Table S1. Single-structure evaluation: Predictive abilities[1] with standard deviation for the multiple-trait model (MTM) and for structural equation models (SEM) including a genomic ($\mathbf{\Lambda}_{\widehat{U}^*}$) or residual ($\mathbf{\Lambda}_{\widehat{E}}$) trait structure denoted by the Bayesian network (BN) algorithm it originates from.

BN giving $\Lambda_{\widehat{U}^*}$	**BN giving $\Lambda_{\widehat{E}}$**	**DMY[2]**	**DMC**	**PH**	**DtTAS**	**DtSILK**
Dent						
-----	GS 3	0.53 (0.05)	0.64 (0.04)	0.69 (0.04)	0.63 (0.05)	0.68 (0.04)
-----	GS 1, 2, 4	0.53 (0.05)	0.64 (0.04)	0.69 (0.04)	0.62 (0.05)	0.68 (0.04)
-----	TABU 1, 2	0.53 (0.05)	0.64 (0.04)	0.69 (0.04)	0.63 (0.05)	0.68 (0.04)
TABU 1	-----	0.52 (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)
TABU 2	-----	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	-----	0.52 (0.05)	0.63 (0.04)	0.69 (0.04)	0.62 (0.04)	0.67 (0.03)
Flint						
-----	TABU 1	0.64 (0.04)	0.67 (0.05)	0.70 (0.04)	0.74 (0.04)	0.76 (0.04)
-----	GS 1, 2, 3, 4	0.64 (0.04)	0.67 (0.05)	0.70 (0.04)	0.74 (0.04)	0.76 (0.04)
-----	TABU 2	0.64 (0.04)	0.67 (0.05)	0.70 (0.04)	0.74 (0.04)	0.76 (0.04)
-----	-----	0.64 (0.04)	0.67 (0.05)	0.70 (0.04)	0.74 (0.04)	0.76 (0.04)
TABU 1, 2	-----	0.62 (0.04)	0.67 (0.05)	0.69 (0.05)	0.74 (0.03)	0.75 (0.03)
GS 1, 2, 3, 4	-----	0.63 (0.04)	0.66 (0.05)	0.67 (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)