

Supplementary tables and figures

For 'Partitioning for genomic variance reveals biological pathways associated with udder health and milk production traits in dairy cattle'

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Kolmogorov-Smirnov Tests

Here, we would like to estimate the difference between our empirically estimated distributions and the χ^2 distributions more statistically, that is with the Kolmogorov-Smirnov test.

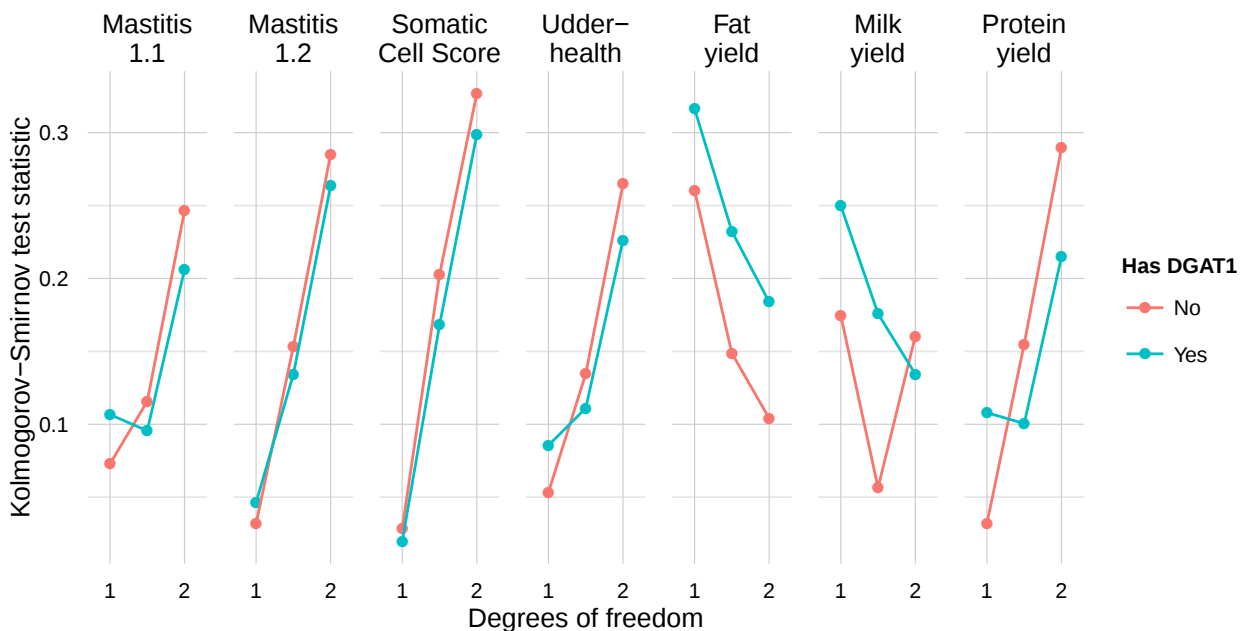


Figure S1: *Distance between observed likelihood ratios and theoretical χ^2 distributions.*

1 Group size vs. H_{set}^2

The figures in this section displays the proportion of explained genetic variance explained by random gene groups, as a function of the number of markers in the groups ('group size'), plotted together with the 50th and 95th percentile. The groups are colour coded by whether the likelihood ratio is larger than 95% of the likelihood ratios of the same trait. The regression lines are coloured by whether they describe groups containing DGAT1 genes; the grey, dashed line corresponds to the naïve expectation of the infinitesimal model, where all genetic markers contribute with the same effect.

1.1 Health traits

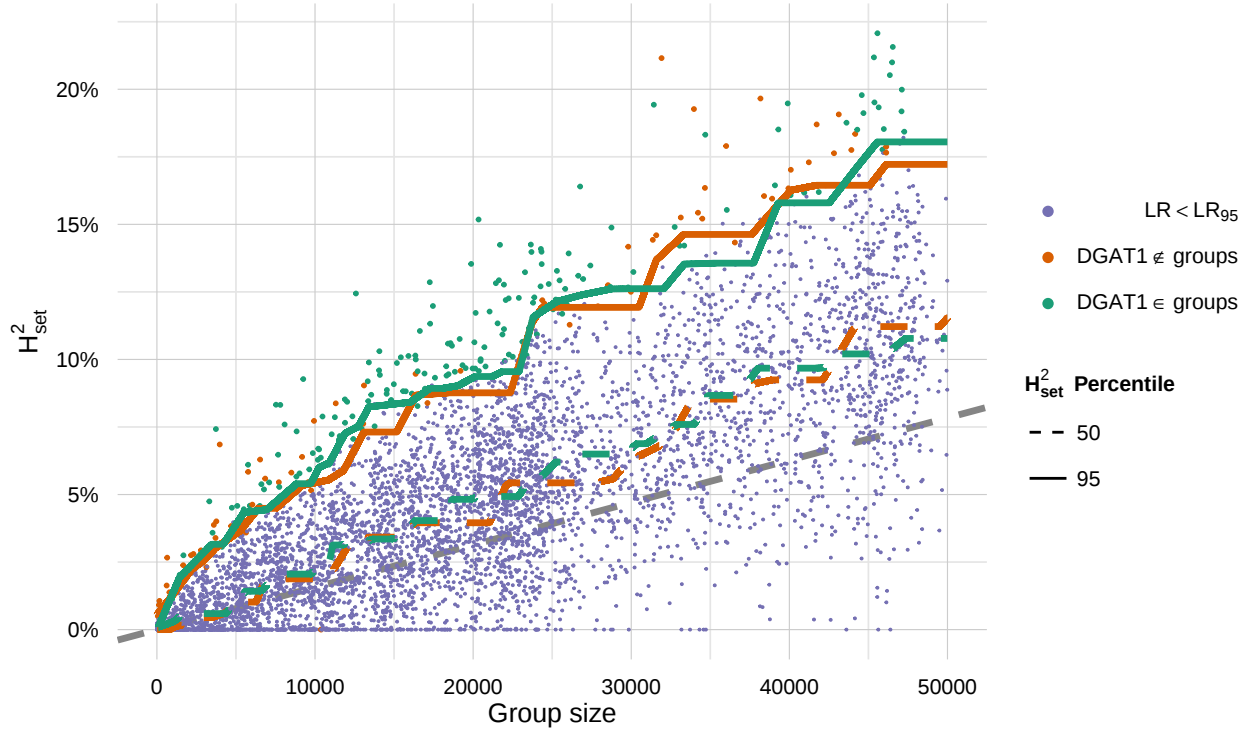


Figure S2: *Mastitis 1.1*

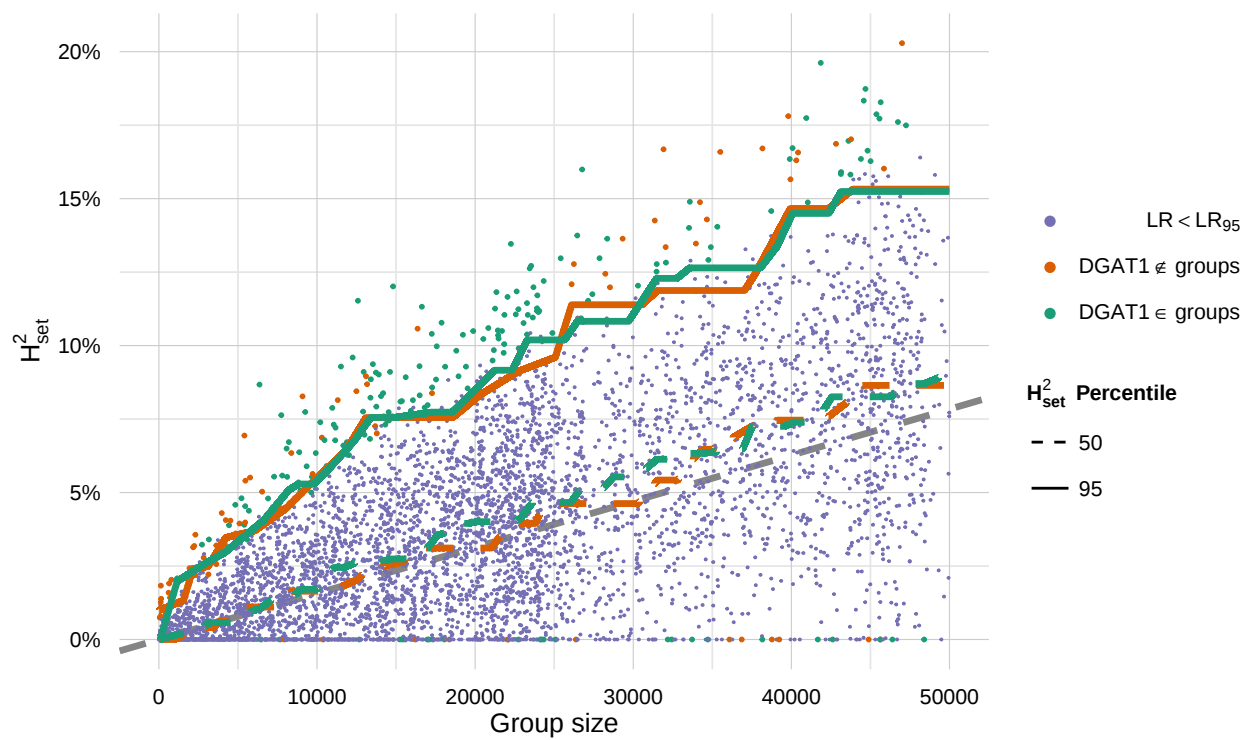


Figure S3: Mastitis 1.2

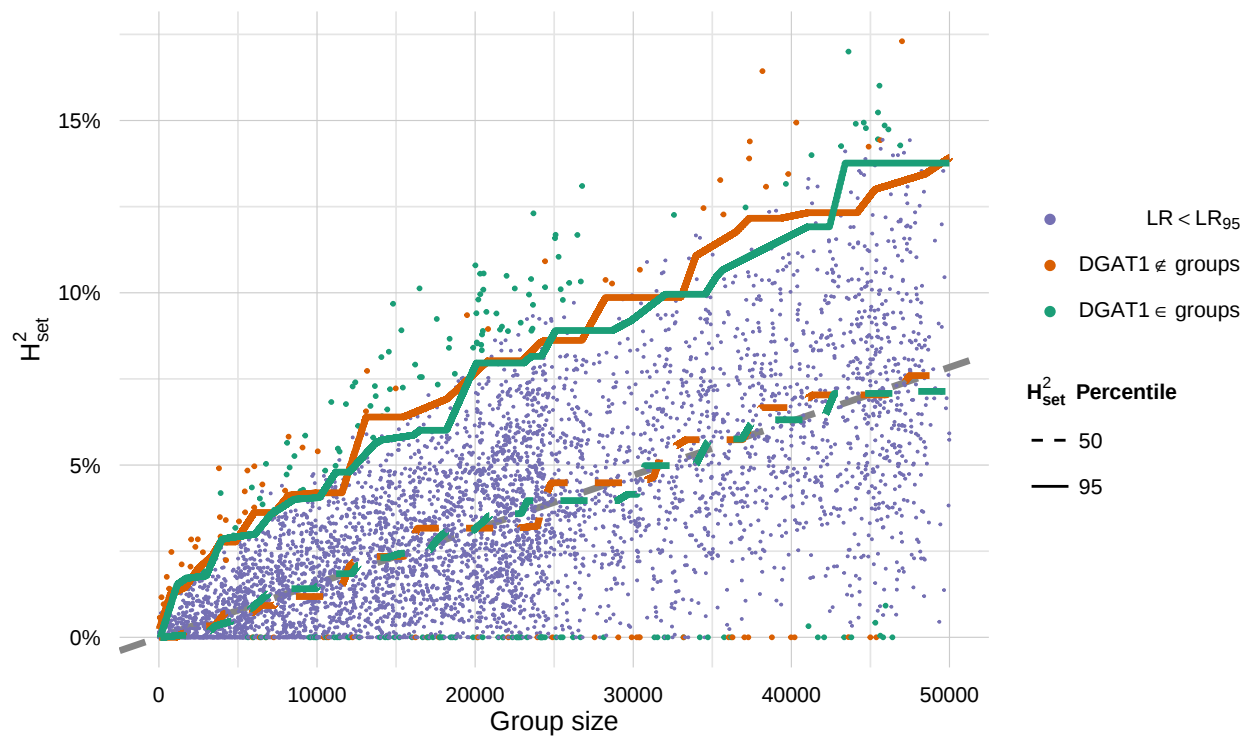


Figure S4: Somatic Cell Score

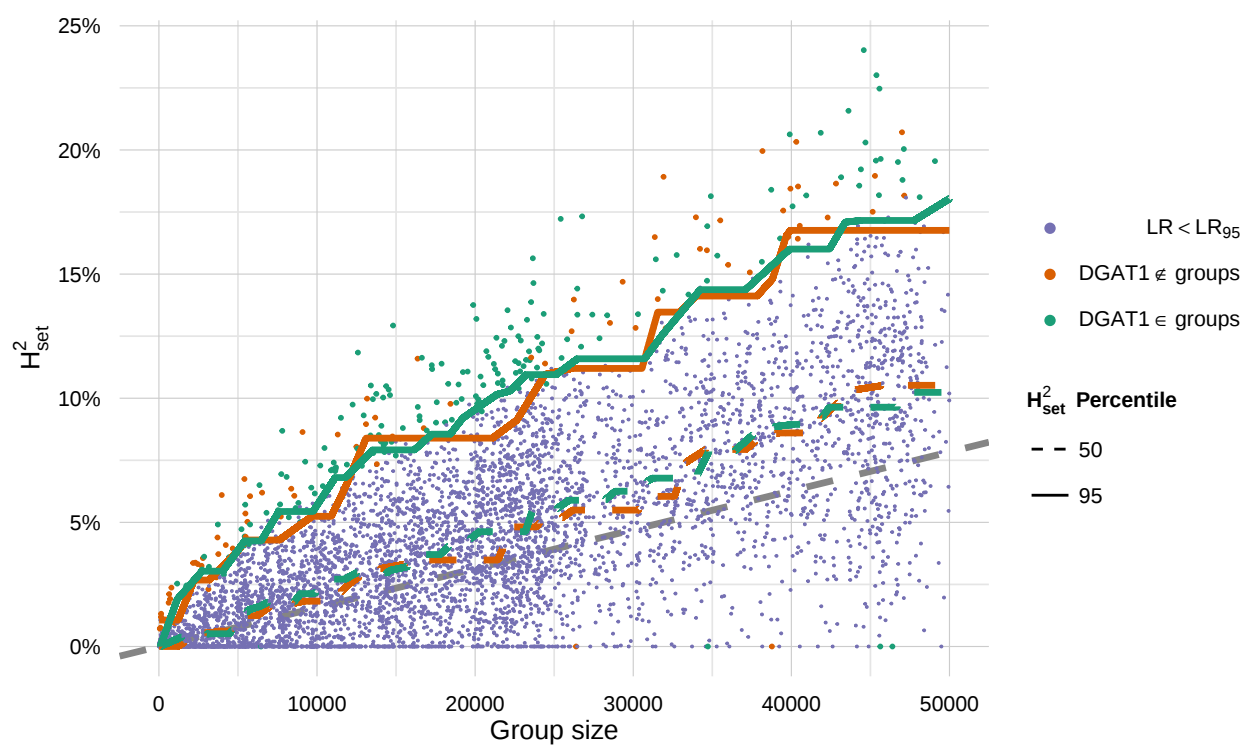


Figure S5: *Udder-health*

1.2 Production traits

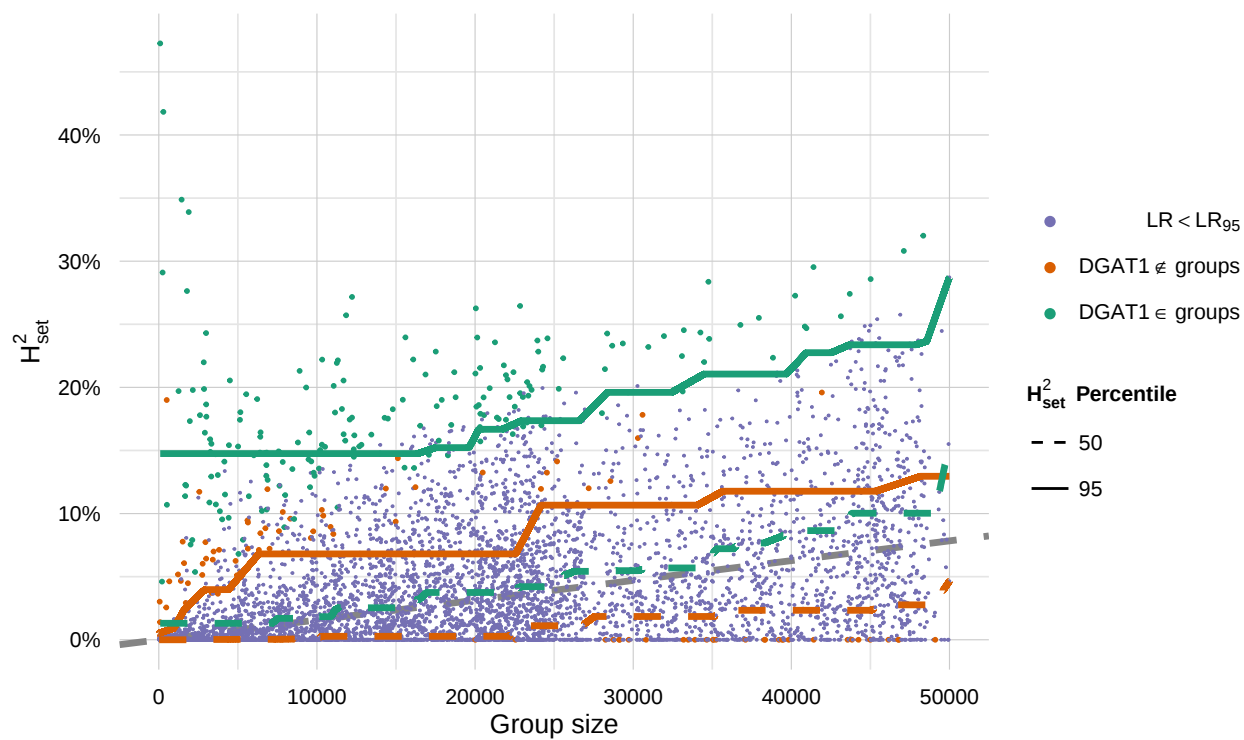


Figure S6: *Fat yield*

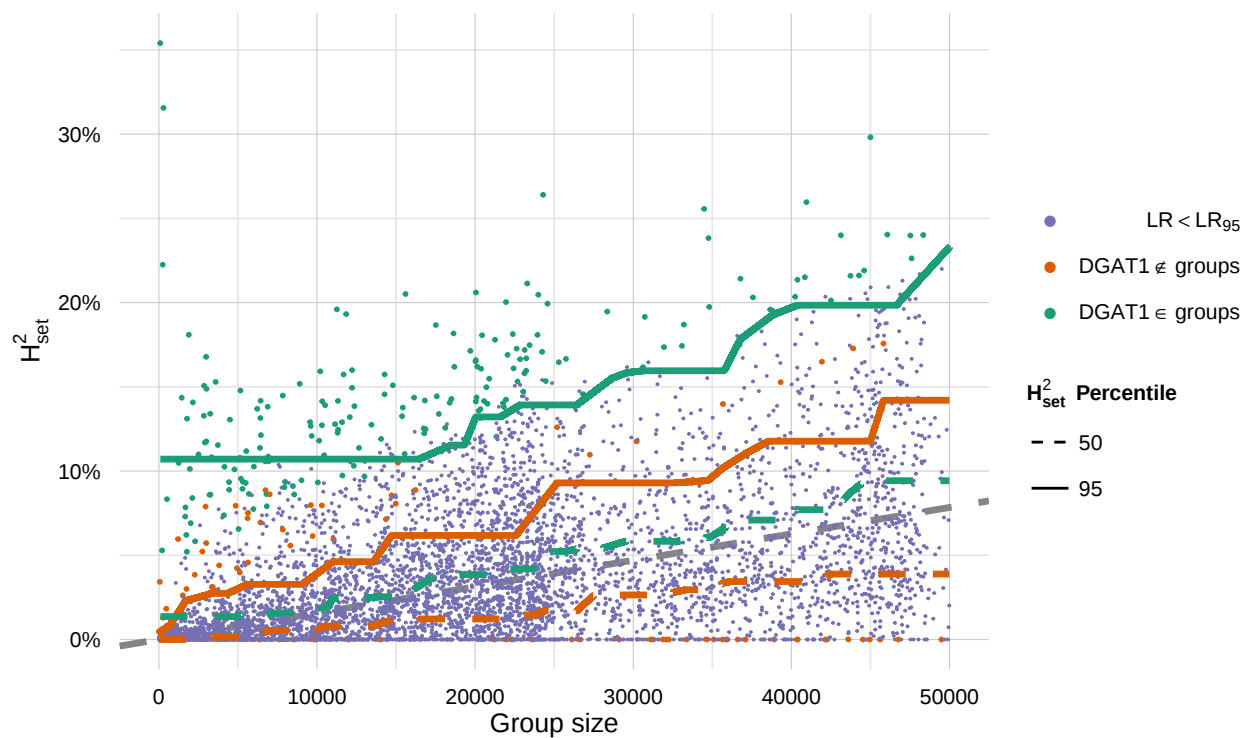


Figure S7: *Milk yield*

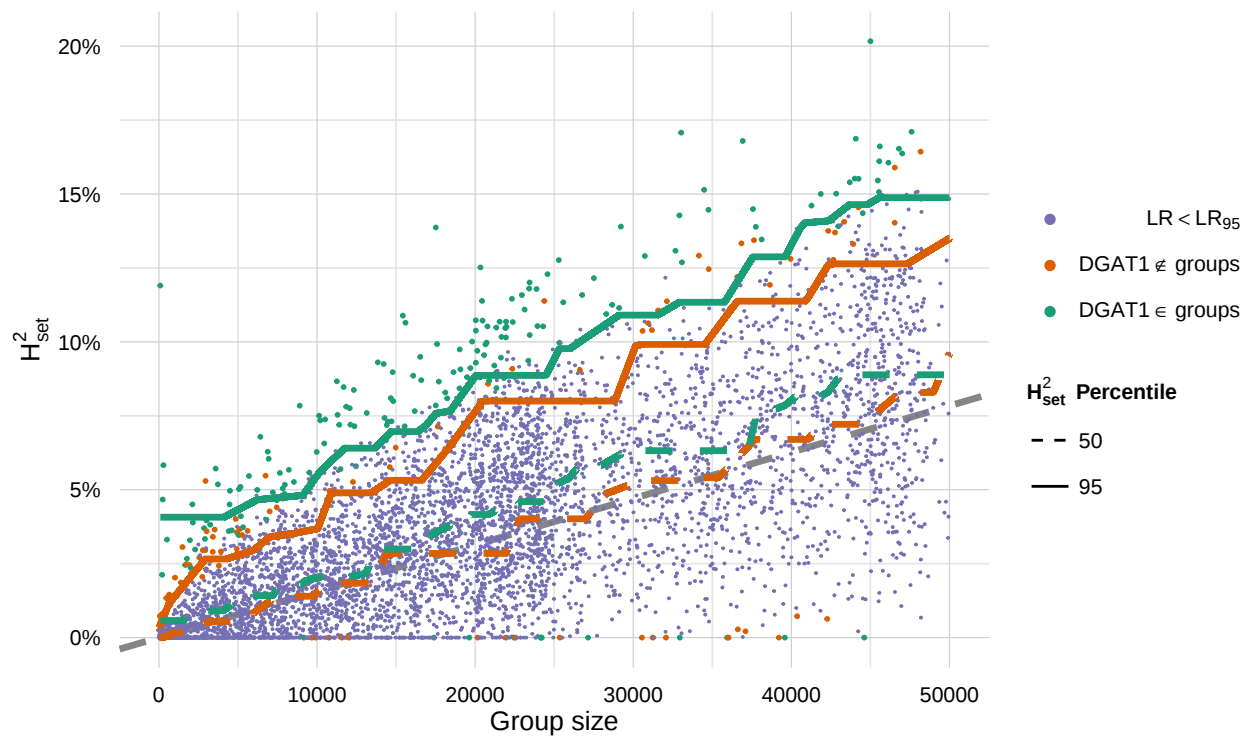


Figure S8: *Protein yield*