Table S2. Double-structure evaluation: Predictive abilities\(^1\) with standard deviation for the multiple-trait model (MTM) and for structural equation models (SEM) including both genomic (\(\Lambda_{G}\)) and residual (\(\Lambda_{E}\)) trait structure denoted by the Bayesian network (BN) algorithms they originate from.

| BN giving \(\Lambda_{E}\) | BN giving \(\Lambda_{G}\) | DMY\(^2\) | DMC | PH | DtTAS | DtSILK |
|------------------------|------------------------|---------|-----|-----|-------|-------|
| Dent                   |                        |         |     |     |       |       |
| TABU 1                 | GS 3                   | 0.53 (0.05) | 0.64 (0.04) | 0.69 (0.04) | 0.63 (0.05) | 0.68 (0.04) |
| TABU 2                 | GS 3                   | 0.53 (0.05) | 0.64 (0.04) | 0.69 (0.04) | 0.63 (0.05) | 0.68 (0.04) |
| TABU 1                 | GS 1, 2, 4             | 0.53 (0.05) | 0.64 (0.04) | 0.69 (0.04) | 0.63 (0.05) | 0.68 (0.04) |
| TABU 1                 | TABU 1, 2              | 0.53 (0.05) | 0.64 (0.04) | 0.69 (0.04) | 0.63 (0.05) | 0.68 (0.04) |
| TABU 2                 | TABU 1, 2              | 0.53 (0.05) | 0.64 (0.04) | 0.69 (0.04) | 0.63 (0.05) | 0.68 (0.04) |
| TABU 2                 | GS 1, 2, 4             | 0.53 (0.05) | 0.64 (0.04) | 0.69 (0.04) | 0.62 (0.05) | 0.68 (0.04) |
| -----                  | -----                  | 0.52 (0.05) | 0.64 (0.04) | 0.69 (0.04) | 0.62 (0.04) | 0.68 (0.04) |
| GS 1, 2, 3, 4          | GS 3                   | 0.53 (0.05) | 0.63 (0.04) | 0.69 (0.04) | 0.62 (0.04) | 0.67 (0.04) |
| GS 1, 2, 3, 4          | GS 1, 2, 4             | 0.53 (0.05) | 0.63 (0.04) | 0.69 (0.04) | 0.62 (0.04) | 0.67 (0.04) |
| GS 1, 2, 3, 4          | TABU 1, 2              | 0.53 (0.05) | 0.63 (0.04) | 0.69 (0.04) | 0.62 (0.04) | 0.67 (0.04) |
| Flint                  |                        |         |     |     |       |       |
| -----                  | -----                  | 0.64 (0.04) | 0.67 (0.05) | 0.70 (0.04) | 0.74 (0.04) | 0.76 (0.04) |
| TABU 1, 2              | TABU 1                 | 0.63 (0.04) | 0.67 (0.05) | 0.70 (0.04) | 0.74 (0.03) | 0.76 (0.03) |
| TABU 1, 2              | GS 1, 2, 3, 4          | 0.63 (0.04) | 0.67 (0.05) | 0.70 (0.04) | 0.74 (0.03) | 0.76 (0.03) |
| TABU 1, 2              | TABU 2                 | 0.63 (0.04) | 0.67 (0.05) | 0.70 (0.05) | 0.74 (0.04) | 0.76 (0.04) |
| GS 1, 2, 3, 4          | TABU 2                 | 0.64 (0.04) | 0.67 (0.05) | 0.68 (0.04) | 0.73 (0.03) | 0.75 (0.03) |
| GS 1, 2, 3, 4          | TABU 1                 | 0.64 (0.04) | 0.67 (0.05) | 0.68 (0.05) | 0.73 (0.04) | 0.75 (0.04) |
| GS 1, 2, 3, 4          | GS 1, 2, 3, 4          | 0.64 (0.04) | 0.67 (0.05) | 0.68 (0.05) | 0.73 (0.04) | 0.75 (0.04) |

For notation of BN algorithms see material and methods, “Learning genomic and residual Bayesian networks”.

\(^1\) Average of 10 random 5-fold cross-validations

\(^2\) Traits: DMY biomass dry matter yield (dt/ha), DMC biomass dry matter content (%), PH plant height (cm), DtTAS days to tasseling (days), DtSILK days to silking (days)