## Table S1 Variance components as a proportion of the total variance.

| Variance Components | P_A* | M_A* | P_AD* | M_AD* | P_A#A* | M_A#A* | P_D#D* | M_D#D* | P_A#D* | M_A#D* |
|---|---|---|---|---|---|---|---|---|---|---|
| Incomplete block | 0.218 | 0.207 | 0.227 | 0.217 | 0.228 | 0.234 | 0.228 | 0.233 | 0.228 | 0.234 |
| Additive (Add) | 0.320 | 0.347 | 0.235 | 0.199 | 0.233 | 0.088 | 0.228 | 0.139 | 0.231 | 0.125 |
| Dominance (Dom) | | | 0.056 | 0.117 | 0.055 | 0.022 | 0.058 | 0.009 | 0.056 | 0.006 |
| Epistasis Add x Add | | | | | 0.000 | 0.154 | | | | |
| Epistasis Dom x Dom | | | | | | | 0.000 | 0.121 | | |
| Epistasis Add x Dom | | | | | | | | | 0.000 | 0.135 |
| Culture x Add | 0.017 | 0.013 | 0.010 | 0.014 | 0.000 | 0.001 | 0.008 | 0.008 | 0.008 | 0.006 |
| Culture x Dom | | | 0.012 | | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |
| culture x (Add x Add) | | | | | 0.026 | 0.025 | | | | |
| culture x (Dom x Dom) | | | | | | | 0.019 | 0.019 | | |
| culture x (Add x Dom) | | | | | | | | | 0.018 | 0.020 |
| Residual variance | 0.445 | 0.433 | 0.460 | 0.452 | 0.459 | 0.475 | 0.458 | 0.471 | 0.459 | 0.473 |
| Total Variance | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 | 1.000 |

*Each column represents a different model. See Table 1 for model description

**Table S2 Estimates of genetic parameters (standard errors in parenthesis) and goodness-of-fit measures using Vitezica *et al.* (2013) parameterization.**

| | P_A | M_A | P_AD | M_AD | P_A#A | M_A#A | P_D#D | M_D#D | P_A#D | M_A#D |
|---|---|---|---|---|---|---|---|---|---|---|
| $h^2$ | 0.32 | 0.347 | 0.235 | 0.239 | 0.233 | 0.10 | 0.228 | 0.162 | 0.231 | 0.149 |
| SE($h^2$) | (0.017) | (0.018) | (0.047) | (0.027) | (0.047) | (0.041) | (0.046) | (0.03) | (0.047) | (0.032) |
| $d^2$ | | | 0.056 | 0.076 | 0.055 | 0.000 | 0.058 | 0.006 | 0.056 | 0.000 |
| SE($d^2$) | na | na | (0.033) | (0.02) | (0.033) | (0.000) | (0.032) | (0.023) | (0.043) | (0.000) |
| $i^2$ | | | | | 0.000 | 0.164 | 0.000 | 0.112 | 0.000 | 0.124 |
| SE($i^2$) | na | na | na | na | (0.000) | (0.032) | (0.000) | (0.031) | (0.000) | (0.024) |
| $H^2$ | 0.32 | 0.347 | 0.29 | 0.315 | 0.288 | 0.265 | 0.286 | 0.280 | 0.288 | 0.273 |
| SE($H^2$) | (0.017) | (0.018) | (0.021) | (0.018) | (0.021) | (0.019) | (0.021) | (0.018) | (0.021) | (0.018) |
| LogL | -1299.40 | -1323.73 | -1295.37 | -1306.69 | -1294.83 | -1293.75 | -1293.90 | -1294.81 | -1294.38 | -1293.55 |
| AIC | 2606.80 | 2655.46 | 2602.74 | 2625.38 | 2605.66 | 2603.50 | 2603.80 | 2605.62 | 2604.76 | 2603.10 |

*Each column represents a different model. See Table 1 for model description

**Table S3 Sampling correlation matrix for all models tested.** Above diagonal pedigree-based and below diagonal marker-based models. additive models 1 and 6 (A),additive plus dominance models 2 and 7 (B), additive plus dominance plus additive-by-additive models 3 and 8 (C), additive plus dominance plus dominance-by-dominance models 4 and 9 (D), and additive plus dominance plus additive-by-dominance models 5 and 10 (E). Estimated effects are Iblock = incomplete block, Add = Additive, Dom = dominance and Culture = silviculture type.

| **A** | Iblock | Add | Culture x Add | Residual |
|---|---|---|---|---|
| Iblock | 1.00 | 0.00 | 0.01 | -0.07 |
| Add | 0.00 | 1.00 | -0.14 | -0.08 |
| Culture x Add | 0.01 | -0.08 | 1.00 | -0.24 |
| Residual | -0.07 | -0.13 | -0.19 | 1.00 |

| **B** | Iblock | Add | Dom | Culture x Add | Culture x Dom | Residual |
|---|---|---|---|---|---|---|
| Iblock | 1.00 | 0.00 | 0.00 | 0.00 | 0.01 | -0.07 |
| Add | 0.00 | 1.00 | -0.90 | -0.08 | 0.05 | -0.04 |
| Dom | 0.00 | -0.70 | 1.00 | 0.09 | -0.15 | 0.02 |
| Culture x Add | 0.00 | -0.12 | 0.12 | 1.00 | -0.62 | 0.02 |
| Culture x Dom | 0.01 | 0.09 | -0.17 | -0.69 | 1.00 | -0.26 |
| Residual | -0.07 | -0.05 | -0.02 | 0.00 | -0.19 | 1.00 |

| **C** | Iblock | Add | Dom | Add x Add* | Culture x Add | Culture x Dom | Culture x (Add x Add) | Residual |
|---|---|---|---|---|---|---|---|---|
| Iblock | 1.00 | 0.00 | 0.00 | - | -0.07 | -0.07 | 0.01 | -0.07 |
| Add | 0.00 | 1.00 | -0.89 | - | -0.02 | -0.02 | -0.04 | -0.02 |
| Dom | 0.00 | -0.31 | 1.00 | - | 0.01 | 0.01 | -0.07 | 0.01 |
| Add x Add | 0.00 | -0.52 | -0.52 | $1.00^{+}$ | - | - | - | - |
| Culture x Add | 0.00 | -0.09 | 0.00 | 0.13 | 1.00 | 1.00 | -0.30 | 1.00 |
| Culture x Dom | -0.07 | 0.01 | 0.00 | -0.02 | 0.13 | 1.00 | -0.30 | 1.00 |
| Culture x (Add x Add) | 0.01 | 0.07 | 0.00 | -0.16 | -0.77 | -0.29 | 1.00 | -0.30 |
| Residual | -0.07 | 0.01 | 0.00 | -0.02 | 0.13 | 1.00 | -0.29 | 1.00 |

| **D** | Iblock | Add | Dom | Dom x Dom* | Culture x Add | Culture x Dom | Culture x (Dom x Dom) | Residual |
|---|---|---|---|---|---|---|---|---|
| Iblock | 1.00 | 0.00 | 0.00 | - | 0.01 | -0.07 | 0.00 | -0.07 |
| Add | 0.00 | 1.00 | -0.89 | - | -0.02 | -0.01 | -0.05 | -0.01 |
| Dom | 0.00 | -0.45 | 1.00 | - | 0.04 | 0.01 | -0.07 | 0.01 |
| Dom x Dom | 0.00 | -0.27 | -0.58 | 1.00[+] | - | - | - | - |
| Culture x Add | 0.00 | -0.09 | 0.00 | 0.11 | 1.00 | 0.02 | -0.48 | 0.02 |
| Culture x Dom | -0.07 | 0.00 | 0.01 | -0.01 | 0.04 | 1.00 | -0.31 | 1.00 |
| Culture x (Dom x Dom) | 0.01 | 0.04 | 0.00 | -0.18 | -0.54 | -0.31 | 1.00 | -0.31 |
| Residual | -0.07 | 0.00 | 0.01 | -0.01 | 0.04 | 1.00 | -0.31 | 1.00 |

| **E** | Iblock | Add | Dom | Add x Dom* | Culture x Add | Culture x Dom | Culture x (Add x Dom) | Residual |
|---|---|---|---|---|---|---|---|---|
| Iblock | 1.00 | 0.00 | 0.00 | - | 0.01 | -0.07 | 0.00 | -0.07 |
| Add | 0.00 | 1.00 | -0.89 | - | -0.03 | -0.02 | -0.02 | -0.02 |
| Dom | 0.00 | -0.40 | 1.00 | - | 0.06 | 0.01 | -0.10 | 0.01 |
| Add x Dom | 0.00 | -0.34 | -0.58 | 1.00[+] | - | - | - | - |
| Culture x Add | 0.00 | -0.09 | 0.00 | 0.12 | 1.00 | 0.03 | -0.54 | 0.03 |
| Culture x Dom | -0.07 | 0.00 | 0.01 | -0.02 | 0.08 | 1.00 | -0.30 | 1.00 |
| Culture x (Add x Dom) | 0.01 | 0.05 | 0.00 | -0.17 | -0.63 | -0.30 | 1.00 | -0.30 |
| Residual | -0.07 | 0.00 | 0.01 | -0.02 | 0.08 | 1.00 | -0.30 | 1.00 |

*Correlation of epistasis with other effects were not calculated in pedigree-based models as epistasis had no variance (See Table 2)

[+] Value from marker-base method