The results below are generated from an R script.

```
# Load results for 15 traits for 266K SNPs
setwd("/home/lima/Sodbo/OmicABEL_paper/final_cut/tables/")
load("3_methods_15_traits_266K_SNPs.RData")

# List of objects
ls()
```

```
## [1] "EMMAX_15traits"    "GWFGLS_15traits"   "OMICABEL_15traits"
```

```
# Head of table containing EMMAX results
head(EMMAX_15traits)
```

```
##                         Chisq    P-value    beta_SNP     se_SNP
## rs3737728_pcp_47  4.36218563 0.03674513 -0.12006189 0.05748481
## rs6687776_pcp_47  0.35498937 0.55130227  0.04012389 0.06734346
## rs12726255_pcp_47 0.01751924 0.89469933  0.00902336 0.06817272
## rs4970362_pcp_47  0.18559329 0.66660987  0.02290982 0.05317905
## rs9660710_pcp_47  0.01372266 0.90674612 -0.01143067 0.09757811
## rs4970420_pcp_47  6.19236104 0.01283029 -0.15935771 0.06403906
```

```
# Create vector of differences between GWFGLS and OmicABEL estimation of
# standart error of SNPs. Using formula (a-b) / b
gwfglsVSomica = abs(GWFGLS_15traits[,"se_SNP"]-OMICABEL_15traits[,"se_SNP"])/
        OMICABEL_15traits[,"se_SNP"]

# Brief summary of differences
summary(gwfglsVSomica)
```

```
##      Min.   1st Qu.    Median      Mean   3rd Qu.      Max.
## 0.0000000 0.0006751 0.0010600 0.0009720 0.0012400 0.1932000
```

```
# Create vector of differences between EMMAX and OmicABEL estimation of
# standart error of SNPs. Using formula (a-b) / b
emmaxVSomica = abs(EMMAX_15traits[,"se_SNP"]-OMICABEL_15traits[,"se_SNP"])/
        OMICABEL_15traits[,"se_SNP"]

# Brief summary of differences
summary(emmaxVSomica)
```

```
##      Min.   1st Qu.    Median      Mean   3rd Qu.      Max.
## 0.0000000 0.0005470 0.0007900 0.0007447 0.0009633 0.1819000
```

```
# Select SNPs for which differences between standart errors are more than 2%
TwoProcDiffSNPs = cbind(OMICABEL_15traits[which(gwfglsVSomica>0.02),2:4],
        diff = gwfglsVSomica[which(gwfglsVSomica>0.02)])

# Print head of TwoProcDiffSNPs
head(TwoProcDiffSNPs)
```

```
##                       P_value   beta_SNP     se_SNP       diff
## rs509360_pcp_25  3.307857e-16  0.4219920 0.05170498 0.04236777
## rs102275_pcp_25  4.336341e-58 -0.8621287 0.05365793 0.18074562
## rs412334_pcp_25  2.314809e-12  0.5587760 0.07966498 0.03076672
## rs174546_pcp_25  1.555490e-61 -0.8925267 0.05392344 0.19322518
## rs174556_pcp_25  2.242274e-53 -0.8894322 0.05783179 0.16397953
## rs968567_pcp_25  2.368272e-14 -0.5830343 0.07642476 0.03674679
```

```r
# Sort DwaProcRaz by differences between standart errors. You can see that
# differences between se_SNP estimdated by OmicABEL and GWFGLS are growing up
# with increasing of Chi-square and beta_SNP.
TwoProcDiffSNPs[order((TwoProcDiffSNPs[,"diff"])),]
```

```
##                                    P_value   beta_SNP     se_SNP       diff
## rs968567_pc_38                6.798219e-09 -0.4391189 0.07576456 0.02048700
## rs12889954_spm_1              5.872073e-09  0.4219019 0.07248725 0.02067360
## rs12221836_pcp_25             5.404342e-09 -0.5351502 0.09172611 0.02077955
## rs1466448_spmp_8              4.557403e-09 -0.3712051 0.06331772 0.02099699
## rs968567_spmp_18_AND_pcp_25   4.341861e-09  0.4517291 0.07694754 0.02105884
## rs1466448_spm_3_AND_spm_8     4.000476e-09  0.3743031 0.06361180 0.02116336
## rs174611_pc_38                2.288916e-09 -0.3294776 0.05513485 0.02187657
## rs12889954_spm_1_AND_spmp_18 4.439378e-10  0.4538860 0.07276446 0.02397772
## rs509360_spmp_18_AND_pcp_25   3.545796e-10 -0.3268071 0.05209896 0.02426633
## rs174611_spmp_18_AND_pcp_25   3.312160e-10  0.3518054 0.05598951 0.02435395
## rs509360_pc_38                3.283283e-10  0.3222979 0.05128231 0.02436518
## rs174450_spmp_18_AND_pcp_25   2.404998e-10 -0.3314577 0.05233852 0.02476523
## rs174449_spmp_18_AND_pcp_25   9.392995e-11  0.3414013 0.05271457 0.02597537
## rs2851682_pc_38               2.327351e-12 -0.5561987 0.07930610 0.03075979
## rs412334_pcp_25               2.314809e-12  0.5587760 0.07966498 0.03076672
## rs2851682_spmp_18_AND_pcp_25 3.700730e-13  0.5853170 0.08055472 0.03315285
## rs4902242_spmp_1              3.078635e-13  0.5337301 0.07320488 0.03339286
## rs174449_pcp_25               2.819387e-13 -0.3824866 0.05237569 0.03350758
## rs174450_pcp_25               1.652445e-13  0.3834552 0.05199907 0.03420491
## rs4902242_spm_1               1.105094e-13  0.5443100 0.07328115 0.03473061
## rs968567_pcp_25               2.368272e-14 -0.5830343 0.07642476 0.03674679
## rs4902242_spm_1_AND_spmp_18   1.270965e-14  0.5666248 0.07350449 0.03756316
## rs174570_pc_38                1.121222e-14 -0.5342898 0.06916647 0.03772775
## rs174570_spmp_18_AND_pcp_25   3.634845e-15  0.5525909 0.07024238 0.03920794
## rs2072114_pc_38               1.378325e-15 -0.5314611 0.06653759 0.04048462
## rs174611_pcp_25               6.787587e-16 -0.4491140 0.05562280 0.04141869
## rs509360_pcp_25               3.307857e-16  0.4219920 0.05170498 0.04236777
## rs2072114_spmp_18_AND_pcp_25 2.992127e-19  0.6060835 0.06757537 0.05168423
## rs2851682_pcp_25              1.438392e-21 -0.7629675 0.07998172 0.05885507
## rs174570_pcp_25               1.745761e-23 -0.6967911 0.06977304 0.06482993
## rs174556_pc_38                4.900701e-29 -0.6410568 0.05732068 0.08238955
## rs2072114_pcp_25              5.699808e-30 -0.7633443 0.06711902 0.08538118
## rs102275_pc_38                2.517949e-33 -0.6397595 0.05318707 0.09620988
## rs1535_pc_38                  2.448529e-34 -0.6592433 0.05395056 0.09950359
## rs174556_spmp_18_AND_pcp_25   7.930555e-35  0.7165727 0.05820723 0.10110172
## rs174546_pc_38                7.587002e-35 -0.6582190 0.05345157 0.10116473
## rs102275_spmp_18_AND_pcp_25   3.525456e-37  0.6881317 0.05401181 0.10882063
## rs174546_spmp_18_AND_pcp_25   2.064136e-38  0.7034822 0.05428126 0.11289388
## rs1535_spmp_18_AND_pcp_25     1.035820e-38  0.7128190 0.05477865 0.11388608
## rs174556_pcp_25               2.242274e-53 -0.8894322 0.05783179 0.16397953
## rs102275_pcp_25               4.336341e-58 -0.8621287 0.05365793 0.18074562
## rs1535_pcp_25                 1.153723e-60 -0.8944834 0.05443985 0.19005464
## rs174546_pcp_25               1.555490e-61 -0.8925267 0.05392344 0.19322518
```

```r
# Let's check this hypothethis by testing linear regresion of
# differences against Chisq and compare results with testing against
# se_SNP and beta_SNP
```

```r
# Linear regression of differences against Chisq
# We can see that there is strong effect of Chisq on se_differences.
# As Chisq is squared (beta_SNP / se_SNP) we can conclude that se_differences
# are growing up with increasing of ratio between beta_SNP and se_SNP.
summary(lm(gwfglsVSomica ~ GWFGLS_15traits[,"Chisq"]))
```

```
##
## Call:
## lm(formula = gwfglsVSomica ~ GWFGLS_15traits[, "Chisq"])
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.001110 -0.000352  0.000147  0.000385  0.134344
##
## Coefficients:
##                              Estimate Std. Error t value Pr(>|t|)
## (Intercept)                 8.339e-04  3.335e-07  2500.4   <2e-16 ***
## GWFGLS_15traits[, "Chisq"] 1.379e-04  1.846e-07   747.2   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0005554 on 4003168 degrees of freedom
## Multiple R-squared:  0.1224,Adjusted R-squared:  0.1224
## F-statistic: 5.582e+05 on 1 and 4003168 DF,  p-value: < 2.2e-16
```

```r
# This is actually what we can see on the plot of minus log10 of p.value
# estimdated by OmicABEL against estimated by GWFGLS
# Let's plot it

# Temporary function to plot y=x line
#my_line <- function(x,y,...){
#    points(x,y,...)
#    abline(a = 0,b = 1,...)
#}
# Plotting minus log10 of pvalue OmicABEL vs GWFGLS
#pairs(cbind(OmicABEL = (-log10(OMICABEL_15traits$P_value)),
# GWFGLS = (-log10(GWFGLS_15traits[,"P-value"]))), lower.panel = my_line,
# upper.panel=my_line,cex.labels=4.0,cex=1.5,cex.main=2.0,cex.axis=2.5,
# )

# What about effect of
# Linear regression of differences against beta_SNP
summary(lm(gwfglsVSomica ~ GWFGLS_15traits[,"beta_SNP"]))
```

```
##
## Call:
## lm(formula = gwfglsVSomica ~ GWFGLS_15traits[, "beta_SNP"])
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.000978 -0.000297  0.000088  0.000268  0.192217
##
## Coefficients:
##                               Estimate Std. Error  t value Pr(>|t|)
## (Intercept)                  9.720e-04  2.963e-07 3280.351   <2e-16 ***
```

```
## GWFGLS_15traits[, "beta_SNP"] -4.003e-05  4.435e-06   -9.027   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0005929 on 4003168 degrees of freedom
## Multiple R-squared:  2.036e-05,Adjusted R-squared:  2.011e-05
## F-statistic: 81.49 on 1 and 4003168 DF,  p-value: < 2.2e-16

# Linear regression of differences against se_SNP
summary(lm(gwfglsVSomica ~ GWFGLS_15traits[,"se_SNP"]))

##
## Call:
## lm(formula = gwfglsVSomica ~ GWFGLS_15traits[, "se_SNP"])
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.000973 -0.000297  0.000088  0.000268  0.192252
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)                  9.764e-04  1.301e-06 750.681  < 2e-16 ***
## GWFGLS_15traits[, "se_SNP"] -6.674e-05  1.945e-05  -3.431 0.000601 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0005929 on 4003168 degrees of freedom
## Multiple R-squared:  2.941e-06,Adjusted R-squared:  2.691e-06
## F-statistic: 11.77 on 1 and 4003168 DF,  p-value: 0.000601
```

The R session information (including the OS info, R version and all packages used):

```
sessionInfo()

## R version 3.2.2 (2015-08-14)
## Platform: x86_64-pc-linux-gnu (64-bit)
## Running under: CentOS Linux 7 (Core)
##
## locale:
##  [1] LC_CTYPE=en_US.UTF-8       LC_NUMERIC=C               LC_TIME=en_US.UTF-8
##  [4] LC_COLLATE=en_US.UTF-8     LC_MONETARY=en_US.UTF-8    LC_MESSAGES=en_US.UTF-8
##  [7] LC_PAPER=en_US.UTF-8       LC_NAME=C                  LC_ADDRESS=C
## [10] LC_TELEPHONE=C             LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
## [1] stats     graphics  grDevices utils     datasets  methods   base
##
## other attached packages:
## [1] knitr_1.11
##
## loaded via a namespace (and not attached):
## [1] magrittr_1.5  formatR_1.2.1 tools_3.2.2   stringi_0.5-5 highr_0.5.1   stringr_1.0.0
## [7] evaluate_0.8

Sys.time()
```

```
## [1] "2015-10-07 04:24:06 NOVT"
```