Table S1: 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.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| QTNa | QGMb | BAc | MASd | RKHSe | SVRf |
| 4 | Adt | 0.48±0.10 | 0.52±0.10 | 0.45±0.10 | 0.46±0.09 |
| 4 | Dom | 0.41±0.09 | 0.58±0.07 | 0.37±0.08 | 0.36±0.08 |
| 4 | Epi | 0.57±0.09 | 0.67±0.07 | 0.50±0.09 | 0.47±0.08 |
| 10 | Adt | 0.50±0.09 | 0.41±0.13 | 0.46±0.10 | 0.43±0.08 |
| 10 | Dom | 0.22±0.10 | 0.42±0.09 | 0.23±0.09 | 0.21±0.09 |
| 10 | Epi | 0.42±0.11 | 0.51±0.08 | 0.41±0.11 | 0.39±0.10 |
| 20 | Adt | 0.46±0.09 | 0.41±0.13 | 0.41±0.10 | 0.32±0.09 |
| 20 | Dom | 0.15±0.10 | 0.31±0.13 | 0.17±0.10 | 0.17±0.09 |
| 20 | Epi | 0.53±0.09 | 0.29±0.12 | 0.52±0.10 | 0.44±0.09 |
| 100 | Adt | 0.51±0.08 | 0.28±0.14 | 0.48±0.09 | 0.35±0.09 |
| 100 | Dom | 0.17±0.10 | 0.00±0.12 | 0.19±0.10 | 0.26±0.09 |
| 100 | Epi | 0.53±0.09 | 0.25±0.13 | 0.52±0.09 | 0.41±0.09 |

aQTN, Quantitative Traits’ Nucleotide(s)

bQGM, Quantitative Genetic Mechanism

cBA, Bayes A

dMAS, Marker-Assisted Selection

eRKHS, Reproducing Kernel Hilbert Space

fSVR, Support Vector Regression

Table S2: 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.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| QTNa | QGMb | BAc | MASd | RKHSe | SVRf |
| 4 | Adt | 0.21±0.15 | 0.25±0.16 | 0.21±0.15 | 0.20±0.15 |
| 4 | Dom | 0.17±0.14 | 0.30±0.15 | 0.17±0.14 | 0.16±0.14 |
| 4 | Epi | 0.23±0.14 | 0.38±0.15 | 0.22±0.14 | 0.21±0.13 |
| 10 | Adt | 0.21±0.14 | 0.13±0.16 | 0.20±0.15 | 0.18±0.14 |
| 10 | Dom | 0.11±0.14 | 0.15±0.17 | 0.12±0.14 | 0.09±0.14 |
| 10 | Epi | 0.19±0.15 | 0.23±0.19 | 0.19±0.15 | 0.17±0.15 |
| 20 | Adt | 0.19±0.14 | 0.11±0.16 | 0.17±0.14 | 0.13±0.14 |
| 20 | Dom | 0.07±0.14 | 0.07±0.17 | 0.09±0.14 | 0.08±0.14 |
| 20 | Epi | 0.25±0.15 | 0.12±0.15 | 0.24±0.15 | 0.20±0.14 |
| 100 | Adt | 0.22±0.14 | 0.13±0.16 | 0.21±0.14 | 0.16±0.14 |
| 100 | Dom | 0.08±0.14 | 0.01±0.14 | 0.10±0.15 | 0.10±0.14 |
| 100 | Epi | 0.25±0.15 | 0.11±0.16 | 0.25±0.15 | 0.20±0.13 |

aQTN, Quantitative Traits’ Nucleotide(s)

bQGM, Quantitative Genetic Mechanism

cBA, Bayes A

dMAS, Marker-Assisted Selection

eRKHS, Reproducing Kernel Hilbert Space

fSVR, Support Vector Regression

Table S3: 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.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| QTNa | QGMb | BAc | MASd | RKHSe | SVRf |
| 4 | Adt | 1.11±0.21 | 0.82±0.15 | 1.62±0.31 | 1.46±0.29 |
| 4 | Dom | 0.88±0.19 | 0.81±0.09 | 1.67±0.30 | 1.10±0.23 |
| 4 | Epi | 1.05±0.17 | 0.90±0.09 | 1.57±0.22 | 1.59±0.26 |
| 10 | Adt | 1.17±0.18 | 0.68±0.21 | 1.74±0.32 | 1.81±0.33 |
| 10 | Dom | 0.60±0.23 | 0.73±0.12 | 1.28±0.33 | 0.87±0.35 |
| 10 | Epi | 0.95±0.22 | 0.85±0.13 | 1.50±0.31 | 1.65±0.41 |
| 20 | Adt | 1.12±0.20 | 0.68±0.21 | 1.83±0.34 | 1.84±0.47 |
| 20 | Dom | 0.42±0.23 | 0.57±0.22 | 1.00±0.41 | 0.88±0.43 |
| 20 | Epi | 1.19±0.18 | 0.50±0.21 | 1.77±0.29 | 2.74±0.54 |
| 100 | Adt | 1.23±0.16 | 0.51±0.24 | 1.88±0.26 | 3.66±0.91 |
| 100 | Dom | 0.52±0.28 | -0.01±0.24 | 1.21±0.52 | 2.52±0.81 |
| 100 | Epi | 1.19±0.18 | 0.47±0.25 | 1.72±0.22 | 5.65±1.13 |

aQTN, Quantitative Traits’ Nucleotide(s)

bQGM, Quantitative Genetic Mechanism

cBA, Bayes A

dMAS, Marker-Assisted Selection

eRKHS, Reproducing Kernel Hilbert Space

fSVR, Support Vector Regression

Table S4: 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.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| QTNa | QGMb | BAc | MASd | RKHSe | SVRf |
| 4 | Adt | 0.62±0.44 | 0.48±0.31 | 1.29±0.97 | 0.81±0.59 |
| 4 | Dom | 0.51±0.39 | 0.57±0.27 | 1.15±0.79 | 0.58±0.51 |
| 4 | Epi | 0.66±0.38 | 0.69±0.26 | 1.36±0.68 | 0.98±0.62 |
| 10 | Adt | 0.62±0.42 | 0.26±0.34 | 1.30±0.94 | 1.05±0.79 |
| 10 | Dom | 0.34±0.42 | 0.29±0.33 | 0.86±0.85 | 0.50±0.76 |
| 10 | Epi | 0.55±0.45 | 0.44±0.37 | 1.25±0.86 | 1.13±0.93 |
| 20 | Adt | 0.57±0.44 | 0.21±0.32 | 1.20±0.94 | 1.08±1.08 |
| 20 | Dom | 0.25±0.43 | 0.14±0.33 | 0.69±0.94 | 0.59±1.05 |
| 20 | Epi | 0.71±0.41 | 0.23±0.30 | 1.53±0.77 | 2.08±1.38 |
| 100 | Adt | 0.66±0.41 | 0.26±0.31 | 1.43±0.81 | 2.46±2.06 |
| 100 | Dom | 0.31±0.48 | 0.04±0.28 | 0.81±1.16 | 1.77±2.08 |
| 100 | Epi | 0.72±0.41 | 0.22±0.30 | 1.49±0.75 | 4.69±2.72 |

aQTN, Quantitative Traits’ Nucleotide(s)

bQGM, Quantitative Genetic Mechanism

cBA, Bayes A

dMAS, Marker-Assisted Selection

eRKHS, Reproducing Kernel Hilbert Space

fSVR, Support Vector Regression

Table S5: 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.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| QTNa | QGMb | BAc | MASd | RKHSe | SVRf |
| 4 | Adt | -0.13±0.25 | 0.21±0.16 | -0.71±0.35 | -0.53±0.33 |
| 4 | Dom | 0.07±0.12 | 0.13±0.06 | -0.43±0.19 | -0.07±0.15 |
| 4 | Epi | -0.03±0.10 | 0.09±0.06 | -0.33±0.13 | -0.31±0.15 |
| 10 | Adt | -0.71±0.73 | 1.25±0.83 | -2.96±1.26 | -3.22±1.29 |
| 10 | Dom | 0.75±0.43 | 0.54±0.24 | -0.55±0.63 | 0.26±0.66 |
| 10 | Epi | 0.11±0.28 | 0.19±0.15 | -0.59±0.38 | -0.72±0.49 |
| 20 | Adt | -1.13±1.75 | 2.84±1.87 | -7.37±2.99 | -7.47±4.18 |
| 20 | Dom | 2.36±0.95 | 1.78±0.92 | -0.04±1.67 | 0.51±1.75 |
| 20 | Epi | -0.69±0.71 | 1.93±0.82 | -2.91±1.13 | -6.42±2.01 |
| 100 | Adt | -10.06±7.22 | 21.67±10.76 | -38.8±11.57 | -117.48±40.32 |
| 100 | Dom | 10.29±6.07 | 21.63±5.10 | -4.45±11.24 | -32.56±17.31 |
| 100 | Epi | -6.08±5.54 | 16.41±7.82 | -22.35±6.96 | -143.78±35.2 |

aQTN, Quantitative Traits’ Nucleotide(s)

bQGM, Quantitative Genetic Mechanism

cBA, Bayes A

dMAS, Marker-Assisted Selection

eRKHS, Reproducing Kernel Hilbert Space

fSVR, Support Vector Regression

Table S6: 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.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| QTNa | QGMb | BAc | MASd | RKHSe | SVRf |
| 4 | Adt | 0.43±0.51 | 0.6±0.36 | -0.32±1.11 | 0.22±0.68 |
| 4 | Dom | 0.31±0.25 | 0.28±0.17 | -0.09±0.51 | 0.26±0.33 |
| 4 | Epi | 0.20±0.23 | 0.18±0.15 | -0.20±0.39 | 0.03±0.36 |
| 10 | Adt | 1.48±1.65 | 2.89±1.33 | -1.18±3.71 | -0.19±3.13 |
| 10 | Dom | 1.26±0.81 | 1.36±0.65 | 0.27±1.65 | 0.96±1.45 |
| 10 | Epi | 0.60±0.58 | 0.70±0.48 | -0.26±1.07 | -0.10±1.13 |
| 20 | Adt | 3.81±3.86 | 6.94±2.85 | -1.75±8.32 | -0.74±9.50 |
| 20 | Dom | 3.05±1.76 | 3.52±1.39 | 1.28±3.87 | 1.67±4.27 |
| 20 | Epi | 1.16±1.59 | 3.01±1.18 | -1.97±3.01 | -3.99±5.31 |
| 100 | Adt | 15.15±18.16 | 32.71±13.77 | -19.14±35.53 | -64.14±90.76 |
| 100 | Dom | 14.87±10.46 | 20.62±5.97 | 4.12±24.91 | -16.42±44.28 |
| 100 | Epi | 8.74±12.78 | 24.45±9.45 | -15.12±23.25 | -114.36±84.98 |

aQTN, Quantitative Traits’ Nucleotide(s)

bQGM, Quantitative Genetic Mechanism

cBA, Bayes A

dMAS, Marker-Assisted Selection

eRKHS, Reproducing Kernel Hilbert Space

fSVR, Support Vector Regression

Table S7: 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.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| QTNa | QGMb | BAc | MASd | RKHSe | SVRf |
| 4 | Adt | 0.29±0.11 | 0.23±0.11 | 0.27±0.11 | 0.29±0.12 |
| 4 | Dom | 0.23±0.12 | 0.19±0.09 | 0.24±0.13 | 0.23±0.12 |
| 4 | Epi | 0.26±0.11 | 0.32±0.12 | 0.24±0.13 | 0.23±0.12 |
| 10 | Adt | 0.24±0.12 | 0.22±0.11 | 0.23±0.14 | 0.21±0.12 |
| 10 | Dom | 0.19±0.11 | 0.18±0.09 | 0.20±0.11 | 0.18±0.10 |
| 10 | Epi | 0.22±0.10 | 0.19±0.09 | 0.21±0.10 | 0.21±0.10 |
| 20 | Adt | 0.28±0.13 | 0.23±0.11 | 0.25±0.13 | 0.19±0.11 |
| 20 | Dom | 0.16±0.10 | 0.16±0.11 | 0.16±0.10 | 0.14±0.09 |
| 20 | Epi | 0.34±0.12 | 0.19±0.12 | 0.33±0.12 | 0.27±0.10 |
| 100 | Adt | 0.31±0.13 | 0.21±0.11 | 0.31±0.13 | 0.25±0.12 |
| 100 | Dom | 0.17±0.11 | 0.09±0.08 | 0.19±0.11 | 0.16±0.10 |
| 100 | Epi | 0.35±0.12 | 0.20±0.13 | 0.35±0.13 | 0.29±0.12 |

aQTN, Quantitative Traits’ Nucleotide(s)

bQGM, Quantitative Genetic Mechanism

cBA, Bayes A

dMAS, Marker-Assisted Selection

eRKHS, Reproducing Kernel Hilbert Space

fSVR, Support Vector Regression

Table S8: 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.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| QTNa | QGMb | BAc | MASd | RKHSe | SVRf |
| 4 | Adt | 0.18±0.12 | 0.17±0.12 | 0.18±0.11 | 0.19±0.11 |
| 4 | Dom | 0.17±0.11 | 0.17±0.11 | 0.19±0.11 | 0.17±0.12 |
| 4 | Epi | 0.19±0.12 | 0.21±0.11 | 0.19±0.13 | 0.17±0.11 |
| 10 | Adt | 0.17±0.11 | 0.15±0.12 | 0.16±0.11 | 0.15±0.10 |
| 10 | Dom | 0.14±0.11 | 0.15±0.11 | 0.14±0.11 | 0.13±0.10 |
| 10 | Epi | 0.17±0.11 | 0.16±0.11 | 0.17±0.11 | 0.16±0.11 |
| 20 | Adt | 0.17±0.10 | 0.15±0.11 | 0.15±0.09 | 0.14±0.11 |
| 20 | Dom | 0.14±0.11 | 0.12±0.10 | 0.14±0.11 | 0.13±0.11 |
| 20 | Epi | 0.21±0.12 | 0.14±0.10 | 0.22±0.12 | 0.18±0.12 |
| 100 | Adt | 0.18±0.11 | 0.15±0.11 | 0.18±0.12 | 0.15±0.11 |
| 100 | Dom | 0.14±0.11 | 0.11±0.09 | 0.14±0.10 | 0.12±0.10 |
| 100 | Epi | 0.22±0.13 | 0.15±0.10 | 0.21±0.12 | 0.19±0.11 |

aQTN, Quantitative Traits’ Nucleotide(s)

bQGM, Quantitative Genetic Mechanism

cBA, Bayes A

dMAS, Marker-Assisted Selection

eRKHS, Reproducing Kernel Hilbert Space

fSVR, Support Vector Regression

Table S9: 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 sugarcane F1 population.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| QTNa | QGMb | BAc | MASd | RKHSe | SVRf |
| 4 | Adt | 0.72±0.04 | 0.67±0.03 | 0.50±0.06 | 0.44±0.05 |
| 4 | Dom | 0.75±0.04 | 0.70±0.04 | 0.52±0.05 | 0.49±0.05 |
| 4 | Epi | 0.73±0.03 | 0.61±0.05 | 0.58±0.05 | 0.52±0.05 |
| 10 | Adt | 0.66±0.05 | 0.54±0.05 | 0.59±0.05 | 0.54±0.05 |
| 10 | Dom | 0.64±0.06 | 0.60±0.07 | 0.56±0.05 | 0.54±0.05 |
| 10 | Epi | 0.66±0.05 | 0.44±0.05 | 0.64±0.04 | 0.63±0.04 |
| 20 | Adt | 0.65±0.04 | 0.41±0.10 | 0.64±0.04 | 0.60±0.04 |
| 20 | Dom | 0.53±0.06 | 0.43±0.10 | 0.51±0.06 | 0.49±0.06 |
| 20 | Epi | 0.65±0.04 | 0.39±0.06 | 0.64±0.04 | 0.64±0.04 |
| 100 | Adt | 0.77±0.03 | 0.36±0.10 | 0.77±0.03 | 0.77±0.03 |
| 100 | Dom | 0.58±0.05 | 0.15±0.09 | 0.58±0.05 | 0.54±0.05 |
| 100 | Epi | 0.75±0.03 | 0.40±0.10 | 0.75±0.03 | 0.75±0.03 |

aQTN, Quantitative Traits’ Nucleotide(s)

bQGM, Quantitative Genetic Mechanism

cBA, Bayes A

dMAS, Marker-Assisted Selection

eRKHS, Reproducing Kernel Hilbert Space

fSVR, Support Vector Regression

Table S10: 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 sugarcane F1 population.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| QTNa | QGMb | BAc | MASd | RKHSe | SVRf |
| 4 | Adt | 0.27±0.11 | 0.42±0.07 | 0.24±0.09 | 0.23±0.10 |
| 4 | Dom | 0.29±0.10 | 0.39±0.08 | 0.27±0.09 | 0.26±0.09 |
| 4 | Epi | 0.32±0.10 | 0.40±0.08 | 0.28±0.09 | 0.27±0.09 |
| 10 | Adt | 0.31±0.09 | 0.29±0.10 | 0.31±0.09 | 0.29±0.09 |
| 10 | Dom | 0.29±0.09 | 0.28±0.12 | 0.29±0.09 | 0.29±0.09 |
| 10 | Epi | 0.36±0.08 | 0.28±0.11 | 0.38±0.08 | 0.36±0.08 |
| 20 | Adt | 0.34±0.09 | 0.22±0.10 | 0.35±0.08 | 0.33±0.09 |
| 20 | Dom | 0.27±0.09 | 0.17±0.12 | 0.26±0.09 | 0.26±0.09 |
| 20 | Epi | 0.37±0.08 | 0.24±0.11 | 0.39±0.07 | 0.38±0.08 |
| 100 | Adt | 0.45±0.07 | 0.23±0.09 | 0.48±0.07 | 0.46±0.07 |
| 100 | Dom | 0.29±0.09 | 0.06±0.09 | 0.28±0.09 | 0.27±0.09 |
| 100 | Epi | 0.44±0.07 | 0.25±0.10 | 0.47±0.06 | 0.45±0.07 |

aQTN, Quantitative Traits’ Nucleotide(s)

bQGM, Quantitative Genetic Mechanism

cBA, Bayes A

dMAS, Marker-Assisted Selection

eRKHS, Reproducing Kernel Hilbert Space

fSVR, Support Vector Regression

Table S11: 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 sugarcane F1 population.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| QTNa | QGMb | BAc | MASd | RKHSe | SVRf |
| 4 | Adt | 1.02±0.05 | 0.98±0.03 | 1.17±0.10 | 1.25±0.14 |
| 4 | Dom | 1.00±0.03 | 0.99±0.04 | 1.13±0.07 | 1.38±0.11 |
| 4 | Epi | 1.00±0.04 | 0.94±0.06 | 1.21±0.09 | 1.41±0.12 |
| 10 | Adt | 1.08±0.06 | 0.91±0.08 | 1.13±0.07 | 1.30±0.10 |
| 10 | Dom | 1.01±0.05 | 0.92±0.06 | 1.12±0.07 | 1.47±0.09 |
| 10 | Epi | 1.01±0.05 | 0.93±0.10 | 1.08±0.05 | 1.21±0.07 |
| 20 | Adt | 1.05±0.06 | 0.75±0.15 | 1.11±0.05 | 1.30±0.09 |
| 20 | Dom | 0.97±0.08 | 0.80±0.14 | 1.08±0.08 | 1.44±0.13 |
| 20 | Epi | 0.98±0.05 | 0.85±0.13 | 1.06±0.04 | 1.20±0.06 |
| 100 | Adt | 0.99±0.03 | 0.66±0.14 | 1.05±0.03 | 1.17±0.04 |
| 100 | Dom | 1.08±0.07 | 0.36±0.22 | 1.18±0.07 | 1.69±0.15 |
| 100 | Epi | 0.98±0.03 | 0.71±0.14 | 1.04±0.03 | 1.14±0.03 |

aQTN, Quantitative Traits’ Nucleotide(s)

bQGM, Quantitative Genetic Mechanism

cBA, Bayes A

dMAS, Marker-Assisted Selection

eRKHS, Reproducing Kernel Hilbert Space

fSVR, Support Vector Regression

Table S12: 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 sugarcane F1 population.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| QTNa | QGMb | BAc | MASd | RKHSe | SVRf |
| 4 | Adt | 0.73±0.23 | 0.87±0.12 | 1.17±0.35 | 0.80±0.31 |
| 4 | Dom | 0.75±0.19 | 0.78±0.14 | 1.26±0.26 | 0.91±0.29 |
| 4 | Epi | 0.80±0.20 | 0.84±0.14 | 1.30±0.30 | 0.94±0.29 |
| 10 | Adt | 0.77±0.18 | 0.62±0.22 | 1.18±0.21 | 0.92±0.26 |
| 10 | Dom | 0.77±0.18 | 0.60±0.23 | 1.30±0.23 | 0.99±0.26 |
| 10 | Epi | 0.82±0.14 | 0.58±0.23 | 1.17±0.13 | 0.98±0.17 |
| 20 | Adt | 0.81±0.16 | 0.47±0.22 | 1.17±0.16 | 0.98±0.22 |
| 20 | Dom | 0.71±0.20 | 0.38±0.25 | 1.24±0.27 | 0.91±0.28 |
| 20 | Epi | 0.82±0.13 | 0.50±0.22 | 1.16±0.12 | 0.98±0.15 |
| 100 | Adt | 0.87±0.10 | 0.44±0.17 | 1.10±0.08 | 1.03±0.12 |
| 100 | Dom | 0.78±0.19 | 0.14±0.21 | 1.33±0.28 | 0.99±0.30 |
| 100 | Epi | 0.85±0.10 | 0.48±0.18 | 1.10±0.08 | 1.01±0.11 |

aQTN, Quantitative Traits’ Nucleotide(s)

bQGM, Quantitative Genetic Mechanism

cBA, Bayes A

dMAS, Marker-Assisted Selection

eRKHS, Reproducing Kernel Hilbert Space

fSVR, Support Vector Regression

Table S13: 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 sugarcane F1 population.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| QTNa | QGMb | BAc | MASd | RKHSe | SVRf |
| 4 | Adt | -0.01±0.03 | 0.01±0.02 | -0.09±0.06 | -0.14±0.08 |
| 4 | Dom | 0.00±0.02 | 0.01±0.03 | -0.09±0.05 | -0.27±0.09 |
| 4 | Epi | 0.01±0.07 | 0.09±0.09 | -0.29±0.13 | -0.53±0.18 |
| 10 | Adt | -0.18±0.16 | 0.23±0.18 | -0.29±0.17 | -0.72±0.25 |
| 10 | Dom | -0.02±0.11 | 0.17±0.13 | -0.25±0.14 | -0.98±0.20 |
| 10 | Epi | -0.02±0.26 | 0.32±0.52 | -0.38±0.24 | -1.00±0.34 |
| 20 | Adt | -0.32±0.37 | 1.55±0.94 | -0.67±0.34 | -1.91±0.55 |
| 20 | Dom | 0.14±0.33 | 0.86±0.61 | -0.35±0.32 | -1.92±0.55 |
| 20 | Epi | 0.21±0.43 | 1.25±1.14 | -0.44±0.37 | -1.55±0.50 |
| 100 | Adt | 0.27±1.3 | 13.31±5.55 | -1.81±1.07 | -6.39±1.50 |
| 100 | Dom | -1.79±1.61 | 14.23±4.82 | -3.87±1.49 | -15.15±3.35 |
| 100 | Epi | 0.7±1.17 | 10.42±5.11 | -1.36±0.99 | -4.94±1.21 |

aQTN, Quantitative Traits’ Nucleotide(s)

bQGM, Quantitative Genetic Mechanism

cBA, Bayes A

dMAS, Marker-Assisted Selection

eRKHS, Reproducing Kernel Hilbert Space

fSVR, Support Vector Regression

Table S14: 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 sugarcane F1 population.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| QTNa | QGMb | BAc | MASd | RKHSe | SVRf |
| 4 | Adt | 0.16±0.14 | 0.08±0.07 | -0.10±0.20 | 0.12±0.18 |
| 4 | Dom | 0.18±0.14 | 0.16±0.10 | -0.18±0.19 | 0.07±0.21 |
| 4 | Epi | 0.30±0.30 | 0.23±0.21 | -0.42±0.44 | 0.13±0.42 |
| 10 | Adt | 0.57±0.45 | 0.93±0.55 | -0.42±0.52 | 0.21±0.63 |
| 10 | Dom | 0.50±0.38 | 0.84±0.48 | -0.63±0.48 | 0.03±0.56 |
| 10 | Epi | 0.92±0.71 | 2.10±1.17 | -0.81±0.68 | 0.16±0.85 |
| 20 | Adt | 1.18±0.98 | 3.34±1.35 | -1.07±1.00 | 0.15±1.37 |
| 20 | Dom | 1.26±0.86 | 2.70±1.10 | -1.05±1.17 | 0.41±1.25 |
| 20 | Epi | 1.59±1.10 | 4.20±1.92 | -1.27±1.03 | 0.25±1.29 |
| 100 | Adt | 5.15±3.75 | 21.74±6.42 | -3.91±2.93 | -1.05±4.56 |
| 100 | Dom | 4.85±4.20 | 18.86±4.71 | -7.20±6.21 | 0.27±6.73 |
| 100 | Epi | 5.13±3.42 | 18.50±6.49 | -3.46±2.87 | -0.20±4.06 |

aQTN, Quantitative Traits’ Nucleotide(s)

bQGM, Quantitative Genetic Mechanism

cBA, Bayes A

dMAS, Marker-Assisted Selection

eRKHS, Reproducing Kernel Hilbert Space

fSVR, Support Vector Regression

Table S15: 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 sugarcane F1 population.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| QTNa | QGMb | BAc | MASd | RKHSe | SVRf |
| 4 | Adt | 0.46±0.09 | 0.23±0.07 | 0.32±0.09 | 0.30±0.07 |
| 4 | Dom | 0.33±0.08 | 0.26±0.09 | 0.24±0.08 | 0.21±0.09 |
| 4 | Epi | 0.37±0.08 | 0.25±0.07 | 0.32±0.08 | 0.33±0.08 |
| 10 | Adt | 0.38±0.08 | 0.22±0.07 | 0.34±0.08 | 0.33±0.09 |
| 10 | Dom | 0.29±0.09 | 0.27±0.08 | 0.25±0.08 | 0.23±0.08 |
| 10 | Epi | 0.48±0.09 | 0.25±0.07 | 0.44±0.09 | 0.45±0.08 |
| 20 | Adt | 0.36±0.08 | 0.18±0.07 | 0.35±0.08 | 0.33±0.09 |
| 20 | Dom | 0.18±0.09 | 0.21±0.08 | 0.17±0.08 | 0.14±0.07 |
| 20 | Epi | 0.41±0.10 | 0.27±0.07 | 0.39±0.09 | 0.39±0.10 |
| 100 | Adt | 0.44±0.10 | 0.19±0.08 | 0.45±0.10 | 0.44±0.09 |
| 100 | Dom | 0.34±0.09 | 0.19±0.08 | 0.34±0.09 | 0.31±0.08 |
| 100 | Epi | 0.46±0.09 | 0.22±0.09 | 0.46±0.10 | 0.47±0.09 |

aQTN, Quantitative Traits’ Nucleotide(s)

bQGM, Quantitative Genetic Mechanism

cBA, Bayes A

dMAS, Marker-Assisted Selection

eRKHS, Reproducing Kernel Hilbert Space

fSVR, Support Vector Regression

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 sugarcane F1 population.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| QTNa | QGMb | BAc | MASd | RKHSe | SVRf |
| 4 | Adt | 0.21±0.09 | 0.19±0.09 | 0.20±0.09 | 0.18±0.08 |
| 4 | Dom | 0.17±0.09 | 0.20±0.08 | 0.16±0.09 | 0.15±0.08 |
| 4 | Epi | 0.21±0.09 | 0.21±0.08 | 0.21±0.08 | 0.20±0.09 |
| 10 | Adt | 0.19±0.09 | 0.16±0.07 | 0.20±0.10 | 0.18±0.08 |
| 10 | Dom | 0.16±0.08 | 0.18±0.09 | 0.17±0.09 | 0.16±0.08 |
| 10 | Epi | 0.25±0.10 | 0.19±0.08 | 0.27±0.10 | 0.27±0.10 |
| 20 | Adt | 0.21±0.10 | 0.15±0.07 | 0.22±0.10 | 0.20±0.09 |
| 20 | Dom | 0.15±0.08 | 0.14±0.08 | 0.15±0.08 | 0.14±0.08 |
| 20 | Epi | 0.26±0.10 | 0.19±0.08 | 0.28±0.10 | 0.27±0.10 |
| 100 | Adt | 0.26±0.10 | 0.15±0.08 | 0.28±0.10 | 0.26±0.09 |
| 100 | Dom | 0.20±0.08 | 0.13±0.07 | 0.19±0.08 | 0.19±0.08 |
| 100 | Epi | 0.27±0.09 | 0.16±0.07 | 0.28±0.09 | 0.28±0.09 |

aQTN, Quantitative Traits’ Nucleotide(s)

bQGM, Quantitative Genetic Mechanism

cBA, Bayes A

dMAS, Marker-Assisted Selection

eRKHS, Reproducing Kernel Hilbert Space

fSVR, Support Vector Regression

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.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| QTNa | QGMb | BAc | MASd | RKHSe | SVRf |
| 4 | Adt | 0.10 | 0.01 | 0.24 | 0.29 |
| 4 | Dom | 0.33 | -0.11 | 0.05 | 0.31 |
| 4 | Epi | 0.73 | 0.18 | 0.18 | 0.30 |
| 10 | Adt | -0.28 | -0.09 | 0.27 | 0.16 |
| 10 | Dom | 0.04 | -0.08 | 0.21 | 0.18 |
| 10 | Epi | -0.58 | 0.15 | 0.30 | 0.30 |
| 20 | Adt | -0.39 | 0.13 | 0.10 | 0.37 |
| 20 | Dom | 0.37 | -0.01 | 0.28 | 0.29 |
| 20 | Epi | 0.54 | 0.17 | 0.41 | 0.14 |
| 100 | Adt | 0.26 | 0.06 | 0.37 | 0.20 |
| 100 | Dom | -0.38 | -0.05 | 0.04 | 0.06 |
| 100 | Epi | 0.34 | -0.02 | 0.38 | -0.05 |

aQTN, Quantitative Traits’ Nucleotide(s)

bQGM, Quantitative Genetic Mechanism

cBA, Bayes A

dMAS, Marker-Assisted Selection

eRKHS, Reproducing Kernel Hilbert Space

fSVR, Support Vector Regression

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.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| QTNa | QGMb | BAc | MASd | RKHSe | SVRf |
| 4 | Adt | 0.20 | 0.22 | 0.04 | 0.06 |
| 4 | Dom | 0.08 | 0.12 | 0.11 | 0.14 |
| 4 | Epi | -0.21 | 0.34 | 0.16 | 0.42 |
| 10 | Adt | 0.22 | 0.01 | 0.26 | 0.19 |
| 10 | Dom | -0.01 | -0.08 | 0.18 | 0.05 |
| 10 | Epi | -0.05 | 0.03 | 0.19 | 0.07 |
| 20 | Adt | -0.21 | -0.06 | 0.27 | -0.01 |
| 20 | Dom | 0.04 | 0.01 | 0.08 | -0.11 |
| 20 | Epi | 0.55 | -0.02 | 0.29 | 0.19 |
| 100 | Adt | -0.35 | -0.03 | 0.20 | 0.16 |
| 100 | Dom | -0.21 | 0.07 | -0.14 | 0.00 |
| 100 | Epi | 0.47 | -0.02 | -0.03 | 0.40 |

aQTN, Quantitative Traits’ Nucleotide(s)

bQGM, Quantitative Genetic Mechanism

cBA, Bayes A

dMAS, Marker-Assisted Selection

eRKHS, Reproducing Kernel Hilbert Space

fSVR, Support Vector Regression

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 sugarcane BC1 populations.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| QTNa | QGMb | BAc | MASd | RKHSe | SVRf |
| 4 | Adt | 0.63 | 0.73 | 0.13 | 0.11 |
| 4 | Dom | 0.69 | 0.63 | 0.26 | 0.22 |
| 4 | Epi | 0.20 | -0.01 | 0.23 | 0.24 |
| 10 | Adt | -0.08 | 0.50 | 0.14 | 0.25 |
| 10 | Dom | 0.29 | 0.40 | 0.04 | 0.27 |
| 10 | Epi | 0.31 | 0.33 | 0.00 | 0.42 |
| 20 | Adt | 0.20 | 0.34 | 0.29 | 0.05 |
| 20 | Dom | 0.04 | 0.22 | 0.15 | -0.11 |
| 20 | Epi | 0.07 | 0.30 | 0.41 | 0.23 |
| 100 | Adt | -0.22 | 0.26 | 0.28 | 0.23 |
| 100 | Dom | 0.16 | 0.08 | 0.19 | 0.04 |
| 100 | Epi | 0.78 | 0.06 | 0.34 | 0.14 |

aQTN, Quantitative Traits’ Nucleotide(s)

bQGM, Quantitative Genetic Mechanism

cBA, Bayes A

dMAS, Marker-Assisted Selection

eRKHS, Reproducing Kernel Hilbert Space

fSVR, Support Vector Regression

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 sugarcane BC1 populations.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| QTNa | QGMb | BAc | MASd | RKHSe | SVRf |
| 4 | Adt | 0.19 | 0.55 | 0.13 | 0.15 |
| 4 | Dom | 0.31 | 0.38 | 0.21 | 0.12 |
| 4 | Epi | 0.30 | 0.14 | 0.31 | 0.28 |
| 10 | Adt | -0.31 | 0.24 | 0.07 | 0.25 |
| 10 | Dom | 0.51 | 0.25 | 0.02 | 0.15 |
| 10 | Epi | 0.52 | 0.14 | 0.10 | 0.08 |
| 20 | Adt | -0.11 | -0.04 | 0.18 | 0.08 |
| 20 | Dom | -0.20 | 0.10 | -0.08 | -0.06 |
| 20 | Epi | -0.30 | 0.10 | 0.25 | 0.43 |
| 100 | Adt | 0.12 | 0.00 | 0.14 | 0.22 |
| 100 | Dom | 0.09 | 0.00 | 0.03 | 0.07 |
| 100 | Epi | 0.20 | 0.04 | 0.11 | 0.17 |

aQTN, Quantitative Traits’ Nucleotide(s)

bQGM, Quantitative Genetic Mechanism

cBA, Bayes A

dMAS, Marker-Assisted Selection

eRKHS, Reproducing Kernel Hilbert Space

fSVR, Support Vector Regression