERMES authors at the discretion of the study team.

Contact

- Sean L. Zheng (sean.zheng17@imperial.ac.uk)
- Albert Henry (albert.henry.16@ucl.ac.uk)
- Tom Lumbers (t.lumbers@ucl.ac.uk)
- James Ware (j.ware@imperial.ac.uk)