

Allelic Imbalance in SZ (Supplemental Material 2)

This is a document containing supplemental figures for the “Comparison of Quantitative Trait Loci Methods: Total Expression and Allelic Imbalance Method in Brain RNA-seq” manuscript. On each page are each gene-snp pair in table 1 in the main manuscript additionally described by graphs and auxillary tests. **A)** Similar to the plot 1B, which is described in the main manuscript. **B)** A regression test of the reference fraction for each genotype group to prove that there is no underlying skew in the distribution of ref/alt alleles, which would bias the aeQTL result. As can be seen in some graphs there is an underlying mapbias where the reference allele has a higher fraction in all genotype groups, but important is that the bias is equally present in each group, and therefore not affecting the aeQTL analysis. **C)** Illustration of the distribution between homozygotes and heterozygotes together with a p-value for a one sided variance test as used by Fogarthy et al. The idea is that the heterozygote group should have a higher variance as it is assumed that all fractions from the homozygote genotype groups are supposed to lie close to 0.50 and the heterozygote group to have a deviation from 0.50 and thereby create a higher variance in the heterozygote group. This approach was largely unsuccessful, as no test showed significance, even though we know that we have several aeQTLs present from our regression analysis. **D)** A QQ-plot for each genotype group’s parent-1 allele fraction value to its theoretical normal distribution quantiles. The grey shading indicates the confidence bands at alpha=0.05. **E)** A residuals versus fitted values plot based on the aeQTL test on parent-1 allele fraction, to inspect heteroscedasticity/homoscedasticity.

AS3MT,BORCS7,BORCS7-ASMT – rs11191419

DLPFC

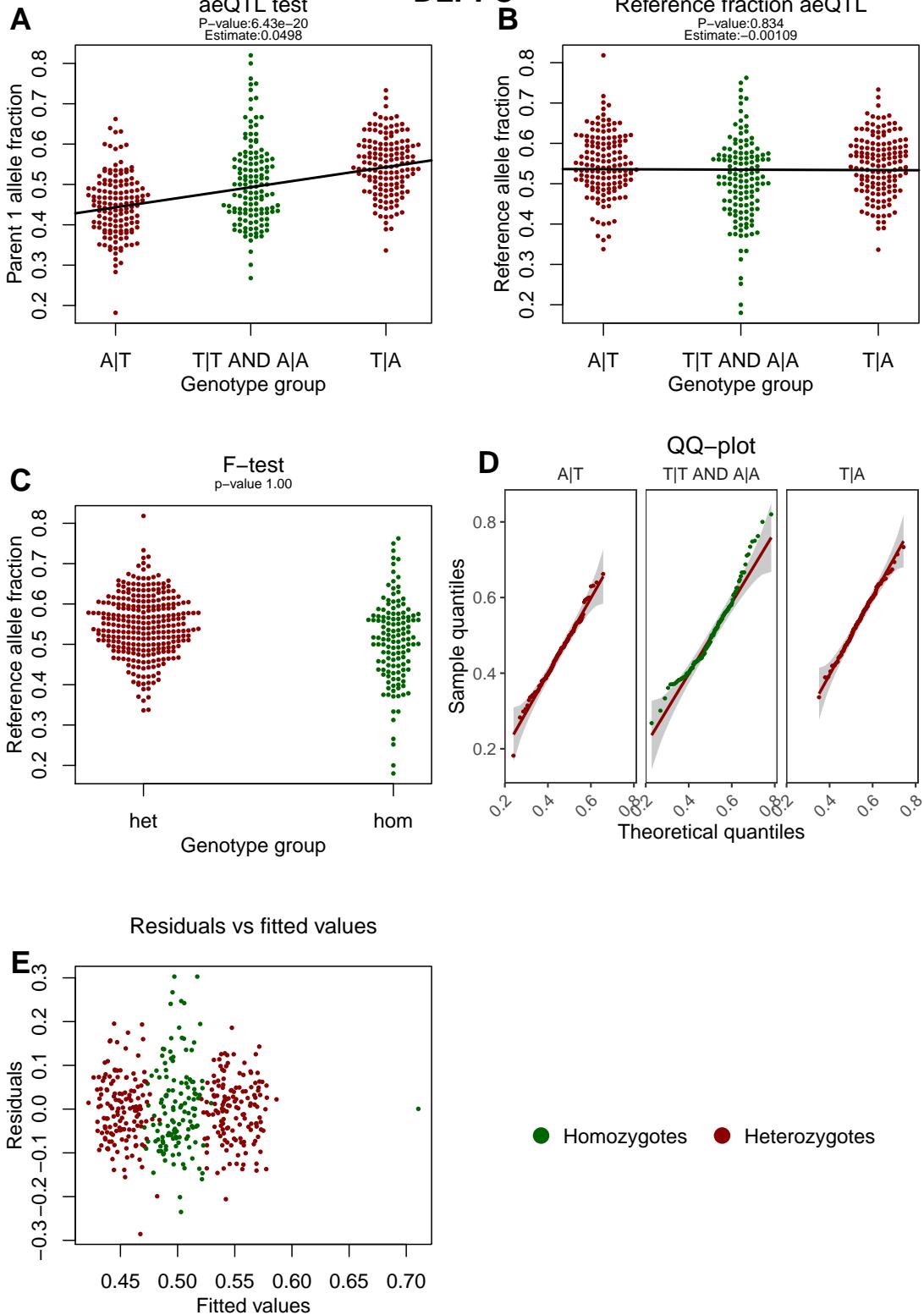


Figure S2–1: More details in the header of this document.

APOPT1 – rs12887734

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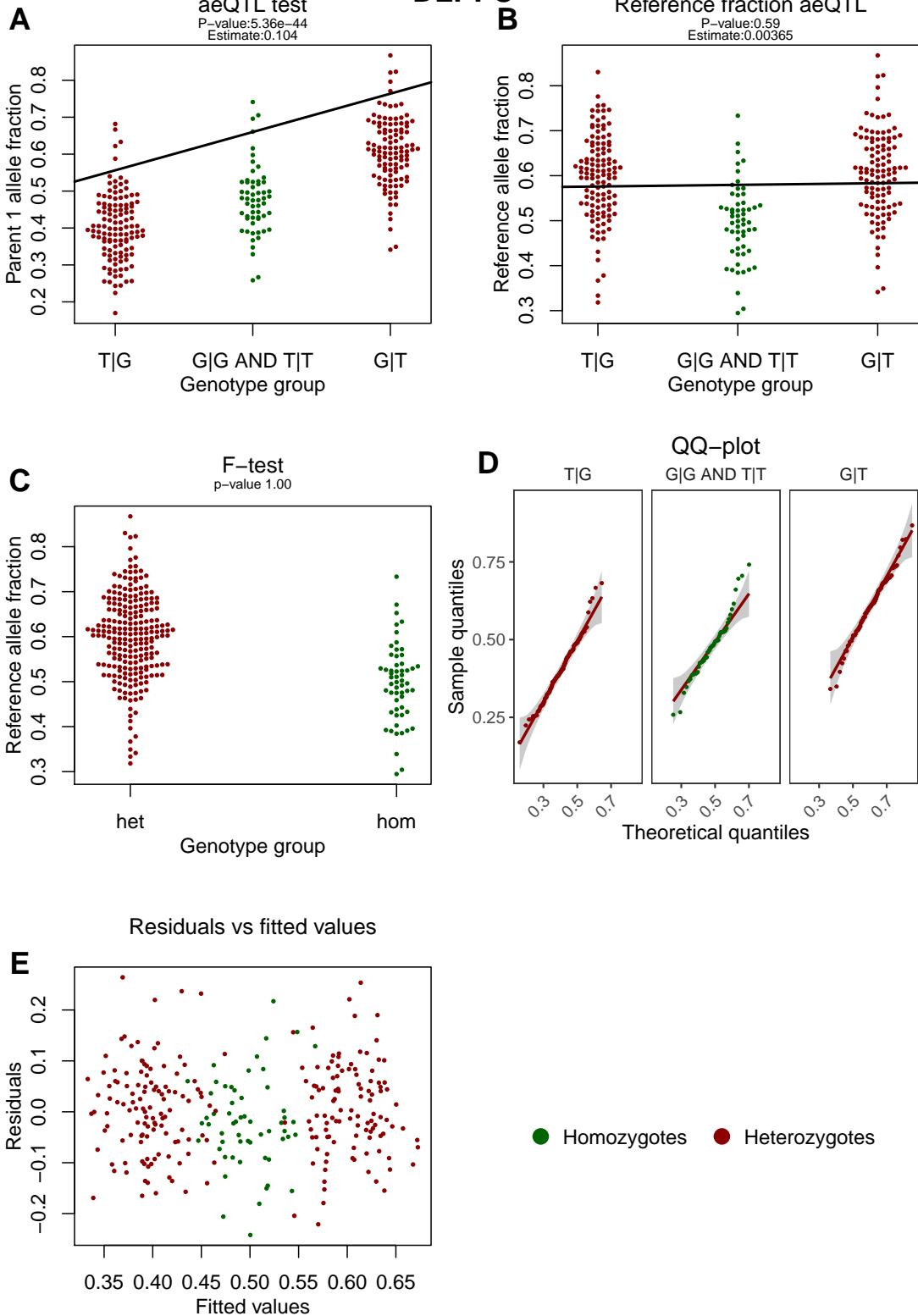


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ZMAT2 - chr5_140143664_I

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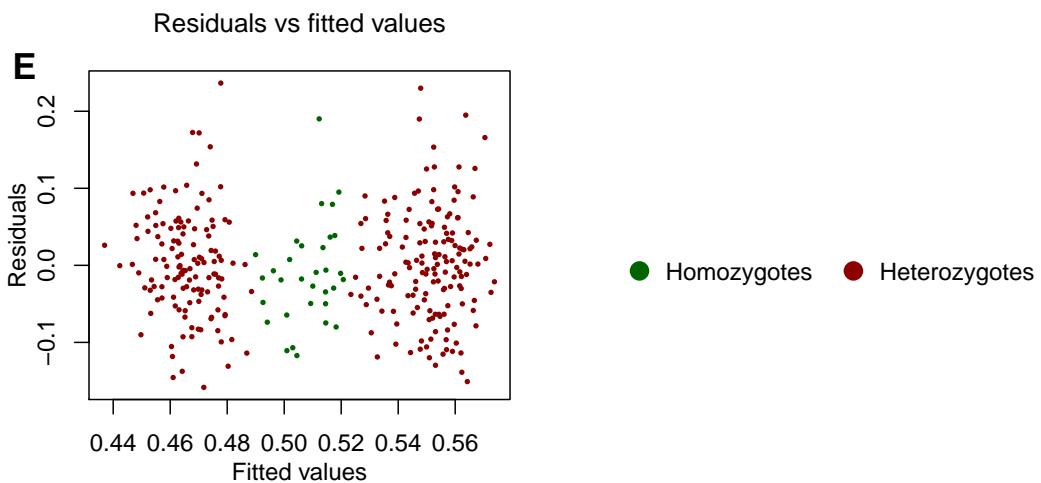
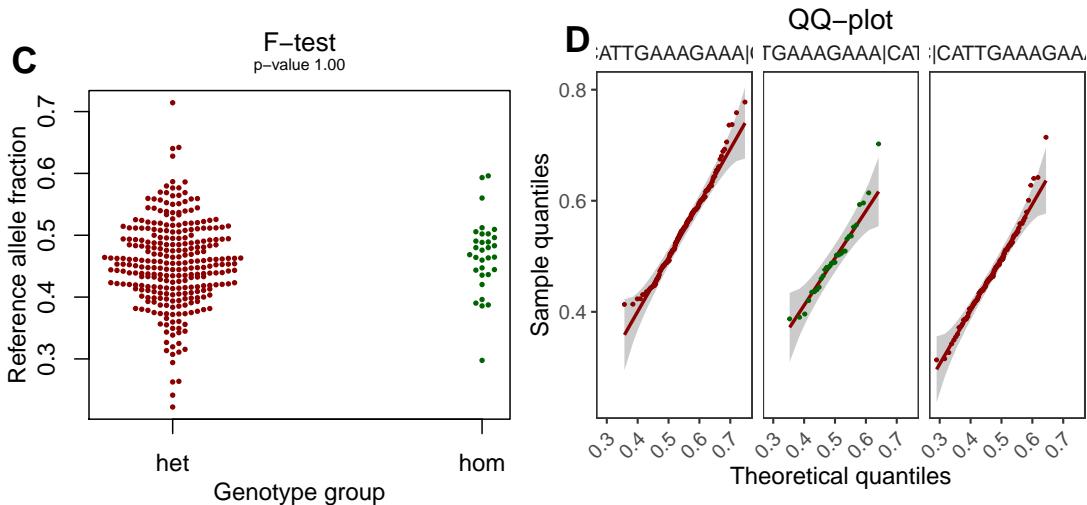
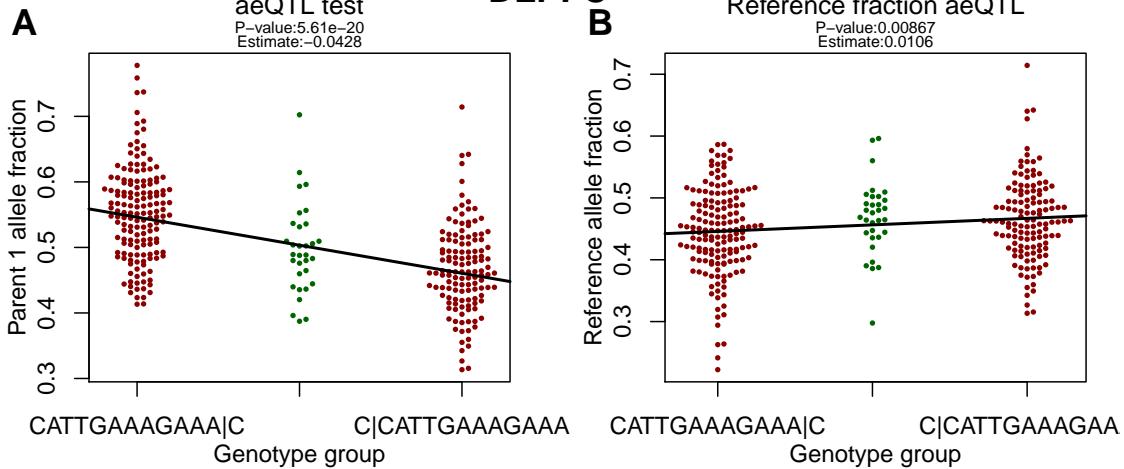


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HAPLN4 – rs2905426

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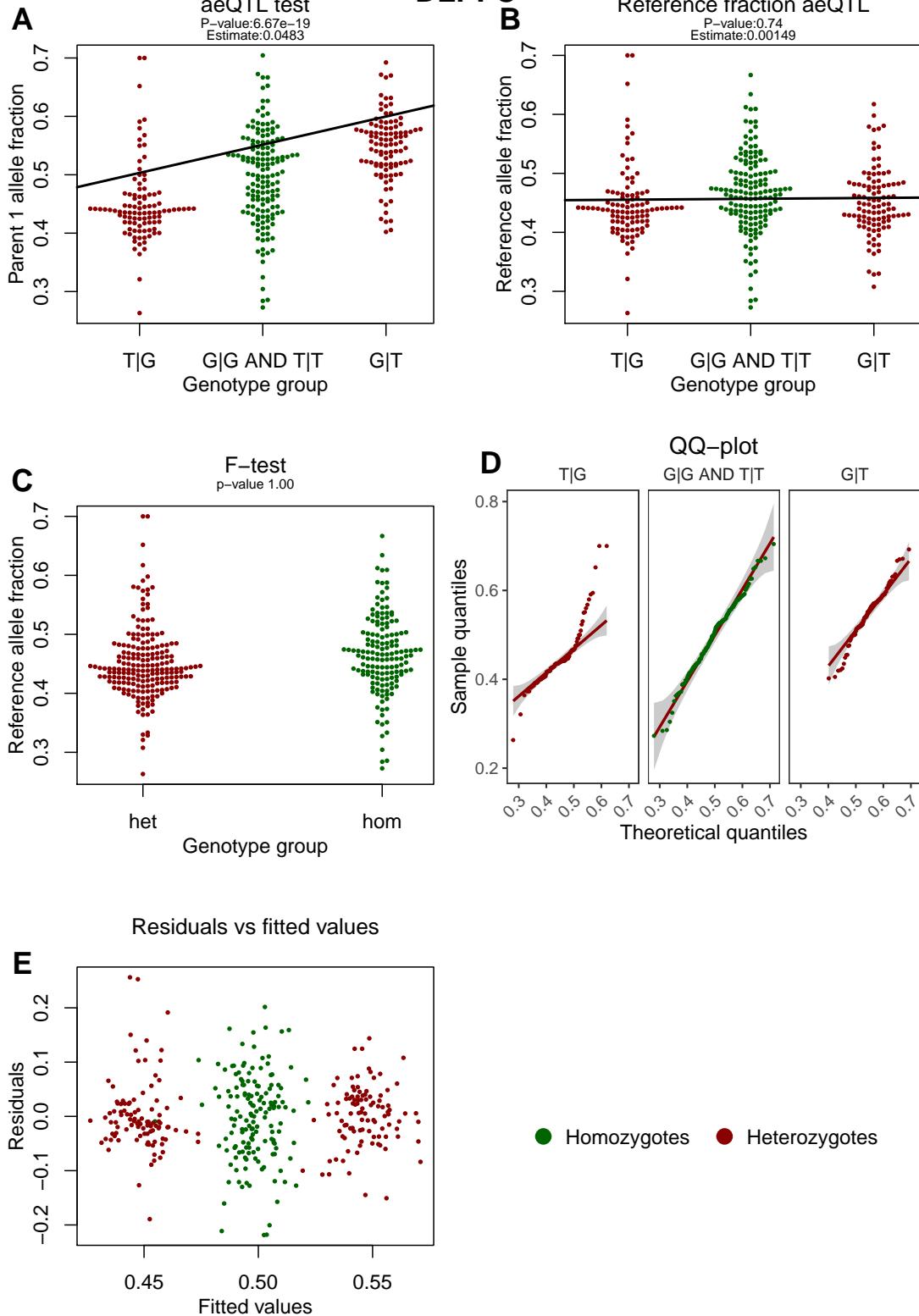


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CD46 – rs7523273

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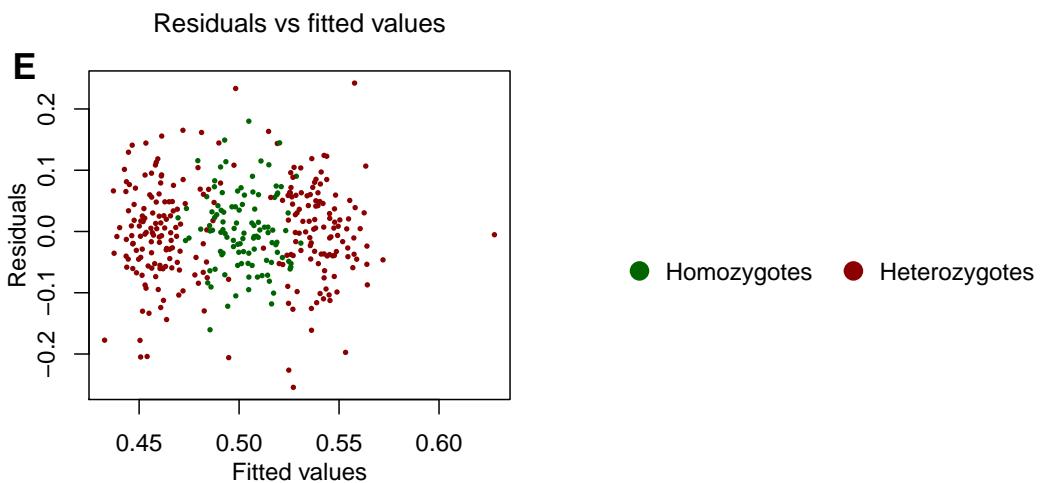
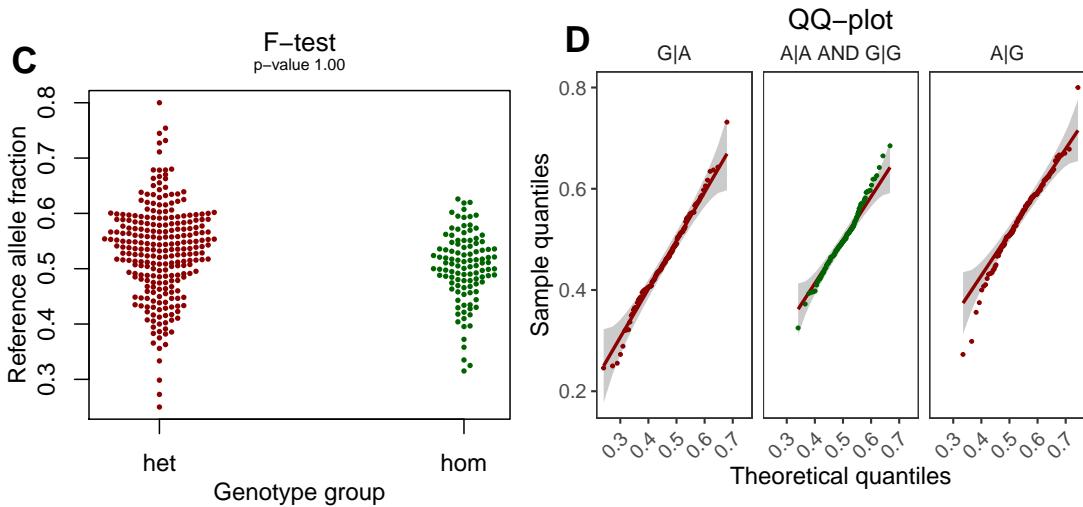
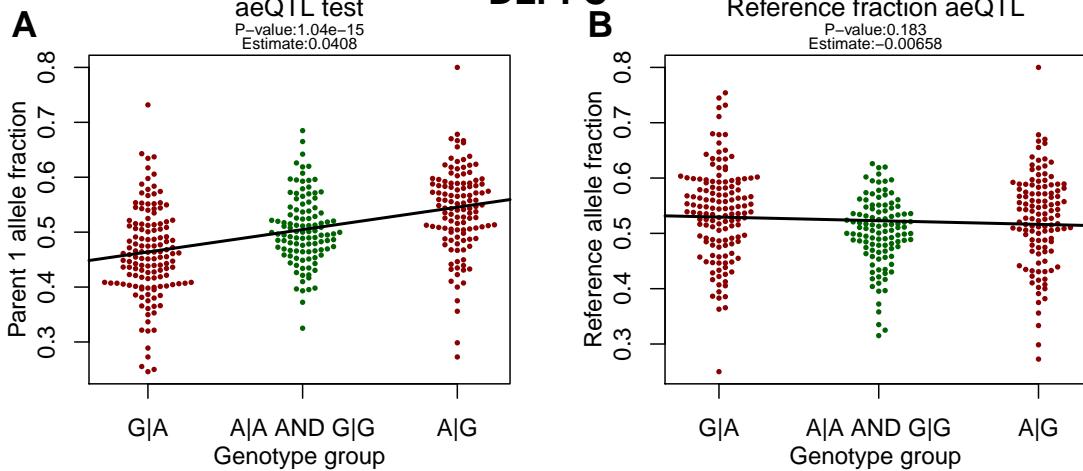


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BRINP2 – rs6670165

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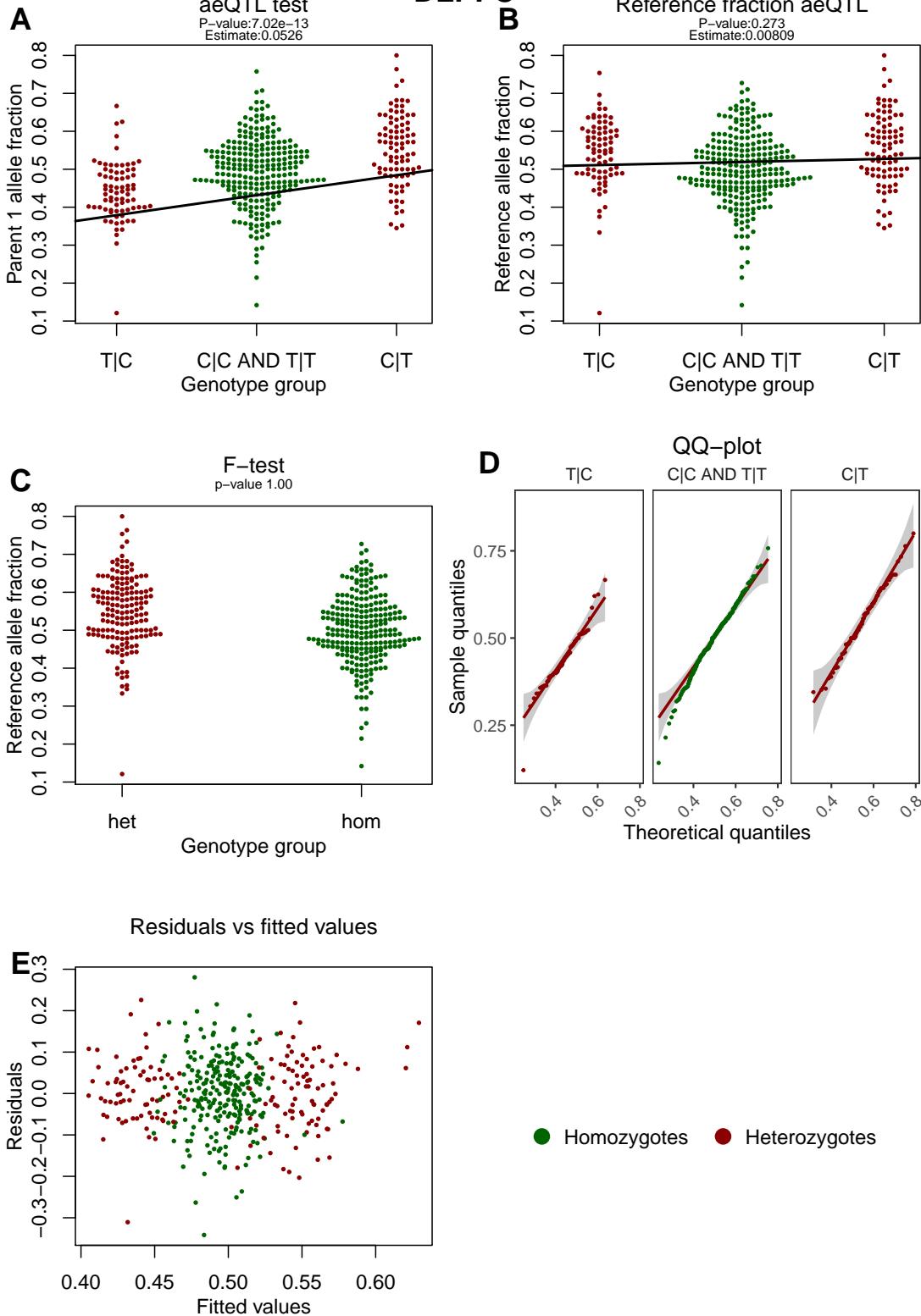


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TOM1L2 – rs8082590

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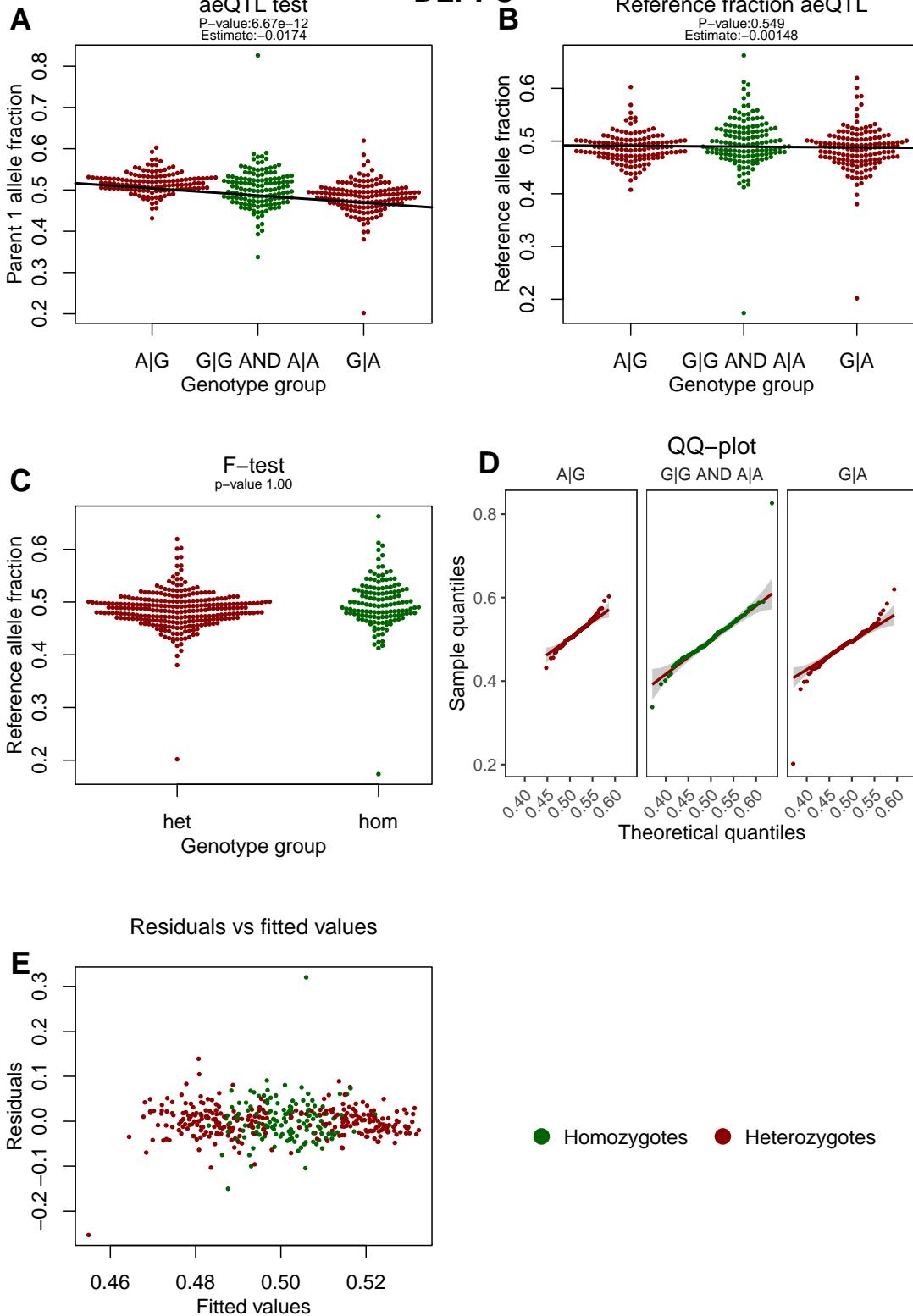


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FURIN – rs4702

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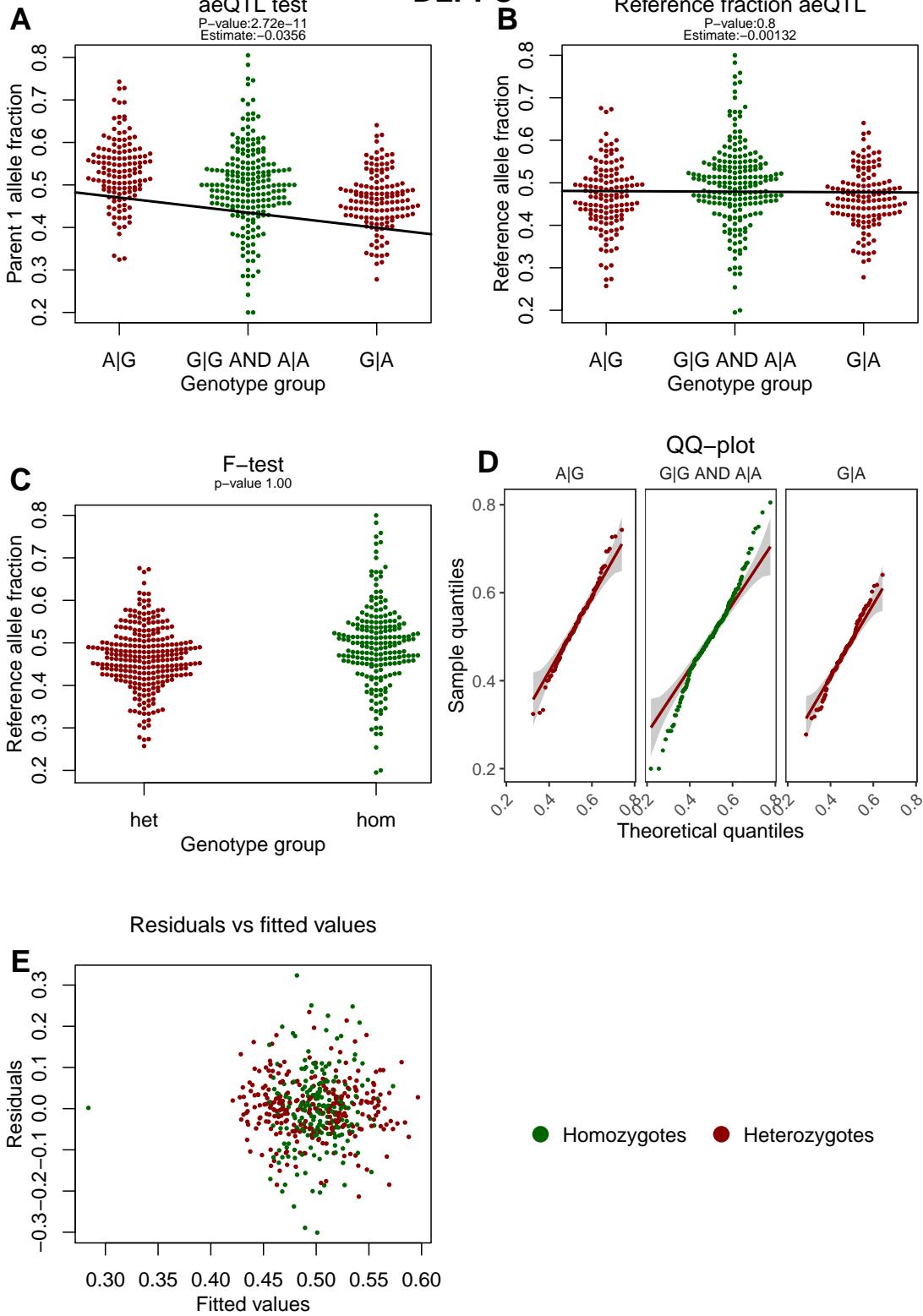


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NDUFA2 – chr5_140143664_I

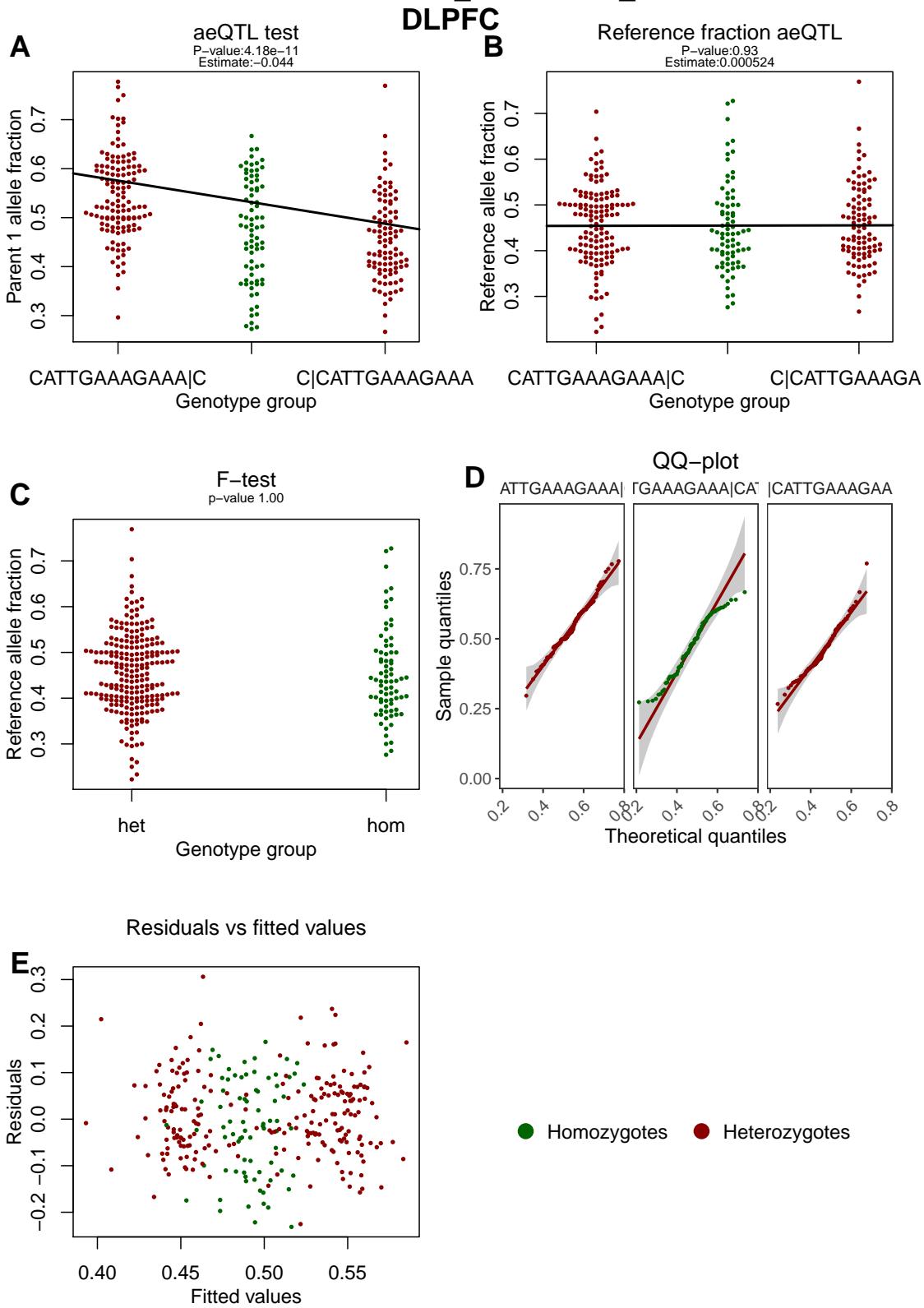


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ANP32E – rs140505938

DLPFC

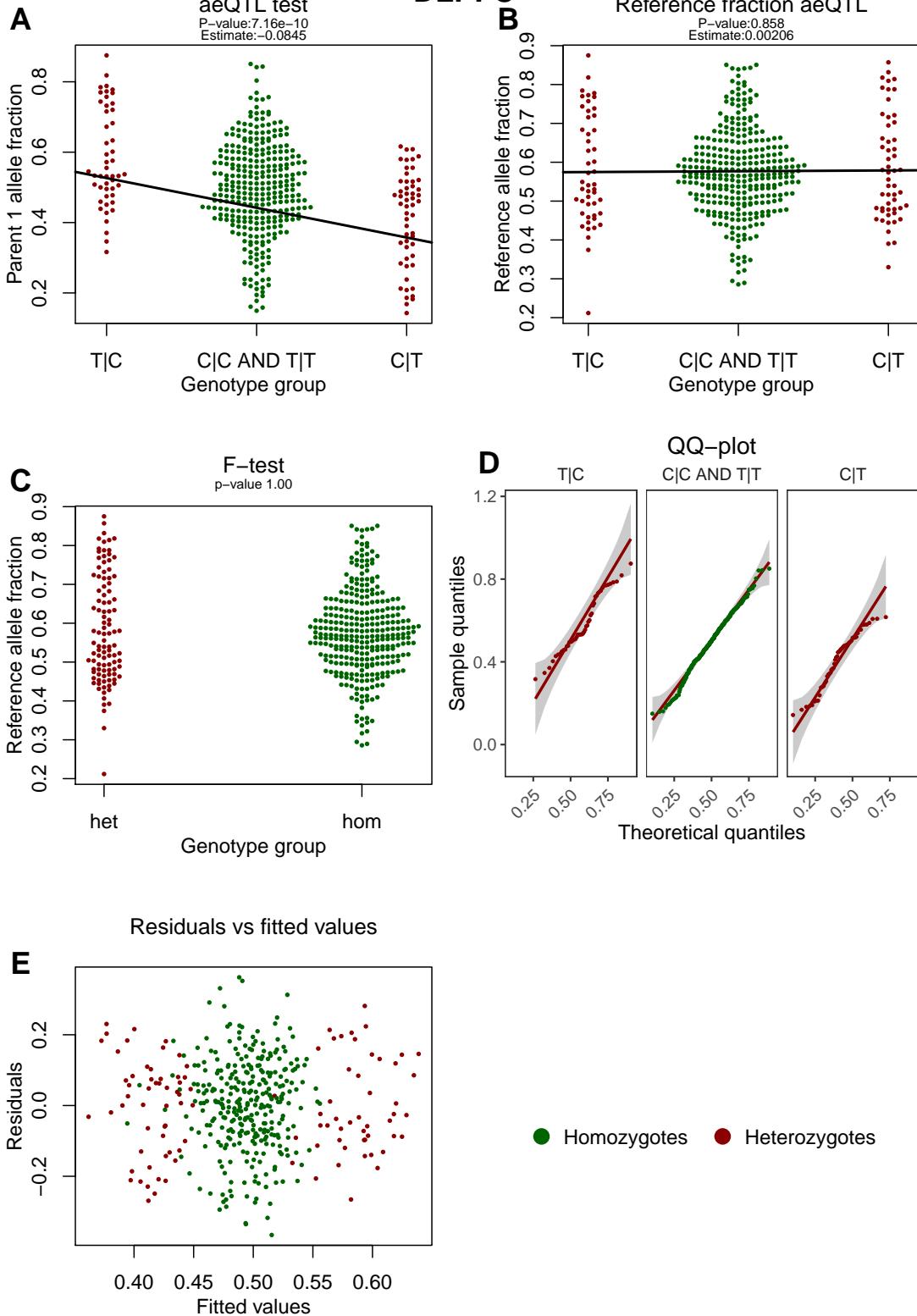


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SPCS1 – rs2535627

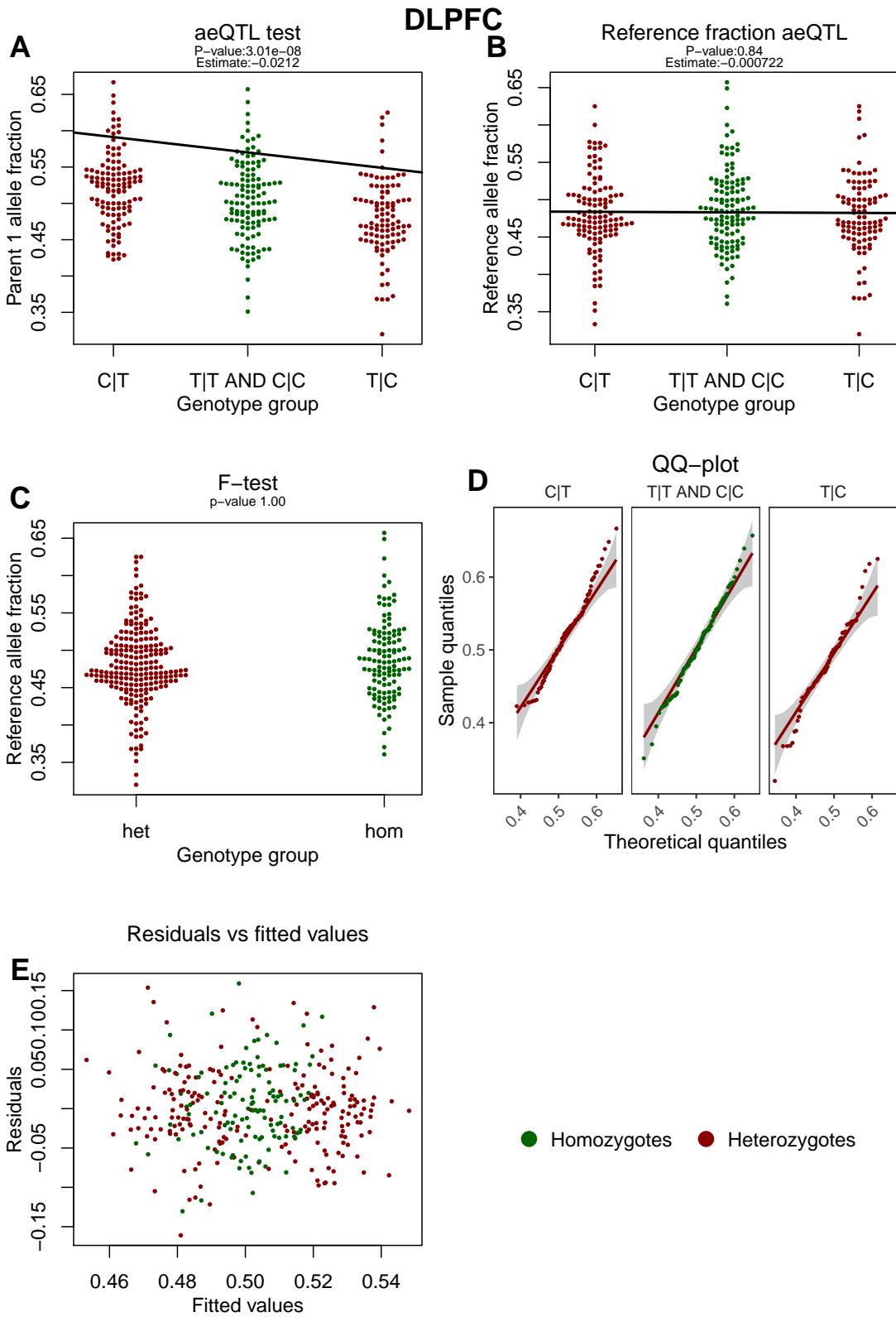


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SNX19 – rs10791097

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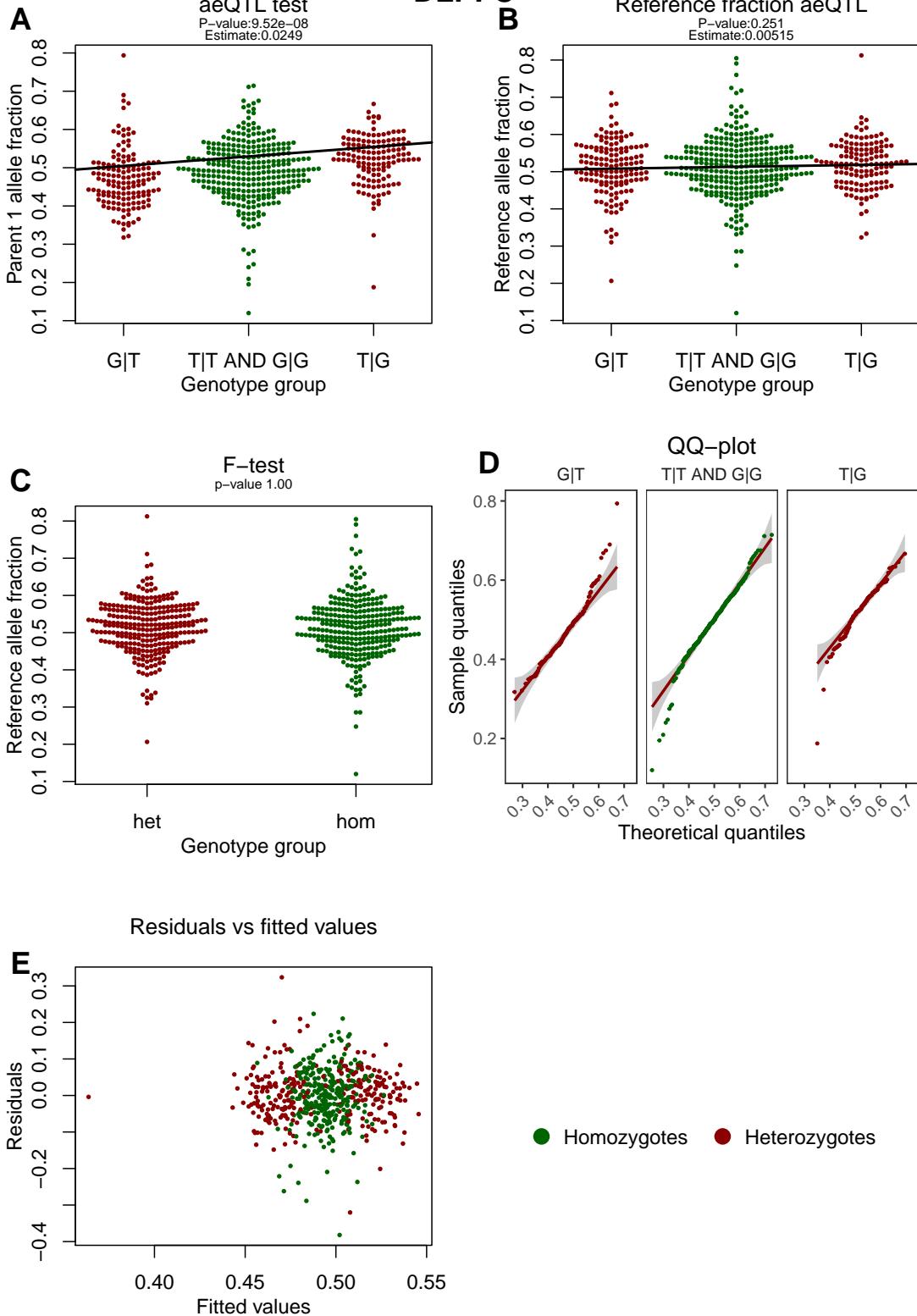


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FAM57B – rs12691307

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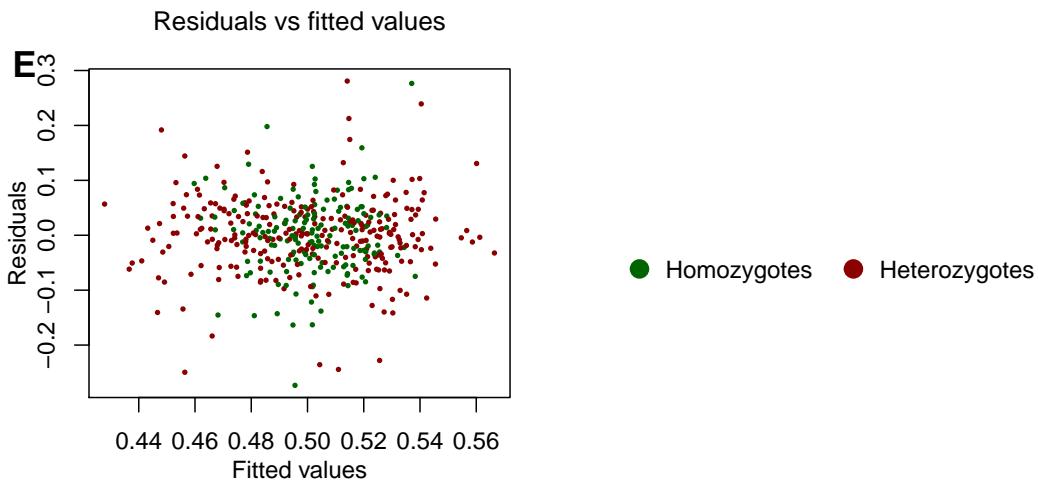
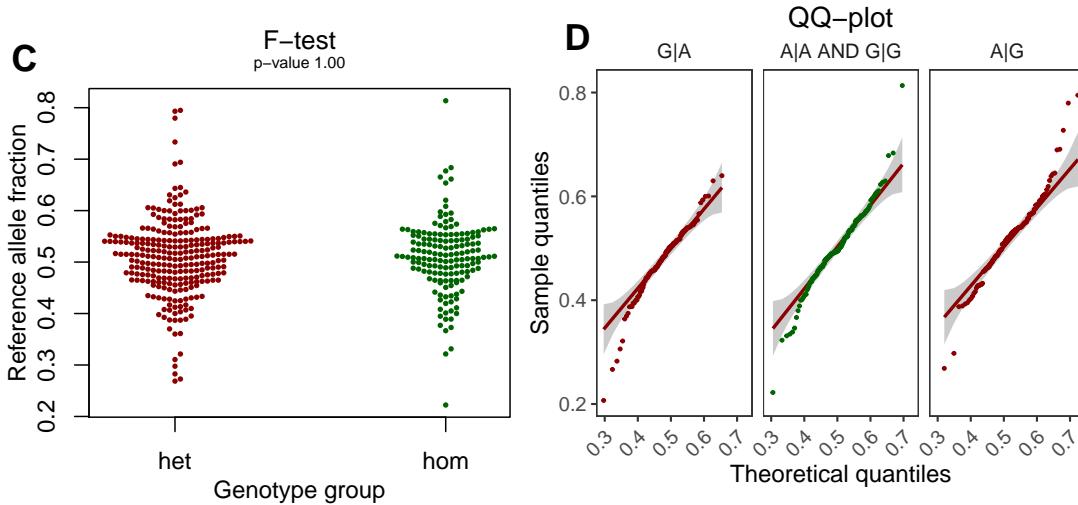
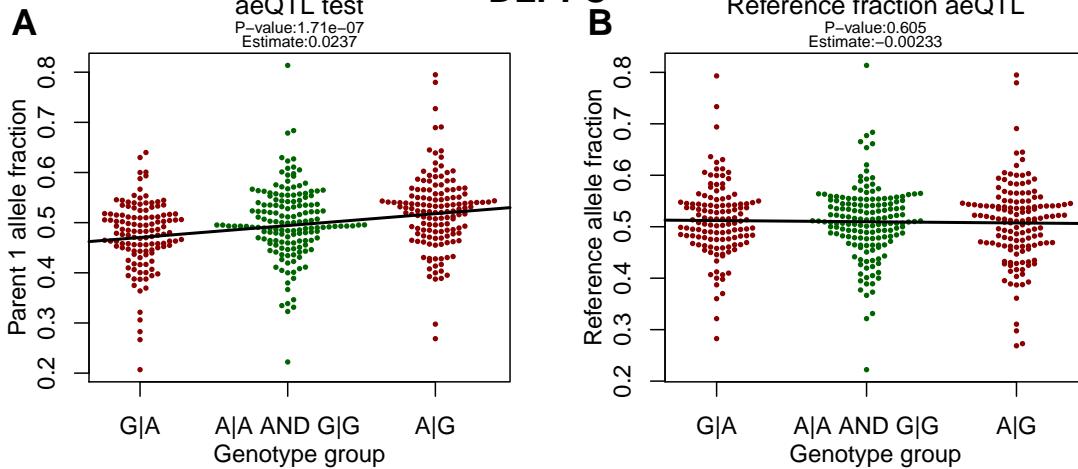


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CKB – rs12887734

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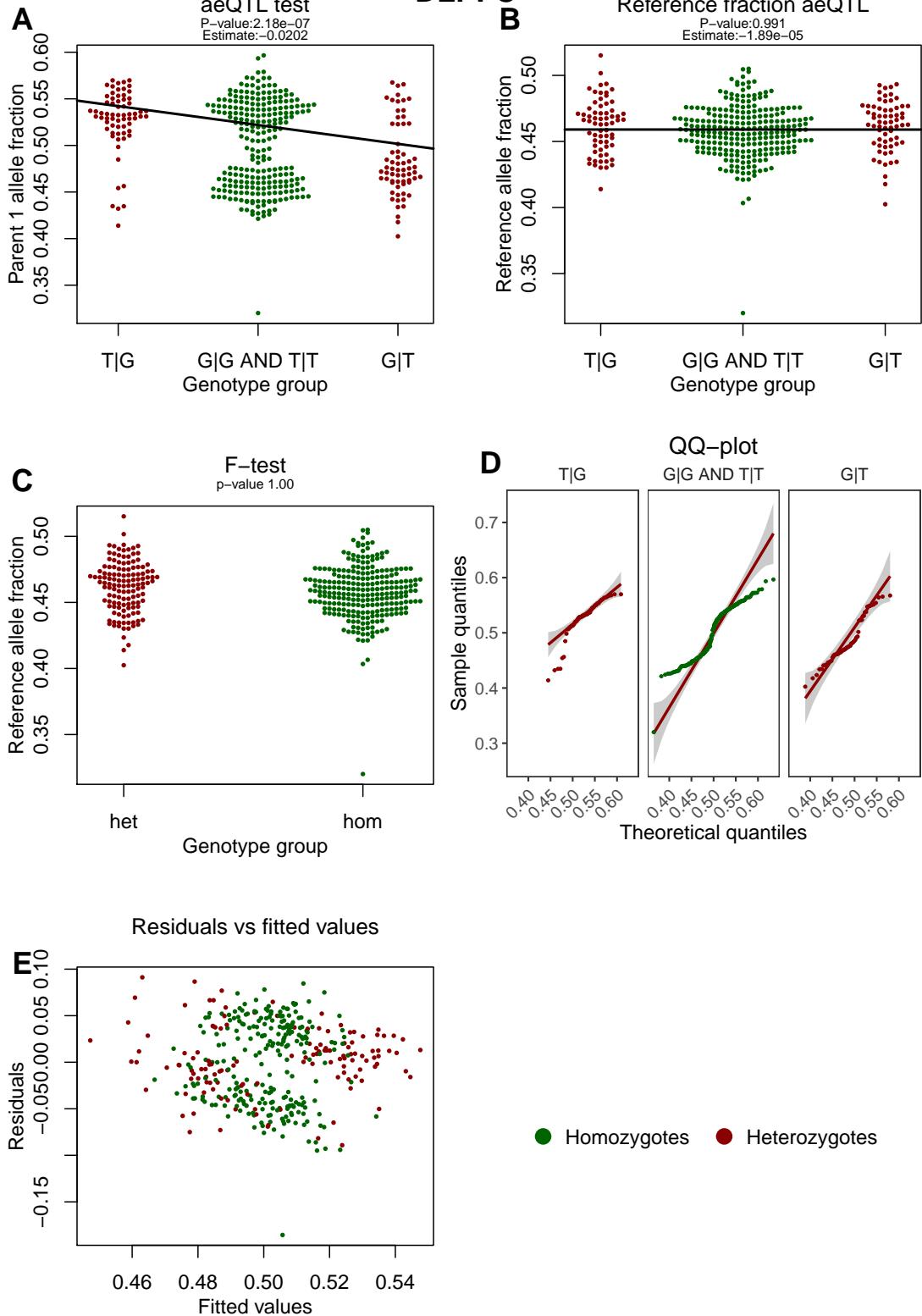


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PTPRF – rs11210892

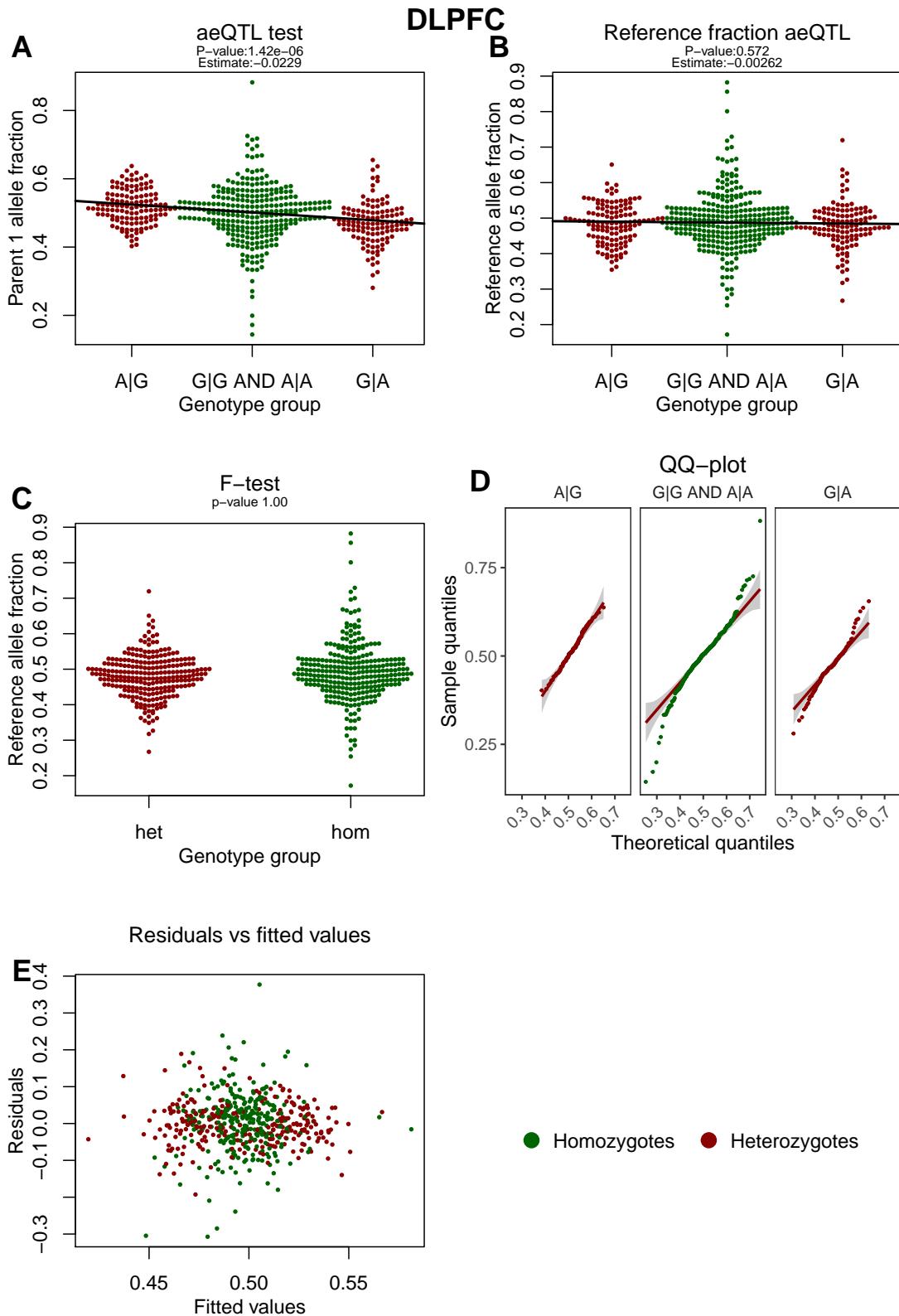


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HSPE1,MOB4,HSPE1-MOB4 – rs6434928

DLPFC

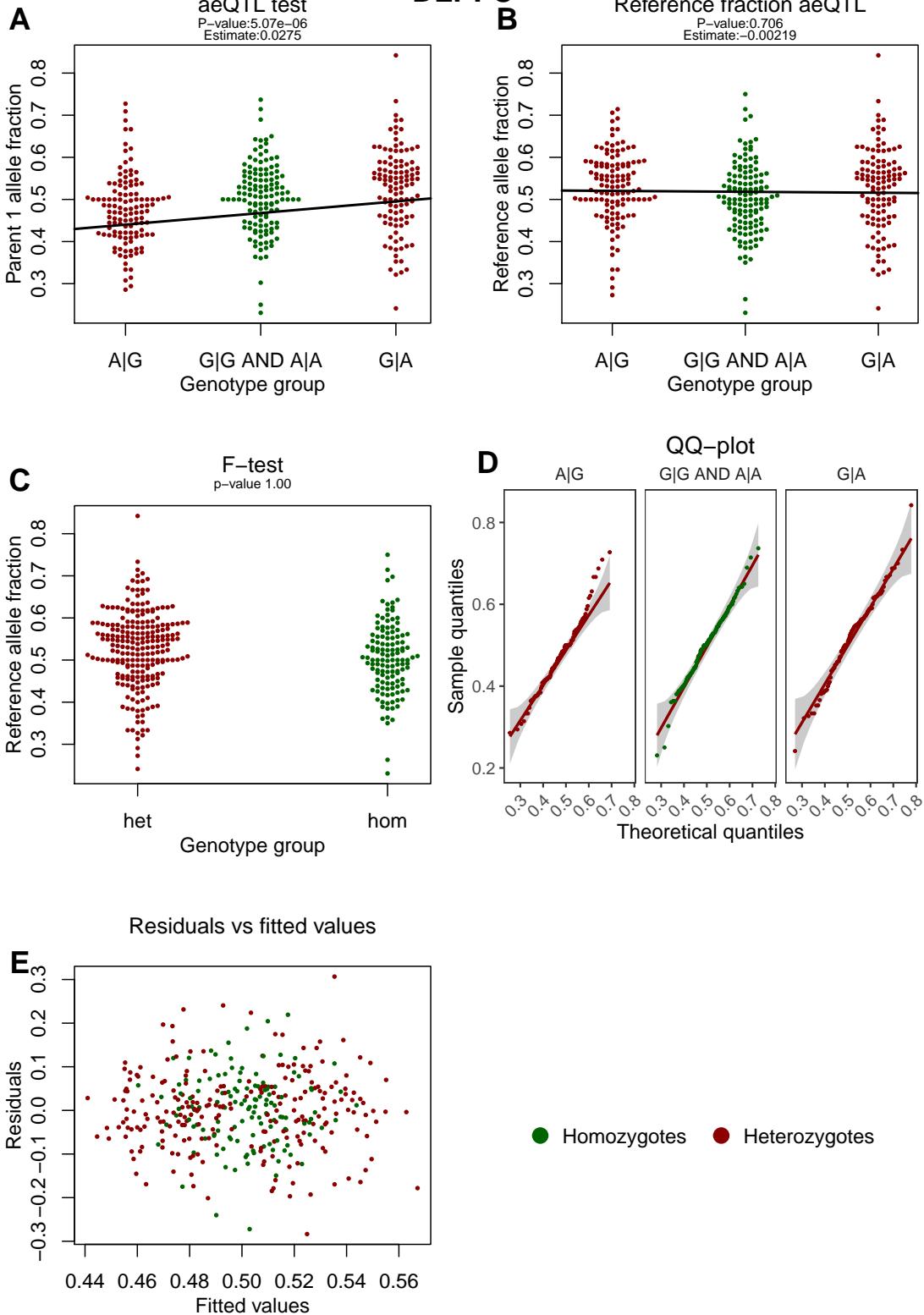


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NEK4 – rs2535627

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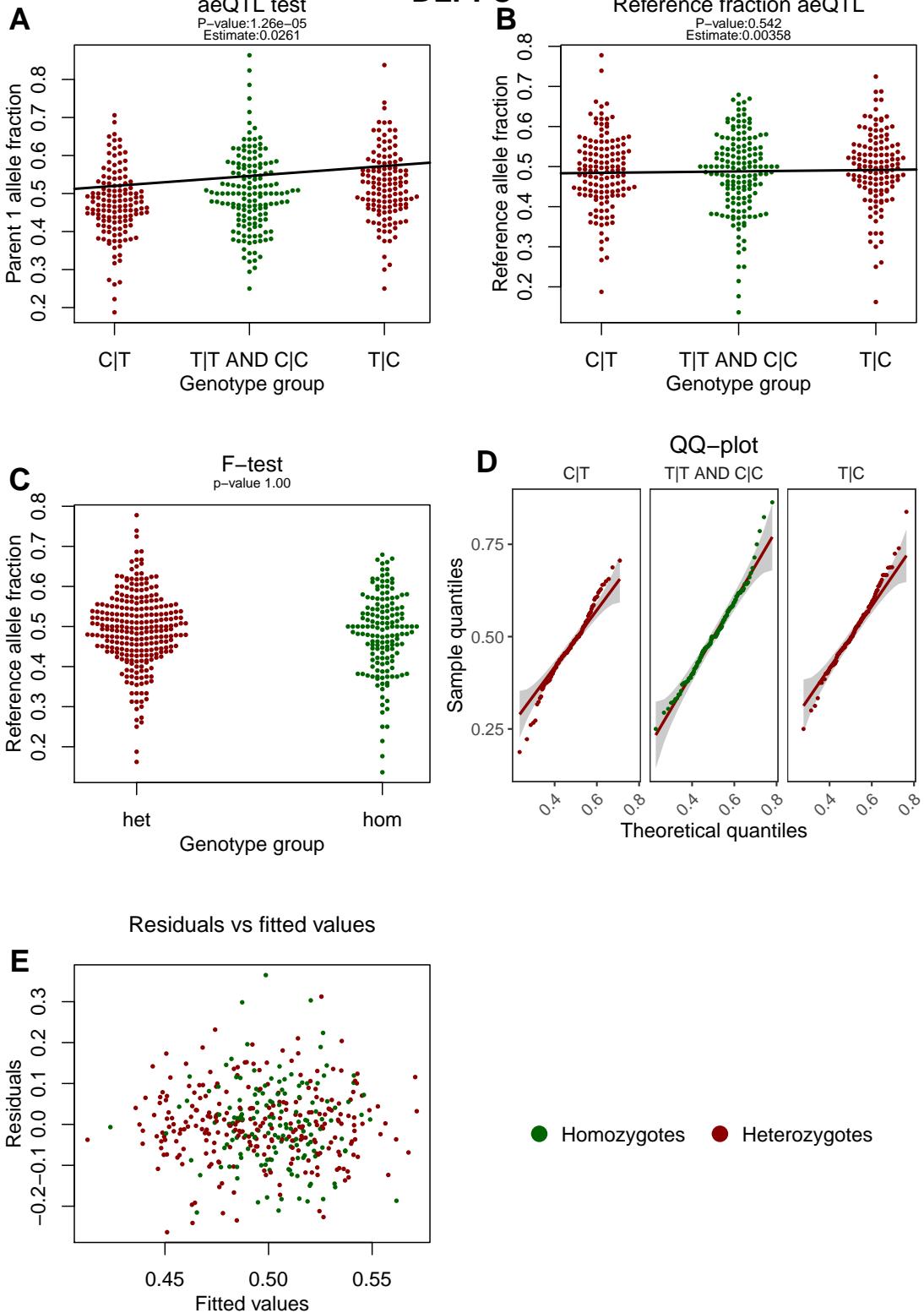


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LRP1,MIR1228 – rs12826178

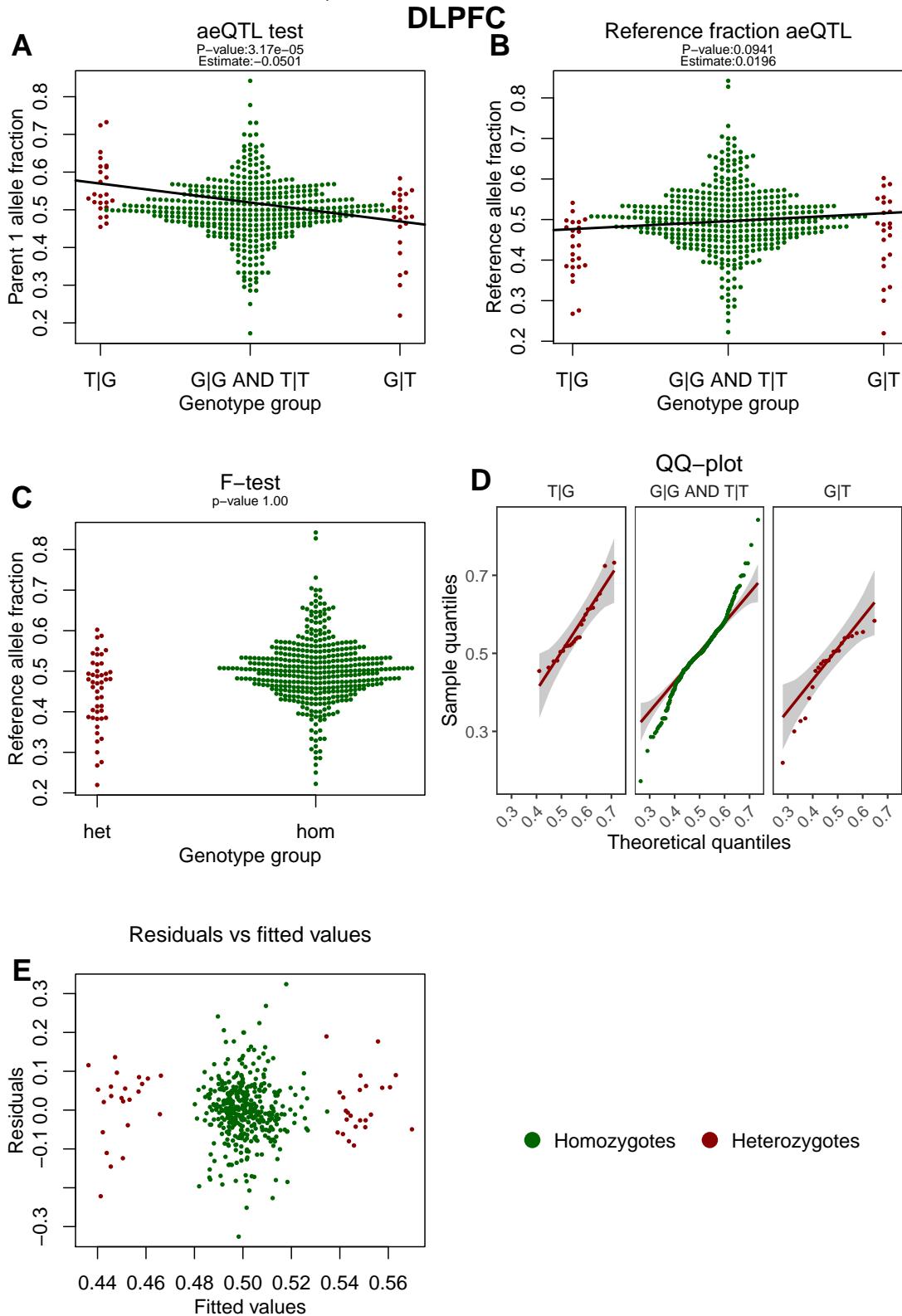


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PRMT7 – rs8044995

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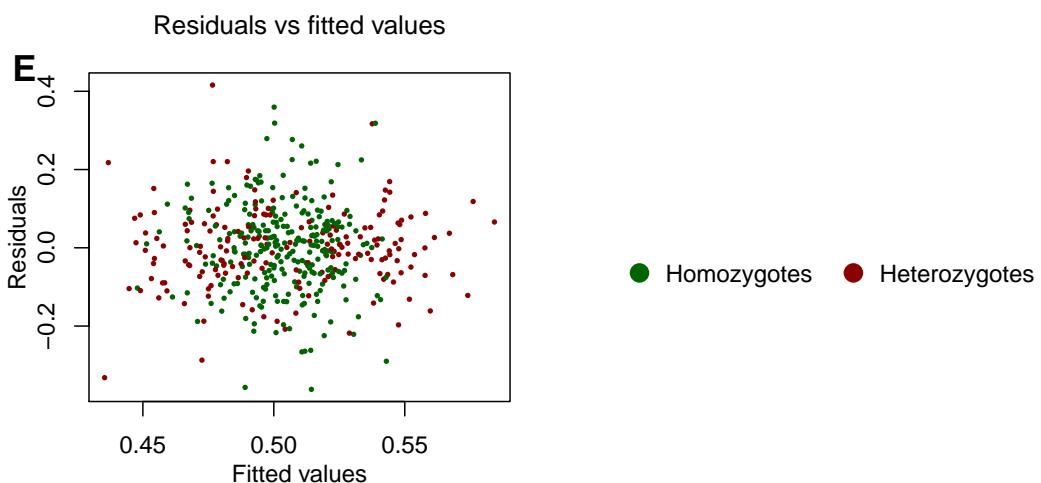
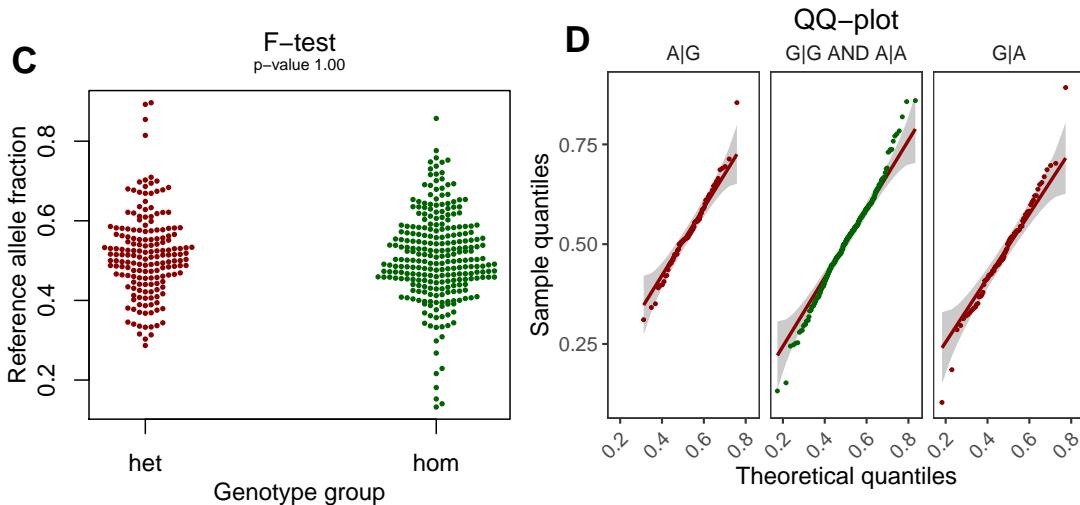
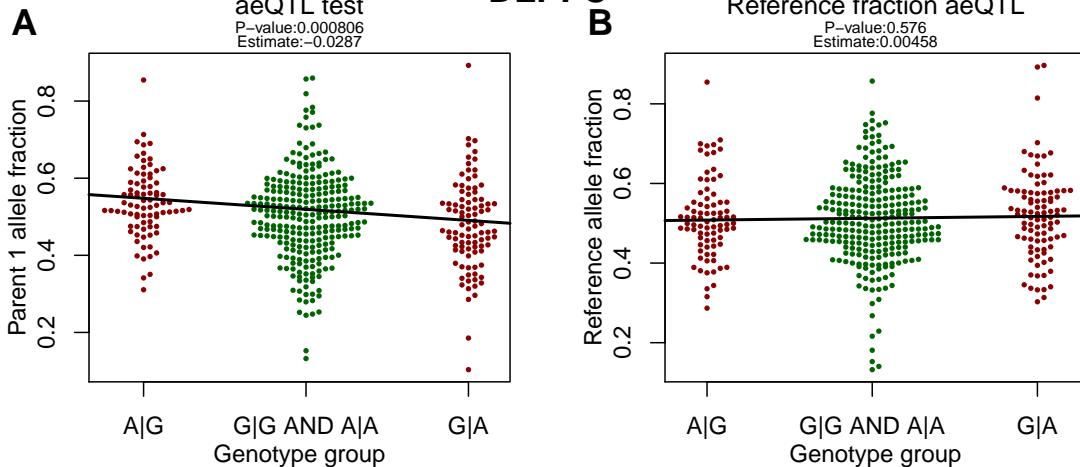


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GATA2A – rs2905426

DLPFC

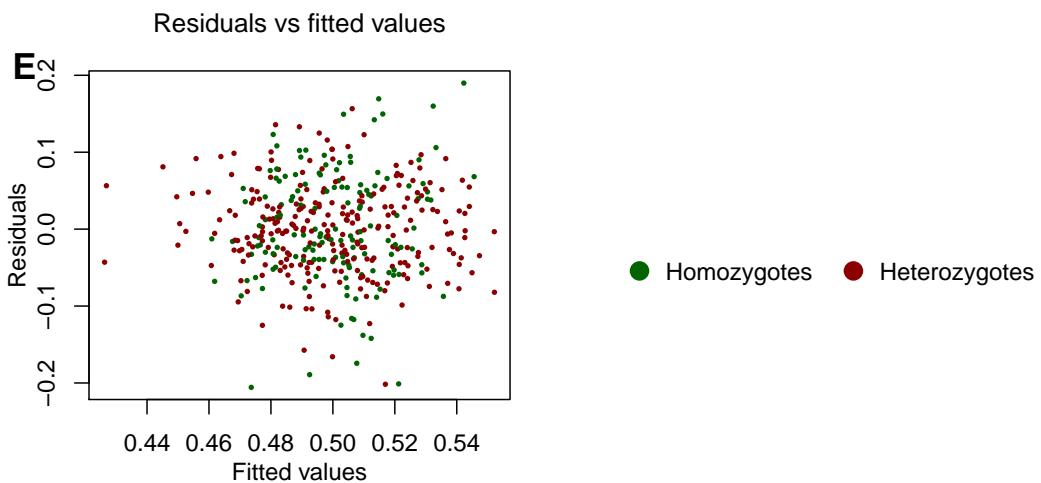
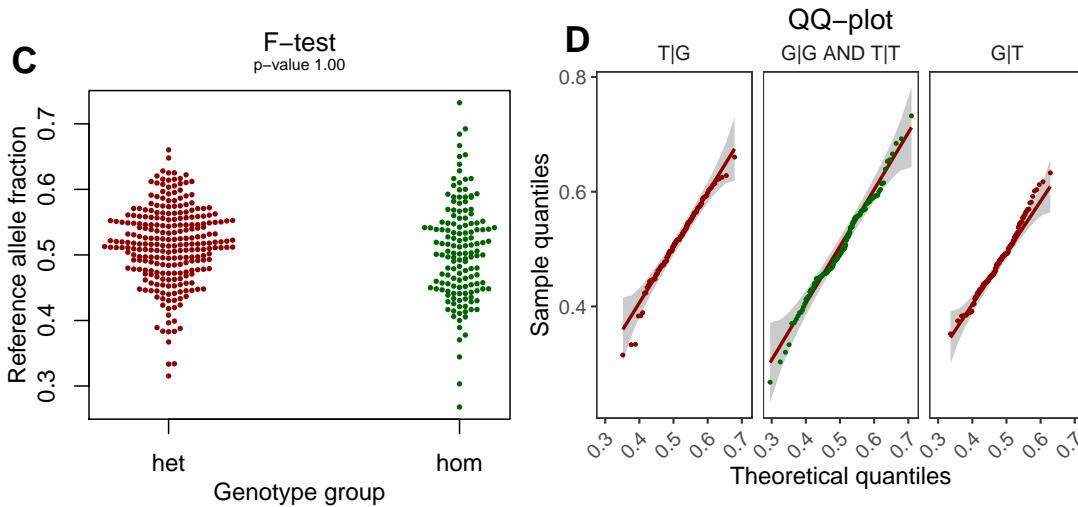
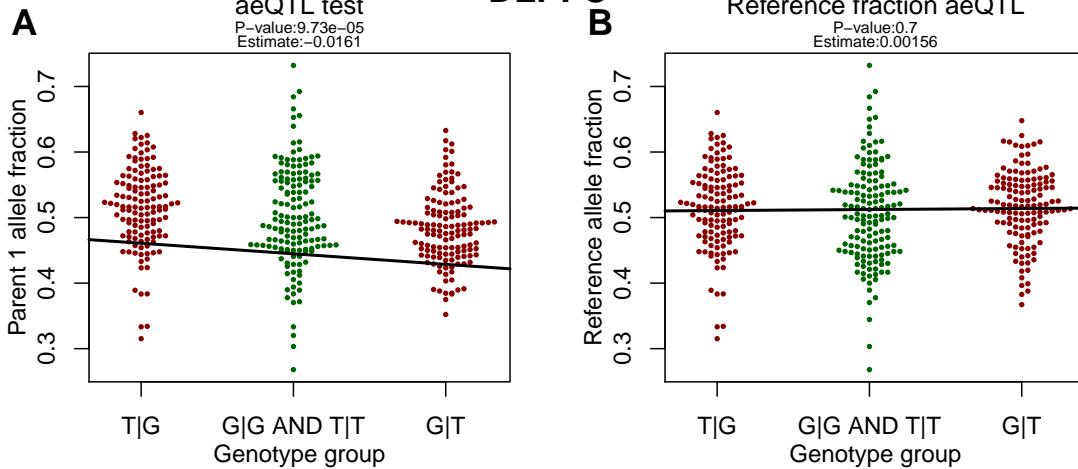


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HSPD1 – rs6434928

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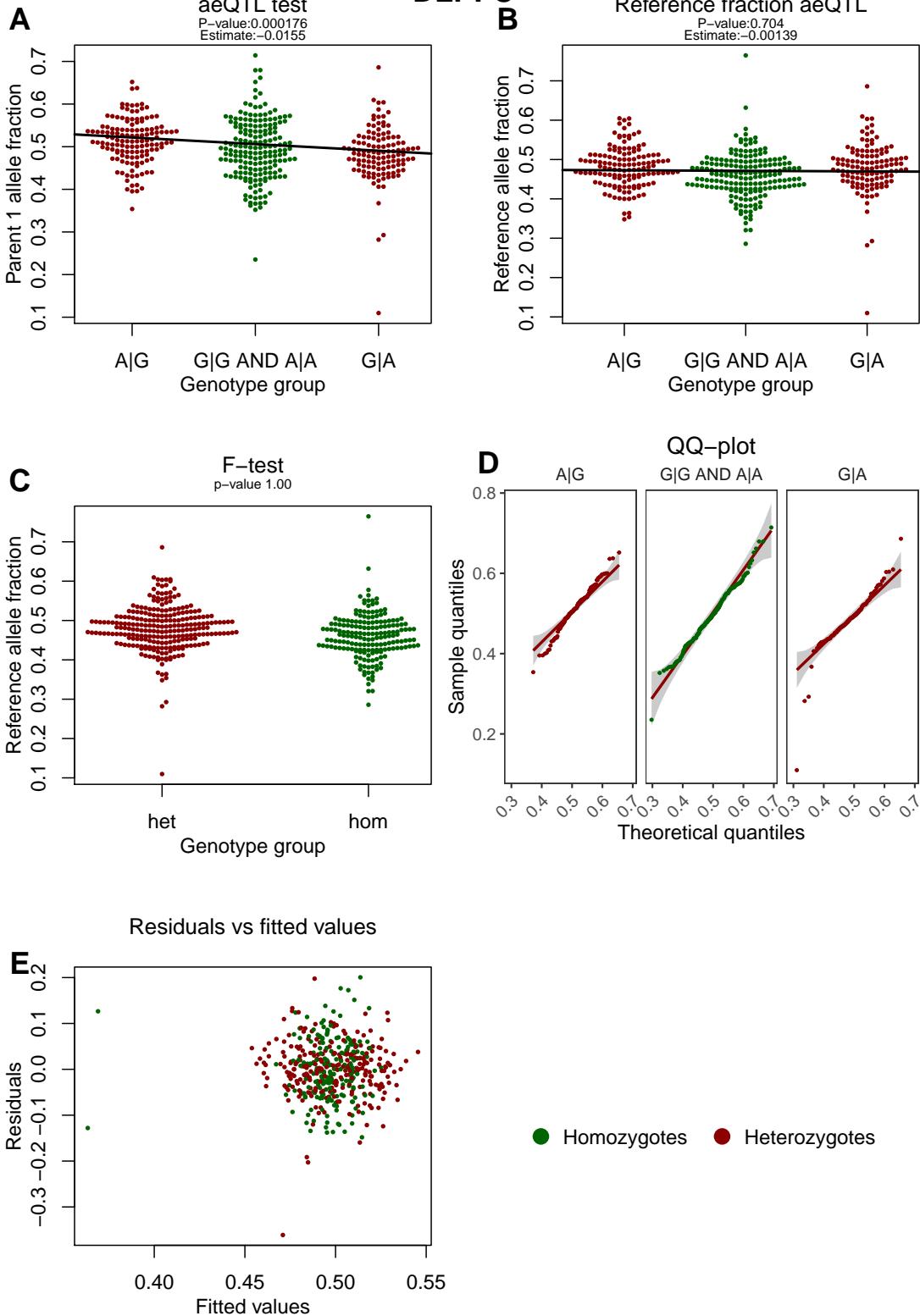


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LCAT,SLC12A4 – rs8044995

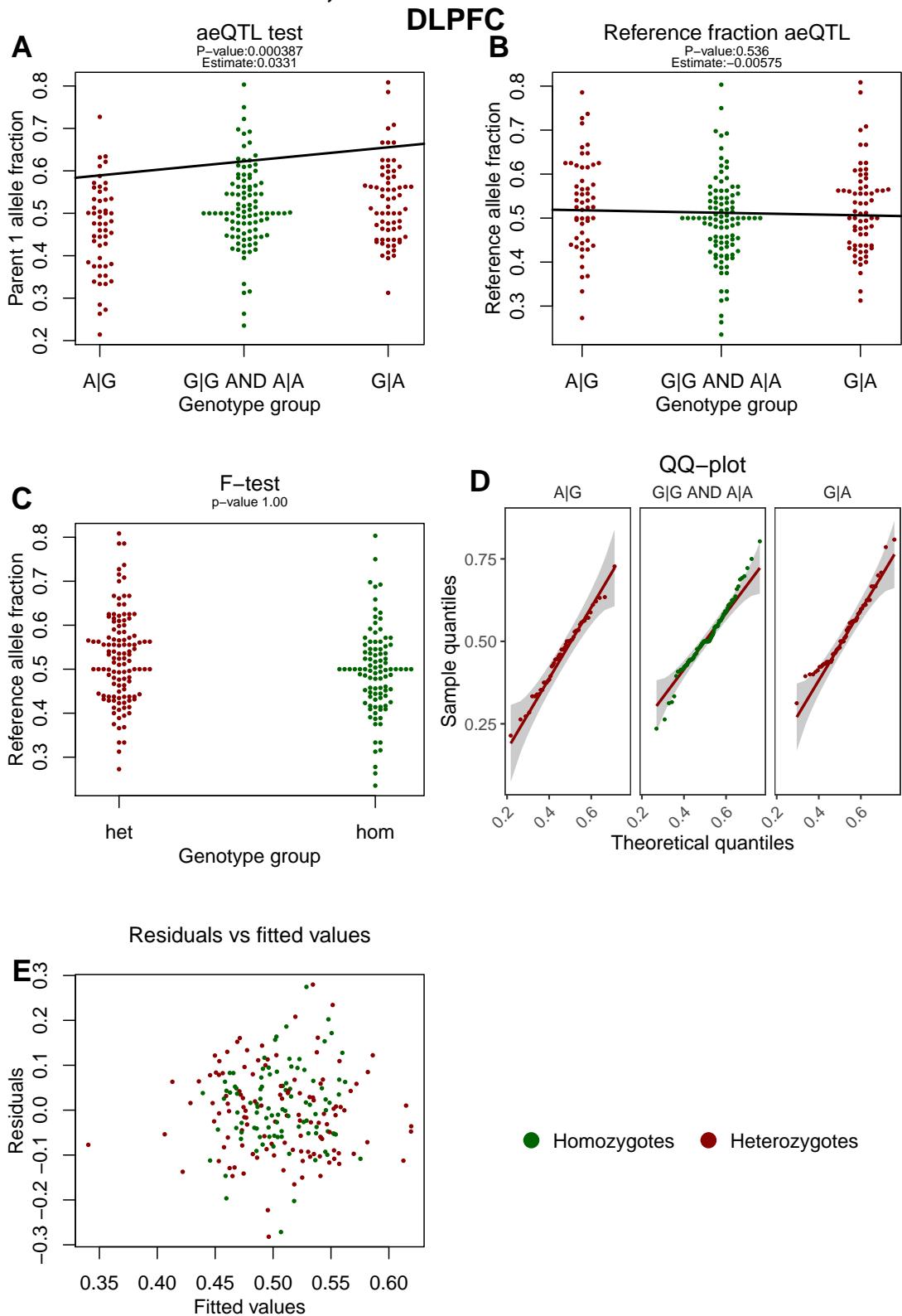


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FAM53C – rs10043984

DLPFC

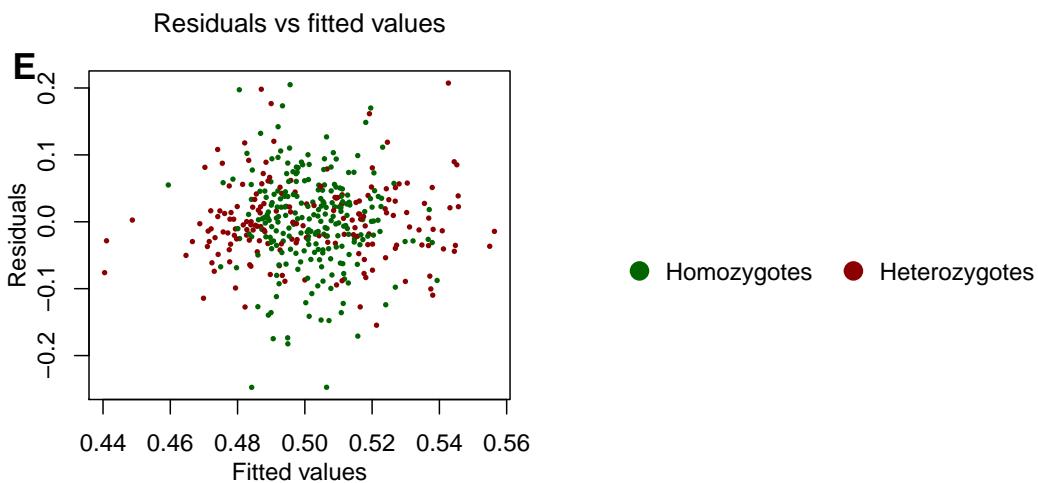
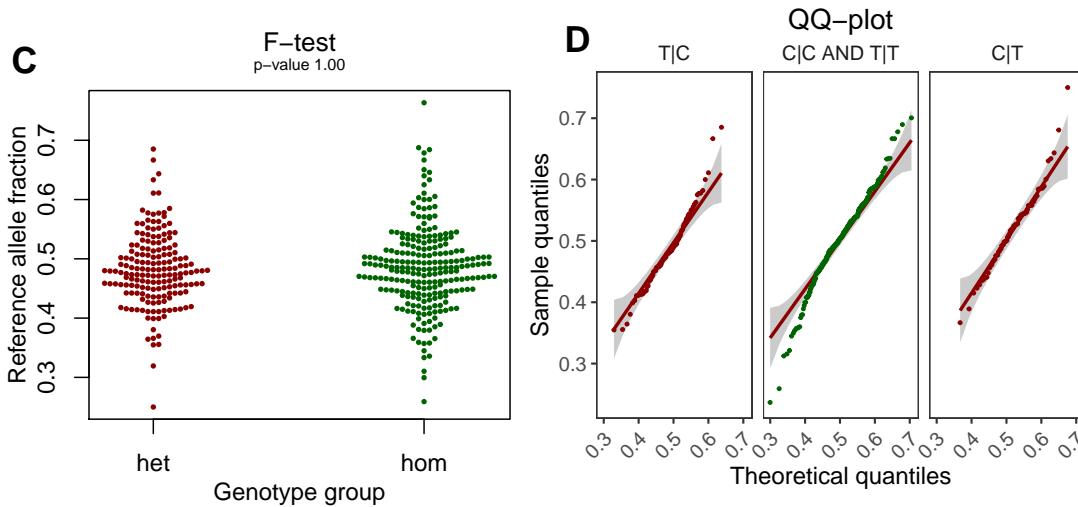
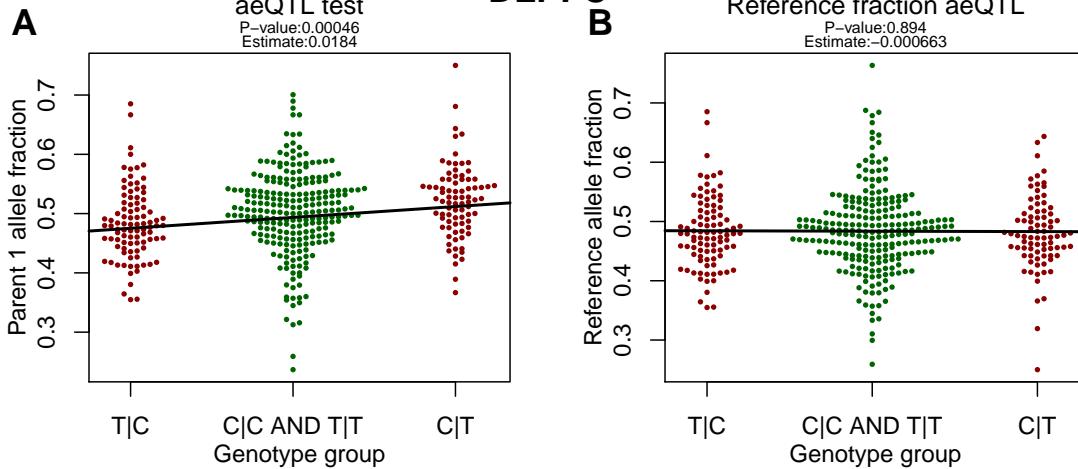


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IK,MIR3655 – chr5_140143664_I

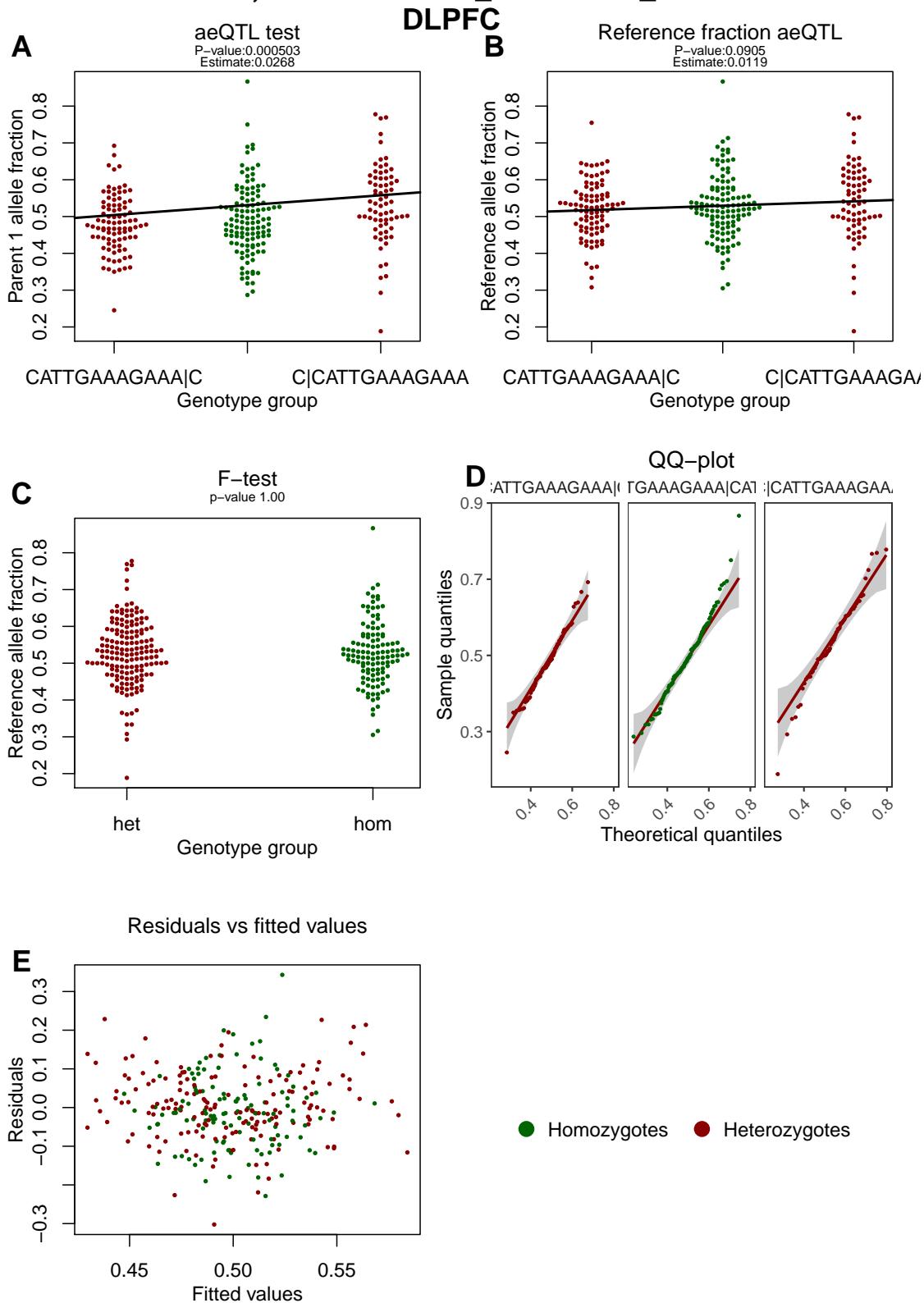


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PPP1R13B – rs12887734

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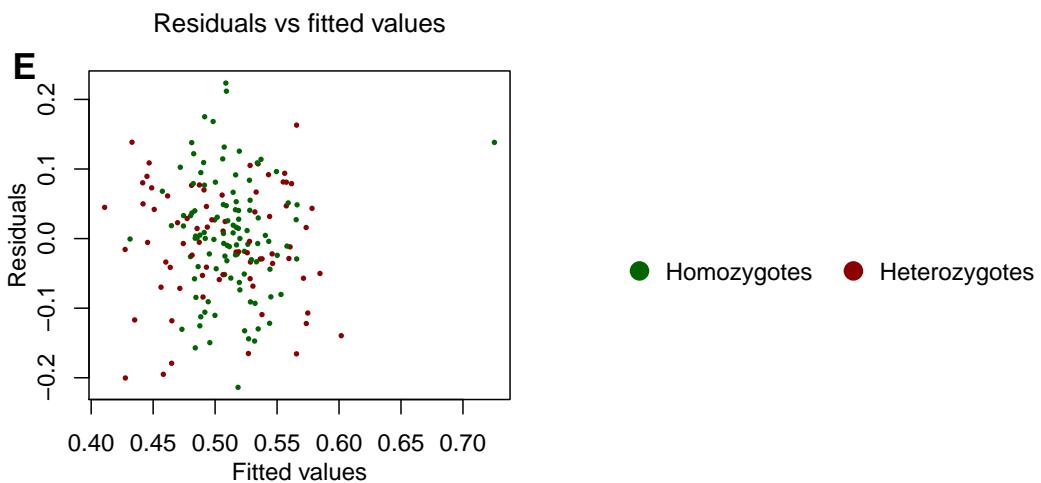
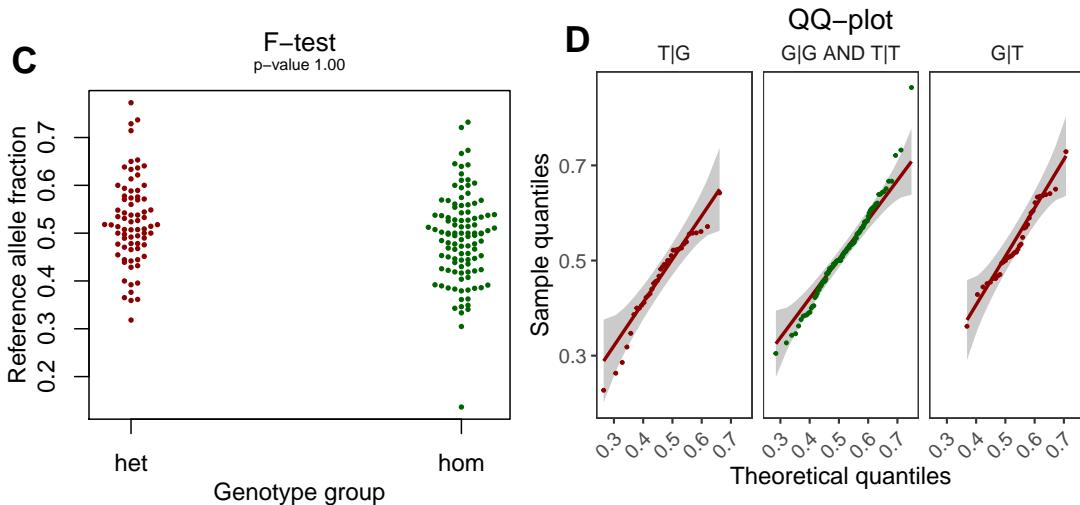
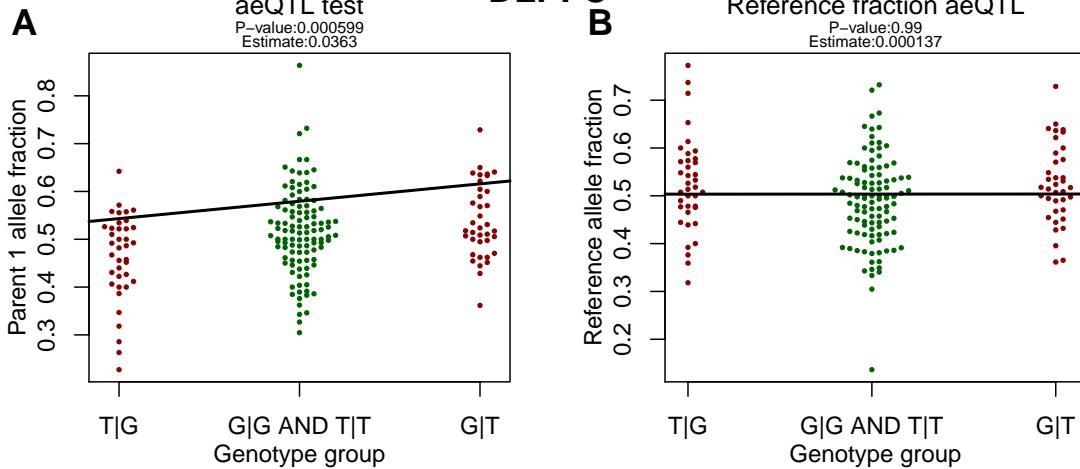


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AS3MT,BORCS7,BORCS7-ASMT – rs55833108

DLPFC

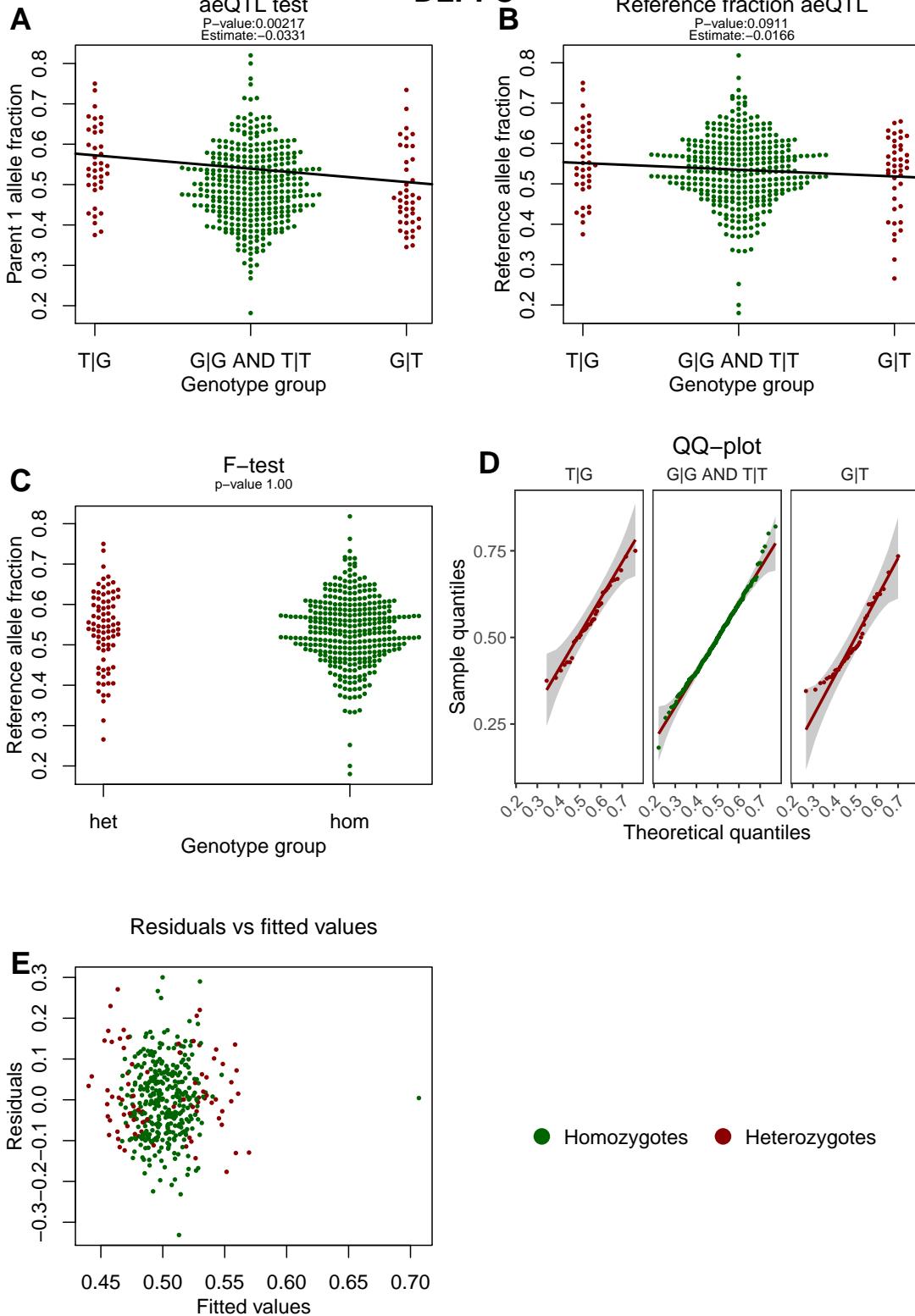


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RIMS1 – rs1339227

DLPFC

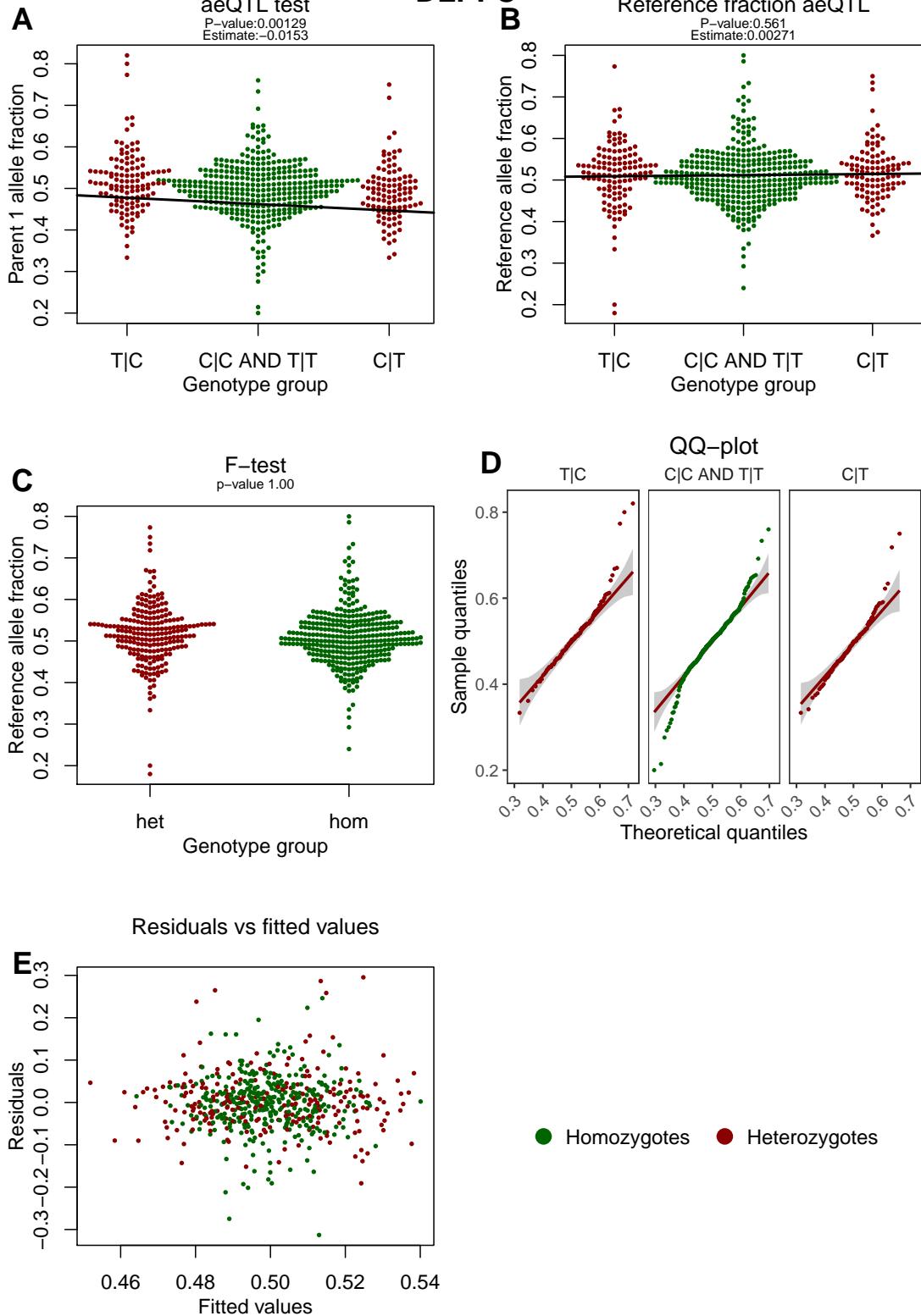


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BUB1B,PAK6 – rs56205728

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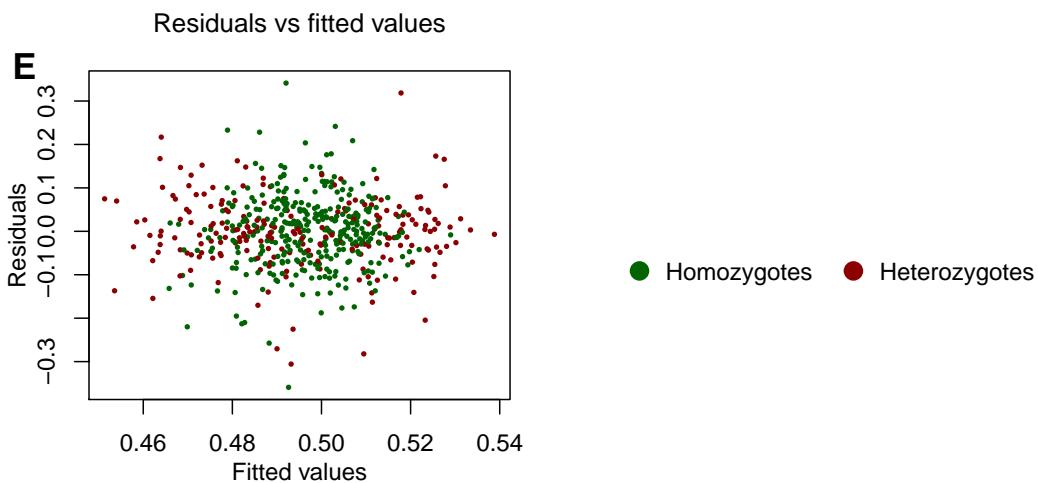
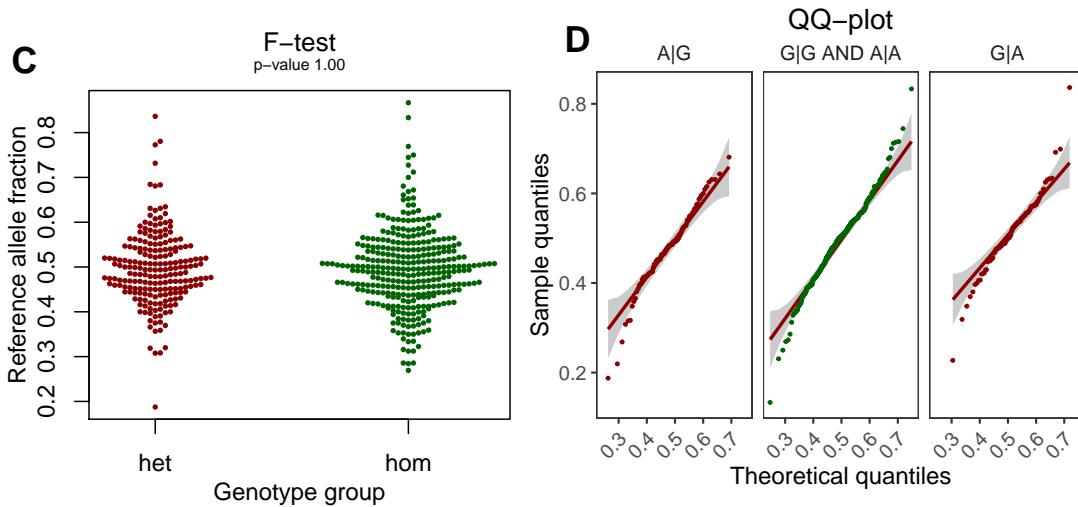
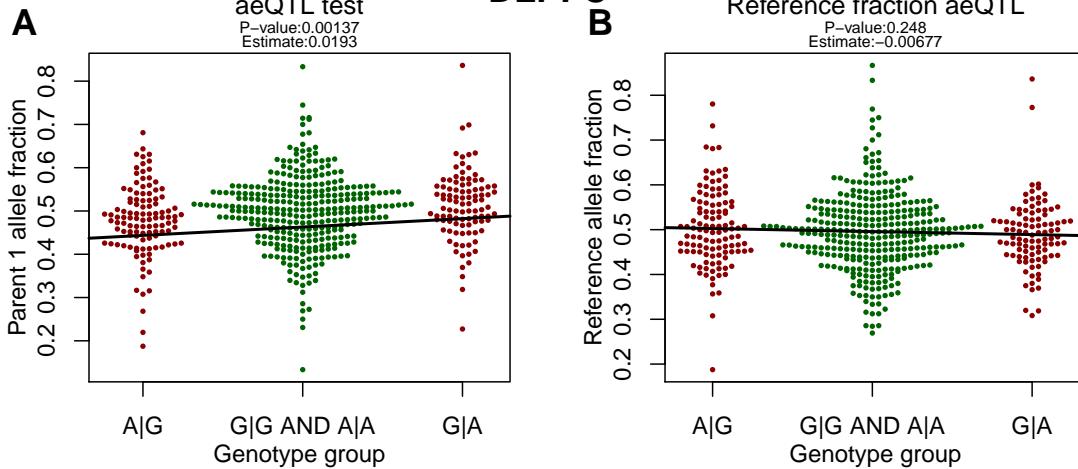


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DNAJC19 – chr3_180594593_I

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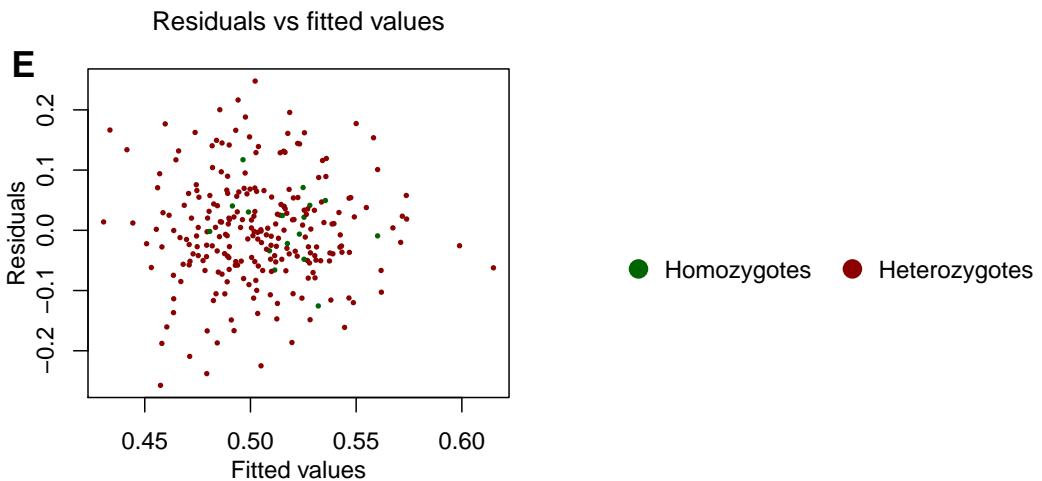
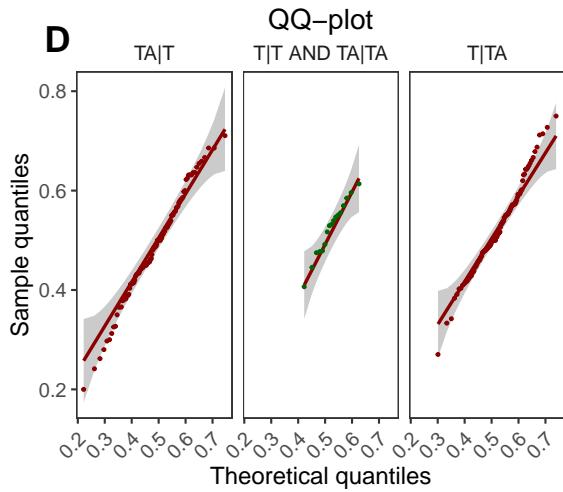
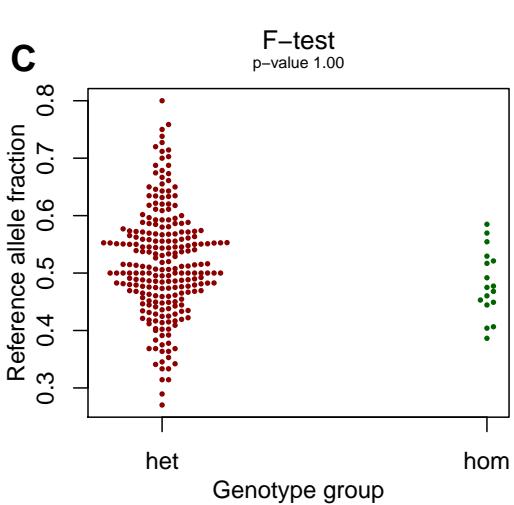
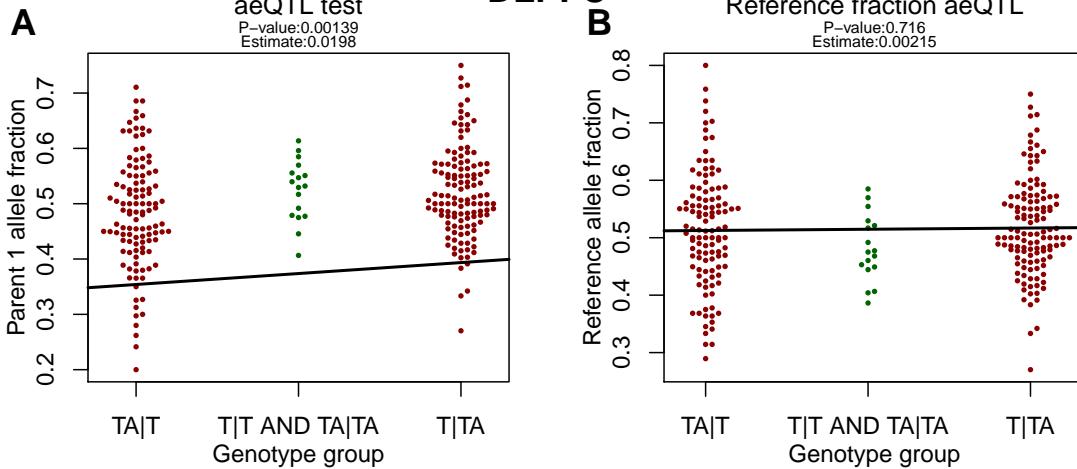


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VPS45 – rs140505938

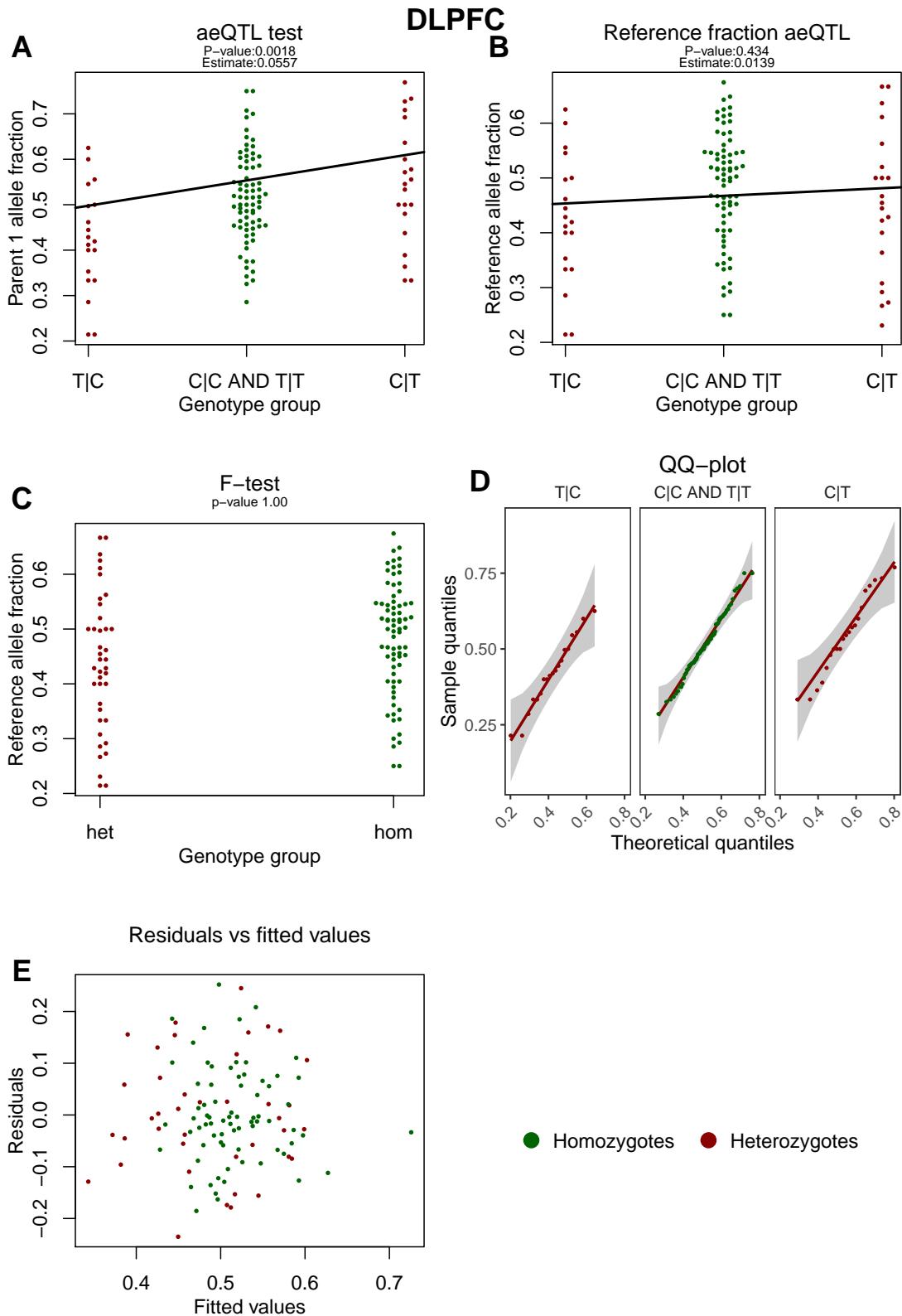


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AS3MT,BORCS7,BORCS7-ASMT – rs11191419

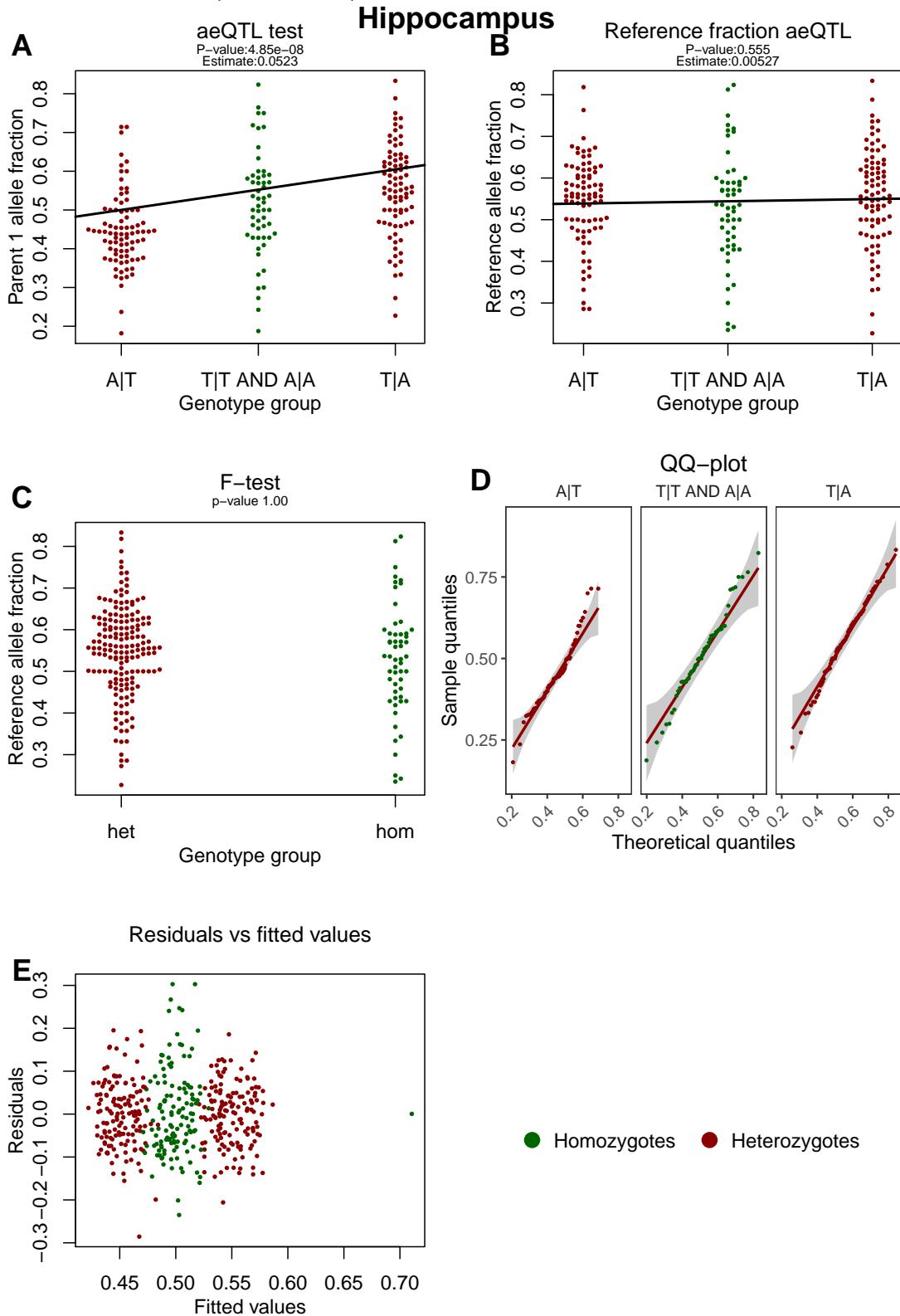


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ZMAT2 – chr5_140143664_I

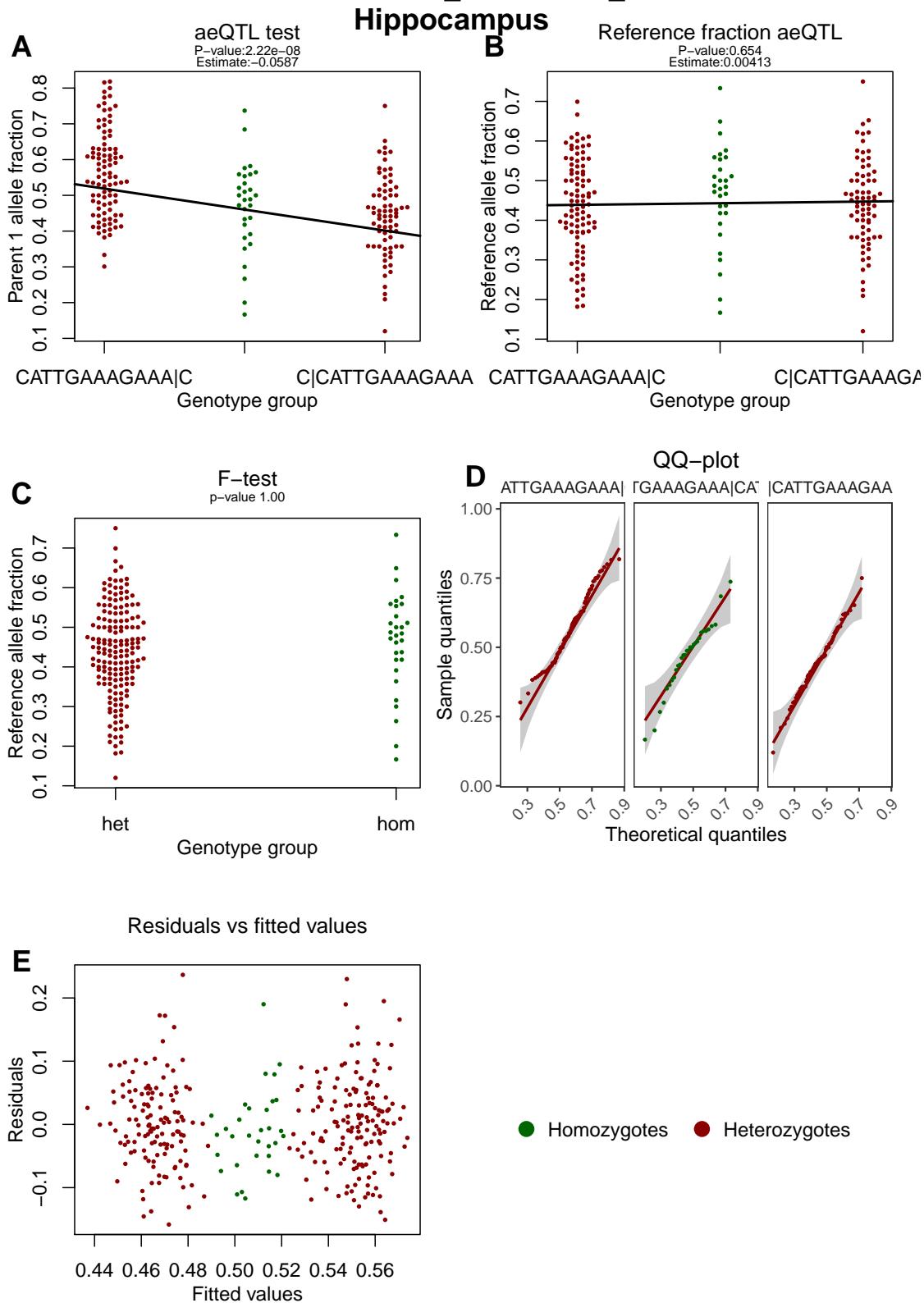


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SNX19 – rs10791097

Hippocampus

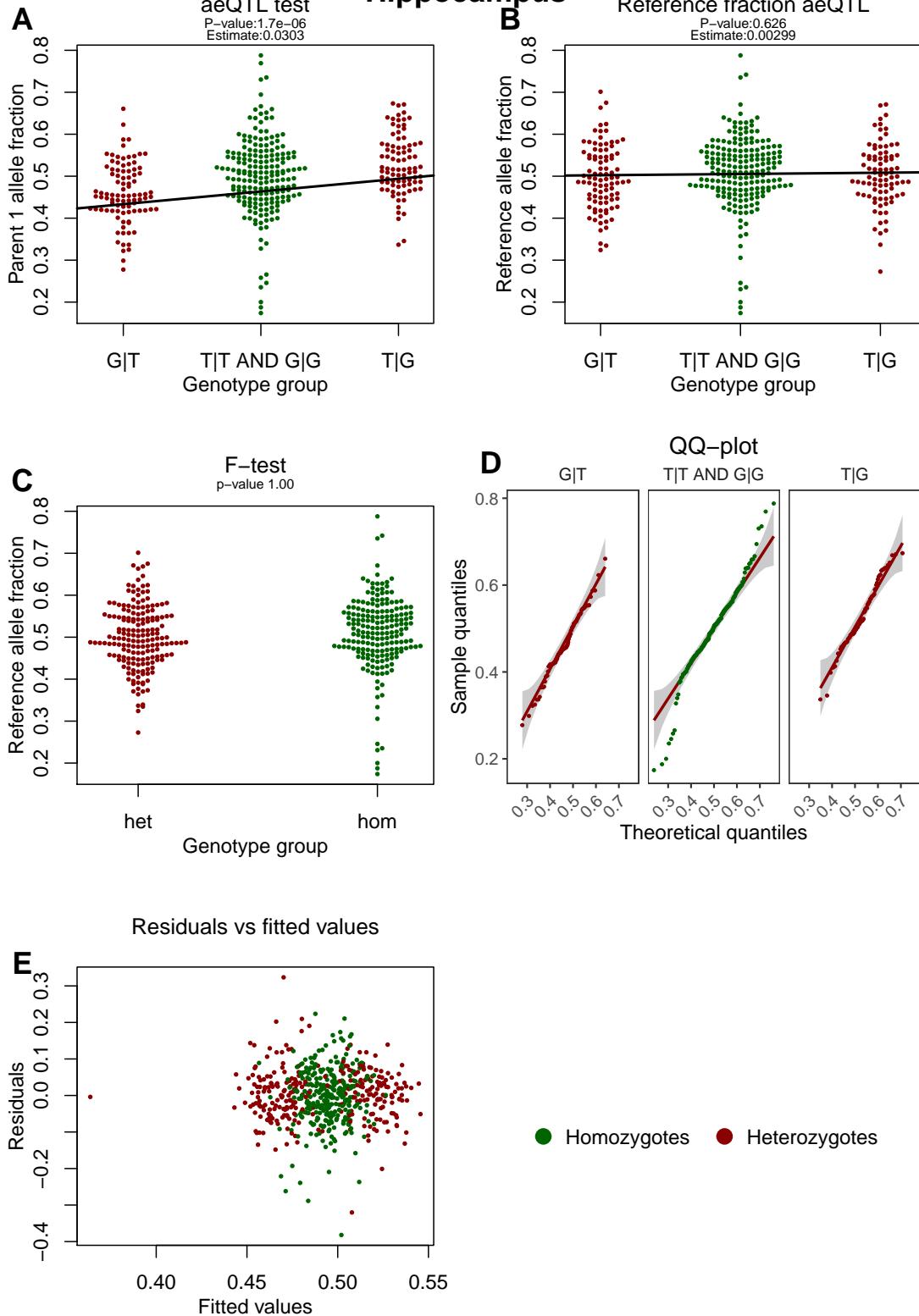


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HSPD1 – rs6434928

Hippocampus

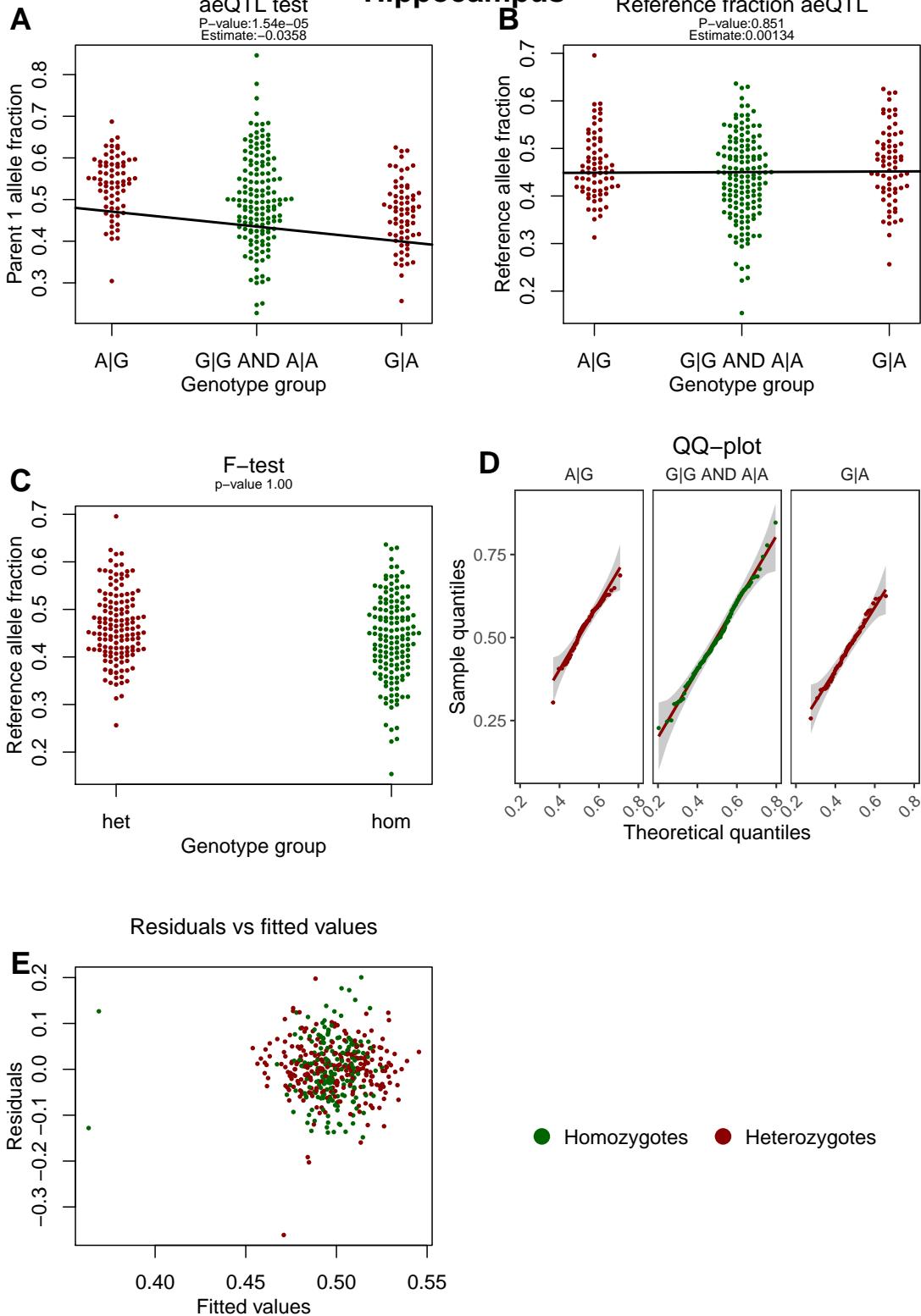


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