File S1: confidence intervals for broad-sense heritability

Confidence intervals for the broad-sense heritability estimates obtain from the ANOVA mean sums of squares are traditionally obtained from the ratio $F = MS(G)/MS(E)$ and the quantiles of the F-distribution with the corresponding degrees of freedom. Given n genotypes with $r_1, \ldots, r_n$ replicates, the intervals are given by

$$\frac{F/F_{\mathrm{df1},\mathrm{df2},0.95} - 1}{F/F_{\mathrm{df1},\mathrm{df2},0.95} + \bar{r} - 1} < H^2 < \frac{F/F_{\mathrm{df1},\mathrm{df2},0.05} - 1}{F/F_{\mathrm{df1},\mathrm{df2},0.05} + \bar{r} - 1},$$

where $\mathrm{df1} = n-1$, $\mathrm{df2} = \sum(r_i - 1)$ and $\bar{r} = (n-1)^{-1}(\sum r_i - (\sum r_i^2)/(\sum r_i))$. In case of a balanced design with $r_i = r$ replicates, this reduces to $\bar{r} = r$ and $\mathrm{df2} = n(r-1)$. See [1] (p.563) or [2].