

Figure S1. Cumulative proportion of variance explained by eigenvalues for models for each of the eight traits. The models considered are only additive effects from the registered pedigree ($P_{exp}A$), pseudo-pedigree (PA) and genomics-based relationships (GA) (left); additive and dominance interaction from registered pedigree ($P_{exp}AD$), pseudo-pedigree (PAD) and genomics-based relationships (GAD) (middle panels); additive, dominance and epistasis interaction from and genomics-based relationships (GAD) (right panels). The diagonal represents an orthogonal correlation matrix where no confounding occurs between variance components.

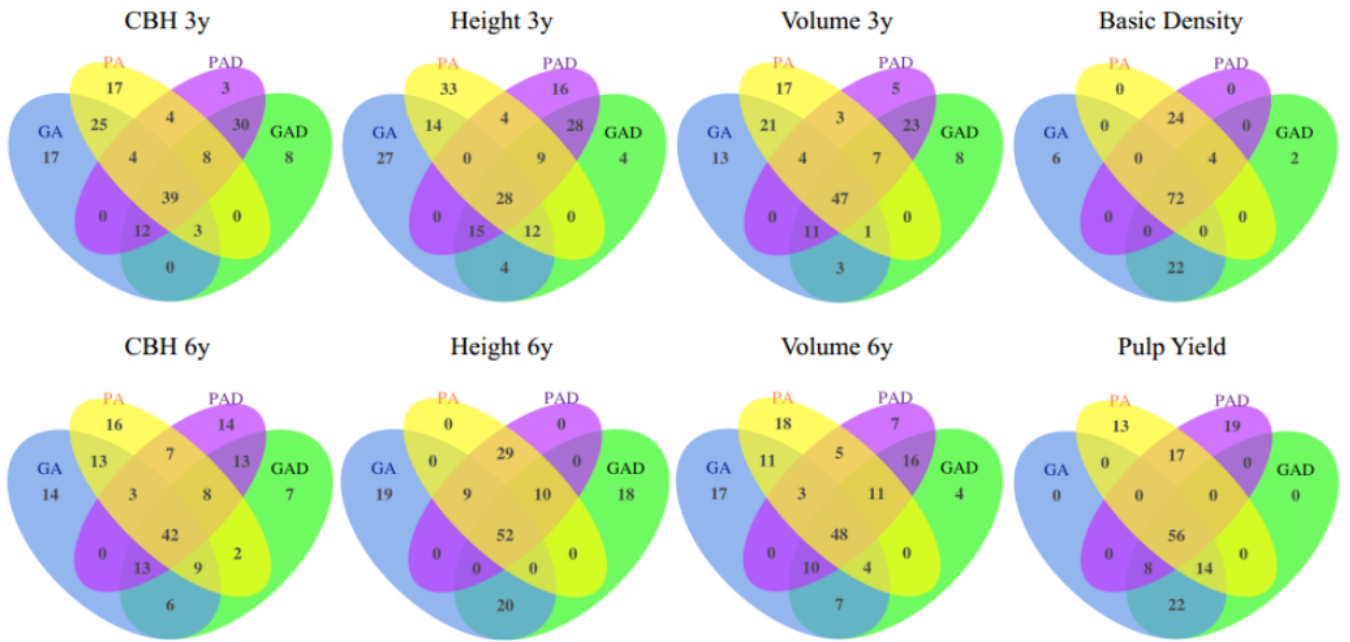


Figure S2. Plots of overlap numbers for the top 100 performing individuals for eight traits, comparing results from GA, GAD, PA and PAD models.

Table S1. Model fit of breeding and genetic values

| Trait | Model | Matrix | | | | | |
|---------------|-------|-------------------------------------|-------------------------------------|-------------------------------------|-------------------------------------|-------------------------------------|-------------------------------------|
| | | G | | P | | P _{exp} | |
| | | $r(\hat{A}_{full}, \hat{Y}_{full})$ | $r(\hat{G}_{full}, \hat{Y}_{full})$ | $r(\hat{A}_{full}, \hat{Y}_{full})$ | $r(\hat{G}_{full}, \hat{Y}_{full})$ | $r(\hat{A}_{full}, \hat{Y}_{full})$ | $r(\hat{G}_{full}, \hat{Y}_{full})$ |
| CBH3y | A | 0.629* | - | 0.679 | - | 0.599 | - |
| | AD | 0.612 | 0.754 | 0.64 | 0.978 | 0.599 | 0.599 |
| | ADE | 0.575 | 0.985 | - | - | - | - |
| CBH6y | A | 0.669 | - | 0.717 | - | 0.664 | - |
| | AD | 0.677 | 0.829 | 0.698 | 0.961 | 0.664 | 0.664 |
| | ADE | 0.664 | 0.908 | - | - | - | - |
| Height3y | A | 0.685 | - | 0.721 | - | 0.614 | - |
| | AD | 0.659 | 0.865 | 0.686 | 1 | 0.609 | 0.941 |
| | ADE | 0.617 | 0.975 | - | - | - | - |
| Height6y | A | 0.674 | - | 0.727 | - | 0.656 | - |
| | AD | 0.673 | 0.811 | 0.727 | 0.727 | 0.656 | 0.656 |
| | ADE | 0.673 | 0.811 | - | - | - | - |
| Volume3y | A | 0.689 | - | 0.736 | - | 0.603 | - |
| | AD | 0.672 | 0.804 | 0.711 | 0.97 | 0.603 | 0.603 |
| | ADE | 0.643 | 0.965 | - | - | - | - |
| Volume6y | A | 0.673 | - | 0.748 | - | 0.638 | - |
| | AD | 0.659 | 0.843 | 0.738 | 0.937 | 0.638 | 0.638 |
| | ADE | 0.648 | 0.922 | - | - | - | - |
| Basic Density | A | 0.775 | - | 0.881 | - | 0.751 | - |
| | AD | 0.764 | 0.822 | 0.881 | 0.881 | 0.742 | 0.857 |
| | ADE | 0.764 | 0.822 | - | - | - | - |
| Pulp Yield | A | 0.842 | - | 0.874 | - | 0.801 | - |
| | AD | 0.842 | 0.842 | 0.877 | 0.992 | 0.79 | 0.988 |
| | ADE | 0.842 | 0.842 | - | - | - | - |

*Model fit: correlation between phenotypes and breeding values/genetic values of full data set