**Table S3 – Summary statistics about genomic inbreeding in Ames-H**

| Feature | Standard deviation | Range | Trait | Effect estimate (p-value) |
|---|---|---|---|---|
| $F$ | 0.059 | (-0.091, 0.55) | DTS | -0.089 (0.93) |
| | | | PH | -2.6 ($2.2 \times 10^{-3}$) |
| | | | GY | -3.6 ($1.4 \times 10^{-3}$) |
| $F^2$ | 0.015 | ($2.2 \times 10^{-9}$, 0.30) | DTS | 7.7 ($7.3 \times 10^{-5}$) |
| | | | PH | 0.97 (0.63) |
| | | | GY | -0.14 (0.96) |

Effects tested were $F$ (linear effect of genomic inbreeding) and $F^2$ (quadratic effect of genomic

inbreeding); standard deviation of genomic inbreeding coefficients were calculated in Ames-H;

p-values were obtained from Wald tests for effects of $F$ or $F^2$ in Ames-H.