Define y=log10(TReCASE p-value)-log10(RASQUAL p-value)

where I first trimmed p-values replacing p-values<1e-20 with 1e-20

(y>0 implies TReCASE p-value less significant than RASQUAL p-value)

y ~ AlleleFrequency + HardyWeinbergEquilibriumLog10Chi2 + DeltaError + PhiBias + #fSNP + #tSNP + log10(NB OD) + log10(BB OD) + MedianPermPval + RasqTrecRat

Estimate Std. Error t value Pr(>|t|)

(Intercept) -1.364e+00 2.505e-01 -5.444 5.28e-08 \*\*\*

AF 7.959e-03 1.184e-01 0.067 0.94640

HWE -9.088e-02 2.882e-02 -3.154 0.00162 \*\*

DErr -2.417e+01 1.383e+01 -1.747 0.08064 .

PhiBeta 1.382e+01 1.176e+00 11.750 < 2e-16 \*\*\*

#fSNP 6.501e-02 4.193e-03 15.506 < 2e-16 \*\*\*

#tSNP 4.484e-04 7.512e-05 5.969 2.44e-09 \*\*\*

log10(NB OD) -1.126e+00 6.848e-02 -16.437 < 2e-16 \*\*\*

log10(BB OD) 7.857e-01 5.346e-02 14.697 < 2e-16 \*\*\*

medPermPval -2.461e+00 3.068e-01 -8.022 1.12e-15 \*\*\*

RasqTrecaseRatio 3.371e-01 3.380e-02 9.972 < 2e-16 \*\*\*

Multiple R-squared: 0.08328, Adjusted R-squared: 0.08264

We can see that with stronger TReCASE p-value are significantly associated with:

- higher NB OD

- higher Chi2 test for Hardy Weinberg Equilibrium,

Stronger RASQUAL p-value are significantly associated with:

- higher BB OD

- more significant permuted p-value

- number fSNPs

- number of test SNPs

- the higher reference bias

- higher number of allele-specific reads produced using SNP-level counts (as opposed to number of allele-specific reads produced using gene-level counts)

Anova Table (Type II tests)

Sum Sq Df F value Pr(>F)

AF 0 1 0.0045 0.946396

HWE 119 1 9.9451 0.001616 \*\*

DErr 37 1 3.0523 0.080642 .

PhiBeta 1654 1 138.0648 < 2.2e-16 \*\*\*

#fSNP 2881 1 240.4485 < 2.2e-16 \*\*\*

#tSNP 427 1 35.6332 2.438e-09 \*\*\*

log10(NB OD) 3238 1 270.1876 < 2.2e-16 \*\*\*

log10(BB OD) 2588 1 215.9974 < 2.2e-16 \*\*\*

medPermPval 771 1 64.3587 1.117e-15 \*\*\*

RasqTrecaseRatio 1192 1 99.4420 < 2.2e-16 \*\*\*

Residuals 171607 14321

ANOVA (type 1):

Df Sum Sq Mean Sq F value Pr(>F)

AF 1 2 2.2 0.1852 0.66697

HWE 1 238 238.3 19.8837 8.292e-06 \*\*\*

DErr 1 96 96.1 8.0212 0.00463 \*\*

PhiBeta 1 1469 1469.1 122.5967 < 2.2e-16 \*\*\*

#fSNP 1 6815 6814.8 568.7112 < 2.2e-16 \*\*\*

#tSNP 1 223 223.0 18.6082 1.616e-05 \*\*\*

log10(NB OD) 1 2506 2506.3 209.1594 < 2.2e-16 \*\*\*

log10(BB OD) 1 2191 2191.0 182.8470 < 2.2e-16 \*\*\*

medPermPval 1 858 858.0 71.6033 < 2.2e-16 \*\*\*

RasqTrecaseRatio 1 1192 1191.6 99.4420 < 2.2e-16 \*\*\*

Residuals 14321 171607 12.0

