**Table S3.** Results of variance component estimation using ASReml for starvation resistance. Different linear models for individual trait records were investigated.

| Starvation Resistance | $\hat{\sigma}^2_{\text{line}}$ | $\hat{\sigma}^2_{\text{sex}*\text{line}}$ | $\hat{\sigma}^{2}_{\text{rep(sex}*\text{line)}}$,[1] | $\hat{\sigma}^2_g$ | $\hat{\sigma}^2_{g\times g}$ | $\hat{\sigma}^2_{\text{residual}}$ | $\ln(L)$[2] | $\hat{H}^{2}_{\text{Model 1}}$,[3] | $\hat{h}^{2}_{\text{Model 2/3}}$,[4] |
|---|---|---|---|---|---|---|---|---|---|
| Model 1 | 87.97[5] (12.74) | 39.65 (5.06) | 17.00 (1.01) | | | 88.00 (1.03) | -46097.51 | 0.59 (0.02) | |
| Model 2 | 0.00 | 39.35 (4.99) | 17.00 (1.01) | 43.13 (6.32) | | 88.00 (1.03) | -46093.63**,[6] | | 0.25 (0.03) |
| Model 3 | 0.00 | 39.35 (4.98) | 17.00 (1.01) | 43.13 (6.32) | 0.00 | 88.00 (1.03) | -46093.63 | | 0.25 (0.03) |
| Model 1 f[7] | 167.62 (19.63) | | 18.22 (1.64) | | | 113.92 (1.88) | -24174.10 | 0.60 (0.03) | |
| Model 2 f | 9.07 (28.35) | | 18.22 (1.64) | 78.24 (18.02) | | 113.92 (1.88) | -24170.31** | | 0.39 (0.11) |
| Model 3 f | 9.08 (28.34) | | 18.22 (1.64) | 78.24 (18.02) | 0.00 | 113.92 (1.88) | -24170.31 | | 0.39 (0.11) |
| Model 1 m[8] | 87.57 (10.40) | | 15.73 (1.21) | | | 61.89 (1.02) | -21617.19 | 0.59 (0.03) | |
| Model 2 m | 5.23 (15.49) | | 15.73 (1.21) | 40.51 (9.68) | | 61.89 (1.02) | -21613.34** | | 0.38 (0.11) |
| Model 3 m | 5.23 (15.49) | | 15.73 (1.21) | 40.51 (9.68) | 0.00 | 61.89 (1.02) | -21613.34 | | 0.38 (0.11) |

[1] or "rep(line)" if factor sex is not included

[2] loglikelihood

[3] broad-sense heritability, standard errors in parentheses

[4] narrow-sense heritability, standard errors in parentheses

[5] estimated variance components, standard errors in parentheses

[6] The superscript ** indicates the 1%-significance of Model 2 compared to the Model 1 without $g$-component based on a likelihood ratio test.

[7] Only measurements of female Drosophila were used.

[8] Only measurements of male Drosophila were used.