bivar\_reml.cpp:124: LOGGER << nms1.size() << " non-missing phenotypes for trait #1 and " << nms2.size() << " for trait #2" << endl;

bivar\_reml.cpp:128: LOGGER << "Note: the residual covariance component is ignored because no individuals were measured for both traits." << endl;

bivar\_reml.cpp:131: LOGGER << "Note: the residual covariance component is ignored because < 10% of individuals were measured for both traits." << endl;

bivar\_reml.cpp:139: if (\_flag\_CC) LOGGER << "for trait #1" << endl;

bivar\_reml.cpp:142: if (\_flag\_CC2) LOGGER << "for trait #2" << endl;

bivar\_reml.cpp:145: if ((\_flag\_CC && prevalence<-1) || (\_flag\_CC2 && prevalence2<-1)) LOGGER << "Note: we can specify the disease prevalence by the option --reml-bivar-prevalence so that GCTA can transform the variance explained to the underlying liability scale." << endl;

bivar\_reml.cpp:231: LOGGER << "There are " << grm\_files.size() << " GRM file names specified in the file [" + grm\_file + "]." << endl;

bivar\_reml.cpp:234: LOGGER << "Reading the GRM from the " << k + 1 << "th file ..." << endl;

bivar\_reml.cpp:304: LOGGER << "Constructing the covariances" << endl;

bivar\_reml.cpp:395: LOGGER << "Note: to constrain the correlation being from -1 to 1, a genetic (or residual) variance-covariance matrix is bended to be positive definite. In this case, the SE is unreliable." << endl;

bivar\_reml.cpp:446: LOGGER << "\nCalculating the logLikelihood for the model with the genetic correlation" << (\_fixed\_rg\_val.size() > 1 ? "s" : "") << " being fixed at ";

bivar\_reml.cpp:447: for (int i = 0; i < \_fixed\_rg\_val.size() - 1; i++) LOGGER << \_fixed\_rg\_val[i] << "\t";

bivar\_reml.cpp:448: LOGGER << \_fixed\_rg\_val[\_fixed\_rg\_val.size() - 1] << endl;

data.cpp:95: LOGGER << "Reading PLINK FAM file from [" + famfile + "]." << endl;

data.cpp:123: LOGGER << \_indi\_num << " individuals to be included from [" + famfile + "]." << endl;

data.cpp:150: LOGGER << "Reading PLINK BIM file from [" + bimfile + "]." << endl;

data.cpp:178: LOGGER << \_snp\_num << " SNPs to be included from [" + bimfile + "]." << endl;

data.cpp:193: LOGGER << "Warning: Duplicated SNP ID \"" + \_snp\_name[i] + "\" ";

data.cpp:227: LOGGER << "Reading PLINK BED file from [" + bedfile + "] in SNP-major format ..." << endl;

data.cpp:255: LOGGER << "Genotype data for " << \_keep.size() << " individuals and " << \_include.size() << " SNPs to be included from [" + bedfile + "]." << endl;

data.cpp:717: LOGGER << "Reading map file of the imputed dosage data from [" + zinfofile + "]." << endl;

data.cpp:752: LOGGER << \_snp\_num << " SNPs to be included from [" + zinfofile + "]." << endl;

data.cpp:767: LOGGER << "Reading map file of the imputed dosage data from [" + infofile + "]." << endl;

data.cpp:799: LOGGER << \_snp\_num << " SNPs to be included from [" + infofile + "]." << endl;

data.cpp:827: LOGGER << "Reading dosage data from [" + zdosefile + "] in individual-major format (Note: may use huge RAM)." << endl;

data.cpp:858: LOGGER << "(Imputed dosage data for " << kp\_it.size() << " individuals detected)." << endl;

data.cpp:875: LOGGER << "Warning: missing values detected in the dosage data." << endl;

data.cpp:890: LOGGER << "Imputed dosage data for " << kept\_id.size() << " individuals are included from [" << zdosefile << "]." << endl;

data.cpp:937: LOGGER << "Reading dosage data from [" + dosefile + "] in individual-major format (Note: may use huge RAM)." << endl;

data.cpp:965: LOGGER << "(Imputed dosage data for " << kp\_it.size() << " individuals detected)." << endl;

data.cpp:982: LOGGER << "Warning: missing values detected in the dosage data." << endl;

data.cpp:996: LOGGER << "Imputed dosage data for " << kept\_id.size() << " individuals are included from [" << dosefile << "]." << endl;

data.cpp:1031: LOGGER << "Reading summary information of the imputed SNPs (BEAGLE output) ..." << endl;

data.cpp:1062: LOGGER << \_snp\_num << " SNPs to be included from [" + zinfofile + "]." << endl;

data.cpp:1084: LOGGER << "Reading imputed dosage scores (BEAGLE output) ..." << endl;

data.cpp:1097: LOGGER << \_indi\_num << " individuals to be included from [" + zdosefile + "]." << endl;

data.cpp:1149: LOGGER << "Writing genotypes to PLINK BED file [" + OutBedFile + "] ..." << endl;

data.cpp:1191: LOGGER << "Writing PLINK FAM file to [" + famfile + "] ..." << endl;

data.cpp:1197: LOGGER << \_keep.size() << " individuals to be saved to [" + famfile + "]." << endl;

data.cpp:1205: LOGGER << "Writing PLINK BIM file to [" + bimfile + "] ..." << endl;

data.cpp:1210: LOGGER << \_include.size() << " SNPs to be saved to [" + bimfile + "]." << endl;

data.cpp:1217: LOGGER << "Converting dosage data into PLINK binary PED format ... " << endl;

data.cpp:1269: LOGGER << "Reading a list of " << msg << " from [" + snplistfile + "]." << endl;

data.cpp:1282: LOGGER << \_include.size() << " SNPs are extracted from [" + snplistfile + "]." << endl;

data.cpp:1291: else LOGGER << "Only the SNP [" + snpname + "] is included in the analysis." << endl;

data.cpp:1296: LOGGER << "Extracting SNPs " << wind\_size/1000 << "kb away from the SNP [" << snpname << "] in either direction ..." << endl;

data.cpp:1312: LOGGER << \_include.size() << " SNPs are extracted." << endl;

data.cpp:1317: LOGGER << "Extracting SNPs " << wind\_size/1000 << "kb away from the position [chr=" << chr <<"; bp="<< bp << "] in either direction ..." << endl;

data.cpp:1326: LOGGER << \_include.size() << " SNPs are extracted." << endl;

data.cpp:1335: LOGGER << prev\_size - \_include.size() << " SNPs are excluded from [" + snplistfile + "] and there are " << \_include.size() << " SNPs remaining." << endl;

data.cpp:1340: LOGGER << "Excluding SNPs " << wind\_size/1000 << "kb away from the SNP [" << snpname << "] in either direction ..." << endl;

data.cpp:1356: LOGGER << \_include.size() << " SNPs have been excluded." << endl;

data.cpp:1361: LOGGER << "Excluding SNPs " << wind\_size/1000 << "kb away from the position [chr=" << chr <<"; bp="<< bp << "] in either direction ..." << endl;

data.cpp:1370: LOGGER << \_include.size() << " SNPs are excludeed." << endl;

data.cpp:1380: else LOGGER << "The SNP [" + snpname + "] has been excluded from the analysis." << endl;

data.cpp:1396: if (chr\_start != chr\_end) LOGGER << \_include.size() << " SNPs from chromosome " << chr\_start << " to chromosome " << chr\_end << " are included in the analysis." << endl;

data.cpp:1397: else LOGGER << \_include.size() << " SNPs on chromosome " << chr\_start << " are included in the analysis." << endl;

data.cpp:1404: LOGGER << "Filtering SNPs with MAF > " << maf << " ..." << endl;

data.cpp:1420: LOGGER << "After filtering SNPs with MAF > " << maf << ", there are " << \_include.size() << " SNPs (" << prev\_size - \_include.size() << " SNPs with MAF < " << maf << ")." << endl;

data.cpp:1428: LOGGER << "Filtering SNPs with MAF < " << max\_maf << " ..." << endl;

data.cpp:1444: LOGGER << "After filtering SNPs with MAF < " << max\_maf << ", there are " << \_include.size() << " SNPs (" << prev\_size - \_include.size() << " SNPs with MAF > " << max\_maf << ")." << endl;

data.cpp:1450: if (\_impRsq.empty()) LOGGER << "Warning: the option --imput-rsq is inactive because GCTA can't find the imputation quality scores for the SNPs. Use the option --update-imput-rsq to input the imputation quality scores." << endl;

data.cpp:1451: LOGGER << "Filtering SNPs with imputation Rsq > " << rsq\_cutoff << " ..." << endl;

data.cpp:1465: LOGGER << "After filtering for imputation Rsq > " << rsq\_cutoff << ", there are " << \_include.size() << " SNPs (" << prev\_size - \_include.size() << " SNPs with imputation Rsq < " << rsq\_cutoff << ")." << endl;

data.cpp:1491: LOGGER << \_keep.size() << " individuals are kept from [" + indi\_list\_file + "]." << endl;

data.cpp:1499: LOGGER << prev\_size - \_keep.size() << " individuals are removed from [" + indi\_list\_file + "] and there are " << \_keep.size() << " individuals remaining." << endl;

data.cpp:1507: LOGGER << "Reading sex information from [" + sex\_file + "]." << endl;

data.cpp:1532: LOGGER << "Sex information for " << icount << " individuals are update from [" + sex\_file + "]." << endl;

data.cpp:1540: LOGGER << "Reading reference alleles of SNPs from [" + ref\_A\_file + "]." << endl;

data.cpp:1561: LOGGER << "Reference alleles of " << icount << " SNPs are updated from [" + ref\_A\_file + "]." << endl;

data.cpp:1562: if (icount != \_snp\_num) LOGGER << "Warning: reference alleles of " << \_snp\_num - icount << " SNPs have not been updated." << endl;

data.cpp:1584: LOGGER << "Calculating allele frequencies ..." << endl;

data.cpp:1650: LOGGER << "Reading imputation Rsq of the SNPs from [" + zinfofile + "]." << endl;

data.cpp:1670: LOGGER << "Imputation Rsq of " << icount << " SNPs are updated from [" + zinfofile + "]." << endl;

data.cpp:1671: if (icount != \_snp\_num) LOGGER << "Warning: imputation Rsq of " << \_snp\_num - icount << " SNPs have not been updated." << endl;

data.cpp:1681: LOGGER << "Reading allele frequencies of the SNPs from [" + freq + "]." << endl;

data.cpp:1706: LOGGER << "Allele frequencies of " << icount << " SNPs are updated from [" + freq + "]." << endl;

data.cpp:1707: if (icount != \_snp\_num) LOGGER << "Warning: allele frequencies of " << \_snp\_num - icount << " SNPs have not been updated." << endl;

data.cpp:1716: LOGGER << "Writing allele frequencies of " << \_include.size() << " SNPs to [" + save\_freq + "]." << endl;

data.cpp:1723: LOGGER << "Allele frequencies of " << \_include.size() << " SNPs have been saved in the file [" + save\_freq + "]." << endl;

data.cpp:1757: LOGGER << "BLUP solution to the total genetic effects for " << \_keep.size() << " individuals have been read from [" + blup\_indi\_file + "]." << endl;

data.cpp:1764: LOGGER << "Recoding genotypes (individual major mode) ..." << endl;

data.cpp:1805: LOGGER << "Recoding genotypes for dominance effects (individual major mode) ..." << endl;

data.cpp:1994: LOGGER << "Saving the recoded genotype matrix to the file [" + X\_zFile + "]." << endl;

data.cpp:2037: LOGGER << "The recoded genotype matrix has been saved in the file [" + X\_zFile + "] (in compressed text format)." << endl;

edata.cpp:20: LOGGER << "Reading gene expression / methylation data from [" + efile + "] ..." << endl;

edata.cpp:186: LOGGER << "Recoding gene expression / methylation data ..." << endl;

edata.cpp:196: LOGGER << "\nCalculating expression relationship matrix (ERM) ... " << endl;

ejma.cpp:70: LOGGER << "Reading correlation matrix of gene expression from [" + eR\_file + "] ..." << endl;

ejma.cpp:91: LOGGER << "\nReading expression-trait association summary-level statistics from [" + e\_metafile + "] ..." << endl;

ejma.cpp:117: LOGGER << "GWAS summary statistics of " << probe\_buf.size() << " probs being read from [" + e\_metafile + "]." << endl;

ejma.cpp:119: LOGGER << "Matching the summary data to the genotype data ..." << endl;

ejma.cpp:164: LOGGER << endl;

ejma.cpp:166: LOGGER << "Performing stepwise model selection on " << \_e\_include.size() << " probes to select association signals ... (p-value cutoff = " << \_ecojo\_p\_cutoff << "; ";

ejma.cpp:167: LOGGER << "collinearity cutoff = " << \_ecojo\_collinear << ")"<< endl;

ejma.cpp:170: LOGGER << "No probe has been selected." << endl;

ejma.cpp:177: LOGGER << "Performing backward selection on " << \_e\_include.size() << " probes at p-value cutoff = " << \_ecojo\_p\_cutoff << " ..." << endl;

ejma.cpp:184: LOGGER << "Performing joint analysis on all the " << slct.size();

ejma.cpp:185: if (joint\_only) LOGGER << " probes ..." << endl;

ejma.cpp:186: else LOGGER << " selected signals ..." << endl;

ejma.cpp:195: if (joint\_only) LOGGER << "Saving the joint analysis result of " << slct.size() << " probes to [" + filename + "] ..." << endl;

ejma.cpp:196: else LOGGER << "Saving the " << slct.size() << " independent signals to [" + filename + "] ..." << endl;

ejma.cpp:222: if (\_ecojo\_p\_cutoff > 1e-3) LOGGER << "Performing forward model selection because the significance level is too low..." << endl;

ejma.cpp:230: if (slct.size() % 5 == 0 && slct.size() > prev\_num) LOGGER << slct.size() << " associated probes have been selected." << endl;

ejma.cpp:234: LOGGER << "Performing backward elimination..." << endl;

ejma.cpp:237: LOGGER << "Finally, " << slct.size() << " associated probes are selected." << endl;

ejma.cpp:416: LOGGER << "Recoding gene expression data ..." << endl;

ejma.cpp:429: LOGGER << "\nPerforming joint analysis on all the " << \_e\_include.size() << " probes ..." << endl;

ejma.cpp:443: LOGGER << "Saving the BLUP analysis result of " << \_e\_include.size() << " probes to [" + filename + "] ..." << endl;

est\_hsq.cpp:72: LOGGER << "Reading phenotypes from [" + phen\_file + "]." << endl;

est\_hsq.cpp:76: if (phen\_num > 1) LOGGER << "There are " << phen\_num << " traits specified in the file [" + phen\_file + "]." << endl;

est\_hsq.cpp:87: if (\_bivar\_reml) LOGGER << "Traits " << mphen << " and " << mphen2 << " are included in the bivariate analysis." << endl;

est\_hsq.cpp:89: if (phen\_num > 1) LOGGER << "Trait #" << mphen << " is included for analysis." << endl;

est\_hsq.cpp:117: LOGGER << "Non-missing phenotypes of " << phen\_buf.size() << " individuals are included from [" + phen\_file + "]." << endl;

est\_hsq.cpp:137: if (qcovar\_flag) LOGGER << "Reading quantitative covariate(s) from [" + covar\_file + "]." << endl;

est\_hsq.cpp:138: else LOGGER << "Reading discrete covariate(s) from [" + covar\_file + "]." << endl;

est\_hsq.cpp:140: if (qcovar\_flag) LOGGER << covar\_num << " quantitative covariate(s) of " << covar\_ID.size() << " individuals are included from [" + covar\_file + "]." << endl;

est\_hsq.cpp:141: else LOGGER << covar\_num << " discrete covariate(s) of " << covar\_ID.size() << " individuals are included from [" + covar\_file + "]." << endl;

est\_hsq.cpp:185: LOGGER << "Reading " << env << " factor(s) for the analysis of GE interaction from [" + GE\_file + "]." << endl;

est\_hsq.cpp:188: LOGGER << GE\_num << " " << env << " factor(s) for " << GE\_ID.size() << " individuals are included from [" + GE\_file + "]." << endl;

est\_hsq.cpp:203: LOGGER << "Reading weights from [" + phen\_file + "]." << endl;

est\_hsq.cpp:207: if (phen\_num > 1) LOGGER << "There are " << phen\_num << " weights specified in the file [" + phen\_file + "], however, only the first one is used." << endl;

est\_hsq.cpp:234: LOGGER << "Non-missing weights of " << phen\_ID.size() << " individuals are included from [" + phen\_file + "]." << endl;

est\_hsq.cpp:327: LOGGER << endl;

est\_hsq.cpp:331: if (!mlmassoc && prevalence<-1) LOGGER << "Note: you can specify the disease prevalence by the option --prevalence so that GCTA can transform the variance explained to the underlying liability scale." << endl;

est\_hsq.cpp:333: LOGGER << "Note: you can specify the prevalences of the two diseases by the option --reml-bivar-prevalence so that GCTA can transform the estimates of variance explained to the underlying liability scale." << endl;

est\_hsq.cpp:355: LOGGER << "Mean of diagonal elements of the GRM = " << diag\_mean << endl;

est\_hsq.cpp:375: LOGGER << "There are " << grm\_files.size() << " GRM file names specified in the file [" + grm\_file + "]." << endl;

est\_hsq.cpp:377: LOGGER << "Reading the GRM from the " << i + 1 << "th file ..." << endl;

est\_hsq.cpp:394: LOGGER << "Mean of diagonal elements of the GRM = " << diag\_mean << endl;

est\_hsq.cpp:509: LOGGER << \_n << " individuals are in common in these files." << endl;

est\_hsq.cpp:554: LOGGER << qcovar\_num << " quantitative variable(s) included as covariate(s)." << endl;

est\_hsq.cpp:567: LOGGER << covar\_num << " discrete variable(s) included as covariate(s)." << endl;

est\_hsq.cpp:638: if (!\_bivar\_reml) LOGGER << "Assuming a disease phenotype for a case-control study: ";

est\_hsq.cpp:639: LOGGER << (int) case\_num << " cases and " << (int) (n - case\_num) << " controls ";

est\_hsq.cpp:643: LOGGER << "Only " << value.size() << " type(s) of phenotype values being observed: ";

est\_hsq.cpp:645: LOGGER << value[i] << "\t";

est\_hsq.cpp:647: LOGGER << std::endl;

est\_hsq.cpp:743: LOGGER << "\nPerforming " << (\_bivar\_reml ? "bivariate" : "") << " REML analysis ... (Note: may take hours depending on sample size)." << endl;

est\_hsq.cpp:745: LOGGER << \_n << " observations, " << \_X\_c << " fixed effect(s), and " << \_r\_indx.size() << " variance component(s)(including residual variance)." << endl;

est\_hsq.cpp:791: LOGGER << "\nSummary result of REML analysis:" << endl;

est\_hsq.cpp:792: LOGGER << "Source\tVariance\tSE" << std::fixed << LOGGER.setprecision(6) << endl;

est\_hsq.cpp:793: for (i = 0; i < \_r\_indx.size(); i++) LOGGER << \_var\_name[i] << "\t" << varcmp[i] << "\t" << sqrt(Hi(i, i)) << endl;

est\_hsq.cpp:795: LOGGER << "Vp\_tr1\t" << Vp << "\t" << sqrt(VarVp) << endl;

est\_hsq.cpp:796: LOGGER << "Vp\_tr2\t" << Vp2 << "\t" << sqrt(VarVp2) << endl;

est\_hsq.cpp:798: LOGGER << \_hsq\_name[j] << "\t" << Hsq[\_bivar\_pos[0][i]] << "\t" << sqrt(VarHsq[\_bivar\_pos[0][i]]) << endl;

est\_hsq.cpp:799: LOGGER << \_hsq\_name[j + 1] << "\t" << Hsq[\_bivar\_pos[1][i]] << "\t" << sqrt(VarHsq[\_bivar\_pos[1][i]]) << endl;

est\_hsq.cpp:802: LOGGER << "Vp\t" << Vp << "\t" << sqrt(VarVp) << endl;

est\_hsq.cpp:803: for (i = 0; i < Hsq.size(); i++) LOGGER << \_hsq\_name[i] << "\t" << Hsq[i] << "\t" << sqrt(VarHsq[i]) << endl;

est\_hsq.cpp:804: if (\_r\_indx.size() > 2) LOGGER << "\nSum of V(G)/Vp\t" << sum\_hsq << "\t" << sqrt(var\_sum\_hsq) << endl;

est\_hsq.cpp:807: LOGGER << "The estimate of variance explained on the observed scale is transformed to that on the underlying liability scale:" << endl;

est\_hsq.cpp:809: if (\_flag\_CC) LOGGER << "Proportion of cases in the sample = " << \_ncase << " for trait #1; User-specified disease prevalence = " << prevalence << " for trait #1" << endl;

est\_hsq.cpp:810: if (\_flag\_CC2) LOGGER << "Proportion of cases in the sample = " << \_ncase2 << " for trait #2; User-specified disease prevalence = " << prevalence2 << " for trait #2" << endl;

est\_hsq.cpp:812: if (\_flag\_CC) LOGGER << \_hsq\_name[j] << "\_L\t" << transform\_hsq\_L(\_ncase, prevalence, Hsq[\_bivar\_pos[0][i]]) << "\t" << transform\_hsq\_L(\_ncase, prevalence, sqrt(VarHsq[\_bivar\_pos[0][i]])) << endl;

est\_hsq.cpp:813: if (\_flag\_CC2) LOGGER << \_hsq\_name[j + 1] << "\_L\t" << transform\_hsq\_L(\_ncase2, prevalence2, Hsq[\_bivar\_pos[1][i]]) << "\t" << transform\_hsq\_L(\_ncase2, prevalence2, sqrt(VarHsq[\_bivar\_pos[1][i]])) << endl;

est\_hsq.cpp:816: LOGGER << "(Proportion of cases in the sample = " << \_ncase << "; User-specified disease prevalence = " << prevalence << ")" << endl;

est\_hsq.cpp:817: for (i = 0; i < Hsq.size(); i++) LOGGER << \_hsq\_name[i] << "\_L\t" << transform\_hsq\_L(\_ncase, prevalence, Hsq[i]) << "\t" << transform\_hsq\_L(\_ncase, prevalence, sqrt(VarHsq[i])) << endl;

est\_hsq.cpp:818: if (\_r\_indx.size() > 2) LOGGER << "\nSum of V(G)\_L/Vp\t" << transform\_hsq\_L(\_ncase, prevalence, sum\_hsq) << "\t" << transform\_hsq\_L(\_ncase, prevalence, sqrt(var\_sum\_hsq)) << endl;

est\_hsq.cpp:827: LOGGER << rg\_name[i] << "\t" << rg[i] << "\t" << sqrt(rg\_var[i]) << endl;

est\_hsq.cpp:831: LOGGER << "\nSampling variance/covariance of the estimates of variance components:" << endl;

est\_hsq.cpp:833: //for (j = 0; j < \_r\_indx.size(); j++) LOGGER << setiosflags(ios::scientific) << Hi(i, j) << "\t";

est\_hsq.cpp:834: for (j = 0; j < \_r\_indx.size(); j++) LOGGER << std::scientific << Hi(i, j) << "\t";

est\_hsq.cpp:835: LOGGER << endl;

est\_hsq.cpp:839: LOGGER << "Estimate" << (\_X\_c > 1 ? "s" : "") << "of fixed effect" << (\_X\_c > 1 ? "s" : "") << ":" << endl;

est\_hsq.cpp:840: LOGGER << "\nSource\tEstimate\tSE" << endl;

est\_hsq.cpp:842: if (i == 0) LOGGER << "mean\t";

est\_hsq.cpp:843: else LOGGER << "X\_" << i + 1 << "\t";

est\_hsq.cpp:844: LOGGER << std::fixed << \_b[i] << "\t" << sqrt(Xt\_Vi\_X\_i(i, i)) << endl;

est\_hsq.cpp:906: LOGGER << "\nSummary result of REML analysis has been saved in the file [" + reml\_rst\_file + "]." << endl;

est\_hsq.cpp:917: LOGGER << "\nBLUP solutions of the genetic effects for " << \_keep.size() << " individuals have been saved in the file [" + rand\_eff\_file + "]." << endl;

est\_hsq.cpp:977: LOGGER << "\ncvBLUP solutions of the genetic effects for " << \_keep.size() << " individuals have been saved in the file [" + rand\_eff\_file + "]." << endl;

est\_hsq.cpp:1036: LOGGER << "\nCalculating the logLikelihood for the reduced model ...\n(variance component" << (multi\_comp ? "s " : " ");

est\_hsq.cpp:1038: if (find(\_r\_indx\_drop.begin(), \_r\_indx\_drop.end(), \_r\_indx[i]) == \_r\_indx\_drop.end()) LOGGER << \_r\_indx[i] + 1 << " ";

est\_hsq.cpp:1040: LOGGER << (multi\_comp ? "are" : "is") << " dropped from the model)" << endl;

est\_hsq.cpp:1073: if(\_reml\_fixed\_var) LOGGER << "Variance components are fixed at: " << varcmp.transpose() << endl;

est\_hsq.cpp:1074: else LOGGER << "Prior values of variance components: " << varcmp.transpose() << endl;

est\_hsq.cpp:1078: LOGGER << "Calculating prior values of variance components by EM-REML ..." << endl;

est\_hsq.cpp:1083: LOGGER << "Running " << mtd\_str[\_reml\_mtd] << " algorithm ..." << "\nIter.\tlogL\t";

est\_hsq.cpp:1084: for (i = 0; i < \_r\_indx.size(); i++) LOGGER << \_var\_name[\_r\_indx[i]] << "\t";

est\_hsq.cpp:1085: LOGGER << endl;

est\_hsq.cpp:1087: //LOGGER << "Iter " << iter << endl;

est\_hsq.cpp:1103: //LOGGER << "calcu\_vi\_bivar returned" << endl;

est\_hsq.cpp:1136: LOGGER << iter << "\t" << std::fixed << LOGGER.setprecision(2) << lgL << "\t";

est\_hsq.cpp:1137: for (i = 0; i < \_r\_indx.size(); i++) LOGGER << LOGGER.setprecision(5) << varcmp[i] << "\t";

est\_hsq.cpp:1138: //LOGGER << time\_vi << "\t" << time\_p << "\t" << time\_reml << "\t";

est\_hsq.cpp:1139: if (constrain\_num > 0) LOGGER << "(" << constrain\_num << " component(s) constrained)" << endl;

est\_hsq.cpp:1140: else LOGGER << endl;

est\_hsq.cpp:1142: if (!prior\_var\_flag) LOGGER << "Updated prior values: " << varcmp.transpose() << endl;

est\_hsq.cpp:1143: LOGGER << "logL: " << lgL << endl;

est\_hsq.cpp:1182: if(\_reml\_fixed\_var) LOGGER << "Warning: the model is evaluated at fixed variance components. The (log-)likelihood might not be maximised." <<endl;

est\_hsq.cpp:1184: if(converged\_flag) LOGGER << "Log-likelihood ratio converged." << endl;

est\_hsq.cpp:1186: if(\_reml\_force\_converge || \_reml\_no\_converge) LOGGER << "Warning: Log-likelihood not converged. Results are not reliable." <<endl;

est\_hsq.cpp:1315: LOGGER << "Still can't be inverted. Try --reml-alg-inv 2 " << endl;

est\_hsq.cpp:1319: LOGGER << "Switching to the \"bending\" approach to invert V. This method hasn't been tested extensively. The results might not be reliable!" << endl;

est\_hsq.cpp:1339: LOGGER << "Still can't be inverted. Try --reml-alg-inv 2 " << endl;

est\_hsq.cpp:1344: LOGGER << "Switching to the \"bending\" approach to invert V. This method hasn't been tested extensively. The results might not be reliable!" << endl;

est\_hsq.cpp:1348: LOGGER << "Try --reml-alg-inv 1 for diagonal addition value or --reml-alg-inv 2 for bending Vi" << endl;

est\_hsq.cpp:1361: LOGGER << "\nSwitching to the \"bending\" approach to invert V. This method hasn't been tested extensively. The results might not be reliable!" << endl;

est\_hsq.cpp:1377: LOGGER << "Switching from Cholesky to LU decomposition approach. The results might not be reliable!" << endl;

est\_hsq.cpp:1414: LOGGER << "Bending the GRM(s) to be positive-definite (may take a while if there are multiple GRMs)..." << endl;

est\_hsq.cpp:1425: LOGGER << "Bending the " << i + 1 << "th GRM completed." << endl;

est\_hsq.cpp:1560: LOGGER << "Warning: the information matrix is not invertible." << endl;

est\_hsq.cpp:1626: LOGGER << "Warning: the information matrix is not invertible." << endl;

est\_hsq.cpp:1726: LOGGER << "Calculating the BLUP solutions to SNP effects ..." << endl;

est\_hsq.cpp:1764: LOGGER << "Calculating the BLUP solutions to SNP effects using imputed dosage scores ... " << endl;

est\_hsq.cpp:1787: LOGGER << "Writing BLUP solutions of SNP effects for " << \_include.size() << " SNPs to [" + o\_b\_snp\_file + "]." << endl;

est\_hsq.cpp:1794: LOGGER << "BLUP solutions of SNP effects for " << \_include.size() << " SNPs have been saved in the file [" + o\_b\_snp\_file + "]." << endl;

est\_hsq.cpp:1855: LOGGER << \_n << " individuals are in common in these files." << endl;

est\_hsq.cpp:1865: LOGGER << "\nPerforming Haseman-Elston regression ...\n" << endl;

est\_hsq.cpp:1868: LOGGER << "Standardising the phenotype ..." << endl;

est\_hsq.cpp:1915: LOGGER << "Constructing ordinary least squares equations ..." << endl;

est\_hsq.cpp:1983: LOGGER << "\nLeft-hand side of OLS equations (X'X)\n" << Lhs << endl << endl;

est\_hsq.cpp:1984: //LOGGER << "vare\_cp " << vare\_cp << endl;

est\_hsq.cpp:1985: //LOGGER << "vare\_sd " << vare\_sd << endl << endl;

est\_hsq.cpp:2090: LOGGER << ss.str() << endl;

est\_hsq.cpp:2095: LOGGER << "Results from Haseman-Elston regression have been saved in [" + ofile + "]." << endl;

est\_hsq.cpp:2160: LOGGER << \_n << " individuals are in common in these files." << endl;

est\_hsq.cpp:2183: //LOGGER << i << " " << idx << " " << phen\_buf[idx][mphen] << " " << atof(phen\_buf[idx][mphen].c\_str()) << endl;

est\_hsq.cpp:2194: LOGGER << y1.size() << " non-missing phenotypes for trait #1 and " << y2.size() << " for trait #2" << endl;

est\_hsq.cpp:2206: LOGGER << "\nPerforming Haseman-Elston regression ...\n" << endl;

est\_hsq.cpp:2209: LOGGER << "Standardising the phenotype ..." << endl;

est\_hsq.cpp:2289: LOGGER << "Constructing ordinary least squares equations ..." << endl;

est\_hsq.cpp:2436: LOGGER << "\n length of covariates:" << endl;

est\_hsq.cpp:2437: LOGGER << "\t trait1: " << count[0] << endl;

est\_hsq.cpp:2438: LOGGER << "\t trait2: " << count[1] << endl;

est\_hsq.cpp:2439: LOGGER << "\t trait12: " << count[2] << endl;

est\_hsq.cpp:2453: LOGGER << "\nLeft-hand side of OLS equations (X'X)\n" << LhsAll << endl << endl;

est\_hsq.cpp:2555: LOGGER << "\nJackknife sampling variance/covariance of the estimates of heritability:" << endl;

est\_hsq.cpp:2567: LOGGER << varcov << endl << endl;

est\_hsq.cpp:2608: LOGGER << ss.str() << endl;

est\_hsq.cpp:2613: LOGGER << "Results from Haseman-Elston regression have been saved in [" + ofile + "]." << endl;

est\_hsq.cpp:2647: LOGGER << "\nPerforming Haseman-Elston regression ...\n" << endl;

est\_hsq.cpp:2661: LOGGER << "Standardising the phenotype ..." << endl;

est\_hsq.cpp:2688: LOGGER << ss.str() << endl;

est\_hsq.cpp:2693: LOGGER << "Results from Haseman-Elston regression have been saved in [" + ofile + "]." << endl;

gbat.cpp:19: LOGGER << "\nReading SNP association results from [" + snpAssoc\_file + "]." << endl;

gbat.cpp:23: LOGGER << "Reading association p-values from [" << snpAssoc\_file << "]." << endl;

gbat.cpp:32: LOGGER << "Association p-values of " << snp\_name.size() << " SNPs have been included." << endl;

gbat.cpp:65: LOGGER << "Reading physical positions of the genes from [" + gAnno\_file + "]." << endl;

gbat.cpp:76: LOGGER << "Physical positions of " << gene\_name.size() << " genes have been included." << endl;

gbat.cpp:133: LOGGER << "Mapping the physical positions of genes to SNP data (gene bounaries: " << wind / 1000 << "Kb away from UTRs) ..." << endl;

gbat.cpp:175: else LOGGER << mapped << " genes have been mapped to SNP data." << endl;

gbat.cpp:191: LOGGER << "\nRunning gene-based association test (GBAT)..." << endl;

gbat.cpp:222: if((i + 1) % 100 == 0 || (i + 1) == gene\_num) LOGGER << i + 1 << " of " << gene\_num << " genes.\r";

gbat.cpp:226: LOGGER << "\nSaving the results of the gene-based association analysis to [" + filename + "] ..." << endl;

gbat.cpp:244: LOGGER << "here simulation starts." << endl;

gbat.cpp:270: LOGGER << "here find starts." << endl;

gbat.cpp:276: LOGGER << "here find ends." << endl;

grm.cpp:63: if (!mlmassoc) LOGGER << "\nCalculating the" << ((grm\_d\_flag) ? " dominance" : "") << " genetic relationship matrix (GRM)" << (grm\_xchr\_flag ? " for the X chromosome" : "") << (\_dosage\_flag ? " using imputed dosage data" : "") << " ... (Note: default speed-optimized mode, may use huge RAM)" << endl;

grm.cpp:64: else LOGGER << "\nCalculating the genetic relationship matrix (GRM) ... " << endl;

grm.cpp:206: LOGGER << "GRM of " << \_keep.size() << " individuals has been saved in the file [" + grm\_file + "] (in binary format)." << endl;

grm.cpp:220: LOGGER << "Number of SNPs to calculate the genetic relationship between each pair of individuals has been saved in the file [" + grm\_N\_file + "] (in binary format)." << endl;

grm.cpp:228: LOGGER << "Saving the genetic relationship matrix to the file [" + grm\_file + "] (in compressed text format)." << endl;

grm.cpp:242: LOGGER << "The genetic relationship matrix has been saved in the file [" + grm\_file + "] (in compressed text format)." << endl;

grm.cpp:250: LOGGER << "IDs for the GRM file [" + grm\_file + "] have been saved in the file [" + famfile + "]." << endl;

grm.cpp:257: if (out\_id\_log) LOGGER << "Reading IDs of the GRM from [" + grm\_id\_file + "]." << endl;

grm.cpp:276: if (out\_id\_log) LOGGER << n << " IDs are read from [" + grm\_id\_file + "]." << endl;

grm.cpp:310: LOGGER << "Reading the GRM from [" + grm\_gzfile + "]." << endl;

grm.cpp:322: if (grm\_N\_buf == 0) LOGGER << "Warning: " << buf << endl;

grm.cpp:335: LOGGER << "GRM for " << n << " individuals are included from [" + grm\_gzfile + "]." << endl;

grm.cpp:348: LOGGER << "Reading the GRM from [" + grm\_binfile + "]." << endl;

grm.cpp:364: LOGGER << "Reading the number of SNPs for the GRM from [" + grm\_Nfile + "]." << endl;

grm.cpp:376: LOGGER << "GRM for " << n << " individuals are included from [" + grm\_binfile + "]." << endl;

grm.cpp:380: LOGGER << "Pruning the GRM with a cutoff of " << grm\_cutoff << " ..." << endl;

grm.cpp:426: LOGGER << "After pruning the GRM, there are " << \_keep.size() << " individuals (" << removed\_ID.size() << " individuals removed)." << endl;

grm.cpp:430: LOGGER << "Adjusting the GRM for sampling errors ..." << endl;

grm.cpp:459: LOGGER << "Parameterizing the GRM under the assumption of ";

grm.cpp:460: if (dosage\_compen == 1) LOGGER << "full dosage compensation ..." << endl;

grm.cpp:461: else if (dosage\_compen == 0) LOGGER << "no dosage compensation ..." << endl;

grm.cpp:532: else LOGGER << \_n << " individuals in common in the GRM files." << endl;

grm.cpp:538: LOGGER << "Reading the GRM from the " << f + 1 << "th file ..." << endl;

grm.cpp:562: LOGGER << "\n" << grm\_files.size() << " GRMs have been merged together." << endl;

grm.cpp:578: else LOGGER << \_n << " individuals are in common in the GRM files." << endl;

grm.cpp:586: LOGGER << "Reading the GRM from the " << f + 1 << "th file ..." << endl;

grm.cpp:618: LOGGER << "\n" << grm\_files.size() << " GRMs have been aligned." << endl;

grm.cpp:633: if (out\_log) LOGGER << "There are " << grm\_files.size() << " GRM file names specified in [" + merge\_grm\_file + "]." << endl;

grm.cpp:659: LOGGER << "\nThe off-diagonals that are < " << threshold << " are set to zero.\n" << endl;

grm.cpp:674: LOGGER << "\nPerforming principal component analysis ..." << endl;

grm.cpp:685: LOGGER << "Eigenvalues of " << n << " individuals have been saved in [" + eval\_file + "]." << endl;

grm.cpp:696: LOGGER << "The first " << out\_pc\_num << " eigenvectors of " << n << " individuals have been saved in [" + evec\_file + "]." << endl;

grm.cpp:709: LOGGER << "Reading eigenvectors from [" + eigenvec\_file + "]." << endl;

grm.cpp:713: LOGGER << eigenvec\_num << " eigenvectors of " << eigenvec\_ID.size() << " individuals are included from [" + eigenvec\_file + "]." << endl;

grm.cpp:716: LOGGER << "\nReading eigenvalues from [" + eigenval\_file + "]." << endl;

grm.cpp:727: LOGGER << eigenval\_num << " eigenvalues are read from [" + eigenval\_file + "]" << endl;

grm.cpp:740: LOGGER << \_n << " individuals in common between the input files are included in the analysis."<<endl;

grm.cpp:754: LOGGER << "\nCalculating SNP loading vectors..." << endl;

grm.cpp:764: LOGGER << "\nSaving the PC loading vectors of " << m << " SNPs to [" + filename + "] ..." << endl;

grm.cpp:793: //LOGGER << "\nOpen the project file [" << out\_filename << "] to write."<< endl;

grm.cpp:797: LOGGER << "Reading SNP loading vectors from [" + f\_pc\_load + "]." << endl;

grm.cpp:803: LOGGER << "Number of PC loading vectors: " << N\_loading\_file << endl;

grm.cpp:813: LOGGER << "Number of SNPs in loading array: " << num\_snp << "." << endl;

grm.cpp:849: LOGGER << "Matching alleles..." << endl;

grm.cpp:859: LOGGER << "Adjusting A1" << endl;

grm.cpp:885: LOGGER << " " << m\_snp\_loading.rows() << " SNPs are included for loading" << endl;

grm.cpp:890: LOGGER << " See [" << miss\_file << "] for details. If there are many missing SNPs, the projection might be biased." << endl;

grm.cpp:899: LOGGER << "Standardizing genotypes and projecting PCs..." << endl;

grm.cpp:900: LOGGER << "Total number of subjects: " << \_keep.size() << "\n" << endl;

grm.cpp:902: LOGGER << "Processing subject number: " << endl;

grm.cpp:906: LOGGER << to\_string(ind\_index+1) + "\r" << flush;

grm.cpp:942: LOGGER << "\nFinished, and the PCs have all been saved to " << out\_filename << endl;

gwas\_simu.cpp:26: LOGGER << "Reading a list of SNPs (as causal variants) from [" + qtl\_file + "]." << endl;

gwas\_simu.cpp:55: LOGGER << qtl\_pos.size() << " SNPs (as causal variants) to be included from [" + qtl\_file + "]." << endl;

gwas\_simu.cpp:68: LOGGER << "Simulated QTL effect(s) have been saved in [" + out\_parfile + "]." << endl;

gwas\_simu.cpp:91: LOGGER << "Simulation parameters:" << endl;

gwas\_simu.cpp:92: LOGGER << "Number of simulation replicate(s) = " << simu\_num << " (Default = 1)" << endl;

gwas\_simu.cpp:93: LOGGER << "Heritability " << (cc\_flag ? "of liability = " : " = ") << hsq << " (Default = 0.1)" << endl;

gwas\_simu.cpp:95: LOGGER << "Disease prevalence = " << K << " (Default = 0.1)" << endl;

gwas\_simu.cpp:96: LOGGER << "Number of cases = " << case\_num << endl;

gwas\_simu.cpp:97: LOGGER << "Number of controls = " << control\_num << endl;

gwas\_simu.cpp:99: LOGGER << endl;

gwas\_simu.cpp:118: if (qtl\_num - num\_gener\_qtl\_eff > 0) LOGGER << qtl\_num - num\_gener\_qtl\_eff << " user-specified QTL effects." << endl;

gwas\_simu.cpp:119: if (num\_gener\_qtl\_eff > 0) LOGGER << num\_gener\_qtl\_eff << " unspecified QTL effects are generated from standard normal distribution." << endl;

gwas\_simu.cpp:164: LOGGER << "Simulating GWAS based on the real genotyped data with " << simu\_num << " replicate(s) ..." << endl;

gwas\_simu.cpp:198: if (cc\_flag) LOGGER << "Simulated " << case\_num\_buf << " cases and " << control\_num << " controls have been saved in [" + \_out + ".phen" + "]." << endl;

gwas\_simu.cpp:199: else LOGGER << "Simulated phenotypes of " << \_keep.size() << " individuals have been saved in [" + \_out + ".phen" + "]." << endl;

gwas\_simu.cpp:206: LOGGER << "Saving the simulated data to the file [" + out\_rstfile + "] (in emBayesB format)." << endl;

gwas\_simu.cpp:217: LOGGER << "Simulated data (" << \_keep.size() << " individuals and " << \_include.size() << " SNPs) has been saved in [" + out\_rstfile + "]." << endl;

gwas\_simu.cpp:560: LOGGER << "Genetic distances have been created, and been saved in [" + out\_bimfile + "]." << endl;

joint\_meta.cpp:20: LOGGER << "\nReading GWAS summary-level statistics from [" + metafile + "] ..." << endl;

joint\_meta.cpp:88: LOGGER << "GWAS summary statistics of " << count << " SNPs read from [" + metafile + "]." << endl;

joint\_meta.cpp:90: LOGGER << "Phenotypic variance estimated from summary statistics of all " << count << " SNPs: " << \_jma\_Vp << " (variance of logit for case-control studies)." << endl;

joint\_meta.cpp:94: LOGGER << "User specified genomic inflation factor: " << \_GC\_val << endl;

joint\_meta.cpp:97: LOGGER << "Genomic inflation factor calculated from " << count << " SNPs: " << \_GC\_val << endl;

joint\_meta.cpp:99: LOGGER << "p-values will be adjusted by the genomic control approach." << endl;

joint\_meta.cpp:102: LOGGER << "Matching the GWAS meta-analysis results to the genotype data ..." << endl;

joint\_meta.cpp:146: LOGGER << "Warning: can't match the reference alleles of " << bad\_snp.size() << " SNPs to those in the genotype data. These SNPs have been saved in [" + badsnpfile + "]." << endl;

joint\_meta.cpp:154: LOGGER << bad\_snp\_freq.size() << " SNP(s) have large difference of allele frequency between the GWAS summary data and the reference sample. These SNPs have been saved in [" << badsnpfile << "]." << endl;

joint\_meta.cpp:158: else LOGGER << \_include.size() << " SNPs are matched to the genotype data." << endl;

joint\_meta.cpp:187: LOGGER << "Calculating the variance of SNP genotypes ..." << endl;

joint\_meta.cpp:220: if (pgiven.size() > 0) LOGGER << pgiven.size() << " of them are matched to the genotype and summary data." << endl;

joint\_meta.cpp:236: LOGGER << "The threshold p-value has been set to 0.5 because of the --cojo-top-SNPs option." << endl;

joint\_meta.cpp:241: LOGGER << endl;

joint\_meta.cpp:243: LOGGER << "Performing "<< ((mld\_slct\_alg==0)?"stepwise":"forward") << " model selection on " << \_include.size() << " SNPs to select association signals ... (p cutoff = " << \_jma\_p\_cutoff << "; ";

joint\_meta.cpp:244: LOGGER << "collinearity cutoff = " << \_jma\_collinear << ")"<< endl;

joint\_meta.cpp:245: if (!\_jma\_actual\_geno) LOGGER << "(Assuming complete linkage equilibrium between SNPs which are more than " << \_jma\_wind\_size / 1e6 << "Mb away from each other)" << endl;

joint\_meta.cpp:248: LOGGER << "No SNPs have been selected." << endl;

joint\_meta.cpp:254: LOGGER << "Performing backward selection on " << \_include.size() << " SNPs at threshold p-value = " << \_jma\_p\_cutoff << " ..." << endl;

joint\_meta.cpp:261: LOGGER << "Performing joint analysis on all the " << slct.size();

joint\_meta.cpp:262: if (joint\_only) LOGGER << " SNPs ..." << endl;

joint\_meta.cpp:263: else LOGGER << " selected signals ..." << endl;

joint\_meta.cpp:268: if (\_jma\_actual\_geno) LOGGER << "Residual variance = " << \_jma\_Ve << endl;

joint\_meta.cpp:274: LOGGER << "(" << \_jma\_snpnum\_backward << " SNPs eliminated by backward selection and " << \_jma\_snpnum\_collienar << " SNPs filtered by collinearity test are not included in the output)" << endl;

joint\_meta.cpp:287: LOGGER << "Performing single-SNP association analysis conditional on the " << pgiven.size() << " given SNPs ... ";

joint\_meta.cpp:288: LOGGER << "(collinearity cutoff = " << \_jma\_collinear << ")" << endl;

joint\_meta.cpp:289: if (!\_jma\_actual\_geno) LOGGER << "(Assuming complete linkage equilibrium between SNPs which are more than " << \_jma\_wind\_size / 1e6 << "Mb away from each other)" << endl;

joint\_meta.cpp:310: if (joint\_only) LOGGER << "Saving the joint analysis result of " << slct.size() << " SNPs to [" + filename + "] ..." << endl;

joint\_meta.cpp:311: else LOGGER << "Saving the " << slct.size() << " independent signals to [" + filename + "] ..." << endl;

joint\_meta.cpp:327: if (joint\_only) LOGGER << "Saving the LD structure of " << slct.size() << " SNPs to [" + filename + "] ..." << endl;

joint\_meta.cpp:328: else LOGGER << "Saving the LD structure of " << slct.size() << " independent signals to [" + filename + "] ..." << endl;

joint\_meta.cpp:351: LOGGER << "Saving the conditional analysis results of " << remain.size() << " remaining SNPs to [" + filename + "] ..." << endl;

joint\_meta.cpp:366: LOGGER << "Restricting output threshold to " << out\_thresh << "." << endl;

joint\_meta.cpp:393: LOGGER << "Switched to perform a forward model selection because the significance level is too low..." << endl;

joint\_meta.cpp:401: if (slct.size() % 5 == 0 && slct.size() > prev\_num) LOGGER << slct.size() << " associated SNPs have been selected." << endl;

joint\_meta.cpp:406: LOGGER << "Performing backward elimination..." << endl;

joint\_meta.cpp:409: LOGGER << "Finally, " << slct.size() << " associated SNPs are selected." << endl;

joint\_meta.cpp:795: LOGGER << "\nPerforming joint analysis on all the " << \_include.size() << " SNPs ..." << endl;

joint\_meta.cpp:796: LOGGER << "(Assuming complete linkage equilibrium between SNPs which are more than " << \_jma\_wind\_size / 1e6 << "Mb away from each other)" << endl;

joint\_meta.cpp:799: LOGGER << "Saving the joint analysis result of " << \_include.size() << " SNPs to [" + filename + "] ..." << endl;

joint\_meta.cpp:839: LOGGER << "Calculating the LD correlation matrix of all the " << \_include.size() << " SNPs..." << endl;

joint\_meta.cpp:876: if((i + 1) % 1000 == 0 || (i + 1) == \_include.size()) LOGGER << i + 1 << " of " << \_include.size() << " SNPs.\r";

joint\_meta.cpp:880: LOGGER << "Estimating the joint effects of all SNPs ..." << endl;

ld.cpp:38: else LOGGER << prev\_target\_snp\_num << " target SNPs are read from [" + snplistfile + "], " << \_ld\_target\_snp.size() << " of which exist in the data." << endl;

ld.cpp:57: LOGGER << "Estimating LD structure..." << endl;

ld.cpp:89: LOGGER << "Results have been saved in [" + \_out + ".rsq.ld]" + ", [" + \_out + ".r.ld]" + " and [" + \_out + ".snp.ld].\n" << endl;

ld.cpp:98: LOGGER << "Parameters used to search for SNPs in LD with the given SNPs: window size=" << (int) (wind\_size \* 0.001) << "Kb, significant level=" << alpha << endl;

ld.cpp:168: LOGGER << i + 1 << " of " << smpl.size() << " target SNPs.\r";

ld.cpp:280: LOGGER << "\nCalculating LD score for SNPs (block size of " << wind\_size / 1000 << "Kb with an overlap of "<<wind\_size/2000<<"Kb between blocks); LD rsq threshold = " << rsq\_cutoff << ") ... " << endl;

ld.cpp:282: if(\_ldscore\_adj) LOGGER << "LD rsq will be adjusted for chance correlation, i.e. rsq\_adj = rsq - (1 - rsq) / (n -2)." << endl;

ld.cpp:304: LOGGER << "LD score for " << m << " SNPs have been saved in the file [" + mrsq\_file + "]." << endl;

ld.cpp:518: LOGGER << "There are " << set\_num << " filenames specified in [" + snpset\_filenames\_file + "]." << endl;

ld.cpp:525: LOGGER << "Reading the list of SNPs from [" + snpset\_filenaems[i] + "]." << endl;

ld.cpp:549: LOGGER << snp\_count << " SNPs included from [" << snpset\_filenaems[i] << "]. " <<endl;

ld.cpp:552: LOGGER << "\nCalculating multi-component LD score for SNPs (block size of " << wind\_size / 1000 << "Kb with an overlap of "<<wind\_size/2000<<"Kb between blocks); LD rsq threshold = " << rsq\_cutoff << ") ... " << endl;

ld.cpp:554: if(\_ldscore\_adj) LOGGER << "LD rsq will be adjusted for chance correlation, i.e. rsq\_adj = rsq - (1 - rsq) / (n -2)." << endl;

ld.cpp:587: LOGGER << "LD score for " << m << " SNPs have been saved in the file [" + mrsq\_file + "]." << endl;

ld.cpp:755: LOGGER << "Reading per-SNP LD score from [" + i\_ld\_file + "] ..." << endl;

ld.cpp:789: LOGGER << "Per-SNP LD score for " << m << " SNPs being read from [" + i\_ld\_file + "]." << endl;

ld.cpp:797: LOGGER << "\nCalculating LD score between SNPs (block size of " << wind\_size / 1000 << "Kb with an overlap of "<<wind\_size / 2000<<"Kb between blocks); LD rsq threshold = " << rsq\_cutoff << ") ... " << endl;

ld.cpp:815: LOGGER << "Calculating regional mean LD score (region width = " << seg\_size / 1000 << "Kb with an overlap of " << seg\_size / 2000 << "Kb between regions) ... " << endl;

ld.cpp:850: LOGGER << "Writing the regional LD score to file ["+ lds\_file +"] ..." << endl;

ld.cpp:912: LOGGER << "Calculating maximum LD rsq between SNPs (block size of " << wind\_size / 1000 << "Kb with an overlap of "<<wind\_size/2000<<"Kb between blocks; LD rsq threshold = " << rsq\_cutoff << ") ... " << endl;

ld.cpp:913: LOGGER << "(Maximum number of SNPs allowed in a block = " << max\_size << " due to computational limitation)" << endl;

ld.cpp:934: LOGGER << "Maximum LD rsq for " << m << " SNPs have been saved in the file [" + max\_rsq\_file + "]." << endl;

ld.cpp:1032: LOGGER << "size = " << size << "; eff\_m = " << eff\_m << endl;

ld.cpp:1050: LOGGER << "size = " << size << "; eff\_m = " << eff\_m << endl;

mkl.cpp:22: LOGGER << "Recoding genotypes (individual major mode) ..." << endl;

mkl.cpp:193: if (!mlmassoc) LOGGER << "\nCalculating the" << ((grm\_d\_flag) ? " dominance" : "") << " genetic relationship matrix (GRM)" << (grm\_xchr\_flag ? " for the X chromosome" : "") << (\_dosage\_flag ? " using imputed dosage data" : "") << " ... (Note: default speed-optimized mode, may use huge RAM)" << endl;

mkl.cpp:194: else LOGGER << "\nCalculating the genetic relationship matrix (GRM) ... " << endl;

mkl.cpp:309: LOGGER << "GRM of " << n << " individuals has been saved in the file [" + grm\_file + "] (in binary format)." << endl;

mkl.cpp:319: LOGGER << "Number of SNPs to calculate the genetic relationship between each pair of individuals has been saved in the file [" + grm\_N\_file + "] (in binary format)." << endl;

mkl.cpp:326: LOGGER << "Saving the genetic relationship matrix to the file [" + grm\_file + "] (in compressed text format)." << endl;

mkl.cpp:333: LOGGER << "The genetic relationship matrix has been saved in the file [" + grm\_file + "] (in compressed text format)." << endl;

mkl.cpp:341: LOGGER << "IDs for the GRM file [" + grm\_file + "] have been saved in the file [" + famfile + "]." << endl;

mkl.cpp:554: LOGGER << "\nPruning SNPs for LD ..." << endl;

mkl.cpp:570: LOGGER << "After LD-pruning, " << m << " SNPs remain." << endl;

mkl.cpp:575: LOGGER << "The list of " << m << " LD-pruned SNPs (pruned in) has been saved in the file [" + pruned\_file + "]." << endl;

mkl.cpp:623: LOGGER << "Calculating mean and maximum LD rsq (window size = at least " << wind\_size / 1000 << "Kb in either direction; LD rsq threshold = " << rsq\_cutoff << ") ... " << endl;

mkl.cpp:637: LOGGER << "Mean and maximum LD rsq for " << m << " SNPs have been saved in the file [" + mrsq\_file + "]." << endl;

mlm\_assoc.cpp:105: LOGGER << "\nReading the primary GRM from [" << grm\_files[1] << "] ..." << endl;

mlm\_assoc.cpp:125: LOGGER << "\nReading the secondary GRM from [" << grm\_files[0] << "] ..." << endl;

mlm\_assoc.cpp:152: LOGGER << "There are " << grm\_files.size() << " GRM file names specified in the file [" + grm\_file + "]." << endl;

mlm\_assoc.cpp:154: LOGGER << "Reading the GRM from the " << i + 1 << "th file ..." << endl;

mlm\_assoc.cpp:198: LOGGER << "\nPerforming MLM association analyses" << (subtract\_grm\_flag?"":" (including the candidate SNP)") << " ..."<<endl;

option.cpp:28: LOGGER << "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*" << endl;

option.cpp:29: LOGGER << "\* Genome-wide Complex Trait Analysis (GCTA)" << endl;

option.cpp:30: LOGGER << "\* version 1.93.3 beta3" << endl;

option.cpp:31: LOGGER << "\* (C) 2010-2021, Westlake University" << endl;

option.cpp:32: LOGGER << "\* MIT License" << endl;

option.cpp:33: LOGGER << "\* Please report bugs to: Jian Yang <jian.yang@westlake.edu.cn>" << endl;

option.cpp:34: LOGGER << "\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*" << endl;

option.cpp:38: LOGGER << "Analysis started: " << ctime(&curr) << endl;

option.cpp:39: LOGGER << "Options:" << endl;

option.cpp:48: LOGGER << "\nAnalysis finished: " << ctime(&curr);

option.cpp:50: LOGGER << "Computational time: " << time\_used / 3600 << ":" << (time\_used % 3600) / 60 << ":" << time\_used % 60 << endl;

option.cpp:178: LOGGER << "Accepted options:" << endl;

option.cpp:182: LOGGER << "--thread-num " << thread\_num << endl;

option.cpp:187: LOGGER << "--threads " << thread\_num << endl;

option.cpp:192: LOGGER << "--raw-files " << argv[i] << endl;

option.cpp:195: LOGGER << "--raw-summary " << argv[i] << endl;

option.cpp:198: LOGGER << "--gencall " << GC\_cutoff << endl;

option.cpp:204: LOGGER << "--bfile " << argv[i] << endl;

option.cpp:208: LOGGER << "--mbfile " << argv[i] << endl;

option.cpp:211: LOGGER << "--make-bed " << endl;

option.cpp:215: LOGGER << "--bfile2 " << argv[i] << endl;

option.cpp:221: LOGGER << "--dosage-mach " << dose\_file << " " << dose\_info\_file << endl;

option.cpp:227: LOGGER << "--dosage-mach-gz " << dose\_file << " " << dose\_info\_file << endl;

option.cpp:234: LOGGER << "--dosage-beagle " << dose\_file << " " << dose\_info\_file << endl;

option.cpp:237: LOGGER << "--imput-rsq " << dose\_Rsq\_cutoff << endl;

option.cpp:241: LOGGER << "--update-imput-rsq " << update\_impRsq\_file << endl;

option.cpp:245: LOGGER << "--update-freq " << update\_freq\_file << endl;

option.cpp:249: LOGGER << "--update-ref-allele " << update\_refA\_file << endl;

option.cpp:253: LOGGER << "--keep " << kp\_indi\_file << endl;

option.cpp:257: LOGGER << "--remove " << rm\_indi\_file << endl;

option.cpp:261: LOGGER << "--update-sex " << update\_sex\_file << endl;

option.cpp:265: LOGGER << "--chr " << extract\_chr\_start << endl;

option.cpp:269: LOGGER << "--autosome-num " << autosome\_num << endl;

option.cpp:273: LOGGER << "--autosome" << endl;

option.cpp:276: LOGGER << "--extract " << extract\_snp\_file << endl;

option.cpp:280: LOGGER << "--exclude " << exclude\_snp\_file << endl;

option.cpp:284: LOGGER << "--extract-snp " << extract\_snp\_name << endl;

option.cpp:288: LOGGER << "--extract-region-snp " << extract\_snp\_name << " " << extract\_region\_wind << "Kb" << endl;

option.cpp:295: LOGGER << "--extract-region-bp " << extract\_region\_chr << " " << extract\_region\_bp << " " << extract\_region\_wind << "Kb" << endl;

option.cpp:300: LOGGER << "--exclude-snp " << exclude\_snp\_name << endl;

option.cpp:304: LOGGER << "--exclude-region-snp " << exclude\_snp\_name << exclude\_region\_wind << "Kb" << endl;

option.cpp:311: LOGGER << "--exclude-region-bp " << exclude\_region\_chr << " " << exclude\_region\_bp << " " << exclude\_region\_wind << "Kb" << endl;

option.cpp:316: LOGGER << "--maf " << maf << endl;

option.cpp:320: LOGGER << "--max-maf " << max\_maf << endl;

option.cpp:324: LOGGER << "--out " << out << endl;

option.cpp:328: LOGGER << "--freq-v1" << endl;

option.cpp:332: LOGGER << "--freq" << endl;

option.cpp:335: LOGGER << "--ssq" << endl;

option.cpp:339: LOGGER << "--recode" << endl;

option.cpp:343: LOGGER << "--recode-nomiss" << endl;

option.cpp:347: LOGGER << "--recode-std" << endl;

option.cpp:350: LOGGER << "--save-ram" << endl;

option.cpp:354: LOGGER << "--paa " << paa\_file << endl;

option.cpp:358: LOGGER << "--ibc" << endl;

option.cpp:361: LOGGER << "--ibc-all" << endl;

option.cpp:365: LOGGER << argv[i - 1] << " " << grm\_file << endl;

option.cpp:371: LOGGER << "--mgrm-gz " << grm\_file << endl;

option.cpp:375: LOGGER << argv[i - 1] << " " << grm\_file << endl;

option.cpp:381: LOGGER << "--grm-gz " << grm\_file << endl;

option.cpp:384: LOGGER << "--rm-high-ld " << rm\_high\_ld\_cutoff << endl;

option.cpp:389: LOGGER << argv[i] << endl;

option.cpp:394: LOGGER << "--make-grm-gz" << endl;

option.cpp:399: LOGGER << "--make-grm-alg " << make\_grm\_mtd << endl;

option.cpp:406: LOGGER << "--make-grm-f3" << endl;

option.cpp:411: LOGGER << argv[i] << endl;

option.cpp:417: LOGGER << "--make-grm-d-gz" << endl;

option.cpp:421: LOGGER <<"--dominance"<< endl;

option.cpp:426: LOGGER << argv[i] << endl;

option.cpp:432: LOGGER << "--make-grm-xchr-gz" << endl;

option.cpp:437: LOGGER << argv[i] << endl;

option.cpp:443: LOGGER << "--make-grm-inbred-gz" << endl;

option.cpp:446: LOGGER << "--grm-adj " << grm\_adj\_fac << endl;

option.cpp:450: LOGGER << "--dc " << dosage\_compen << endl;

option.cpp:454: if (grm\_cutoff >= -1 && grm\_cutoff <= 2) LOGGER << "--grm-cutoff" << grm\_cutoff << endl;

option.cpp:462: else LOGGER << "--make-bK " << bK\_threshold << endl;

option.cpp:471: LOGGER << "--pca " << out\_pc\_num << endl;

option.cpp:478: LOGGER << "--pc-loading " << pc\_file << endl;

option.cpp:485: LOGGER << "--project-loading " << project\_file << " " << project\_N << endl;

option.cpp:492: LOGGER << "--ld " << LD\_file << endl;

option.cpp:497: LOGGER << "--ld-step " << LD\_step << endl;

option.cpp:501: LOGGER << argv[i - 1] << " " << LD\_wind << endl;

option.cpp:510: LOGGER << "--ld-sig " << LD\_sig << endl;

option.cpp:514: LOGGER << "--ld-i" << endl;

option.cpp:518: LOGGER << "--ld-pruning " << LD\_prune\_rsq << endl;

option.cpp:523: LOGGER << "--ld-score" << endl;

option.cpp:526: LOGGER << "--ld-score-adj" << endl;

option.cpp:531: LOGGER << "--ld-score-multi " << ld\_score\_multi\_file << endl;

option.cpp:535: LOGGER << "--ld-rsq-cutoff " << LD\_rsq\_cutoff << endl;

option.cpp:544: LOGGER << "--ld-max-rsq" << endl;

option.cpp:553: LOGGER << "--ld-score-region" << endl;

option.cpp:558: LOGGER << "--ld-file " << LD\_file << endl;

option.cpp:563: LOGGER << "--simu-qt" << endl;

option.cpp:568: LOGGER << "--simu-cc " << simu\_case\_num << " " << simu\_control\_num << endl;

option.cpp:573: LOGGER << "--simu-rep " << simu\_rep << endl;

option.cpp:577: LOGGER << "--simu-hsq " << simu\_h2 << endl;

option.cpp:581: LOGGER << "--simu-k " << simu\_K << endl;

option.cpp:585: LOGGER << "--simu-causal-loci " << simu\_causal << endl;

option.cpp:589: LOGGER << "--simu-embayesb" << endl;

option.cpp:592: LOGGER << "--simu-output-causal" << endl;

option.cpp:595: LOGGER << "--simu-seed " << simu\_seed << endl;

option.cpp:599: LOGGER << "--simu-eff-mod " << simu\_eff\_mod << endl;

option.cpp:605: LOGGER << "--hapmap-genet-dst " << hapmap\_genet\_dst\_file << endl;

option.cpp:610: LOGGER << "--HEreg" << endl;

option.cpp:630: LOGGER << "--HEreg-bivar " << mphen << " " << mphen2 << endl;

option.cpp:634: LOGGER << "--reml" << endl;

option.cpp:639: LOGGER << "--prevalence " << prevalence << endl;

option.cpp:643: LOGGER << "--reml-pred-rand" << endl;

option.cpp:646: LOGGER << "--cvblup" << endl;

option.cpp:649: LOGGER << "--reml-est-fix" << endl;

option.cpp:652: LOGGER << "--reml-alg " << reml\_mtd << endl;

option.cpp:657: LOGGER << "--reml-no-constrain" << endl;

option.cpp:665: LOGGER << "--reml-priors ";

option.cpp:668: LOGGER << reml\_priors[j] << " ";

option.cpp:671: LOGGER << endl;

option.cpp:682: LOGGER << s\_buf << " ";

option.cpp:685: LOGGER << reml\_priors\_var[j] << " ";

option.cpp:688: LOGGER << endl;

option.cpp:692: LOGGER << "--reml-no-lrt" << endl;

option.cpp:703: LOGGER << "--reml-lrt ";

option.cpp:706: LOGGER << reml\_drop[j] << " ";

option.cpp:709: LOGGER << endl;

option.cpp:713: LOGGER << "--reml-maxit " << MaxIter << endl;

option.cpp:717: LOGGER << "--reml-bendV " << endl;

option.cpp:720: LOGGER << "--reml-force-converge " << endl;

option.cpp:723: LOGGER << "--reml-allow-no-converge " << endl;

option.cpp:726: LOGGER << "--reml-bending " << endl;

option.cpp:729: LOGGER << "--reml-amzvc" << endl;

option.cpp:732: LOGGER << "--reml-diag-one " << endl;

option.cpp:735: LOGGER << "--reml-diagV-adj " << reml\_diagV\_adj << endl;

option.cpp:738: LOGGER << "--reml-diag-mul " << reml\_diag\_mul << endl;

option.cpp:741: LOGGER << "--reml-inv-mtd " << reml\_inv\_method << endl;

option.cpp:744: LOGGER << "--pheno " << phen\_file << endl;

option.cpp:748: LOGGER << "--mpheno " << mphen << endl;

option.cpp:752: LOGGER << "--qcovar " << qcovar\_file << endl;

option.cpp:756: LOGGER << "--covar " << covar\_file << endl;

option.cpp:760: LOGGER << "--reml-res-diag " << weight\_file << endl;

option.cpp:764: LOGGER << "--gxqe " << qgxe\_file << endl;

option.cpp:768: LOGGER << "--gxe " << gxe\_file << endl;

option.cpp:773: LOGGER << "--blup-snp " << blup\_indi\_file << endl;

option.cpp:778: LOGGER << "--reml-wfam " << endl;

option.cpp:798: LOGGER << "--reml-bivar " << mphen << " " << mphen2 << endl;

option.cpp:810: LOGGER << "--reml-bivar-prevalence " << K\_buf[0] << " " << K\_buf[1] << endl;

option.cpp:815: LOGGER << "--reml-bivar-prevalence " << K\_buf[0] << endl;

option.cpp:820: LOGGER << "--reml-bivar-nocove" << endl;

option.cpp:828: LOGGER << "--reml-bivar-lrt-rg ";

option.cpp:831: LOGGER << fixed\_rg\_val[j] << " ";

option.cpp:834: LOGGER << endl;

option.cpp:843: LOGGER << "--reml-bivar-no-constrain" << endl;

option.cpp:846: LOGGER << "--cojo-file " << massoc\_file << endl;

option.cpp:851: LOGGER << "--cojo-slct" << endl;

option.cpp:855: LOGGER << "--cojo-stepwise" << endl;

option.cpp:859: LOGGER << "--cojo-forward" << endl;

option.cpp:863: LOGGER << "--cojo-backward" << endl;

option.cpp:867: LOGGER << "--cojo-top-SNPs " << massoc\_top\_SNPs << endl;

option.cpp:871: LOGGER << "--cojo-actual-geno is deprecated currently." << endl;

option.cpp:874: LOGGER << "--cojo-p " << massoc\_p << endl;

option.cpp:880: LOGGER << "--cojo-collinear " << massoc\_collinear << endl;

option.cpp:884: LOGGER << "--cojo-wind " << massoc\_wind << endl;

option.cpp:893: LOGGER << "--cojo-joint" << endl;

option.cpp:896: LOGGER << "--cojo-cond " << massoc\_cond\_snplist << endl;

option.cpp:907: LOGGER << "--cojo-gc " << ((massoc\_gc\_val < 0) ? "" : argv[i]) << endl;

option.cpp:911: LOGGER << "--cojo-sblup " << massoc\_sblup\_fac << endl;

option.cpp:917: LOGGER << "--mlma " << endl;

option.cpp:920: LOGGER << "--mlma-subtract-grm " << subtract\_grm\_file << endl;

option.cpp:925: LOGGER << "--mlma-loco " << endl;

option.cpp:928: LOGGER << "--mlma-no-adj-covar (use --mlma-no-preadj-covar instead)" << endl;

option.cpp:931: LOGGER << "--mlma-no-preadj-covar" << endl;

option.cpp:934: LOGGER << "--fst " << endl;

option.cpp:937: LOGGER << "--sub-popu " << subpopu\_file << endl;

option.cpp:941: LOGGER << "--fastBAT-ld-cutoff " << sbat\_ld\_cutoff << endl;

option.cpp:945: LOGGER << "--fastBAT-write-snpset" << endl;

option.cpp:948: LOGGER << "--fastBAT " << sbat\_sAssoc\_file << endl;

option.cpp:952: LOGGER << "--fastBAT-gene-list " << sbat\_gAnno\_file << endl;

option.cpp:956: LOGGER << "--fastBAT-set-list " << sbat\_snpset\_file << endl;

option.cpp:960: LOGGER << "--fastBAT-wind " << sbat\_wind << endl;

option.cpp:971: LOGGER << "--fastBAT-seg " << sbat\_seg\_size << endl;

option.cpp:978: LOGGER << "--efile " << efile << endl;

option.cpp:984: LOGGER << "--e-cor " << eR\_file << endl;

option.cpp:989: LOGGER << "--ecojo " << ecojo\_ma\_file << endl;

option.cpp:994: LOGGER << "--ecojo-slct" << endl;

option.cpp:998: LOGGER << "--ecojo-p " << ecojo\_p << endl;

option.cpp:1003: LOGGER << "--ecojo-collinear " << ecojo\_collinear << endl;

option.cpp:1009: LOGGER << "--ecojo-blup " << ecojo\_lambda << endl;

option.cpp:1015: LOGGER << argv[i] << endl;

option.cpp:1021: LOGGER << "--make-erm-gz" << endl;

option.cpp:1027: LOGGER << "--make-erm-alg " << make\_erm\_mtd << endl;

option.cpp:1044: LOGGER << "--gsmr-file " << expo\_file\_list << " " << outcome\_file\_list << endl;

option.cpp:1049: LOGGER << "--gsmr2-beta" << endl;

option.cpp:1054: LOGGER << "--gsmr-direction " << gsmr\_alg\_flag << endl;

option.cpp:1062: LOGGER << "--gsmr-so " << gsmr\_so\_alg << endl;

option.cpp:1065: LOGGER << "--effect-plot" << endl;

option.cpp:1069: LOGGER << "--mtcojo-file " << mtcojolist\_file << endl;

option.cpp:1073: LOGGER << "--mtcojo-bxy " << mtcojo\_bxy\_file << endl;

option.cpp:1087: LOGGER << "--ref-ld-chr " << ref\_ld\_dirt << endl;

option.cpp:1100: LOGGER << "--w-ld-chr " << w\_ld\_dirt << endl;

option.cpp:1162: LOGGER << "--gwas-adj-pc " << pcadjust\_list\_file << endl;

option.cpp:1166: LOGGER << "--gwas-adj-pc-wind " << pc\_adj\_wind\_size << endl;

option.cpp:1176: LOGGER << endl;

option.cpp:1182: LOGGER << "Warning: --grm option suppressed by the --mgrm option." << endl;

option.cpp:1186: LOGGER << "Warning: --grm-cutoff option suppressed by the --mgrm option." << endl;

option.cpp:1192: LOGGER << "Warning: --grm-adj option suppressed by the --pca option." << endl;

option.cpp:1195: LOGGER << "Warning: --dosage-compen option suppressed by the --pca option." << endl;

option.cpp:1199: LOGGER << "Warning: --gxe option is ignored because there is no --grm or --mgrm option specified." << endl;

option.cpp:1203: LOGGER << "Warning: --reml-pred-rand option is ignored because there is no --grm or --mgrm option specified." << endl;

option.cpp:1207: LOGGER << "Warning: --cvblup option is ignored because there is no --grm or --mgrm option specified." << endl;

option.cpp:1211: LOGGER << "Warning: --reml-pred-rand options is ignored because --cvblup does more than this option" << endl;

option.cpp:1220: if (!gxe\_file.empty()) LOGGER << "Warning: the option --gxe option is disabled in this analysis." << endl;

option.cpp:1221: if (!update\_sex\_file.empty()) LOGGER << "Warning: the option --update-sex option is disabled in this analysis." << endl;

option.cpp:1222: if (grm\_adj\_fac>-1.0) LOGGER << "Warning: the option --grm-adj option is disabled in this analysis." << endl;

option.cpp:1223: if (dosage\_compen>-1.0) LOGGER << "Warning: the option --dc option is disabled in this analysis." << endl;

option.cpp:1224: if (est\_fix\_eff) LOGGER << "Warning: the option --reml-est-fix option is disabled in this analysis." << endl;

option.cpp:1225: if (pred\_rand\_eff) LOGGER << "Warning: the option --reml-pred-rand option is disabled in this analysis." << endl;

option.cpp:1226: if(cv\_blup) LOGGER << "Warning: the option --cvblup option is disabled in this analysis." << endl;

option.cpp:1227: if (reml\_lrt\_flag) LOGGER << "Warning: the option --reml-lrt option is disabled in this analysis." << endl;

option.cpp:1251: if (thread\_num == 1) LOGGER << "Note: This is a multi-thread program. You could specify the number of threads by the --thread-num option to speed up the computation if there are multiple processors in your machine." << endl;

option.cpp:1252: else LOGGER << "Note: the program will be running on " << thread\_num << " threads." << endl;

option.cpp:1258: LOGGER << "Warning: --autosome option omitted. You have specified the chromosome to analysis." << endl;

option.cpp:1267: LOGGER << endl;

option.cpp:1300: LOGGER << "There are two datasets specified (in PLINK binary PED format).\nReading dataset 1 ..." << endl;

option.cpp:1387: if (extract\_chr\_start > 0) LOGGER << "Warning: the option --chr, --autosome or --nonautosome is inactive for dosage data." << endl;

pc\_adjust.cpp:485: LOGGER << "PC" << i << ", bxy = " << bxy\_hat(i-1) << endl;

sbat.cpp:19: LOGGER << "\nReading SNP association results from [" + snpAssoc\_file + "]." << endl;

sbat.cpp:37: LOGGER << "Association p-values of " << snp\_name.size() << " SNPs have been included." << endl;

sbat.cpp:70: LOGGER << "Reading physical positions of the genes from [" + gAnno\_file + "]." << endl;

sbat.cpp:81: LOGGER << "Physical positions of " << gene\_name.size() << " genes have been include." << endl;

sbat.cpp:115: LOGGER << "Mapping the physical positions of genes to SNP data (gene boundaries: " << wind / 1000 << "Kb away from UTRs) ..." << endl;

sbat.cpp:157: else LOGGER << mapped << " genes have been mapped to SNP data." << endl;

sbat.cpp:161: LOGGER << "\nRunning fastBAT analysis for genes ..." << endl;

sbat.cpp:162: if (sbat\_ld\_cutoff < 1) LOGGER << "Pruning SNPs with LD rsq cutoff = " << sbat\_ld\_cutoff\*sbat\_ld\_cutoff << endl;

sbat.cpp:222: if((i + 1) % 100 == 0 || (i + 1) == gene\_num) LOGGER << i + 1 << " of " << gene\_num << " genes.\r";

sbat.cpp:226: LOGGER << "\nSaving the results of the fastBAT analysis to [" + filename + "] ..." << endl;

sbat.cpp:239: LOGGER << "The SNP sets have been saved in file [" << rgoodsnpfile << "]." << endl;

sbat.cpp:248: LOGGER << "\nReading SNP sets from [" + snpset\_file + "]." << endl;

sbat.cpp:271: LOGGER << snp\_name.size() << " SNPs in " << snpset.size() << " sets have been included." << endl;

sbat.cpp:295: LOGGER << "\nRunning fastBAT analysis ..." << endl;

sbat.cpp:296: if (sbat\_ld\_cutoff < 1) LOGGER << "Pruning SNPs with maximum LD cutoff " << sbat\_ld\_cutoff << endl;

sbat.cpp:360: if((i + 1) % 100 == 0 || (i + 1) == set\_num) LOGGER << i + 1 << " of " << set\_num << " sets.\r";

sbat.cpp:364: LOGGER << "\nSaving the results of the fastBAT analysis to [" + filename + "] ..." << endl;

sbat.cpp:375: LOGGER << "The SNP sets have been saved in file [" << rgoodsnpfile << "]." << endl;

sbat.cpp:395: LOGGER << "\nRunning fastBAT analysis at genomic segments with a length of " << seg\_size/1000 << "Kb ..." << endl;

sbat.cpp:396: if (sbat\_ld\_cutoff < 1) LOGGER << "Pruning SNPs with maximum LD cutoff " << sbat\_ld\_cutoff << endl;

sbat.cpp:456: if((i + 1) % 100 == 0 || (i + 1) == set\_num) LOGGER << i + 1 << " of " << set\_num << " sets.\r";

sbat.cpp:460: LOGGER << "\nSaving the results of the segment-based fastBAT analysis to [" + filename + "] ..." << endl;

sbat.cpp:473: LOGGER << "The SNP sets have been saved in file [" << rgoodsnpfile << "]." << endl;