GWAS summary statistics for 25 hydroxyvitamin D (25OHD)

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Below is a description of the summary statistics for the 25OHD GWAS published in Wang et al. (2023) PLOS Genetics. Summary statistics are based on UK Biobank (UKB) data.

Wang_2023_25OHD_[AFR|EAS|SAS].gz: Summary statistics generated with rank-based inverse normal transformed (RINT) 25OHD levels from individuals of African (N_{AFR}= 8,306), East Asian (N_{EAS}= 2,279), and South Asian (N_{SAS}= 9,983) ancestry. Covariates, accounted for in the linear mixed model implemented in fastGWA, were age, sex, month of assessment, supplement intake (variable with four levels, namely: “no information”, “never taken”, “other supplements”, ”25OHD supplements”), and the first 10 within-ancestry PCs.
Columns are:

- CHR: chromosome
- SNP: variant rs ID
- POS: base pair position (hg19)
- A1: effect allele
- A2: other allele
- N: sample size
- AF1: frequency of A1
- BETA: effect size of A1
- SE: standard error BETA
- P: *P*-value

Wang_2023_25OHD_EUR_DomGWAS.gz: Summary statistics from a dominance GWAS in unrelated individuals of European ancestry. The phenotype was regressed of confounder effects and normalised with a RINT. Variables regressed were age, sex, genotyping batch, assessment centre, assessment month, use of supplements and the first 20 within-ancestry PCs. Dominance effects were assessed with PLINK2.0 (--glm genotypic) in a model fitting both the additive effects (with genotypes coded as 0, 1, 2) and dominance effects (with genotypes coded as 0, 1, 0).
Columns are:

- CHROM: chromosome
- POS: base pair position (hg19)
- ID: variant rs ID
- REF: reference allele
- ALT: alternative allele
- A1: effect allele
- TEST: Type of test (all dominant)
- OBS_CT: sample size
- BETA: effect size of A1
- SE: standard error BETA
- T_OR_F_STAT: Test statistic
- P: *P*-value

Wang_2023_25OHD_EUR_[Dark|Light]_skin.gz: Summary statistics of GWAS in European-ancestry individuals stratified by self-reported skin colour. Individuals who reported “very fair” and “fair” skin were classed as having “light skin colour” (light skin GWAS), and those that reported “light olive”, “dark olive”, or “brown” were classed as having “dark skin colour” (dark skin GWAS). Information on self-reported skin colour was obtained from UKB data-field 1717. RINT 25OHD levels were analysed

with a linear mixed model. Covariates were age at assessment, sex, assessment month, supplement intake, assessment centre, genotyping batch and 40 within-ancestry PCs.
Columns are as described for Wang_2023_25OHD_[AFR|EAS|SAS].gz.

Wang_2023_25OHD_EUR_SCS_meta.gz: Results from a fixed-effect inverse-variance weighted meta-analysis of the skin colour stratified GWAS.
Columns are:

- SNP: variant rs ID
- A1: Effect allele
- A2: Other allele
- Freq: frequency of A1
- B: effect size of A1
- Se: standard error BETA
- P: *P*-value
- N: sample size