Table S 1: Prediction accuracy means and standard deviation values in five-fold cross validation across 100 replicates in traits simulated with 4, 10, 20, and 100 QTNs under the additive (Adt), dominance (Dom), and epistasis (Epi) mechanisms under heritability of 0.7 in *Miscanthus* F1 population.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| QTN | QGM | ADE | BA | MAS | RKHS | SVR |
| 4 | Adt | 0.47±0.1 | 0.48±0.1 | 0.52±0.1 | 0.45±0.1 | 0.46±0.09 |
| 4 | Dom | 0.43±0.11 | 0.41±0.09 | 0.58±0.07 | 0.37±0.08 | 0.36±0.08 |
| 4 | Epi | 0.52±0.09 | 0.57±0.09 | 0.67±0.07 | 0.5±0.09 | 0.47±0.08 |
| 10 | Adt | 0.49±0.11 | 0.5±0.09 | 0.41±0.13 | 0.46±0.1 | 0.43±0.08 |
| 10 | Dom | 0.28±0.13 | 0.22±0.1 | 0.42±0.09 | 0.23±0.09 | 0.21±0.09 |
| 10 | Epi | 0.45±0.1 | 0.42±0.11 | 0.51±0.08 | 0.41±0.11 | 0.39±0.1 |
| 20 | Adt | 0.43±0.14 | 0.46±0.09 | 0.41±0.13 | 0.41±0.1 | 0.32±0.09 |
| 20 | Dom | 0.27±0.12 | 0.15±0.1 | 0.31±0.13 | 0.17±0.1 | 0.17±0.09 |
| 20 | Epi | 0.53±0.09 | 0.53±0.09 | 0.29±0.12 | 0.52±0.1 | 0.44±0.09 |
| 100 | Adt | 0.49±0.11 | 0.51±0.08 | 0.28±0.14 | 0.48±0.09 | 0.35±0.09 |
| 100 | Dom | 0.26±0.12 | 0.17±0.1 | 0±0.12 | 0.19±0.1 | 0.26±0.09 |
| 100 | Epi | 0.51±0.11 | 0.53±0.09 | 0.25±0.13 | 0.52±0.09 | 0.41±0.09 |

Table S 2: Prediction accuracy means and standard deviation values in five fold cross validation across 100 replicates in traits simulated with 4, 10, 20, and 100 QTNs under the additive (Adt), dominance (Dom), and epistasis (Epi) mechanisms under heritability of 0.3 in *Miscanthus* F1 population.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| QTN | QGM | ADE | BA | MAS | RKHS | SVR |
| 4 | Adt | 0.17±0.16 | 0.21±0.15 | 0.25±0.16 | 0.21±0.15 | 0.2±0.15 |
| 4 | Dom | 0.13±0.18 | 0.17±0.14 | 0.3±0.15 | 0.17±0.14 | 0.16±0.14 |
| 4 | Epi | 0.2±0.17 | 0.23±0.14 | 0.38±0.15 | 0.22±0.14 | 0.21±0.13 |
| 10 | Adt | 0.14±0.17 | 0.21±0.14 | 0.13±0.16 | 0.2±0.15 | 0.18±0.14 |
| 10 | Dom | 0.09±0.16 | 0.11±0.14 | 0.15±0.17 | 0.12±0.14 | 0.09±0.14 |
| 10 | Epi | 0.17±0.18 | 0.19±0.15 | 0.23±0.19 | 0.19±0.15 | 0.17±0.15 |
| 20 | Adt | 0.11±0.18 | 0.19±0.14 | 0.11±0.16 | 0.17±0.14 | 0.13±0.14 |
| 20 | Dom | 0.08±0.16 | 0.07±0.14 | 0.07±0.17 | 0.09±0.14 | 0.08±0.14 |
| 20 | Epi | 0.22±0.19 | 0.25±0.15 | 0.12±0.15 | 0.24±0.15 | 0.2±0.14 |
| 100 | Adt | 0.14±0.19 | 0.22±0.14 | 0.13±0.16 | 0.21±0.14 | 0.16±0.14 |
| 100 | Dom | 0.11±0.17 | 0.08±0.14 | 0.01±0.14 | 0.1±0.15 | 0.1±0.14 |
| 100 | Epi | 0.18±0.19 | 0.25±0.15 | 0.11±0.16 | 0.25±0.15 | 0.2±0.13 |

Table S 3: Slope (measure of bias) means and standard deviation values in five fold cross validation across 100 replicates in traits simulated with 4, 10, 20, and 100 QTNs under the additive (Adt), dominance (Dom), and epistasis (Epi) mechanisms under heritability of 0.7 in *Miscanthus* F1 population.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| QTN | QGM | ADE | BA | MAS | RKHS | SVR |
| 4 | Adt | 1.17±0.26 | 1.11±0.21 | 0.82±0.15 | 1.62±0.31 | 1.46±0.29 |
| 4 | Dom | 1.07±0.23 | 0.88±0.19 | 0.81±0.09 | 1.67±0.3 | 1.1±0.23 |
| 4 | Epi | 0.99±0.14 | 1.05±0.17 | 0.9±0.09 | 1.57±0.22 | 1.59±0.26 |
| 10 | Adt | 1.2±0.47 | 1.17±0.18 | 0.68±0.21 | 1.74±0.32 | 1.81±0.33 |
| 10 | Dom | 0.83±1.22 | 0.6±0.23 | 0.73±0.12 | 1.28±0.33 | 0.87±0.35 |
| 10 | Epi | 0.96±0.17 | 0.95±0.22 | 0.85±0.13 | 1.5±0.31 | 1.65±0.41 |
| 20 | Adt | 1.23±0.72 | 1.12±0.2 | 0.68±0.21 | 1.83±0.34 | 1.84±0.47 |
| 20 | Dom | 1±0.41 | 0.42±0.23 | 0.57±0.22 | 1±0.41 | 0.88±0.43 |
| 20 | Epi | 1.06±0.17 | 1.19±0.18 | 0.5±0.21 | 1.77±0.29 | 2.74±0.54 |
| 100 | Adt | 1.13±0.35 | 1.23±0.16 | 0.51±0.24 | 1.88±0.26 | 3.66±0.91 |
| 100 | Dom | 1.04±0.66 | 0.52±0.28 | -0.01±0.24 | 1.21±0.52 | 2.52±0.81 |
| 100 | Epi | 1.16±0.2 | 1.19±0.18 | 0.47±0.25 | 1.72±0.22 | 5.65±1.13 |

Table S 4: Slope (measure of bias) means and standard deviation values in five fold cross validation across 100 replicates in traits simulated with 4, 10, 20, and 100 QTNs under the additive (Adt), dominance (Dom), and epistasis (Epi) mechanisms under heritability of 0.3 in *Miscanthus* F1 poplation.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| QTN | QGM | ADE | BA | MAS | RKHS | SVR |
| 4 | Adt | 1.11±1.64 | 0.62±0.44 | 0.48±0.31 | 1.29±0.97 | 0.81±0.59 |
| 4 | Dom | 1.26±7.92 | 0.51±0.39 | 0.57±0.27 | 1.15±0.79 | 0.58±0.51 |
| 4 | Epi | 2.98±19.96 | 0.66±0.38 | 0.69±0.26 | 1.36±0.68 | 0.98±0.62 |
| 10 | Adt | 0.83±5.3 | 0.62±0.42 | 0.26±0.34 | 1.3±0.94 | 1.05±0.79 |
| 10 | Dom | 0.75±1.69 | 0.34±0.42 | 0.29±0.33 | 0.86±0.85 | 0.5±0.76 |
| 10 | Epi | 1±2.28 | 0.55±0.45 | 0.44±0.37 | 1.25±0.86 | 1.13±0.93 |
| 20 | Adt | 0.15±16.75 | 0.57±0.44 | 0.21±0.32 | 1.2±0.94 | 1.08±1.08 |
| 20 | Dom | 1.65±11.07 | 0.25±0.43 | 0.14±0.33 | 0.69±0.94 | 0.59±1.05 |
| 20 | Epi | 1.17±2.19 | 0.71±0.41 | 0.23±0.3 | 1.53±0.77 | 2.08±1.38 |
| 100 | Adt | 2.43±9.74 | 0.66±0.41 | 0.26±0.31 | 1.43±0.81 | 2.46±2.06 |
| 100 | Dom | -0.92±21.39 | 0.31±0.48 | 0.04±0.28 | 0.81±1.16 | 1.77±2.08 |
| 100 | Epi | 0.33±4.01 | 0.72±0.41 | 0.22±0.3 | 1.49±0.75 | 4.69±2.72 |

Table S 5: Intercept (measure of bias) means and standard deviation values in five fold cross validation across 100 replicates in traits simulated with 4, 10, 20, and 100 QTNs under the additive (Adt), dominance (Dom), and epistasis (Epi) mechanisms under heritability of 0.7 in *Miscanthus* F1 population.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| QTN | QGM | ADE | BA | MAS | RKHS | SVR |
| 4 | Adt | -0.2±0.3 | -0.13±0.25 | 0.21±0.16 | -0.71±0.35 | -0.53±0.33 |
| 4 | Dom | -0.05±0.15 | 0.07±0.12 | 0.13±0.06 | -0.43±0.19 | -0.07±0.15 |
| 4 | Epi | -0.01±0.09 | -0.03±0.1 | 0.09±0.06 | -0.33±0.13 | -0.31±0.15 |
| 10 | Adt | -0.77±1.9 | -0.71±0.73 | 1.25±0.83 | -2.96±1.26 | -3.22±1.29 |
| 10 | Dom | 0.32±2.34 | 0.75±0.43 | 0.54±0.24 | -0.55±0.63 | 0.26±0.66 |
| 10 | Epi | 0.07±0.22 | 0.11±0.28 | 0.19±0.15 | -0.59±0.38 | -0.72±0.49 |
| 20 | Adt | -1.41±6.64 | -1.13±1.75 | 2.84±1.87 | -7.37±2.99 | -7.47±4.18 |
| 20 | Dom | -0.02±1.71 | 2.36±0.95 | 1.78±0.92 | -0.04±1.67 | 0.51±1.75 |
| 20 | Epi | -0.17±0.67 | -0.69±0.71 | 1.93±0.82 | -2.91±1.13 | -6.42±2.01 |
| 100 | Adt | -5.7±15.73 | -10.06±7.22 | 21.67±10.76 | -38.8±11.57 | -117.48±40.32 |
| 100 | Dom | -0.77±14.12 | 10.29±6.07 | 21.63±5.1 | -4.45±11.24 | -32.56±17.31 |
| 100 | Epi | -4.84±6.32 | -6.08±5.54 | 16.41±7.82 | -22.35±6.96 | -143.78±35.2 |

Table S 6: Intercept (measure of bias) means and standard deviation values in five fold cross validation across 100 replicates in traits simulated with 4, 10, 20, and 100 QTNs under the additive (Adt), dominance (Dom), and epistasis (Epi) mechanisms under heritability of 0.3 in *Miscanthus* F1 population.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| QTN | QGM | ADE | BA | MAS | RKHS | SVR |
| 4 | Adt | 0.13±2.75 | 0.43±0.51 | 0.6±0.36 | -0.32±1.11 | 0.22±0.68 |
| 4 | Dom | -0.19±5.37 | 0.31±0.25 | 0.28±0.17 | -0.09±0.51 | 0.26±0.33 |
| 4 | Epi | -0.95±10.12 | 0.2±0.23 | 0.18±0.15 | -0.2±0.39 | 0.03±0.36 |
| 10 | Adt | 0.86±19.87 | 1.48±1.65 | 2.89±1.33 | -1.18±3.71 | -0.19±3.13 |
| 10 | Dom | 0.55±3.5 | 1.26±0.81 | 1.36±0.65 | 0.27±1.65 | 0.96±1.45 |
| 10 | Epi | 0.02±2.82 | 0.6±0.58 | 0.7±0.48 | -0.26±1.07 | -0.1±1.13 |
| 20 | Adt | 5.82±142.77 | 3.81±3.86 | 6.94±2.85 | -1.75±8.32 | -0.74±9.5 |
| 20 | Dom | -4.98±53.43 | 3.05±1.76 | 3.52±1.39 | 1.28±3.87 | 1.67±4.27 |
| 20 | Epi | -0.22±8.35 | 1.16±1.59 | 3.01±1.18 | -1.97±3.01 | -3.99±5.31 |
| 100 | Adt | -57.63±418.1 | 15.15±18.16 | 32.71±13.77 | -19.14±35.53 | -64.14±90.76 |
| 100 | Dom | 37.08±431.74 | 14.87±10.46 | 20.62±5.97 | 4.12±24.91 | -16.42±44.28 |
| 100 | Epi | 20.67±123.41 | 8.74±12.78 | 24.45±9.45 | -15.12±23.25 | -114.36±84.98 |

Table S 7: Coincidence index means and standard deviation values in five fold cross validation across 100 replicates in traits simulated with 4, 10, 20, and 100 QTNs under the additive (Adt), dominance (Dom), and epistasis (Epi) mechanisms under heritability of 0.7 in *Miscanthus* F1 population.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| QTN | QGM | ADE | BA | MAS | RKHS | SVR |
| 4 | Adt | 0.28±0.11 | 0.29±0.11 | 0.23±0.11 | 0.27±0.11 | 0.29±0.12 |
| 4 | Dom | 0.27±0.12 | 0.23±0.12 | 0.19±0.09 | 0.24±0.13 | 0.23±0.12 |
| 4 | Epi | 0.24±0.13 | 0.26±0.11 | 0.32±0.12 | 0.24±0.13 | 0.23±0.12 |
| 10 | Adt | 0.25±0.14 | 0.24±0.12 | 0.22±0.11 | 0.23±0.14 | 0.21±0.12 |
| 10 | Dom | 0.23±0.11 | 0.19±0.11 | 0.18±0.09 | 0.2±0.11 | 0.18±0.1 |
| 10 | Epi | 0.22±0.12 | 0.22±0.1 | 0.19±0.09 | 0.21±0.1 | 0.21±0.1 |
| 20 | Adt | 0.27±0.12 | 0.28±0.13 | 0.23±0.11 | 0.25±0.13 | 0.19±0.11 |
| 20 | Dom | 0.18±0.12 | 0.16±0.1 | 0.16±0.11 | 0.16±0.1 | 0.14±0.09 |
| 20 | Epi | 0.31±0.13 | 0.34±0.12 | 0.19±0.12 | 0.33±0.12 | 0.27±0.1 |
| 100 | Adt | 0.3±0.12 | 0.31±0.13 | 0.21±0.11 | 0.31±0.13 | 0.25±0.12 |
| 100 | Dom | 0.21±0.12 | 0.17±0.11 | 0.09±0.08 | 0.19±0.11 | 0.16±0.1 |
| 100 | Epi | 0.35±0.12 | 0.35±0.12 | 0.2±0.13 | 0.35±0.13 | 0.29±0.12 |

Table S 8: Coincidence index means and standard deviation values in five fold cross validation across 100 replicates in traits simulated with 4, 10, 20, and 100 QTNs under the additive (Adt), dominance (Dom), and epistasis (Epi) mechanisms under heritability of 0.3 in *Miscanthus* F1 population.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| QTN | QGM | ADE | BA | MAS | RKHS | SVR |
| 4 | Adt | 0.16±0.11 | 0.18±0.12 | 0.17±0.12 | 0.18±0.11 | 0.19±0.11 |
| 4 | Dom | 0.15±0.1 | 0.17±0.11 | 0.17±0.11 | 0.19±0.11 | 0.17±0.12 |
| 4 | Epi | 0.16±0.12 | 0.19±0.12 | 0.21±0.11 | 0.19±0.13 | 0.17±0.11 |
| 10 | Adt | 0.14±0.09 | 0.17±0.11 | 0.15±0.12 | 0.16±0.11 | 0.15±0.1 |
| 10 | Dom | 0.14±0.12 | 0.14±0.11 | 0.15±0.11 | 0.14±0.11 | 0.13±0.1 |
| 10 | Epi | 0.15±0.12 | 0.17±0.11 | 0.16±0.11 | 0.17±0.11 | 0.16±0.11 |
| 20 | Adt | 0.12±0.1 | 0.17±0.1 | 0.15±0.11 | 0.15±0.09 | 0.14±0.11 |
| 20 | Dom | 0.14±0.11 | 0.14±0.11 | 0.12±0.1 | 0.14±0.11 | 0.13±0.11 |
| 20 | Epi | 0.17±0.11 | 0.21±0.12 | 0.14±0.1 | 0.22±0.12 | 0.18±0.12 |
| 100 | Adt | 0.15±0.12 | 0.18±0.11 | 0.15±0.11 | 0.18±0.12 | 0.15±0.11 |
| 100 | Dom | 0.14±0.11 | 0.14±0.11 | 0.11±0.09 | 0.14±0.1 | 0.12±0.1 |
| 100 | Epi | 0.18±0.13 | 0.22±0.13 | 0.15±0.1 | 0.21±0.12 | 0.19±0.11 |

Table S 9: Prediction accuracy means and standard deviation values in five fold cross validation across 100 replicates in traits simulated with 4, 10, 20, and 100 QTNs under the additive (Adt), dominance (Dom), and epistasis (Epi) mechanisms under high heritability in energycane F1 population.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| QTN | QGM | ADE | BA | MAS | RKHS | SVR |
| 4 | Adt | 0.5±0.07 | 0.72±0.04 | 0.67±0.03 | 0.5±0.06 | 0.44±0.05 |
| 4 | Dom | 0.51±0.05 | 0.75±0.04 | 0.7±0.04 | 0.52±0.05 | 0.49±0.05 |
| 4 | Epi | 0.57±0.06 | 0.73±0.03 | 0.61±0.05 | 0.58±0.05 | 0.52±0.05 |
| 10 | Adt | 0.59±0.06 | 0.66±0.05 | 0.54±0.05 | 0.59±0.05 | 0.54±0.05 |
| 10 | Dom | 0.56±0.05 | 0.64±0.06 | 0.6±0.07 | 0.56±0.05 | 0.54±0.05 |
| 10 | Epi | 0.62±0.06 | 0.66±0.05 | 0.44±0.05 | 0.64±0.04 | 0.63±0.04 |
| 20 | Adt | 0.63±0.05 | 0.65±0.04 | 0.41±0.1 | 0.64±0.04 | 0.6±0.04 |
| 20 | Dom | 0.51±0.06 | 0.53±0.06 | 0.43±0.1 | 0.51±0.06 | 0.49±0.06 |
| 20 | Epi | 0.62±0.06 | 0.65±0.04 | 0.39±0.06 | 0.64±0.04 | 0.64±0.04 |
| 100 | Adt | 0.74±0.04 | 0.77±0.03 | 0.36±0.1 | 0.77±0.03 | 0.77±0.03 |
| 100 | Dom | 0.58±0.06 | 0.58±0.05 | 0.15±0.09 | 0.58±0.05 | 0.54±0.05 |
| 100 | Epi | 0.73±0.04 | 0.75±0.03 | 0.4±0.1 | 0.75±0.03 | 0.75±0.03 |

Table S 10: Prediction accuracy means and standard deviation values in five fold cross validation across 100 replicates in traits simulated with 4, 10, 20, and 100 QTNs under the additive (Adt), dominance (Dom), and epistasis (Epi) mechanisms under heritability of 0.3 in energycane F1 population.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| QTN | QGM | ADE | BA | MAS | RKHS | SVR |
| 4 | Adt | 0.17±0.12 | 0.27±0.11 | 0.42±0.07 | 0.24±0.09 | 0.23±0.1 |
| 4 | Dom | 0.22±0.12 | 0.29±0.1 | 0.39±0.08 | 0.27±0.09 | 0.26±0.09 |
| 4 | Epi | 0.21±0.12 | 0.32±0.1 | 0.4±0.08 | 0.28±0.09 | 0.27±0.09 |
| 10 | Adt | 0.23±0.12 | 0.31±0.09 | 0.29±0.1 | 0.31±0.09 | 0.29±0.09 |
| 10 | Dom | 0.24±0.13 | 0.29±0.09 | 0.28±0.12 | 0.29±0.09 | 0.29±0.09 |
| 10 | Epi | 0.27±0.12 | 0.36±0.08 | 0.28±0.11 | 0.38±0.08 | 0.36±0.08 |
| 20 | Adt | 0.25±0.14 | 0.34±0.09 | 0.22±0.1 | 0.35±0.08 | 0.33±0.09 |
| 20 | Dom | 0.21±0.12 | 0.27±0.09 | 0.17±0.12 | 0.26±0.09 | 0.26±0.09 |
| 20 | Epi | 0.26±0.12 | 0.37±0.08 | 0.24±0.11 | 0.39±0.07 | 0.38±0.08 |
| 100 | Adt | 0.34±0.13 | 0.45±0.07 | 0.23±0.09 | 0.48±0.07 | 0.46±0.07 |
| 100 | Dom | 0.23±0.11 | 0.29±0.09 | 0.06±0.09 | 0.28±0.09 | 0.27±0.09 |
| 100 | Epi | 0.32±0.13 | 0.44±0.07 | 0.25±0.1 | 0.47±0.06 | 0.45±0.07 |

Table S 11: Slope (measure of bias) means and standard deviation values in five fold cross validation across 100 replicates in traits simulated with 4, 10, 20, and 100 QTNs under the additive (Adt), dominance (Dom), and epistasis (Epi) mechanisms under heritability of 0.7 in energycane F1 population.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| QTN | QGM | ADE | BA | MAS | RKHS | SVR |
| 4 | Adt | 0.97±0.11 | 1.02±0.05 | 0.98±0.03 | 1.17±0.1 | 1.25±0.14 |
| 4 | Dom | 1.03±0.09 | 1±0.03 | 0.99±0.04 | 1.13±0.07 | 1.38±0.11 |
| 4 | Epi | 1.06±0.1 | 1±0.04 | 0.94±0.06 | 1.21±0.09 | 1.41±0.12 |
| 10 | Adt | 0.97±0.08 | 1.08±0.06 | 0.91±0.08 | 1.13±0.07 | 1.3±0.1 |
| 10 | Dom | 1.05±0.08 | 1.01±0.05 | 0.92±0.06 | 1.12±0.07 | 1.47±0.09 |
| 10 | Epi | 0.94±0.07 | 1.01±0.05 | 0.93±0.1 | 1.08±0.05 | 1.21±0.07 |
| 20 | Adt | 0.94±0.07 | 1.05±0.06 | 0.75±0.15 | 1.11±0.05 | 1.3±0.09 |
| 20 | Dom | 1.01±0.09 | 0.97±0.08 | 0.8±0.14 | 1.08±0.08 | 1.44±0.13 |
| 20 | Epi | 0.92±0.08 | 0.98±0.05 | 0.85±0.13 | 1.06±0.04 | 1.2±0.06 |
| 100 | Adt | 0.92±0.05 | 0.99±0.03 | 0.66±0.14 | 1.05±0.03 | 1.17±0.04 |
| 100 | Dom | 1.06±0.54 | 1.08±0.07 | 0.36±0.22 | 1.18±0.07 | 1.69±0.15 |
| 100 | Epi | 0.93±0.05 | 0.98±0.03 | 0.71±0.14 | 1.04±0.03 | 1.14±0.03 |

Table S 12: Slope (measure of bias) means and standard deviation values in five fold cross validation across 100 replicates in traits simulated with 4, 10, 20, and 100 QTNs under the additive (Adt), dominance (Dom), and epistasis (Epi) mechanisms under heritability of 0.3 in energycane F1 population.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| QTN | QGM | ADE | BA | MAS | RKHS | SVR |
| 4 | Adt | -0.22±7.4 | 0.73±0.23 | 0.87±0.12 | 1.17±0.35 | 0.8±0.31 |
| 4 | Dom | 0.97±0.91 | 0.75±0.19 | 0.78±0.14 | 1.26±0.26 | 0.91±0.29 |
| 4 | Epi | 0.97±1.4 | 0.8±0.2 | 0.84±0.14 | 1.3±0.3 | 0.94±0.29 |
| 10 | Adt | 0.76±0.86 | 0.77±0.18 | 0.62±0.22 | 1.18±0.21 | 0.92±0.26 |
| 10 | Dom | -0.13±10.69 | 0.77±0.18 | 0.6±0.23 | 1.3±0.23 | 0.99±0.26 |
| 10 | Epi | 0.77±0.65 | 0.82±0.14 | 0.58±0.23 | 1.17±0.13 | 0.98±0.17 |
| 20 | Adt | 0.63±0.43 | 0.81±0.16 | 0.47±0.22 | 1.17±0.16 | 0.98±0.22 |
| 20 | Dom | 0.82±0.84 | 0.71±0.2 | 0.38±0.25 | 1.24±0.27 | 0.91±0.28 |
| 20 | Epi | 0.69±0.72 | 0.82±0.13 | 0.5±0.22 | 1.16±0.12 | 0.98±0.15 |
| 100 | Adt | 0.6±0.25 | 0.87±0.1 | 0.44±0.17 | 1.1±0.08 | 1.03±0.12 |
| 100 | Dom | 1.04±1.27 | 0.78±0.19 | 0.14±0.21 | 1.33±0.28 | 0.99±0.3 |
| 100 | Epi | 0.57±0.32 | 0.85±0.1 | 0.48±0.18 | 1.1±0.08 | 1.01±0.11 |

Table S 13: Intercept (measure of bias) means and standard deviation values in five fold cross validation across 100 replicates in traits simulated with 4, 10, 20, and 100 QTNs under the additive (Adt), dominance (Dom), and epistasis (Epi) mechanisms under heritability of 0.7 in energycane F1 population.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| QTN | QGM | ADE | BA | MAS | RKHS | SVR |
| 4 | Adt | 0.02±0.07 | -0.01±0.03 | 0.01±0.02 | -0.09±0.06 | -0.14±0.08 |
| 4 | Dom | -0.02±0.07 | 0±0.02 | 0.01±0.03 | -0.09±0.05 | -0.27±0.09 |
| 4 | Epi | -0.07±0.15 | 0.01±0.07 | 0.09±0.09 | -0.29±0.13 | -0.53±0.18 |
| 10 | Adt | 0.1±0.21 | -0.18±0.16 | 0.23±0.18 | -0.29±0.17 | -0.72±0.25 |
| 10 | Dom | -0.08±0.16 | -0.02±0.11 | 0.17±0.13 | -0.25±0.14 | -0.98±0.2 |
| 10 | Epi | 0.33±0.37 | -0.02±0.26 | 0.32±0.52 | -0.38±0.24 | -1±0.34 |
| 20 | Adt | 0.38±0.46 | -0.32±0.37 | 1.55±0.94 | -0.67±0.34 | -1.91±0.55 |
| 20 | Dom | -0.02±0.38 | 0.14±0.33 | 0.86±0.61 | -0.35±0.32 | -1.92±0.55 |
| 20 | Epi | 0.71±0.67 | 0.21±0.43 | 1.25±1.14 | -0.44±0.37 | -1.55±0.5 |
| 100 | Adt | 3.26±1.93 | 0.27±1.3 | 13.31±5.55 | -1.81±1.07 | -6.39±1.5 |
| 100 | Dom | -1.39±11.95 | -1.79±1.61 | 14.23±4.82 | -3.87±1.49 | -15.15±3.35 |
| 100 | Epi | 2.48±1.87 | 0.7±1.17 | 10.42±5.11 | -1.36±0.99 | -4.94±1.21 |

Table S 14: Intercept (measure of bias) means and standard deviation values in five fold cross validation across 100 replicates in traits simulated with 4, 10, 20, and 100 QTNs under the additive (Adt), dominance (Dom), and epistasis (Epi) mechanisms under heritability of 0.3 in energycane F1 population.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| QTN | QGM | ADE | BA | MAS | RKHS | SVR |
| 4 | Adt | 0.69±3.95 | 0.16±0.14 | 0.08±0.07 | -0.1±0.2 | 0.12±0.18 |
| 4 | Dom | 0.06±0.72 | 0.18±0.14 | 0.16±0.1 | -0.18±0.19 | 0.07±0.21 |
| 4 | Epi | 0.09±2.06 | 0.3±0.3 | 0.23±0.21 | -0.42±0.44 | 0.13±0.42 |
| 10 | Adt | 0.74±3.32 | 0.57±0.45 | 0.93±0.55 | -0.42±0.52 | 0.21±0.63 |
| 10 | Dom | 2.24±20.92 | 0.5±0.38 | 0.84±0.48 | -0.63±0.48 | 0.03±0.56 |
| 10 | Epi | 1.27±3.28 | 0.92±0.71 | 2.1±1.17 | -0.81±0.68 | 0.16±0.85 |
| 20 | Adt | 2.53±2.98 | 1.18±0.98 | 3.34±1.35 | -1.07±1 | 0.15±1.37 |
| 20 | Dom | 0.8±3.61 | 1.26±0.86 | 2.7±1.1 | -1.05±1.17 | 0.41±1.25 |
| 20 | Epi | 2.66±6.11 | 1.59±1.1 | 4.2±1.92 | -1.27±1.03 | 0.25±1.29 |
| 100 | Adt | 15.6±9.68 | 5.15±3.75 | 21.74±6.42 | -3.91±2.93 | -1.05±4.56 |
| 100 | Dom | 0.46±30.35 | 4.85±4.2 | 18.86±4.71 | -7.2±6.21 | 0.27±6.73 |
| 100 | Epi | 15.27±11.28 | 5.13±3.42 | 18.5±6.49 | -3.46±2.87 | -0.2±4.06 |

Table S 15: Coincidence index means and standard deviation values in five fold cross validation across 100 replicates in traits simulated with 4, 10, 20, and 100 QTNs under the additive (Adt), dominance (Dom), and epistasis (Epi) mechanisms under heritability of 0.7 in energycane F1 population.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| QTN | QGM | ADE | BA | MAS | RKHS | SVR |
| 4 | Adt | 0.32±0.09 | 0.46±0.09 | 0.23±0.07 | 0.32±0.09 | 0.3±0.07 |
| 4 | Dom | 0.23±0.08 | 0.33±0.08 | 0.26±0.09 | 0.24±0.08 | 0.21±0.09 |
| 4 | Epi | 0.32±0.09 | 0.37±0.08 | 0.25±0.07 | 0.32±0.08 | 0.33±0.08 |
| 10 | Adt | 0.33±0.09 | 0.38±0.08 | 0.22±0.07 | 0.34±0.08 | 0.33±0.09 |
| 10 | Dom | 0.23±0.08 | 0.29±0.09 | 0.27±0.08 | 0.25±0.08 | 0.23±0.08 |
| 10 | Epi | 0.43±0.09 | 0.48±0.09 | 0.25±0.07 | 0.44±0.09 | 0.45±0.08 |
| 20 | Adt | 0.35±0.09 | 0.36±0.08 | 0.18±0.07 | 0.35±0.08 | 0.33±0.09 |
| 20 | Dom | 0.16±0.08 | 0.18±0.09 | 0.21±0.08 | 0.17±0.08 | 0.14±0.07 |
| 20 | Epi | 0.4±0.09 | 0.41±0.1 | 0.27±0.07 | 0.39±0.09 | 0.39±0.1 |
| 100 | Adt | 0.42±0.11 | 0.44±0.1 | 0.19±0.08 | 0.45±0.1 | 0.44±0.09 |
| 100 | Dom | 0.34±0.09 | 0.34±0.09 | 0.19±0.08 | 0.34±0.09 | 0.31±0.08 |
| 100 | Epi | 0.45±0.09 | 0.46±0.09 | 0.22±0.09 | 0.46±0.1 | 0.47±0.09 |

Table S16: Coincidence index means and standard deviation values in fivefold cross validation across 100 replicates in traits simulated with 4, 10, 20, and 100 QTNs under the additive (Adt), dominance (Dom), and epistasis (Epi) mechanisms under heritability of 0.3 in energycane F1 population.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| QTN | QGM | ADE | BA | MAS | RKHS | SVR |
| 4 | Adt | 0.16±0.08 | 0.21±0.09 | 0.19±0.09 | 0.2±0.09 | 0.18±0.08 |
| 4 | Dom | 0.15±0.09 | 0.17±0.09 | 0.2±0.08 | 0.16±0.09 | 0.15±0.08 |
| 4 | Epi | 0.17±0.08 | 0.21±0.09 | 0.21±0.08 | 0.21±0.08 | 0.2±0.09 |
| 10 | Adt | 0.16±0.09 | 0.19±0.09 | 0.16±0.07 | 0.2±0.1 | 0.18±0.08 |
| 10 | Dom | 0.15±0.09 | 0.16±0.08 | 0.18±0.09 | 0.17±0.09 | 0.16±0.08 |
| 10 | Epi | 0.22±0.09 | 0.25±0.1 | 0.19±0.08 | 0.27±0.1 | 0.27±0.1 |
| 20 | Adt | 0.17±0.08 | 0.21±0.1 | 0.15±0.07 | 0.22±0.1 | 0.2±0.09 |
| 20 | Dom | 0.14±0.09 | 0.15±0.08 | 0.14±0.08 | 0.15±0.08 | 0.14±0.08 |
| 20 | Epi | 0.22±0.09 | 0.26±0.1 | 0.19±0.08 | 0.28±0.1 | 0.27±0.1 |
| 100 | Adt | 0.21±0.1 | 0.26±0.1 | 0.15±0.08 | 0.28±0.1 | 0.26±0.09 |
| 100 | Dom | 0.17±0.08 | 0.2±0.08 | 0.13±0.07 | 0.19±0.08 | 0.19±0.08 |
| 100 | Epi | 0.22±0.09 | 0.27±0.09 | 0.16±0.07 | 0.28±0.09 | 0.28±0.09 |

Table S17: Prediction accuracy values in traits simulated with 4, 10, 20, and 100 QTNs under the additive (Adt), dominance (Dom), and epistasis (Epi) mechanisms under heritability of 0.7 in *Miscanthus* BC1 populations.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| QTN | QGM | ADE | BA | MAS | RKHS | SVR |
| 4 | Adt | 0.2 | 0.1 | 0.01 | 0.24 | 0.29 |
| 4 | Dom | 0.29 | 0.33 | -0.11 | 0.05 | 0.31 |
| 4 | Epi | 0.4 | 0.73 | 0.18 | 0.18 | 0.3 |
| 10 | Adt | 0.04 | -0.28 | -0.09 | 0.27 | 0.16 |
| 10 | Dom | 0.1 | 0.04 | -0.08 | 0.21 | 0.18 |
| 10 | Epi | 0.06 | -0.58 | 0.15 | 0.3 | 0.3 |
| 20 | Adt | 0.25 | -0.39 | 0.13 | 0.1 | 0.37 |
| 20 | Dom | 0.33 | 0.37 | -0.01 | 0.28 | 0.29 |
| 20 | Epi | 0.29 | 0.54 | 0.17 | 0.41 | 0.14 |
| 100 | Adt | -0.08 | 0.26 | 0.06 | 0.37 | 0.2 |
| 100 | Dom | -0.01 | -0.38 | -0.05 | 0.04 | 0.06 |
| 100 | Epi | 0.34 | 0.34 | -0.02 | 0.38 | -0.05 |

Table S18: Prediction accuracy values in traits simulated with 4, 10, 20, and 100 QTNs under the additive (Adt), dominance (Dom), and epistasis (Epi) mechanisms under heritability of 0.3 in *Miscanthus* BC1 populations.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| QTN | QGM | ADE | BA | MAS | RKHS | SVR |
| 4 | Adt | 0.15 | 0.2 | 0.22 | 0.04 | 0.06 |
| 4 | Dom | 0.17 | 0.08 | 0.12 | 0.11 | 0.14 |
| 4 | Epi | -0.01 | -0.21 | 0.34 | 0.16 | 0.42 |
| 10 | Adt | 0.16 | 0.22 | 0.01 | 0.26 | 0.19 |
| 10 | Dom | 0.1 | -0.01 | -0.08 | 0.18 | 0.05 |
| 10 | Epi | -0.01 | -0.05 | 0.03 | 0.19 | 0.07 |
| 20 | Adt | 0.09 | -0.21 | -0.06 | 0.27 | -0.01 |
| 20 | Dom | -0.01 | 0.04 | 0.01 | 0.08 | -0.11 |
| 20 | Epi | 0.22 | 0.55 | -0.02 | 0.29 | 0.19 |
| 100 | Adt | 0.11 | -0.35 | -0.03 | 0.2 | 0.16 |
| 100 | Dom | -0.13 | -0.21 | 0.07 | -0.14 | 0 |
| 100 | Epi | 0.03 | 0.47 | -0.02 | -0.03 | 0.4 |

Table S19: Prediction accuracy values in traits simulated with 4, 10, 20, and 100 QTNs under the additive (Adt), dominance (Dom), and epistasis (Epi) mechanisms under heritability of 0.7 in energycane BC1 populations.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| QTN | QGM | ADE | BA | MAS | RKHS | SVR |
| 4 | Adt | 0.14 | 0.63 | 0.73 | 0.13 | 0.11 |
| 4 | Dom | 0.18 | 0.69 | 0.63 | 0.26 | 0.22 |
| 4 | Epi | 0.39 | 0.2 | -0.01 | 0.23 | 0.24 |
| 10 | Adt | 0.3 | -0.08 | 0.5 | 0.14 | 0.25 |
| 10 | Dom | 0.19 | 0.29 | 0.4 | 0.04 | 0.27 |
| 10 | Epi | 0.46 | 0.31 | 0.33 | 0 | 0.42 |
| 20 | Adt | 0.24 | 0.2 | 0.34 | 0.29 | 0.05 |
| 20 | Dom | 0.25 | 0.04 | 0.22 | 0.15 | -0.11 |
| 20 | Epi | 0.47 | 0.07 | 0.3 | 0.41 | 0.23 |
| 100 | Adt | 0.35 | -0.22 | 0.26 | 0.28 | 0.23 |
| 100 | Dom | 0.12 | 0.16 | 0.08 | 0.19 | 0.04 |
| 100 | Epi | 0.31 | 0.78 | 0.06 | 0.34 | 0.14 |

Table S20: Prediction accuracy values in traits simulated with 4, 10, 20, and 100 QTNs under the additive (Adt), dominance (Dom), and epistasis (Epi) mechanisms under heritability of 0.3 in energycane BC1 populations.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| QTN | QGM | ADE | BA | MAS | RKHS | SVR |
| 4 | Adt | 0.1 | 0.19 | 0.55 | 0.13 | 0.15 |
| 4 | Dom | 0.14 | 0.31 | 0.38 | 0.21 | 0.12 |
| 4 | Epi | 0.2 | 0.3 | 0.14 | 0.31 | 0.28 |
| 10 | Adt | 0.14 | -0.31 | 0.24 | 0.07 | 0.25 |
| 10 | Dom | 0.14 | 0.51 | 0.25 | 0.02 | 0.15 |
| 10 | Epi | 0.36 | 0.52 | 0.14 | 0.1 | 0.08 |
| 20 | Adt | 0.1 | -0.11 | -0.04 | 0.18 | 0.08 |
| 20 | Dom | 0.11 | -0.2 | 0.1 | -0.08 | -0.06 |
| 20 | Epi | 0.17 | -0.3 | 0.1 | 0.25 | 0.43 |
| 100 | Adt | 0.25 | 0.12 | 0 | 0.14 | 0.22 |
| 100 | Dom | 0.09 | 0.09 | 0 | 0.03 | 0.07 |
| 100 | Epi | 0.15 | 0.2 | 0.04 | 0.11 | 0.17 |