bivar\_reml.cpp:81: LOGGER.i(0, to\_string(\_n) + " individuals are in common in these files.");

data.cpp:383: LOGGER.i(0, "There are " + to\_string(multi\_bfiles.size()) + " PLINK genotype files specified in [" + bfile\_list + "].");

data.cpp:390: if(msg\_flag) LOGGER.i(0, "Reading PLINK FAM file from [" + famfile + "].");

data.cpp:415: LOGGER.i(0, to\_string(indi\_num) + " individuals to be included from [" + famfile + "].");

data.cpp:421: LOGGER.i(0, "\nReading the PLINK FAM files ....");

data.cpp:441: LOGGER.i(0, to\_string(\_indi\_num) + " individuals have been included from the PLINK FAM files.");

data.cpp:498: LOGGER.w(0, "Duplicated SNP ID " + strbuf + " has been changed to " + tsnp\_name + ".");

data.cpp:531: if(msg\_flag) LOGGER.i(0, "Reading PLINK BIM file from [" + bimfile + "].");

data.cpp:555: LOGGER.i(0, to\_string(snp\_num) + " SNPs to be included from [" + bimfile + "].");

data.cpp:561: LOGGER.i(0, "Reading the PLINK BIM files ...");

data.cpp:585: LOGGER.i(0, to\_string(\_snp\_num) + " SNPs to be included from PLINK BIM files.");

data.cpp:628: if(msg\_flag) LOGGER.i(0, "Reading PLINK BED file from [" + bedfile + "] in SNP-major format ...");

data.cpp:660: if(msg\_flag) LOGGER.i(0, "Genotype data for " + to\_string(nindi\_chr) + " individuals and " + to\_string(nsnp\_chr) + " SNPs to be included from [" + bedfile + "].");

data.cpp:672: LOGGER.i(0, "Reading PLINK BED files ...");

data.cpp:695: LOGGER.i(0, "Skip reading " + multi\_bfiles[i] + ".bed, no SNPs retained on this chromosome.");

data.cpp:702: LOGGER.i(0, "Genotype data for " + to\_string(\_keep.size()) + " individuals and " + to\_string(\_include.size()) + " SNPs have been included.");

data.cpp:1603: LOGGER.w(0, "gender information (the 5th column of the .fam file) is required for analysis on chromosome X. GCTA assumes that those missing samples are females.");

est\_hsq.cpp:229: LOGGER.w(0, "ignored line #" + to\_string(line) + ".");

est\_hsq.cpp:1152: LOGGER.w(0, "more than half of the variance components are constrained.");

grm.cpp:888: LOGGER.w(0, to\_string(missnp\_list.size()) + " SNPs are not found or alleles mismatch in the target genotype");

gsmr.cpp:98: LOGGER.i(0, "\nReading GWAS summary data for exposure(s) from [" + expo\_file\_list + "].");

gsmr.cpp:119: LOGGER.i(0, "Reading GWAS summary data for outcome(s) from [" + outcome\_file\_list + "].");

gsmr.cpp:156: LOGGER.i(0, to\_string(nsnp) + " genome-wide significant SNPs in common between the exposure(s) and the outcome(s).");

gsmr.cpp:182: LOGGER.i(0, "Filtering out SNPs with multiple alleles or missing value ...");

gsmr.cpp:197: else LOGGER.i(0, to\_string(nsnp) + " SNPs are retained after filtering.");

gsmr.cpp:208: LOGGER.i(0, to\_string(\_include.size()) + " genome-wide significant SNPs with p < " + ss.str() + " are in common among the exposure(s), the outcome(s) and the LD reference sample.\n");

gsmr.cpp:253: LOGGER.i(0, "LD score regression analysis to estimate sample overlap between each pair of exposure and outcome ...");

gsmr.cpp:258: LOGGER.i(0, "Univariate LD score regression analysis ...");

gsmr.cpp:263: LOGGER.i(0, "Bivariate LD score regression analysis ...");

gsmr.cpp:281: LOGGER.i(0, "Intercept:");

gsmr.cpp:287: LOGGER.i(0, ss.str());

gsmr.cpp:289: LOGGER.i(0, "LD score regression analysis completed.");

gsmr.cpp:303: LOGGER.i(0, "Using correlation of SNP effects to estimate sample overlap between each pair of exposure and outcome ...");

gsmr.cpp:340: LOGGER.i(0, "Correlation:");

gsmr.cpp:346: LOGGER.i(0, ss.str());

gsmr.cpp:348: LOGGER.i(0, "Correlation computation completed.");

gsmr.cpp:461: LOGGER.i(0, "Checking allele frequencies among the GWAS summary data and the reference sample...");

gsmr.cpp:505: LOGGER.i(0, "");

gsmr.cpp:515: LOGGER.i(0, "The pleiotropic SNPs filtered by HEIDI-outlier analysis have been saved in [" + pleio\_snpfile + "].");

gsmr.cpp:528: LOGGER.i(0, "Saving the SNP instruments for the GSMR plots to [" + output\_filename + "] ...");

gsmr.cpp:535: LOGGER.w(0, "Not enough SNP instruments to be saved in the compressed text file.");

gsmr.cpp:541: LOGGER.i(0, "Saving the GSMR analyses results of " + to\_string(\_expo\_num) + " exposure(s) and "

gsmr.cpp:547: LOGGER.i(0, "\nGSMR analyses completed.");

gsmr.cpp:566: LOGGER.i(0, "\nForward GSMR analysis for exposure #" + to\_string(i+1) + " and outcome #" + to\_string(j+1) + " ...");

gsmr.cpp:570: LOGGER.w(0, err\_msg);

gsmr.cpp:572: LOGGER.i(0, "Forward GSMR analysis for exposure #" + to\_string(i+1) + " and outcome #" + to\_string(j+1) + " completed.");

gsmr.cpp:603: LOGGER.i(0, "\nReverse GSMR analysis for exposure #" + to\_string(j+1) + " and outcome #" + to\_string(i+1) + " ...");

gsmr.cpp:607: LOGGER.w(0, err\_msg);

gsmr.cpp:609: LOGGER.i(0, "Reverse GSMR analysis for exposure #" + to\_string(j+1) + " and outcome #" + to\_string(i+1) + " completed.");

mtcojo.cpp:618: LOGGER.i(0, to\_string(nbadsnps) + " SNPs have missing value or mismatched alleles. These SNPs have been saved in [" + badsnpfile + "].");

mtcojo.cpp:670: LOGGER.i(0, to\_string(nafsnps) + " SNP(s) have large difference of allele frequency between the GWAS summary data and the reference sample. These SNPs have been saved in [" + afsnpfile + "].");

mtcojo.cpp:689: if(n\_raresnp > 0) LOGGER.w(0, "There are " + to\_string(n\_raresnp) + " SNPs with MAF < 0.01 in the reference sample.");

mtcojo.cpp:698: LOGGER.i(0, to\_string(nafsnps) + " monomorphic SNP(s) have been saved in [" + afsnpfile + "].");

mtcojo.cpp:729: LOGGER.i(0, "\nReading GWAS summary data from [" + mtcojolist\_file + "] ...");

mtcojo.cpp:770: LOGGER.i(0, to\_string(nsnp) + " SNPs in common between the target trait and the covariate trait(s).");

mtcojo.cpp:807: LOGGER.i(0, "Filtering out SNPs with multiple alleles or missing value ...");

mtcojo.cpp:823: else LOGGER.i(0, to\_string(nsnp) + " SNPs are retained after filtering.");

mtcojo.cpp:833: LOGGER.i(0, "There are " + to\_string(\_include.size()) + " genome-wide significant SNPs with p < " + ss.str() + ".\n");

mtcojo.cpp:834: if(keptsnps.size() < nsnp\_gsmr) LOGGER.w(0, "We will use LD score regression to estimate bxy, because there are not enough significant SNPs for GSMR analysis. At least " + to\_string(nsnp\_gsmr) + " SNPs are required.\n");

mtcojo.cpp:1524: //LOGGER.i(0, to\_string(n\_indices\_snp) + " index SNPs are obtained from the clumping analysis of the " + nsnp + " genome-wide significant SNPs.");

mtcojo.cpp:1530: LOGGER.i(0, to\_string(n\_indices\_snp) + " index SNPs are obtained from the clumping analysis with p < " + ss1.str() + " and LD r2 < " + ss2.str() + ".");

mtcojo.cpp:1566: LOGGER.i(0, to\_string(n\_indices\_snp) + " index SNPs are obtained from the clumping analysis with p < " + ss1.str() + " and LD r2 < " + ss2.str() + ".");

mtcojo.cpp:1689: LOGGER.i(0, to\_string(npleio) + " pleiotropic SNPs are filtered by HEIDI-outlier analysis.");

mtcojo.cpp:1695: LOGGER.i(0, to\_string(n\_indices\_snp) + " index SNPs are retained after HEIDI-outlier analysis.");

mtcojo.cpp:2109: LOGGER.w(0, "Only " + to\_string(nsnp\_cm\_trait[i]) + " are retained in the univariate LD score regression analysis for "

mtcojo.cpp:2126: LOGGER.i(0, trait\_name[i] + ": " + to\_string(rst\_ldsc[0]) + " " + to\_string(rst\_ldsc[1]));

mtcojo.cpp:2149: LOGGER.w(0, "Only " + to\_string(n\_cm\_snps\_buf) + " are retained in the bivariate LD score regression analysis for "

mtcojo.cpp:2213: LOGGER.i(0, "\nUnivariate LD score regression analysis to estimate SNP-based heritability ...");

mtcojo.cpp:2221: LOGGER.i(0, "Bivariate LD score regression analysis to estimate genetic correlation between each pair of traits ...");

mtcojo.cpp:2237: LOGGER.i(0, "Intercept:");

mtcojo.cpp:2242: LOGGER.i(0, ss.str());

mtcojo.cpp:2244: LOGGER.i(0, "rg:");

mtcojo.cpp:2249: LOGGER.i(0, ss.str());

mtcojo.cpp:2251: LOGGER.i(0, "The LD score regression analyses completed.");

mtcojo.cpp:2346: LOGGER.i(0, "Checking the difference in allele frequency between the GWAS summary datasets and the LD reference sample...");

mtcojo.cpp:2392: LOGGER.i(0, "\nGSMR analysis for covariate #" + to\_string(i) + " (" + trait\_name[i] + ")" + " ...");

mtcojo.cpp:2396: LOGGER.w(0, err\_msg);

mtcojo.cpp:2397: LOGGER.i(0, "bxy is estimated from rg.");

mtcojo.cpp:2399: LOGGER.i(0, "bxy " + to\_string(gsmr\_rst[0]) + " " + to\_string(gsmr\_rst[1]));

mtcojo.cpp:2407: LOGGER.i(0, "bxy " + to\_string(gsmr\_rst[0]) + " " + to\_string(gsmr\_rst[1]));

mtcojo.cpp:2408: LOGGER.i(0, "GSMR analysis for covariate #" + to\_string(i) + " (" + trait\_name[i] + ") completed.");

mtcojo.cpp:2416: LOGGER.i(0, "The pleiotropic SNPs filtered by HEIDI-outlier analysis have been saved in [" + pleio\_snpfile + "].");

mtcojo.cpp:2443: LOGGER.i(0, "\nmtCOJO analysis ...");

mtcojo.cpp:2444: LOGGER.i(0, "There are " + to\_string(nsnp) + " SNPs in common between the target trait and all the covariate trait(s).");

mtcojo.cpp:2453: LOGGER.i(0, "Saving the mtCOJO analysis results of " + to\_string(nsnp) + " remaining SNPs to [" + output\_filename + "] ...");

mtcojo.cpp:2454: LOGGER.i(0, "mtCOJO analysis completed.");

option.cpp:1233: if(gsmr\_snp\_update\_flag) LOGGER.w(0, "--gsmr-snp has been superseded by --gsmr-snp-min.");

option.cpp:1234: if(nsnp\_gsmr < 5) LOGGER.w(0, "The number of SNP instruments included in the analysis is too small. There might not be enough SNPs to perform the HEIDI-outlier analysis.");

option.cpp:1241: LOGGER.w(0, "The threshold of multi-SNP-based HEIDI-outlier analysis is not specified. The default value is " + to\_string(global\_heidi\_thresh).substr(0,5) + ".");

option.cpp:1244: LOGGER.w(0, "--gsmr2-beta is not specified. GCTA will perform single-SNP-based HEIDI-outlier analysis, which was published in Zhu et al. 2018 Nature Communications. The threshold of multi-SNP-based HEIDI-outlier analysis will not be accepted.");

pc\_adjust.cpp:13: LOGGER.i(0, "\nReading eigenvalues from [" + eigenvalue\_file + "]...");

pc\_adjust.cpp:26: LOGGER.w(0, "Only the first element would be accepted. File [" + eigenvalue\_file + "], line " + to\_string(line\_number) + ".");

pc\_adjust.cpp:43: LOGGER.w(0, "Only the first element would be accepted. File [" + pcadjust\_list\_file + "], line " + to\_string(line\_number) + ".");

pc\_adjust.cpp:85: LOGGER.i(0, to\_string(nsnp) + " SNPs in common between the summary data and the PC loading(s).");

pc\_adjust.cpp:113: LOGGER.i(0, "Filtering out SNPs with multiple alleles or missing value ...");

pc\_adjust.cpp:128: else LOGGER.i(0, to\_string(nsnp) + " SNPs are retained after filtering.");

pc\_adjust.cpp:129: LOGGER.i(0, to\_string(\_include.size()) + " SNPs are in common between the summary data and the LD reference sample.");

pc\_adjust.cpp:180: LOGGER.i(0, to\_string(nafsnps) + " SNP(s) do not have allele frequency information. These SNPs have been saved in [" + afsnpfile + "].");

pc\_adjust.cpp:455: LOGGER.i(0, "Checking differences in allele frequencies between the GWAS summary data and the reference sample...");

pc\_adjust.cpp:463: LOGGER.i(0, "Update allele frequencies for the GWAS summary data ...");