

Identification of strong candidate genes for backfat and intramuscular fatty acid composition in three crosses based on the Iberian pig

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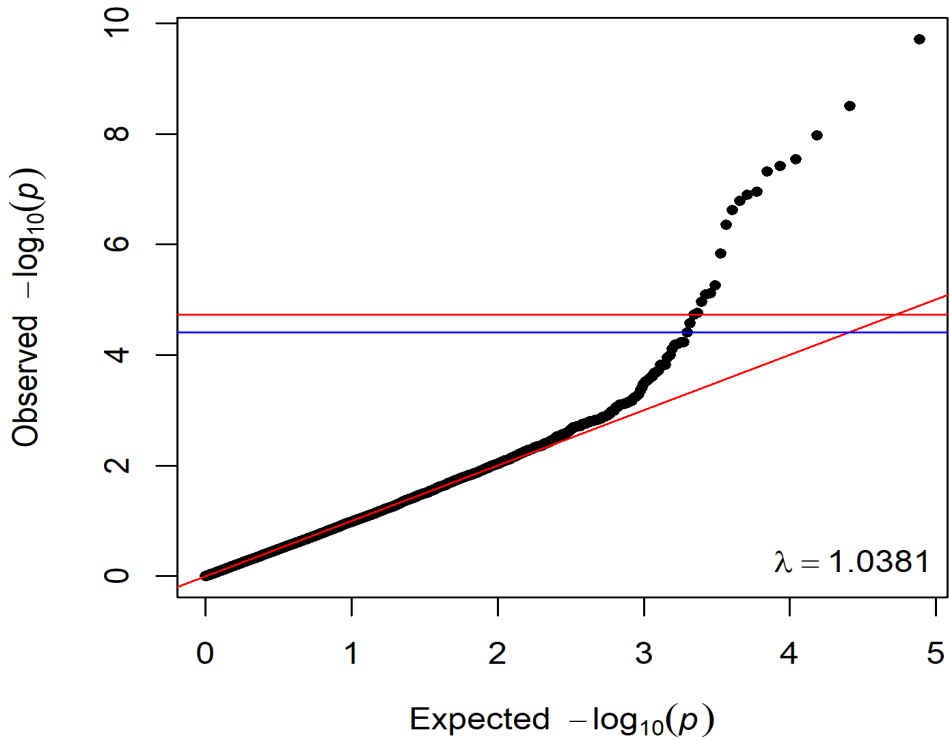
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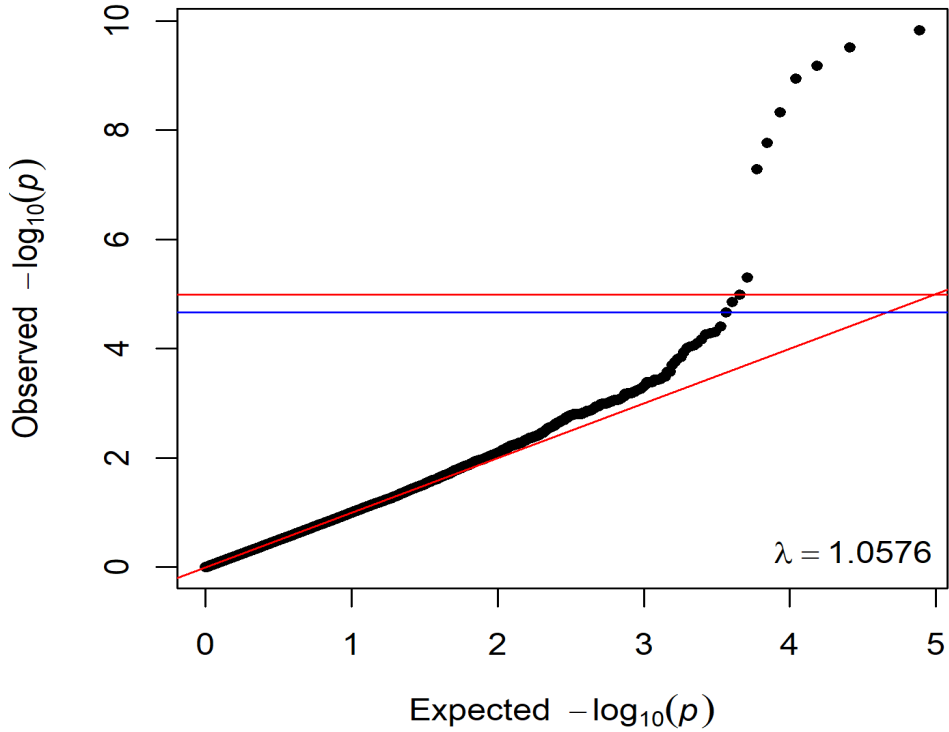
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Supplementary Information S1. Quantile-quantile (Q-Q) plot of the association analysis between the 18 traits in backfat (BF) or *longissimus dorsi* muscle (LD) with significant SNPs. Trait and tissue are specified on the title of each figure. Red and blue lines indicate those SNPs that are below the genome-wide significance threshold ($FDR \leq 0.05$ and $FDR \leq 0.1$, respectively). Genomic inflation factor (λ) is indicated in the legend.

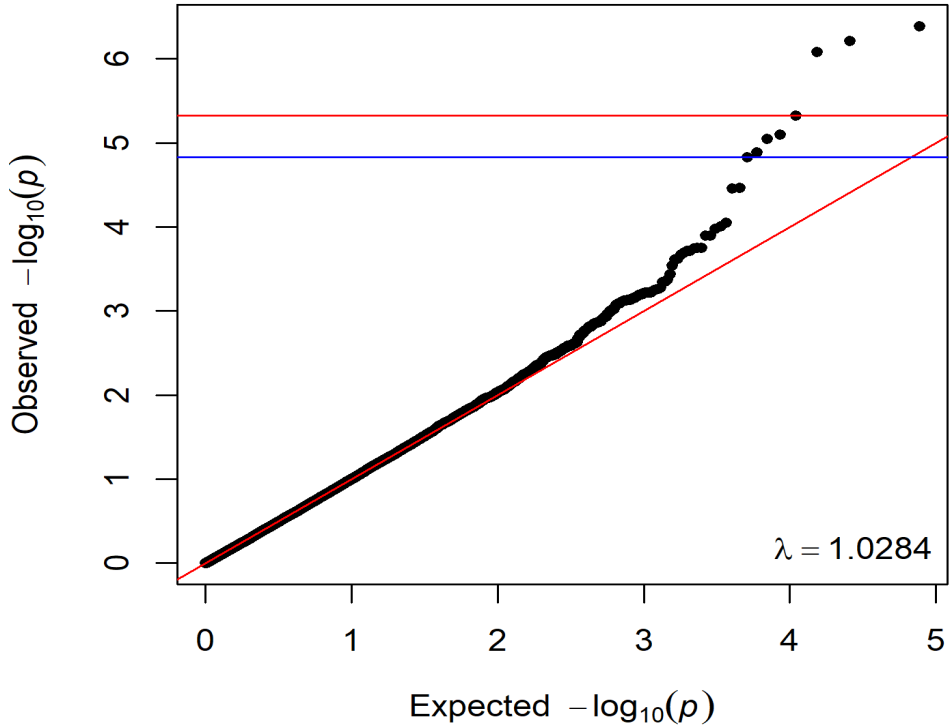
C14:0 in BF



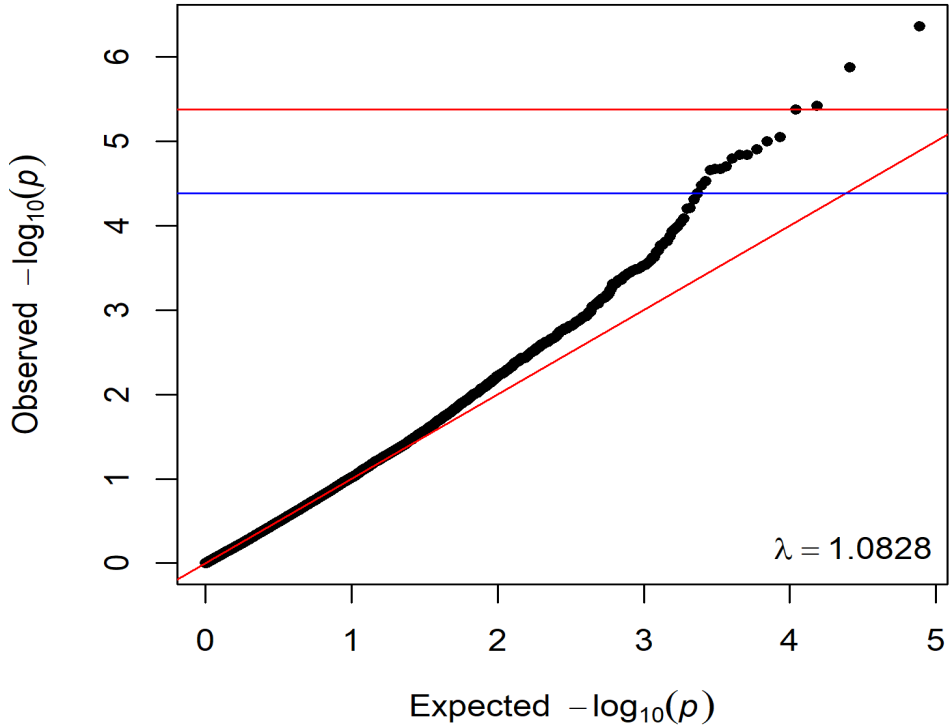
C16:0 in BF



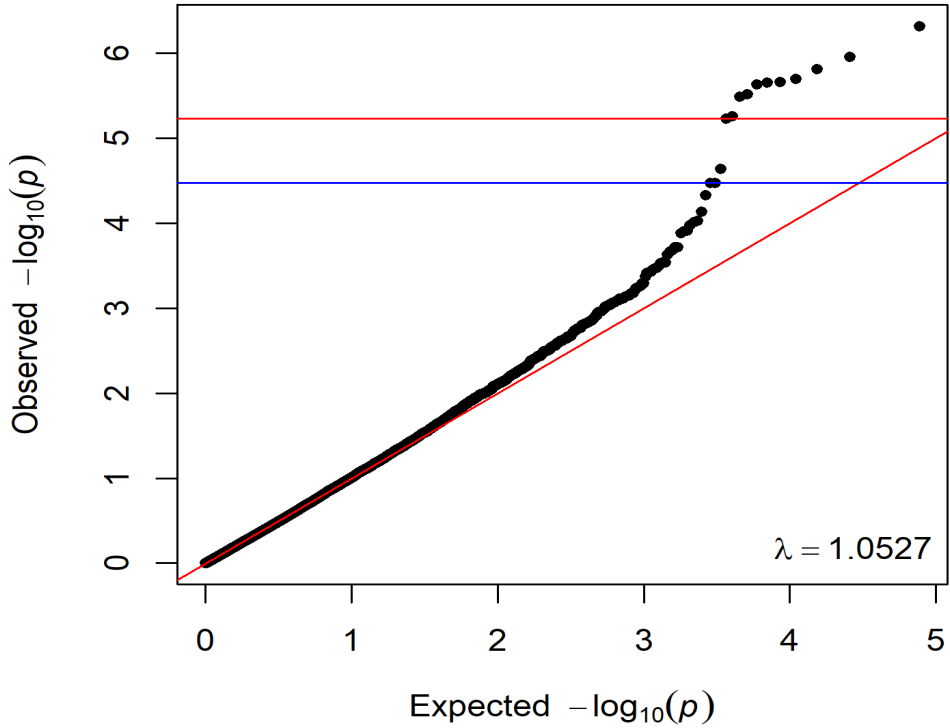
C16:1(n-7) in BF



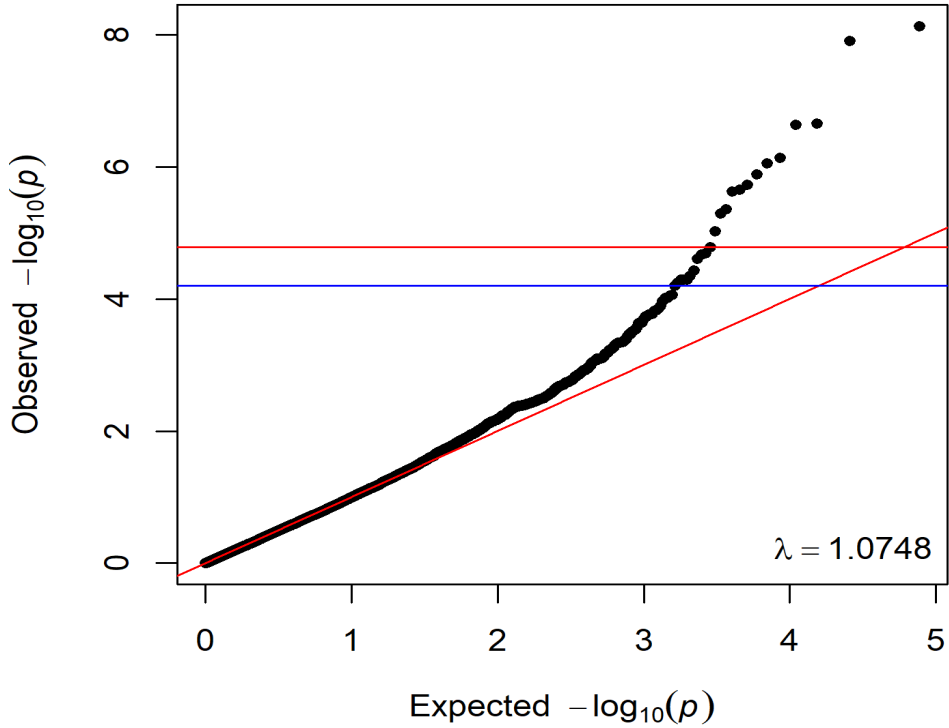
C16:1(n-9) in BF



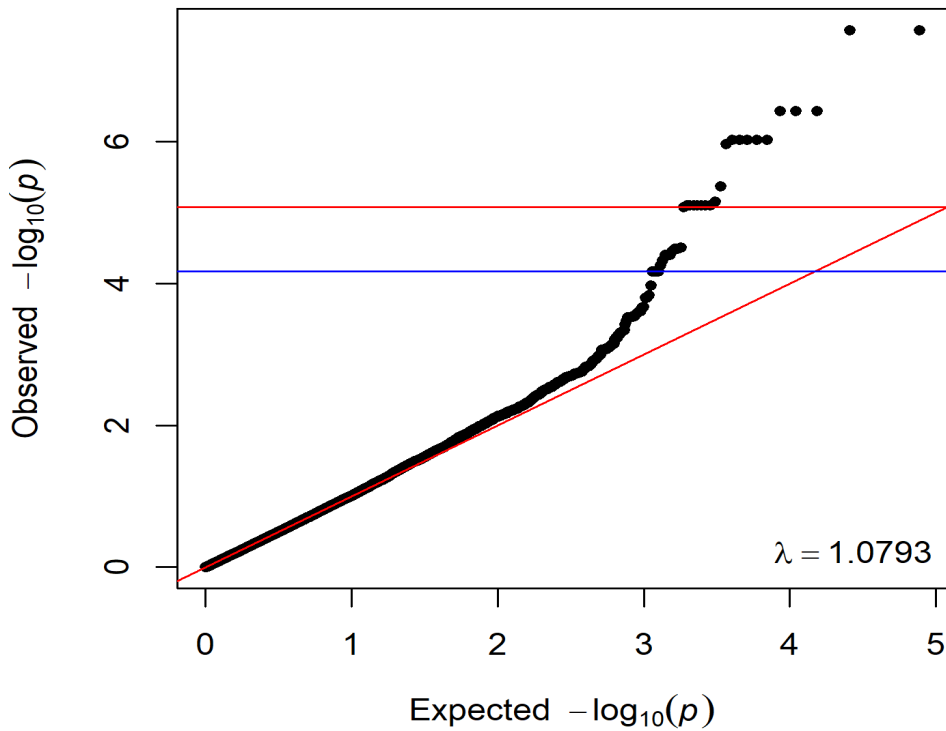
C18:1(n-9) in BF



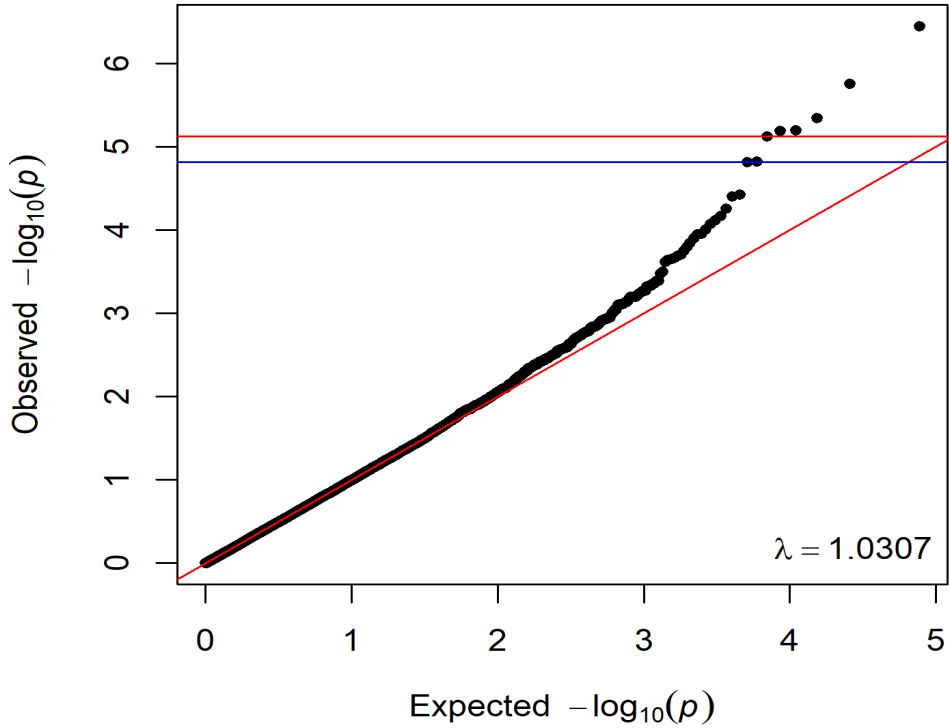
C18:2(n-6) in BF



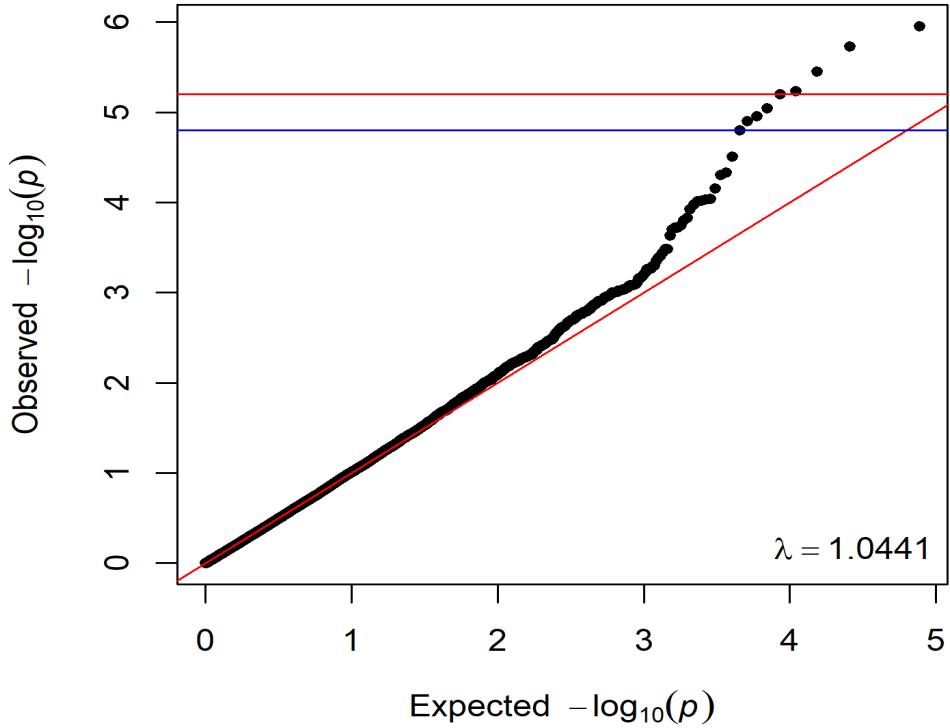
C20:1(n-9)/C20:0 in BF



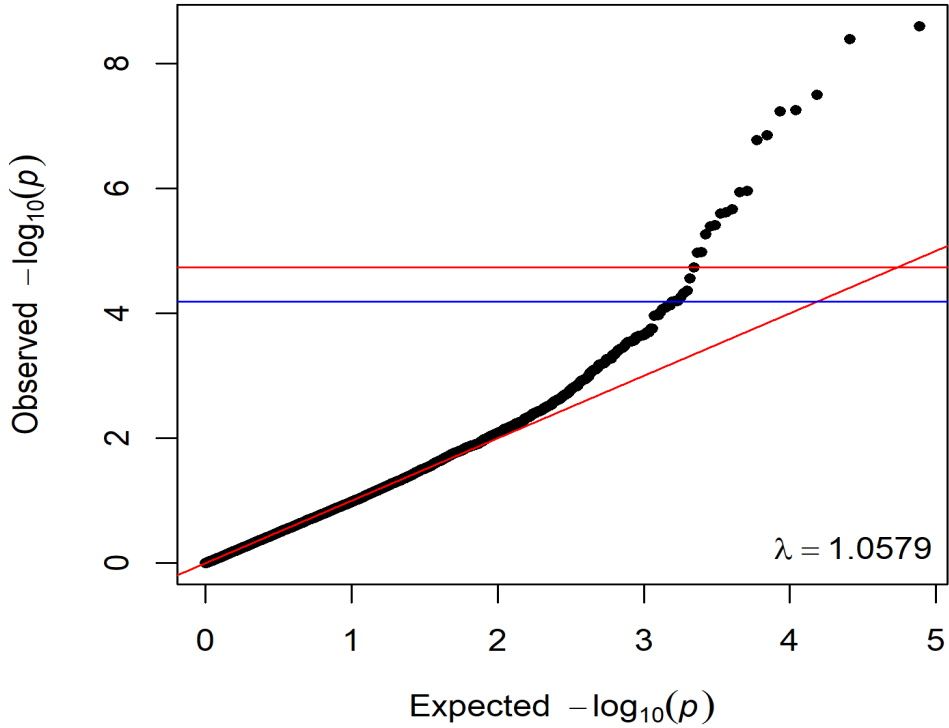
C20:3(n-6) in BF



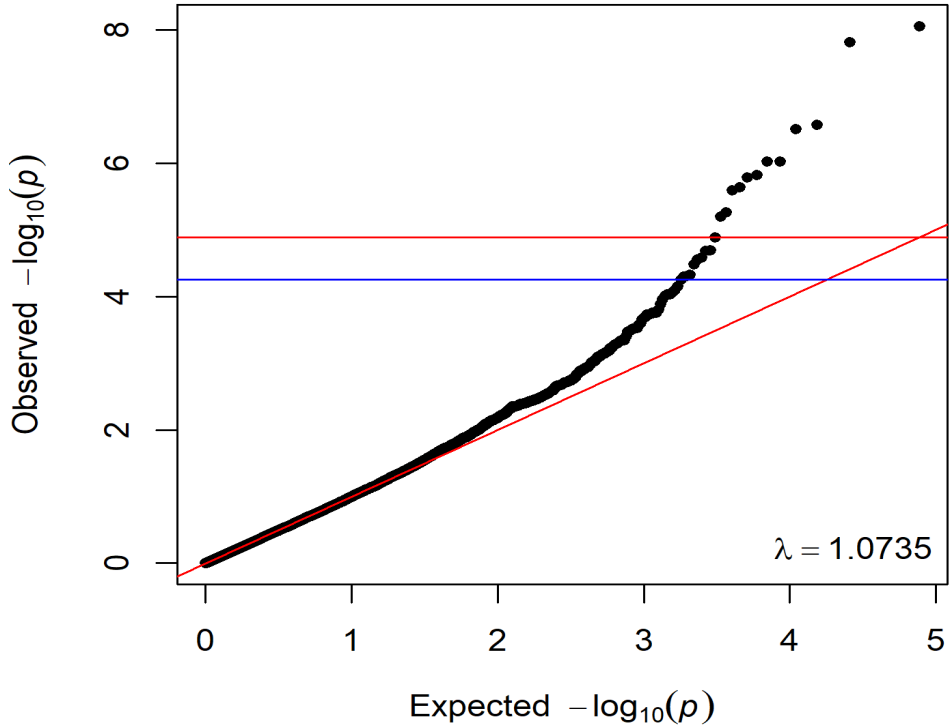
MUFA in BF



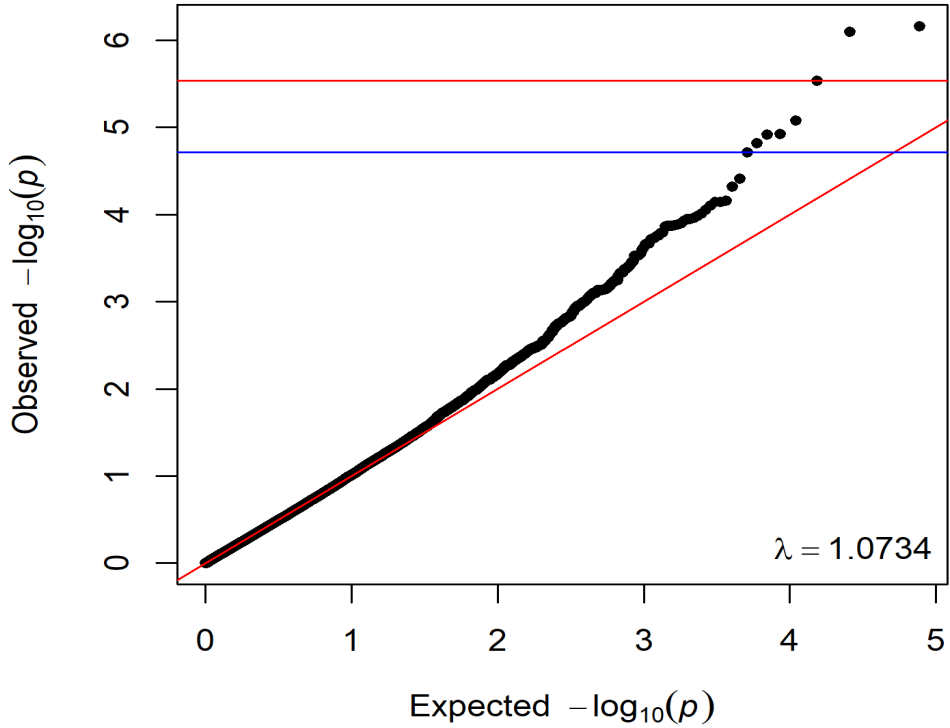
MUFA/PUFA in BF



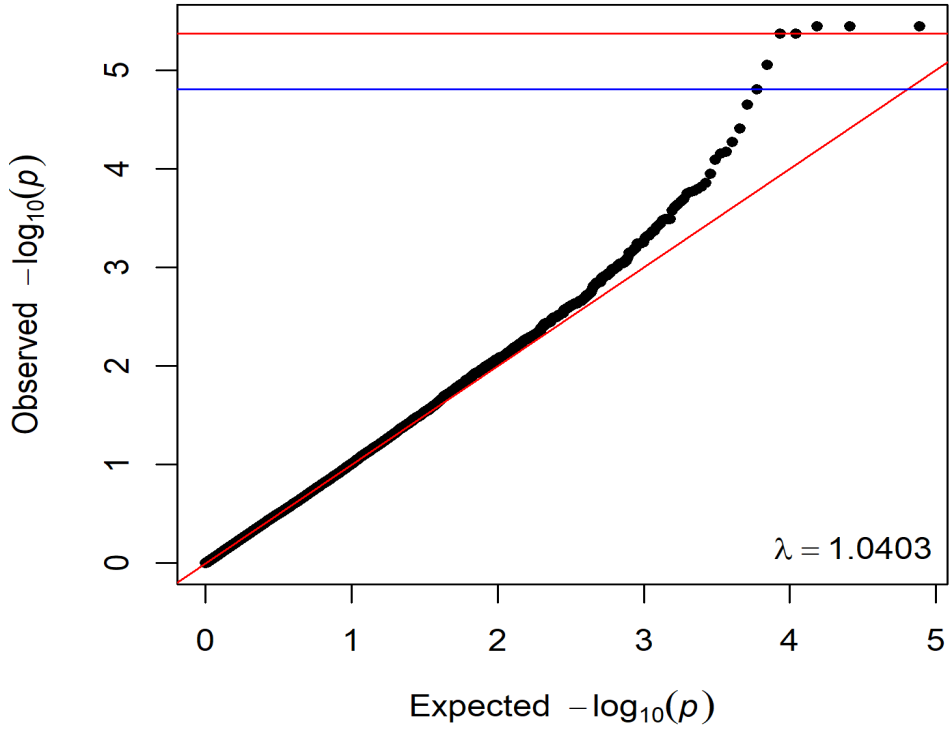
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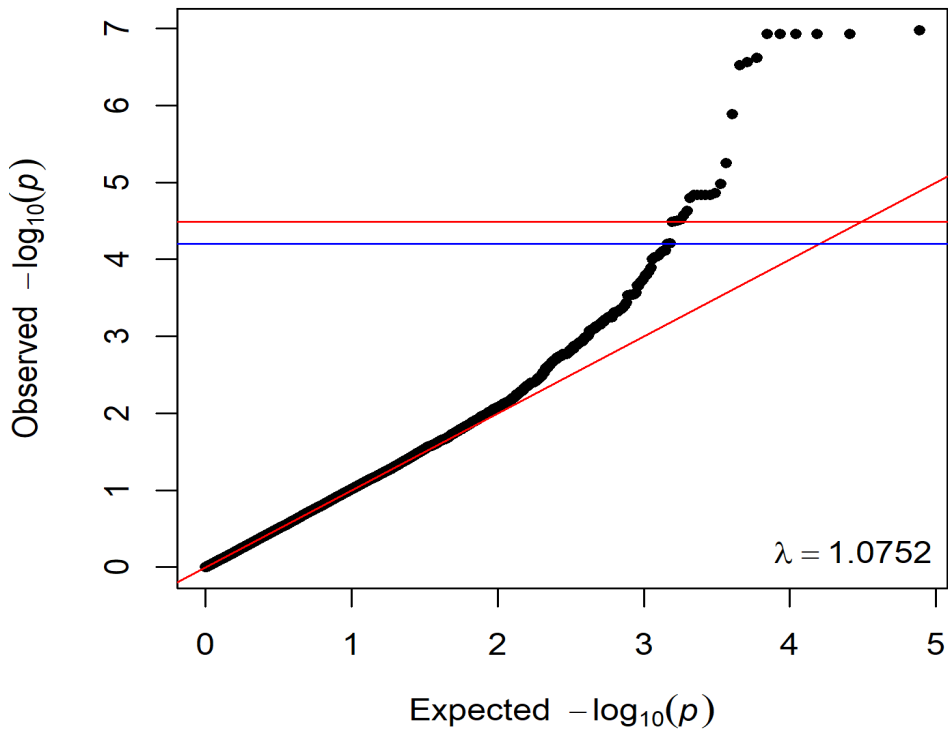
PUFA/SFA in BF



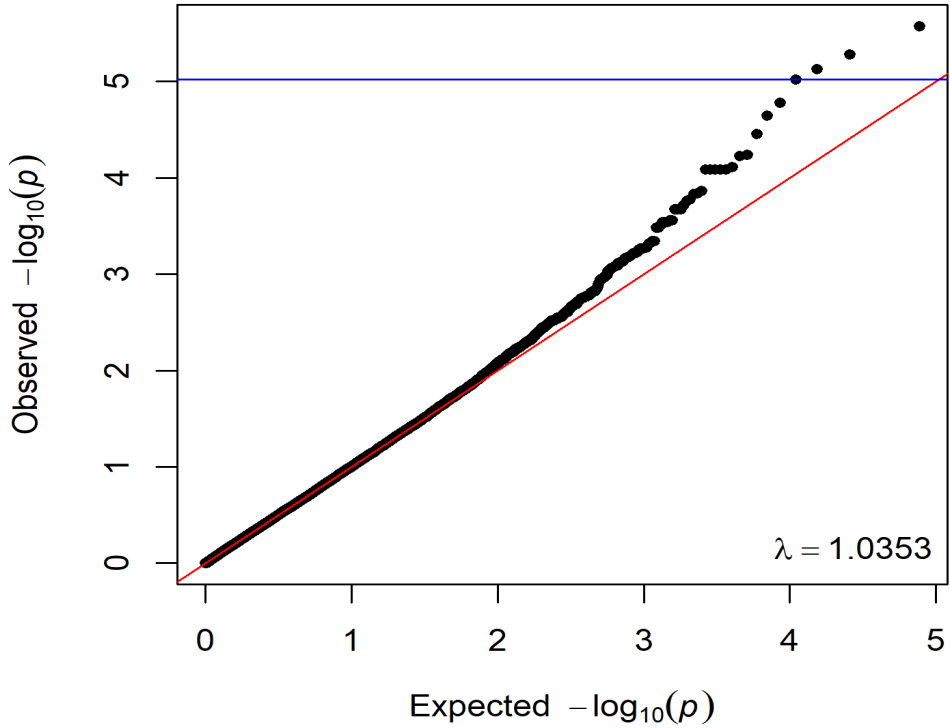
C18:0 in LD



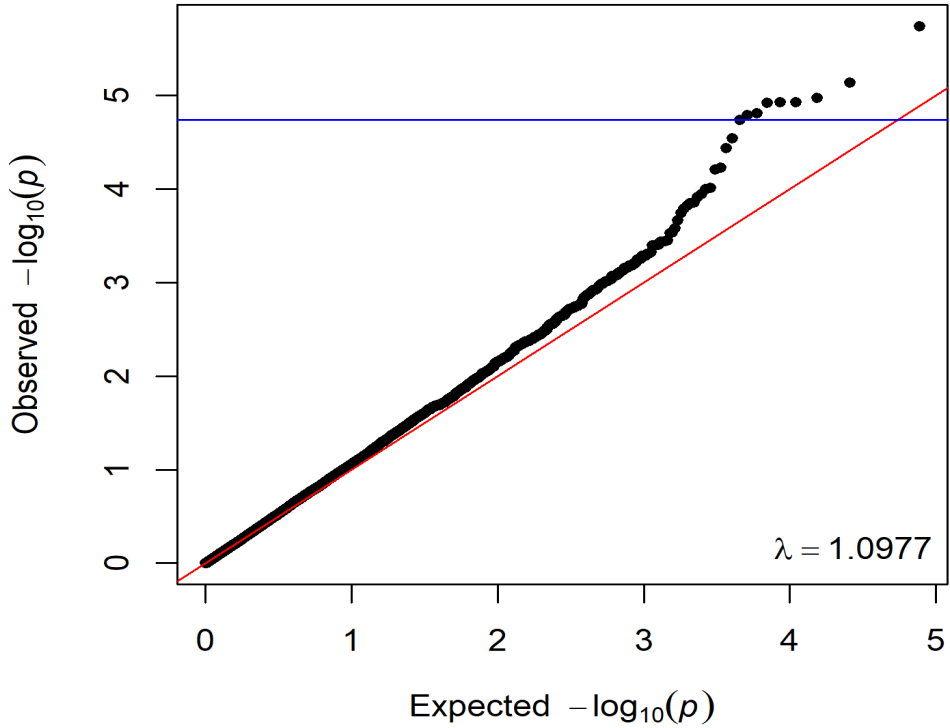
C18:1(n-9)/C18:0 in LD



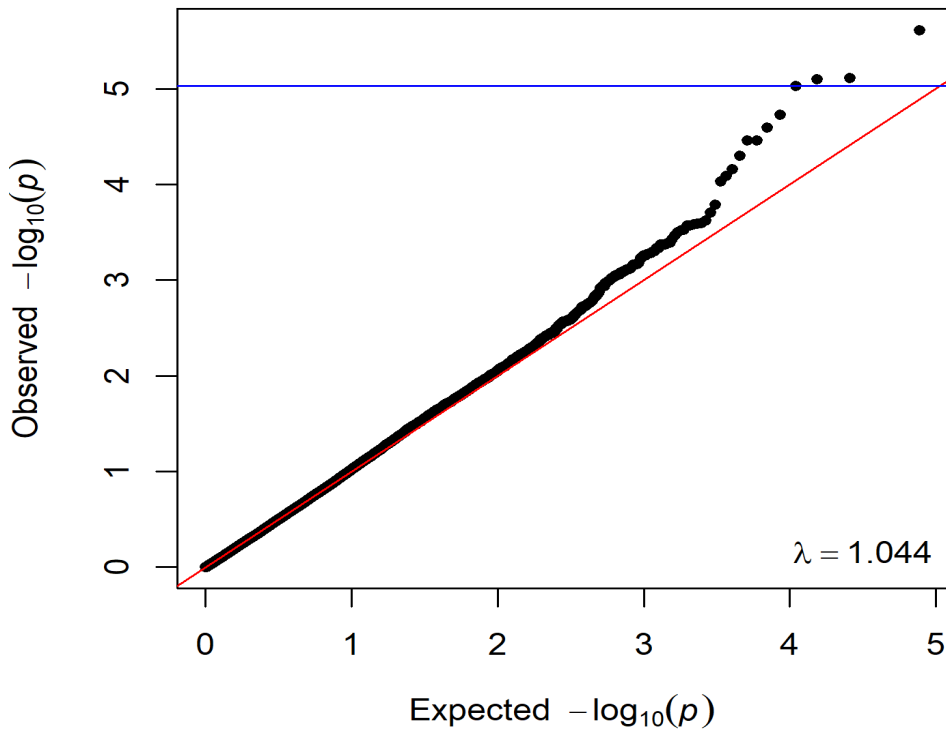
C20:0 in LD



C20:3(n-3) in LD



C20:4(n-6)/C20:3(n-6) in LD



MUFA/SFA in LD

