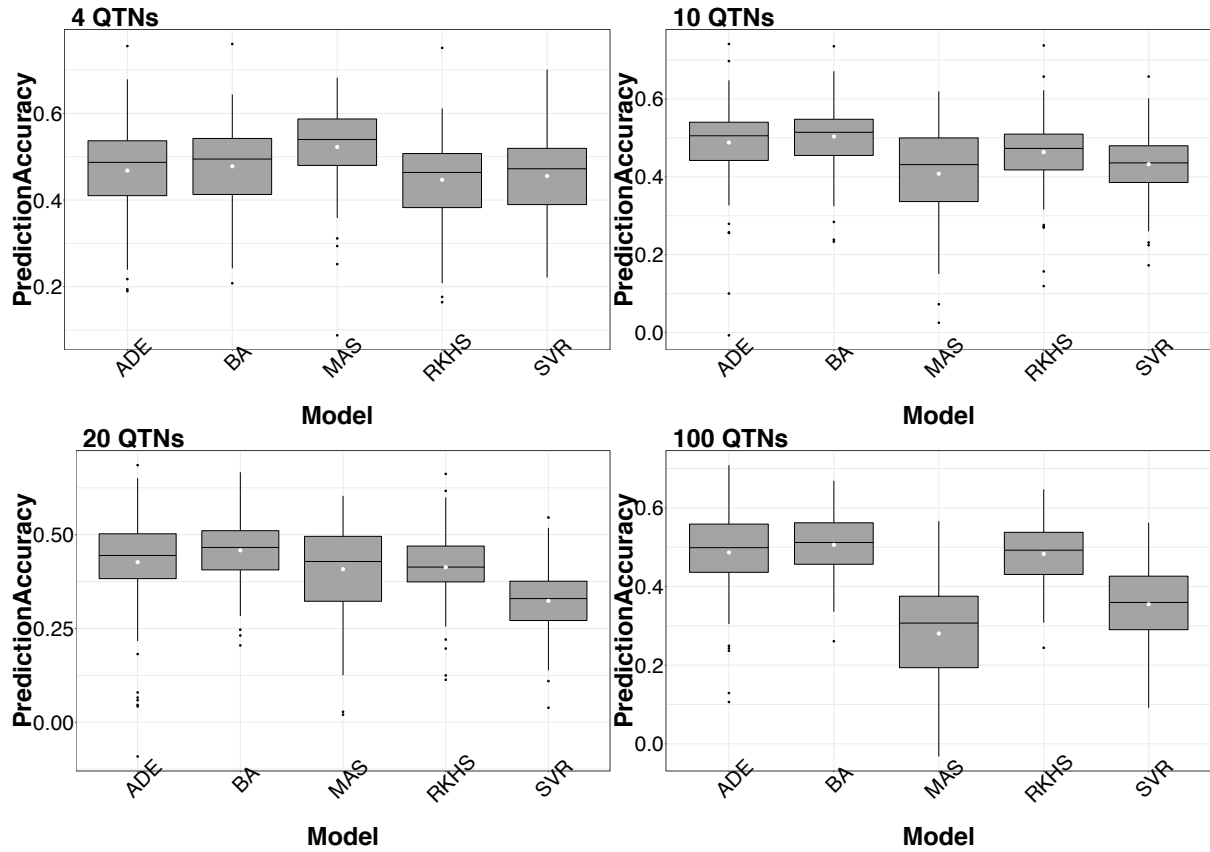
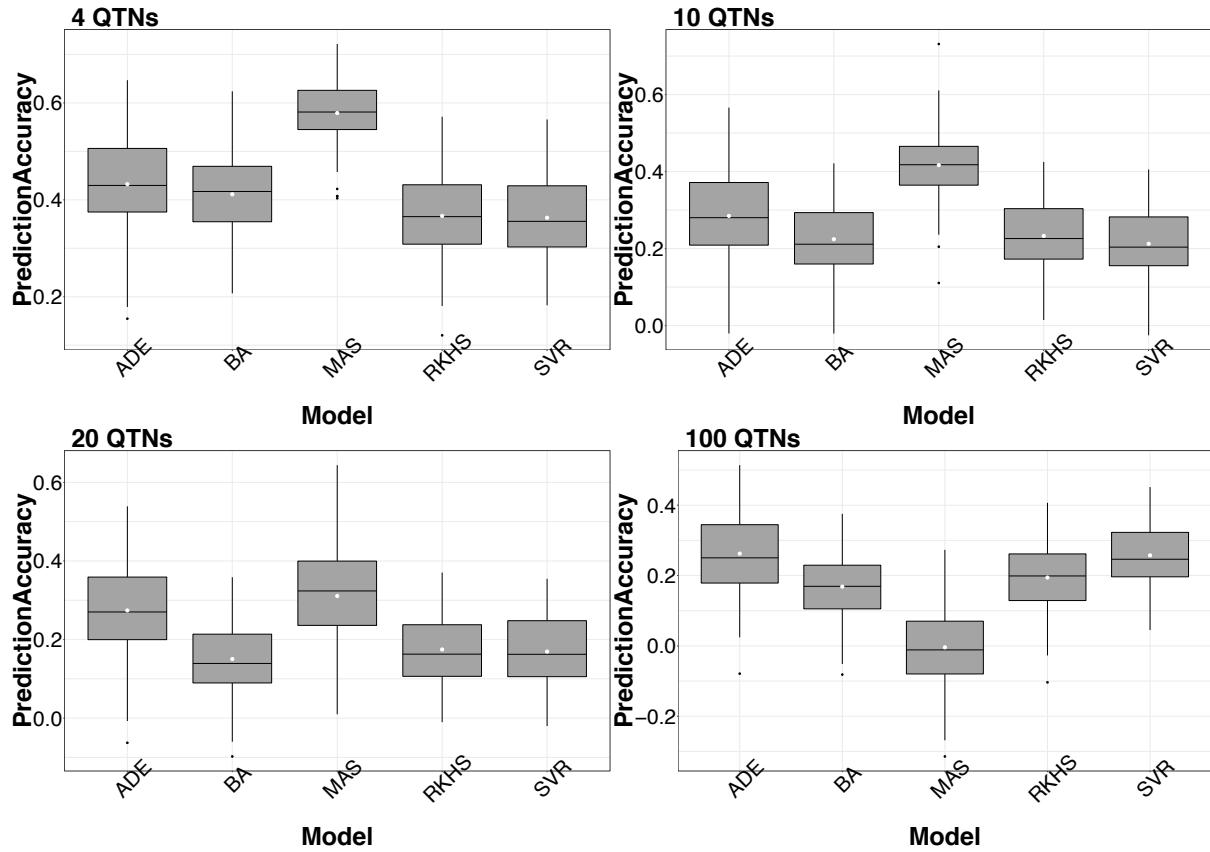


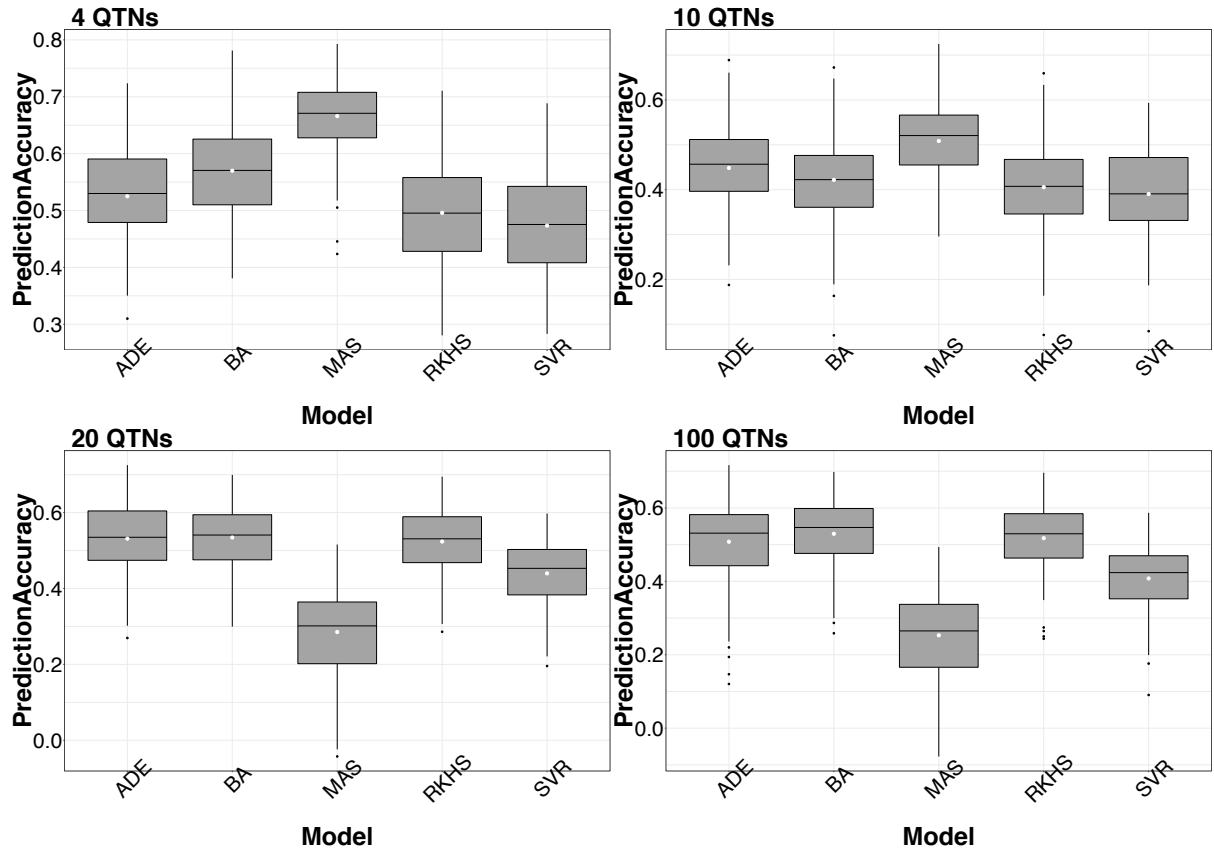
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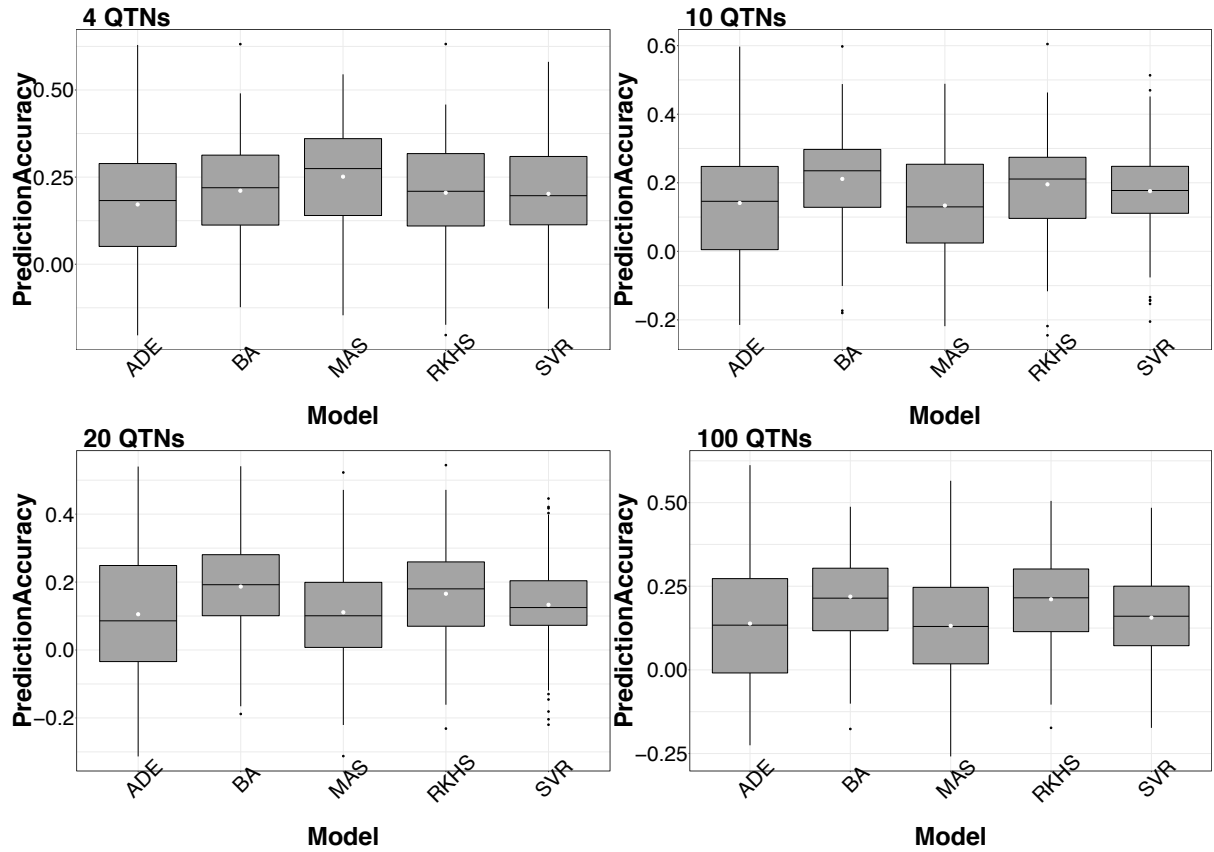
**Figure S1: Comparison among GS models and MAS for traits simulated with 4, 10, 20, and 100 QTNs under additive mechanism and heritability of 0.7 in *Miscanthus* F<sub>1</sub> population.** On x-axis are the GS models [Additive-Dominance-Epistasis (ADE), Bayes A (BA), Reproducing Kernel Hilbert Space (RKHS), and Support Vector Regression (SVR)] and Marker-Assisted Selection model (MAS). On the y-axis is the prediction accuracy. The white dot in the middle each boxplot represents the position of the mean of the distribution of prediction accuracies across 100 replicates using five-fold cross validation approach.



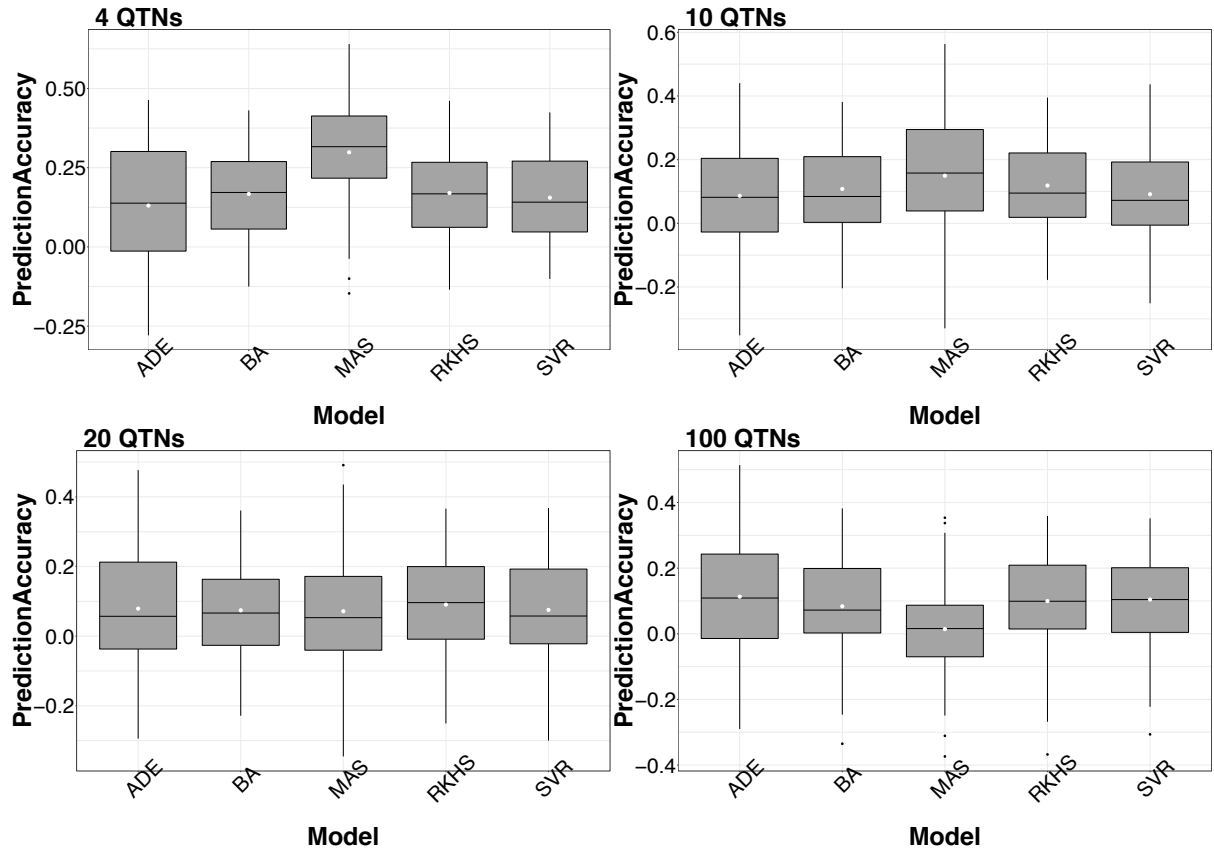
**Figure S2: Comparison among GS models and MAS for traits simulated with 4, 10, 20, and 100 QTNs under dominance mechanism and heritability of 0.7 in *Miscanthus* F<sub>1</sub> population.** On x-axis are the GS models [Additive-Dominance-Epistasis (ADE), Bayes A (BA), Reproducing Kernel Hilbert Space (RKHS), and Support Vector Regression (SVR)] and Marker-Assisted Selection model (MAS). On the y-axis is the prediction accuracy. The white dot in the middle each boxplot represents the position of the mean of the distribution of prediction accuracies across 100 replicates using five-fold cross validation approach.



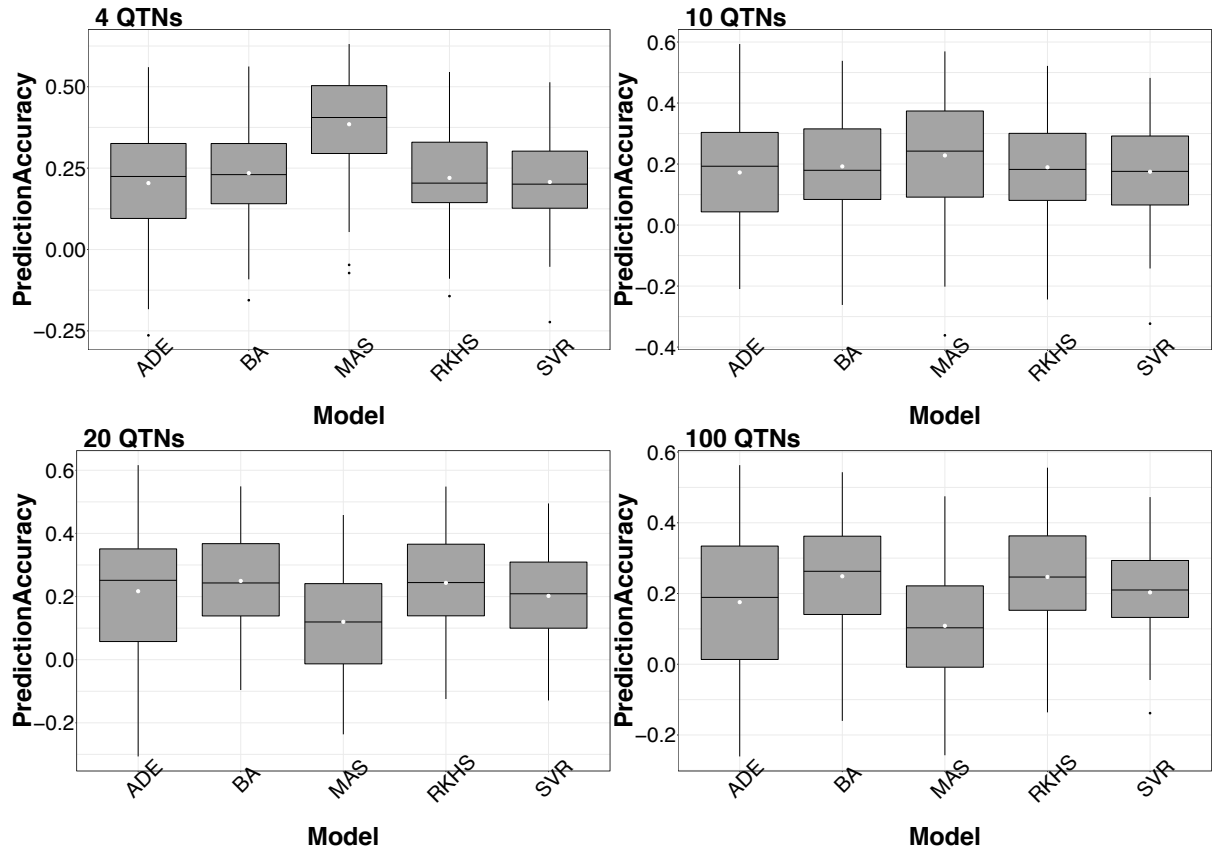
**Figure S3: Comparison among GS models and MAS for traits simulated with 4, 10, 20, and 100 QTNs under epistasis mechanism and heritability of 0.7 in *Miscanthus* F<sub>1</sub> population.** On x-axis are the GS models [Additive-Dominance-Epistasis (ADE), Bayes A (BA), Reproducing Kernel Hilbert Space (RKHS), and Support Vector Regression (SVR)] and Marker-Assisted Selection model (MAS). On the y-axis is the prediction accuracy. The white dot in the middle each boxplot represents the position of the mean of the distribution of prediction accuracies across 100 replicates using five-fold cross validation approach.



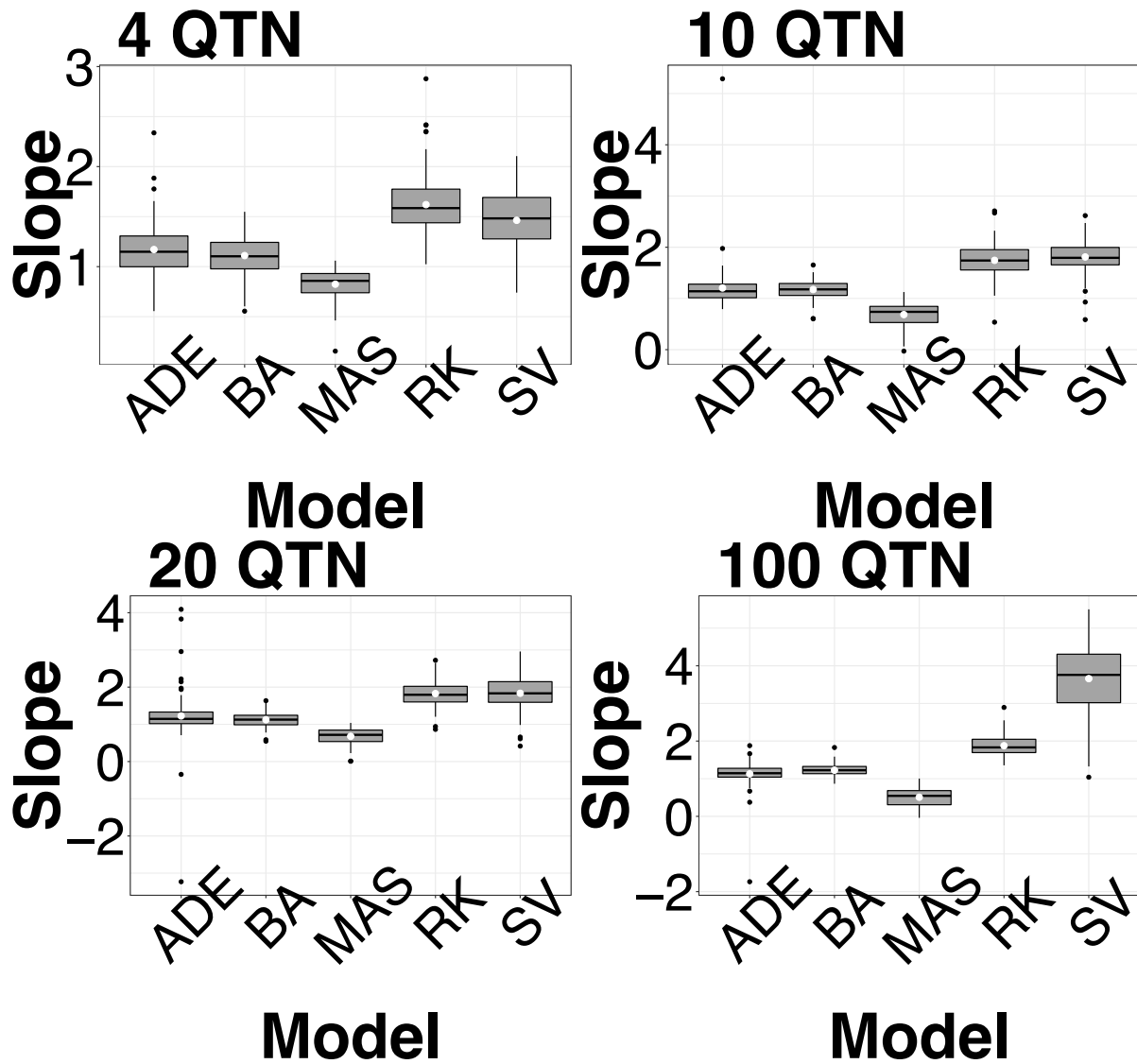
**Figure S4: Comparison among GS models and MAS for traits simulated with 4, 10, 20, and 100 QTNs under additive mechanism and heritability of 0.3 in *Miscanthus* F<sub>1</sub> population.** On x-axis are the GS models [Additive-Dominance-Epistasis (ADE), Bayes A (BA), Reproducing Kernel Hilbert Space (RKHS), and Support Vector Regression (SVR)] and Marker-Assisted Selection model (MAS). On the y-axis is the prediction accuracy. The white dot in the middle each boxplot represents the position of the mean of the distribution of prediction accuracies across 100 replicates using five-fold cross validation approach.



**Figure S5: Comparison among GS models and MAS for traits simulated with 4, 10, 20, and 100 QTNs under dominance mechanism and heritability of 0.3 in *Miscanthus* F<sub>1</sub> population.** On x-axis are the GS models [Additive-Dominance-Epistasis (ADE), Bayes A (BA), Reproducing Kernel Hilbert Space (RKHS), and Support Vector Regression (SVR)] and Marker-Assisted Selection model (MAS). On the y-axis is the prediction accuracy. The white dot in the middle each boxplot represents the position of the mean of the distribution of prediction accuracies across 100 replicates using five-fold cross validation approach.

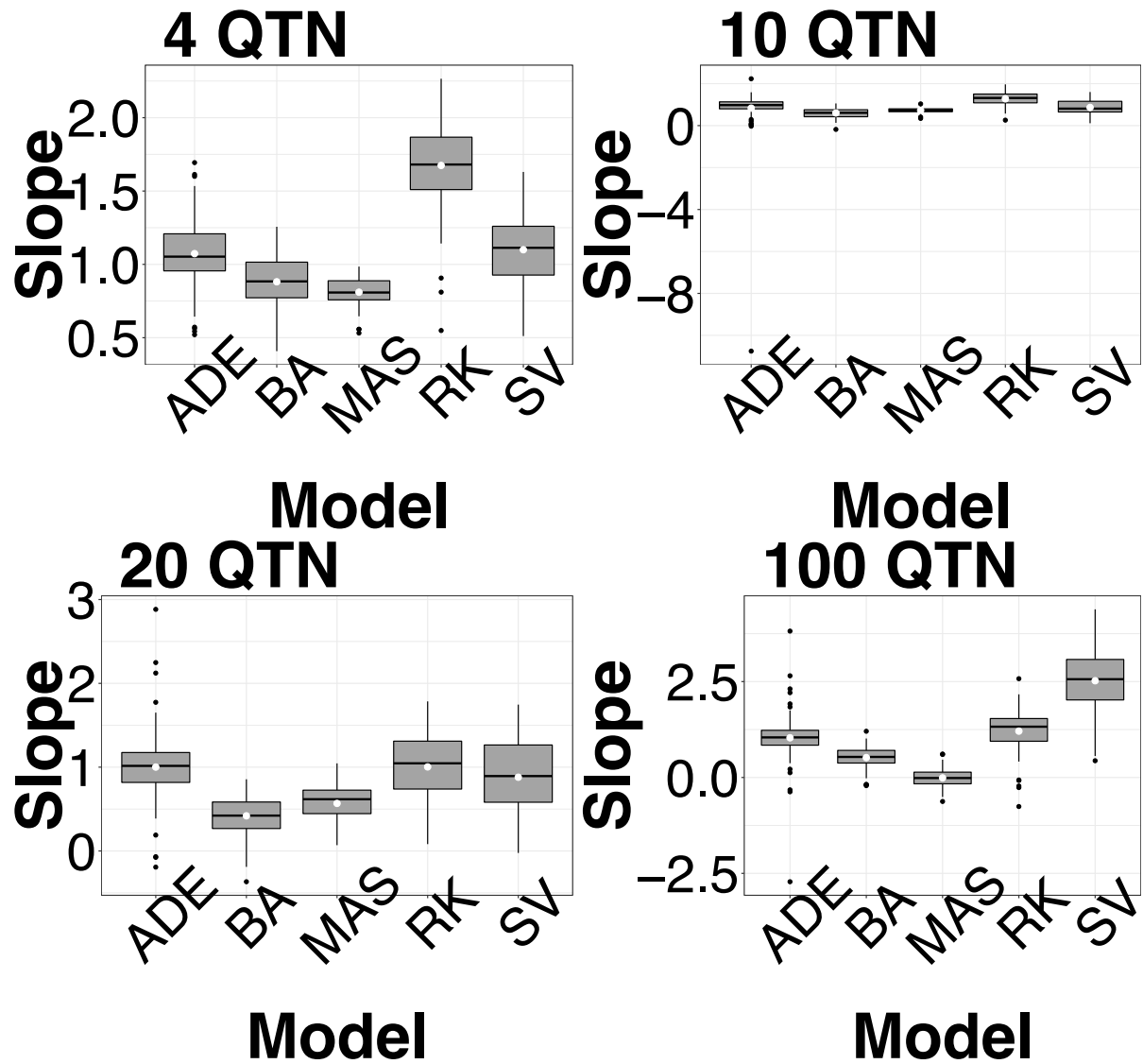


**Figure S6: Comparison among GS models and MAS for traits simulated with 4, 10, 20, and 100 QTNs under epistasis mechanism and heritability of 0.3 in *Miscanthus* F<sub>1</sub> population.** On x-axis are the GS models [Additive-Dominance-Epistasis (ADE), Bayes A (BA), Reproducing Kernel Hilbert Space (RKHS), and Support Vector Regression (SVR)] and Marker-Assisted Selection model (MAS). On the y-axis is the prediction accuracy. The white dot in the middle each boxplot represents the position of the mean of the distribution of prediction accuracies across 100 replicates using five-fold cross validation approach.

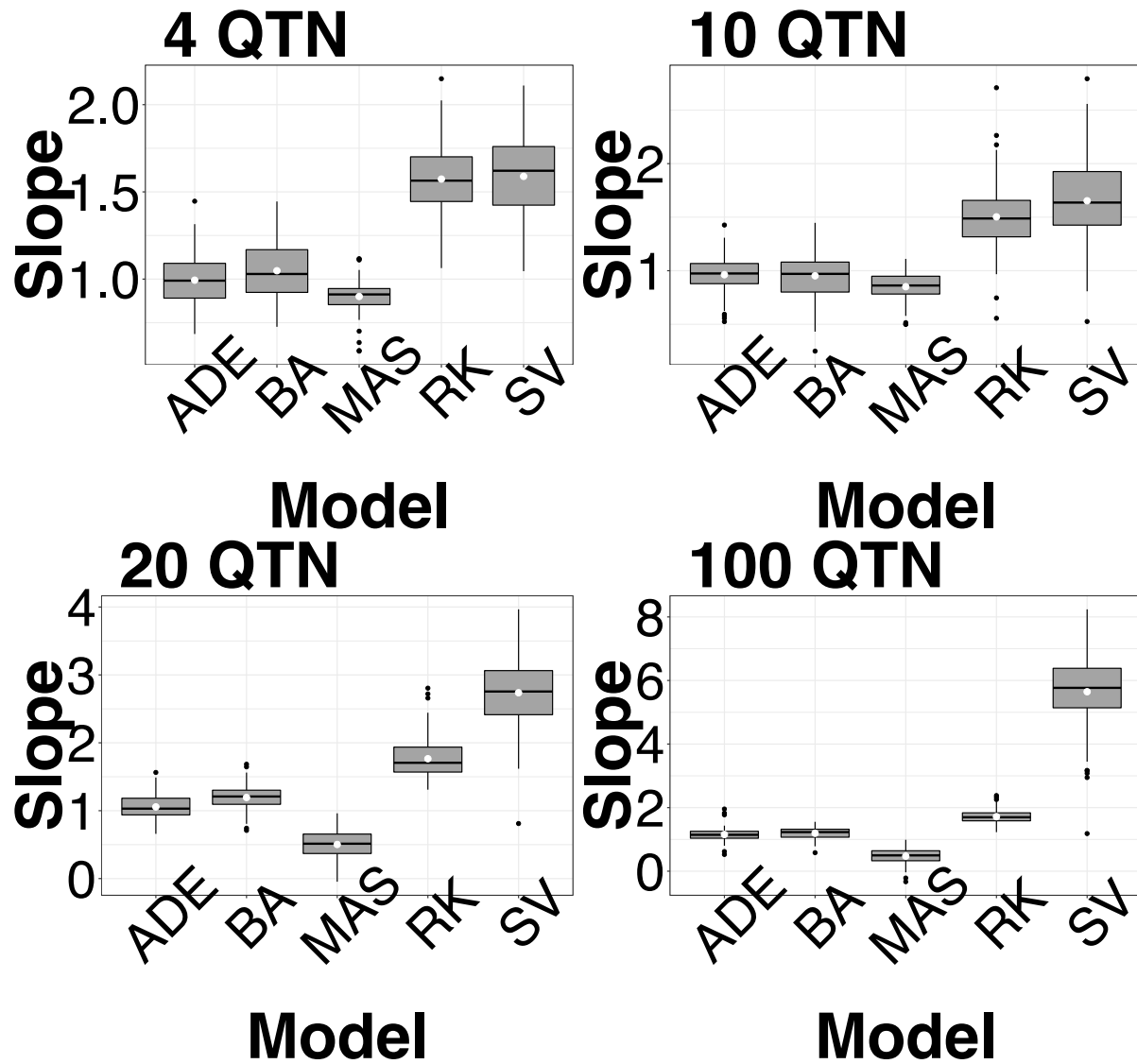


**Figure S7: Comparison of slope values across GS and MAS models under additive mechanism and heritability of 0.7 in *Miscanthus* F<sub>1</sub> population for traits simulated with 4, 10, 20, and 100 QTNs.** Slope values for the regression model between simulated trait and GEBVs (Genomic Estimated Breeding Values) for GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] and MAS (Marker Assisted Selection) model for cross validation folds and 100 replicates. The white dots in the boxplots represent the mean of the distribution in each model.

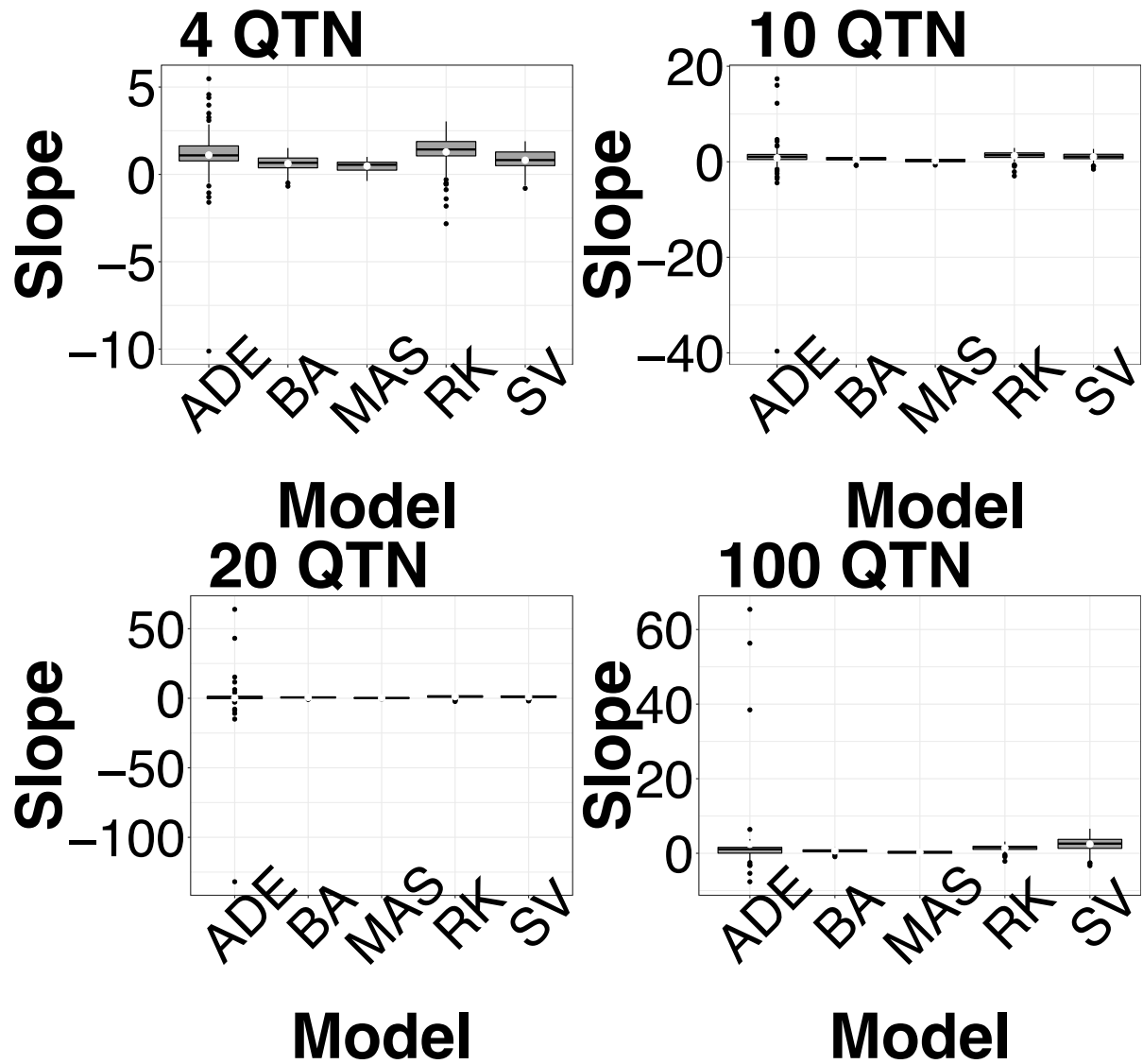




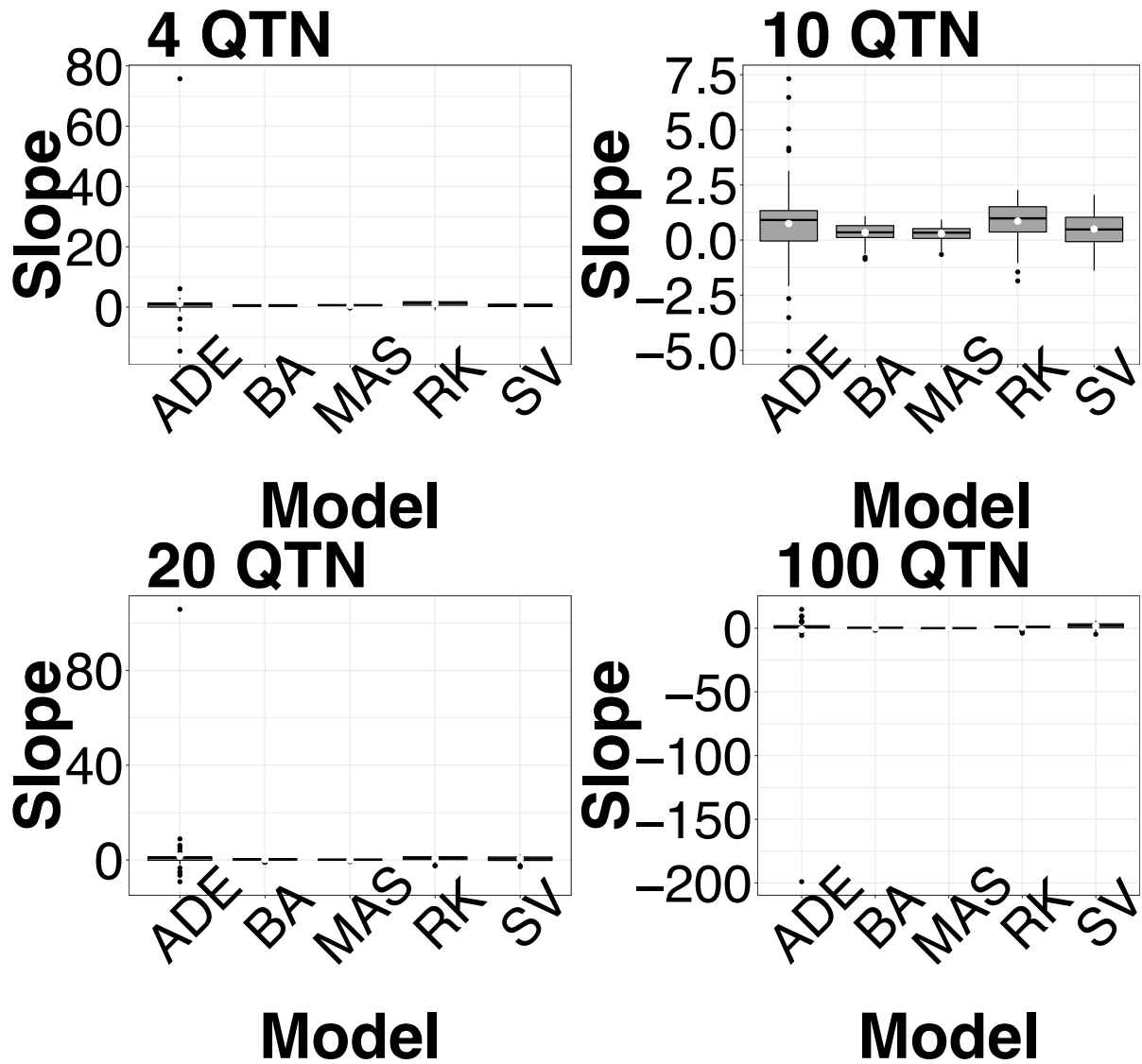
**Figure S8: Comparison of slope values across GS and MAS models under dominance mechanism and heritability of 0.7 in *Miscanthus* F<sub>1</sub> population for traits simulated with 4, 10, 20, and 100 QTNs.** Slope values for the regression model between simulated trait and GEBVs (Genomic Estimated Breeding Values) for GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] and MAS (Marker Assisted Selection) model for cross validation folds and 100 replicates. The white dots in the boxplots represent the mean of the distribution in each model.



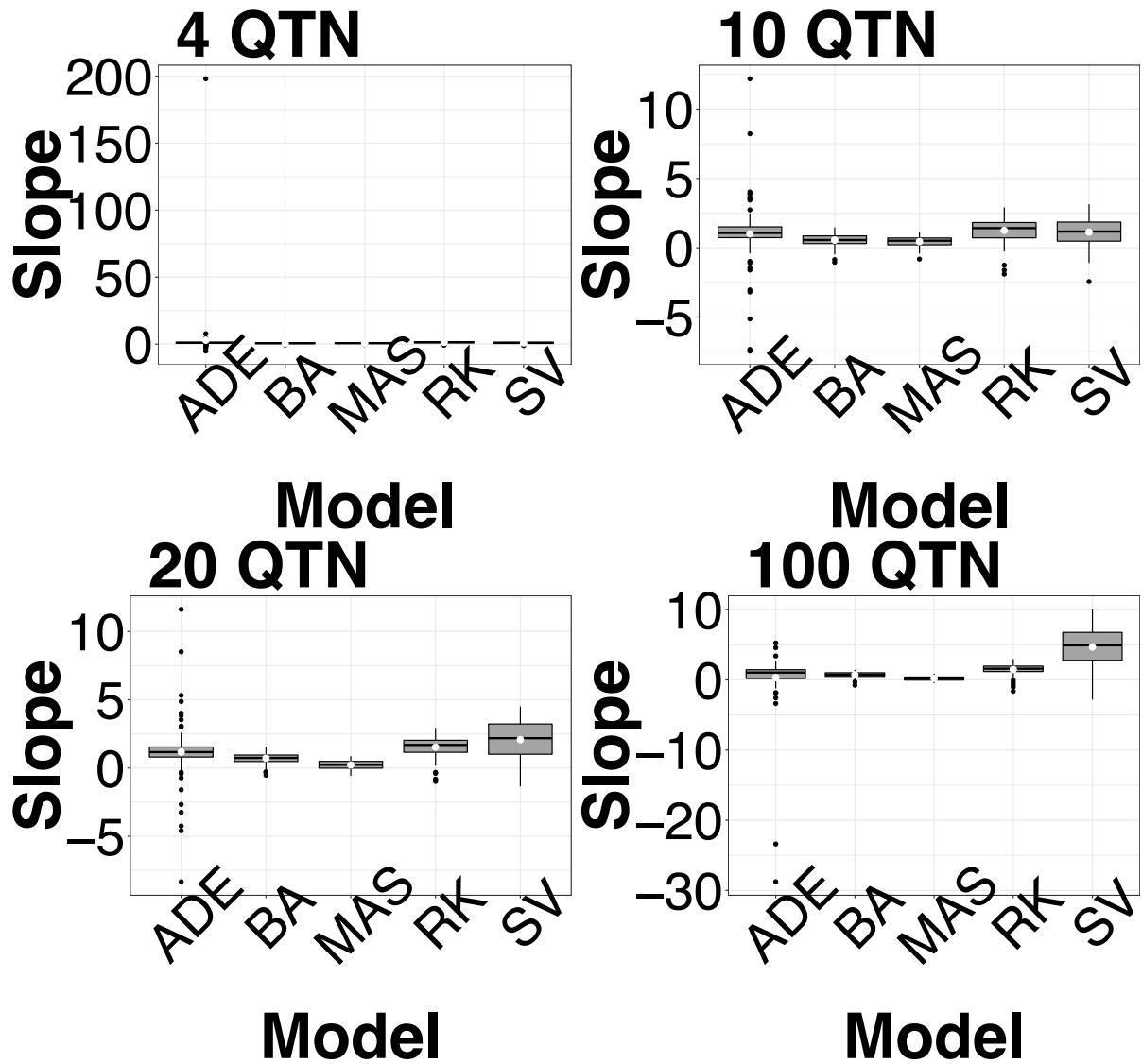
**Figure S9: Comparison of slope values across GS and MAS models under epistasis mechanism and heritability of 0.7 in *Miscanthus* F<sub>1</sub> population for traits simulated with 4, 10, 20, and 100 QTNs.** Slope values for the regression model between simulated trait and GEBVs (Genomic Estimated Breeding Values) for GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] and MAS (Marker Assisted Selection) model for cross validation folds and 100 replicates. The white dots in the boxplots represent the mean of the distribution in each model.



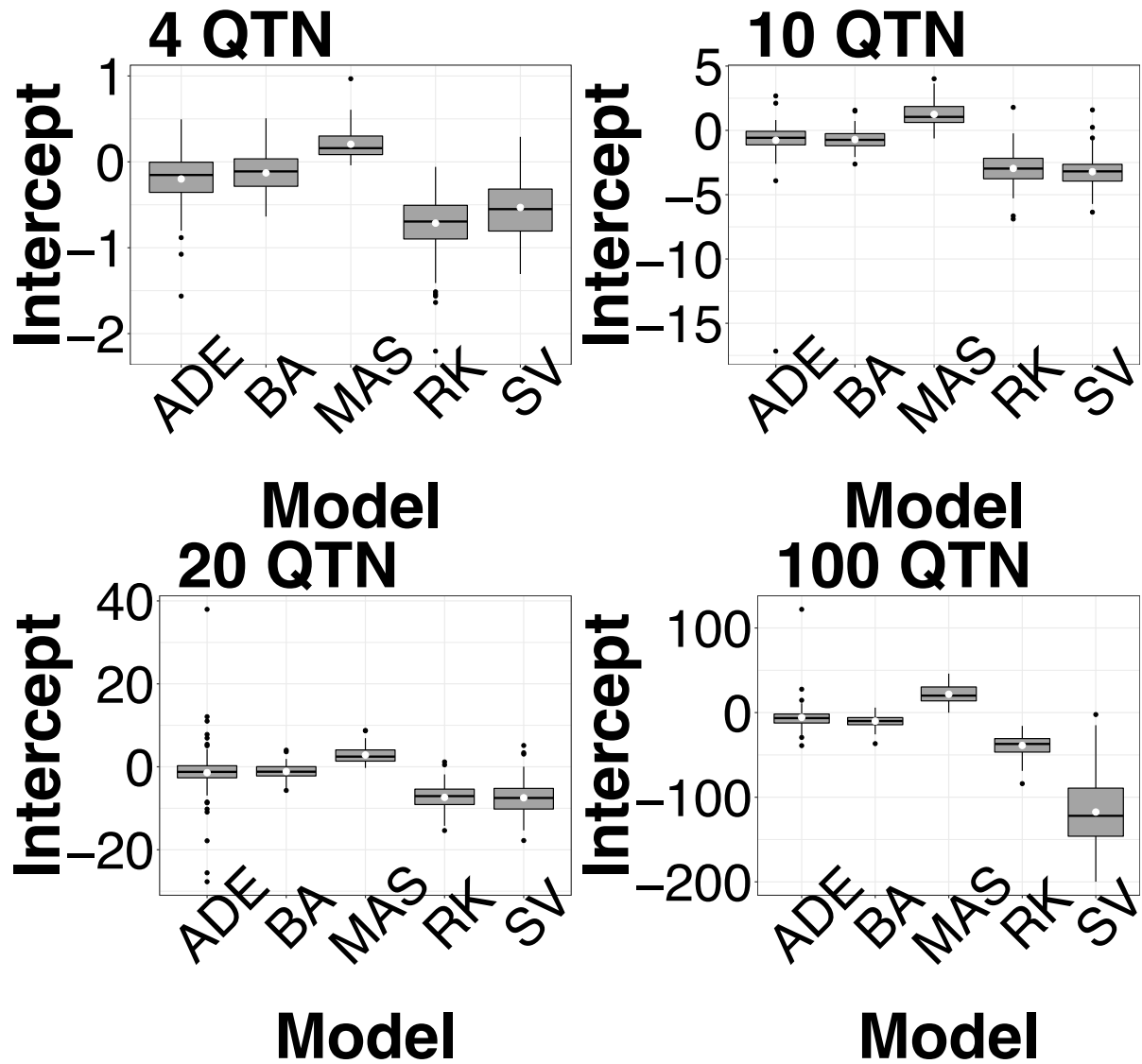
**Figure S10: Comparison of slope values across GS and MAS models under additive mechanism and heritability of 0.3 in *Miscanthus* F<sub>1</sub> population for traits simulated with 4, 10, 20, and 100 QTNs.** Slope values for the regression model between simulated trait and GEBVs (Genomic Estimated Breeding Values) for GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] and MAS (Marker Assisted Selection) model for cross validation folds and 100 replicates. The white dots in the boxplots represent the mean of the distribution in each model.



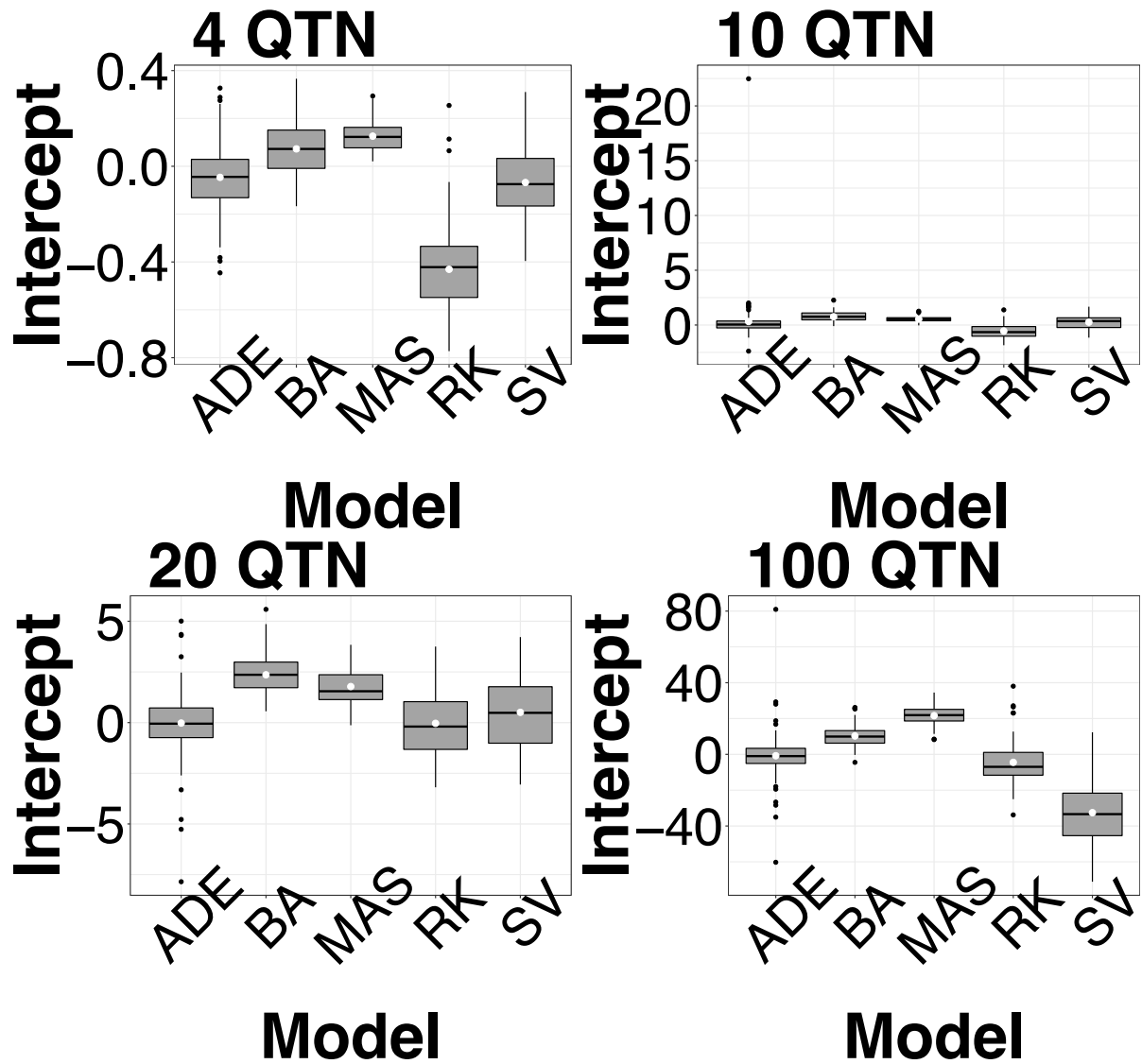
**Figure S11: Comparison of slope values across GS and MAS models under dominance mechanism and heritability of 0.3 in *Miscanthus* F<sub>1</sub> population for traits simulated with 4, 10, 20, and 100 QTNs.** Slope values for the regression model between simulated trait and GEBVs (Genomic Estimated Breeding Values) for GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] and MAS (Marker Assisted Selection) model for cross validation folds and 100 replicates. The white dots in the boxplots represent the mean of the distribution in each model.



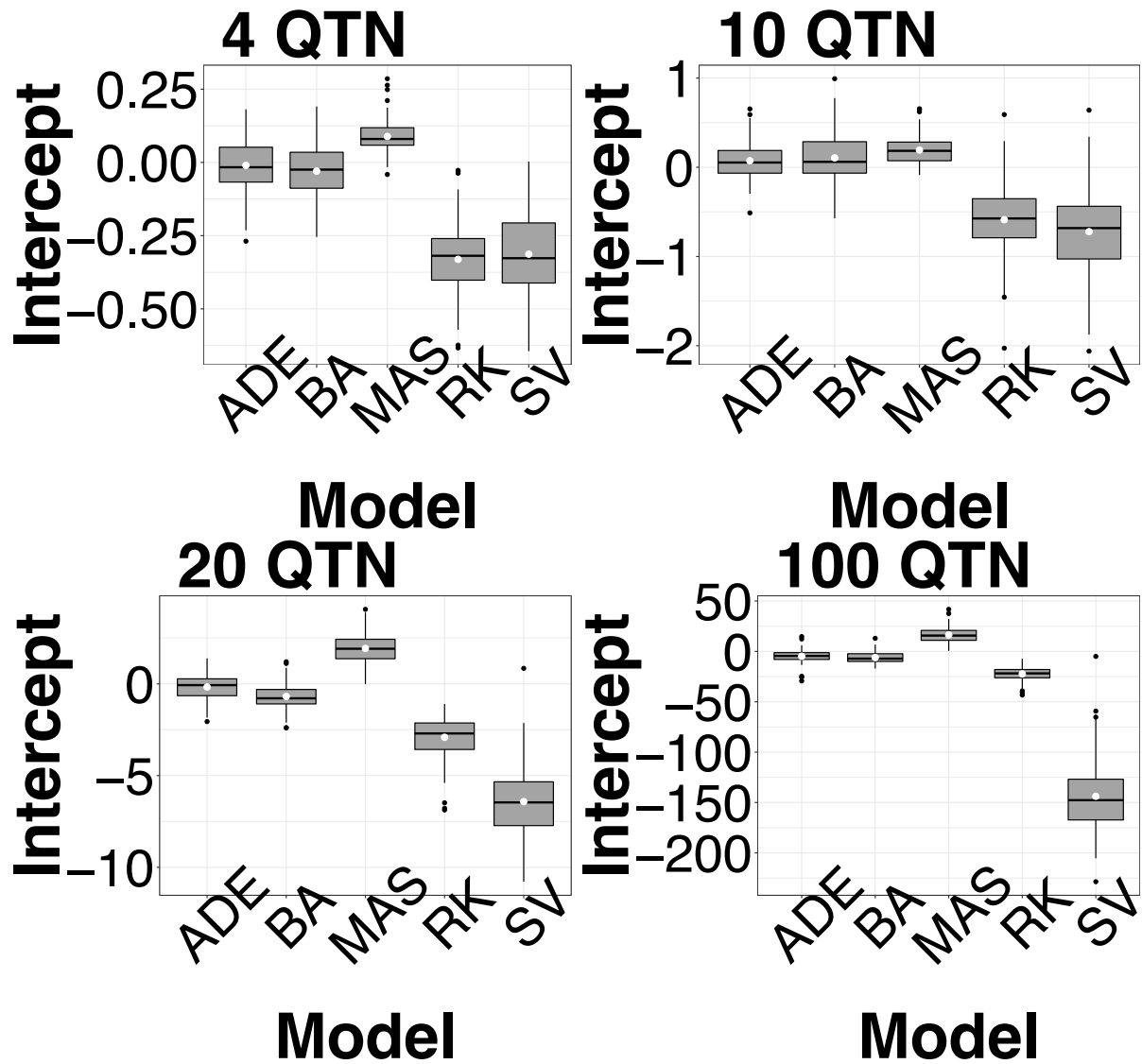
**Figure S12: Comparison of slope values across GS and MAS models under epistasis mechanism and heritability of 0.3 in *Miscanthus* F<sub>1</sub> population for traits simulated with 4, 10, 20, and 100 QTNs.** Slope values for the regression model between simulated trait and GEBVs (Genomic Estimated Breeding Values) for GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] and MAS (Marker Assisted Selection) model for cross validation folds and 100 replicates. The white dots in the boxplots represent the mean of the distribution in each model.



**Figure S13: Comparison of intercept values across GS and MAS models under additive mechanism and heritability of 0.7 in *Miscanthus* F<sub>1</sub> population for traits simulated with 4, 10, 20, and 100 QTNs.** Slope values for the regression model between simulated trait and GEBVs (Genomic Estimated Breeding Values) for GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] and MAS (Marker Assisted Selection) model for cross validation folds and 100 replicates. The white dots in the boxplots represent the mean of the distribution in each model.

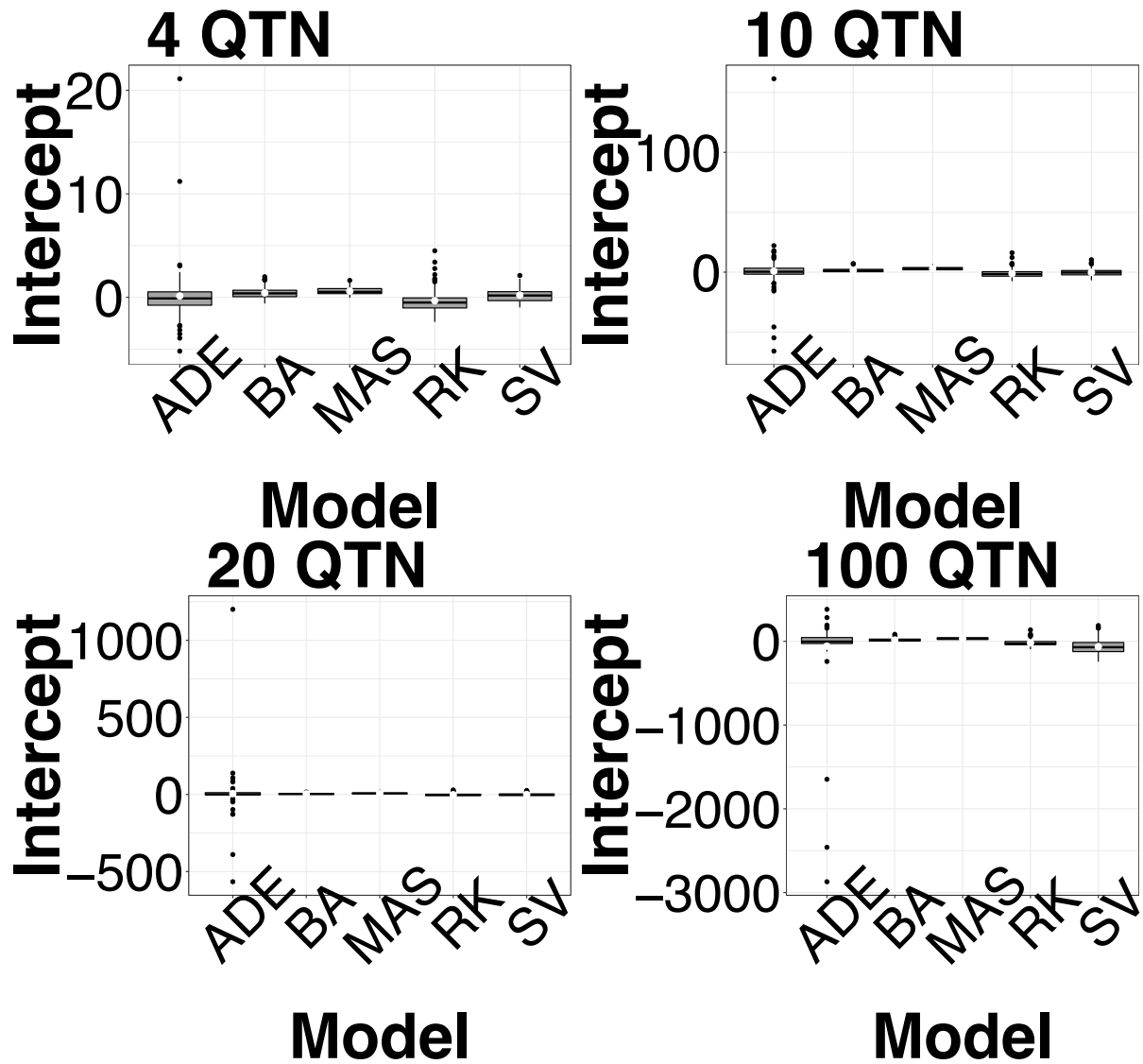


**Figure S14: Comparison of intercept values across GS and MAS models under dominance mechanism and heritability of 0.7 in *Miscanthus* F<sub>1</sub> population for traits simulated with 4, 10, 20, and 100 QTNs.** Slope values for the regression model between simulated trait and GEBVs (Genomic Estimated Breeding Values) for GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] and MAS (Marker Assisted Selection) model for cross validation folds and 100 replicates. The white dots in the boxplots represent the mean of the distribution in each model.

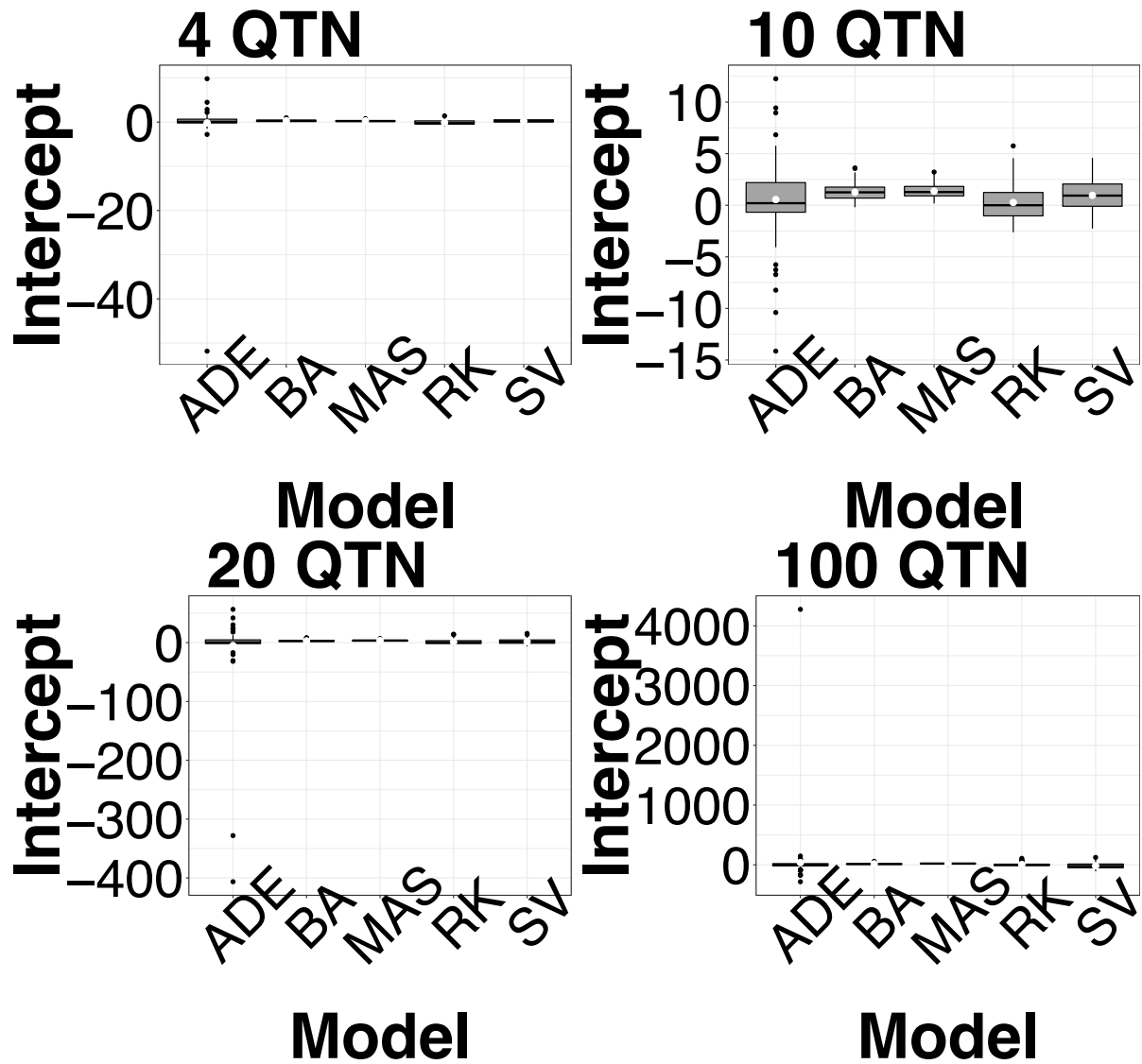


**Figure S15: Comparison of intercept values across GS and MAS models under epistasis mechanism and heritability of 0.7 in *Miscanthus* F<sub>1</sub> population for traits simulated with 4, 10, 20, and 100 QTNs.** Slope values for the regression model between simulated trait and GEBVs (Genomic Estimated Breeding Values) for GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] and MAS (Marker Assisted Selection) model for cross validation folds and 100 replicates. The white dots in the boxplots represent the mean of the distribution in each model.

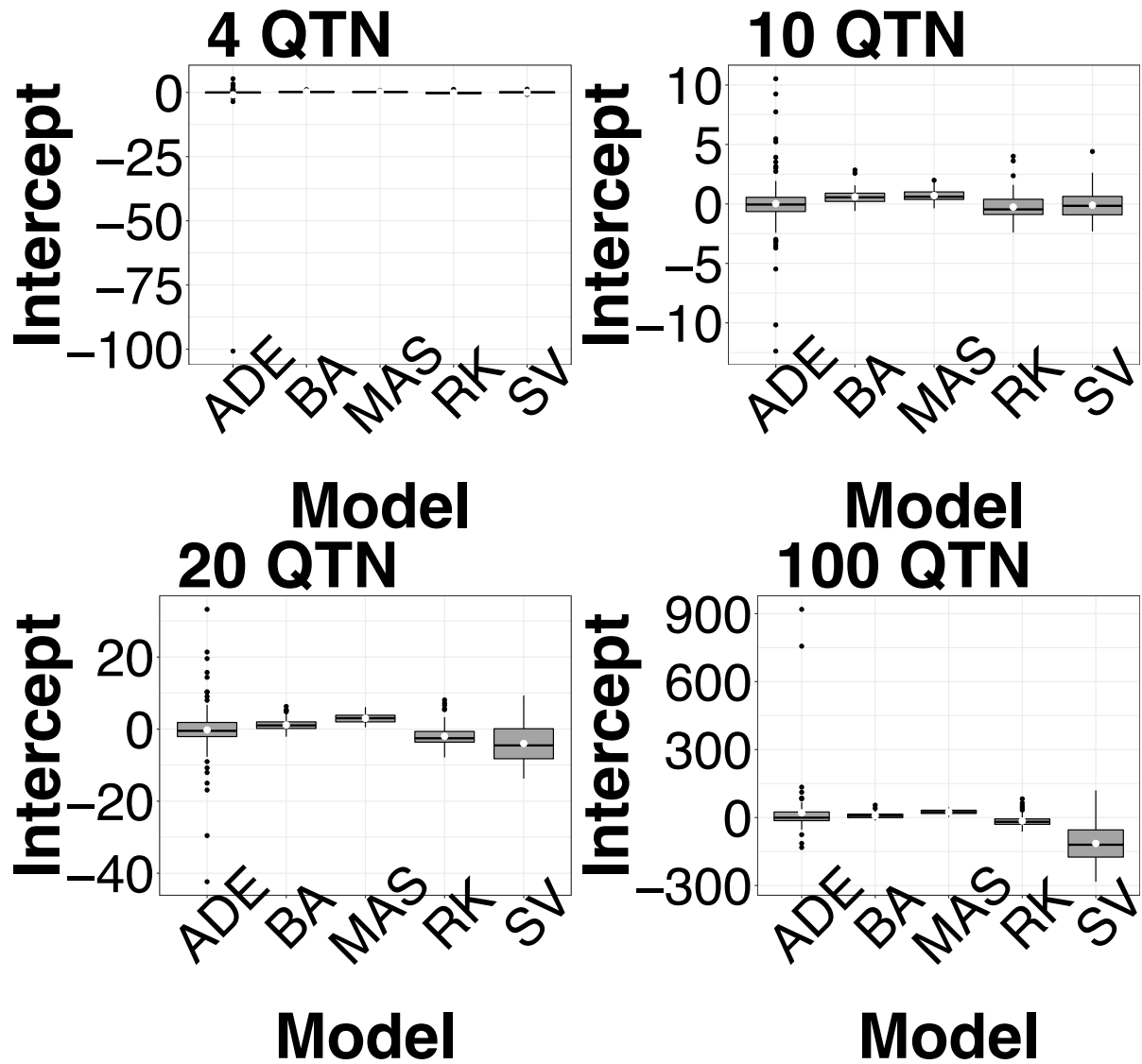




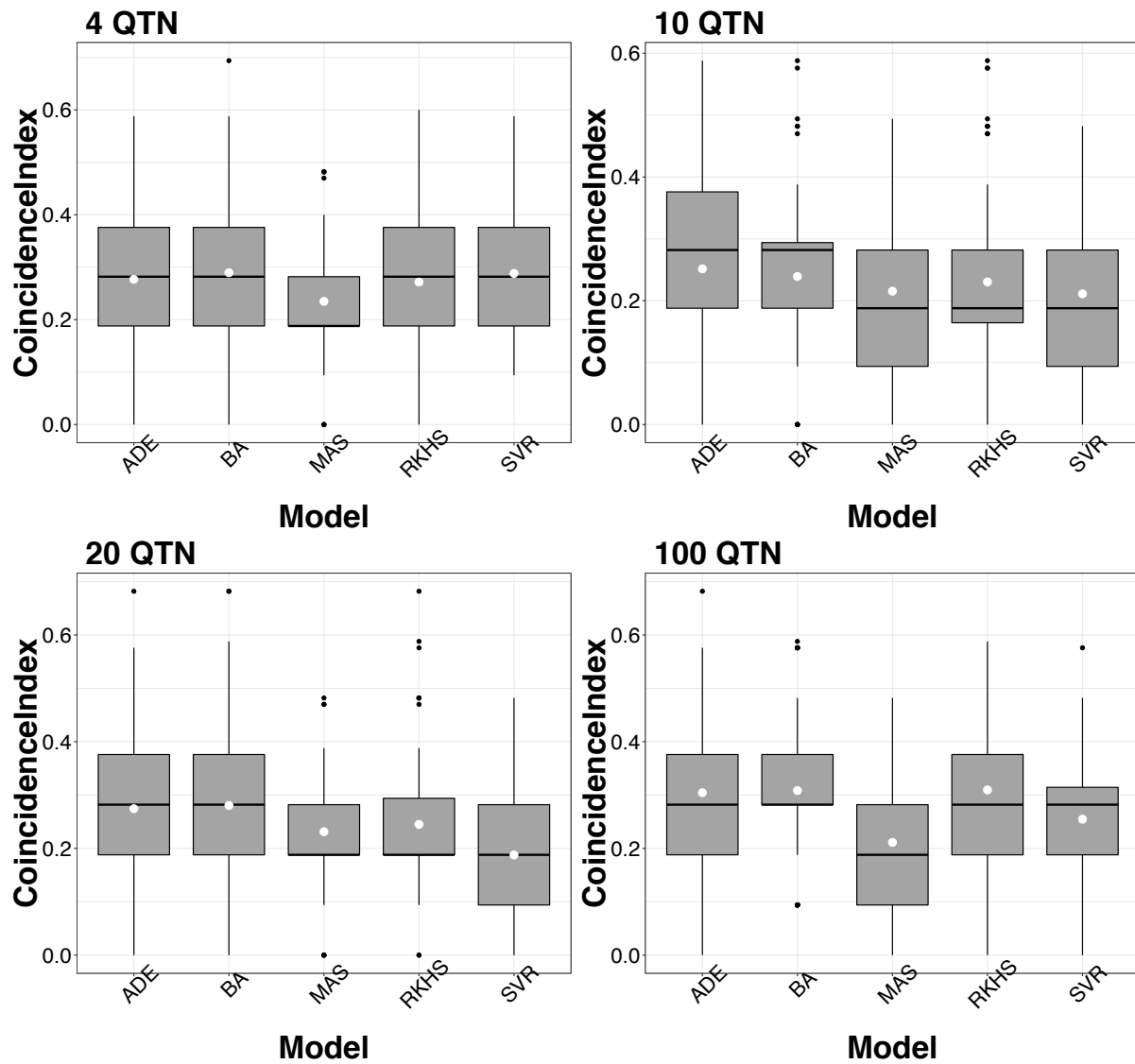
**Figure S16: Comparison of intercept values across GS and MAS models under additive mechanism and heritability of 0.3 in *Miscanthus* F<sub>1</sub> population for traits simulated with 4, 10, 20, and 100 QTNs.** Slope values for the regression model between simulated trait and GEBVs (Genomic Estimated Breeding Values) for GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] and MAS (Marker Assisted Selection) model for cross validation folds and 100 replicates. The white dots in the boxplots represent the mean of the distribution in each model.



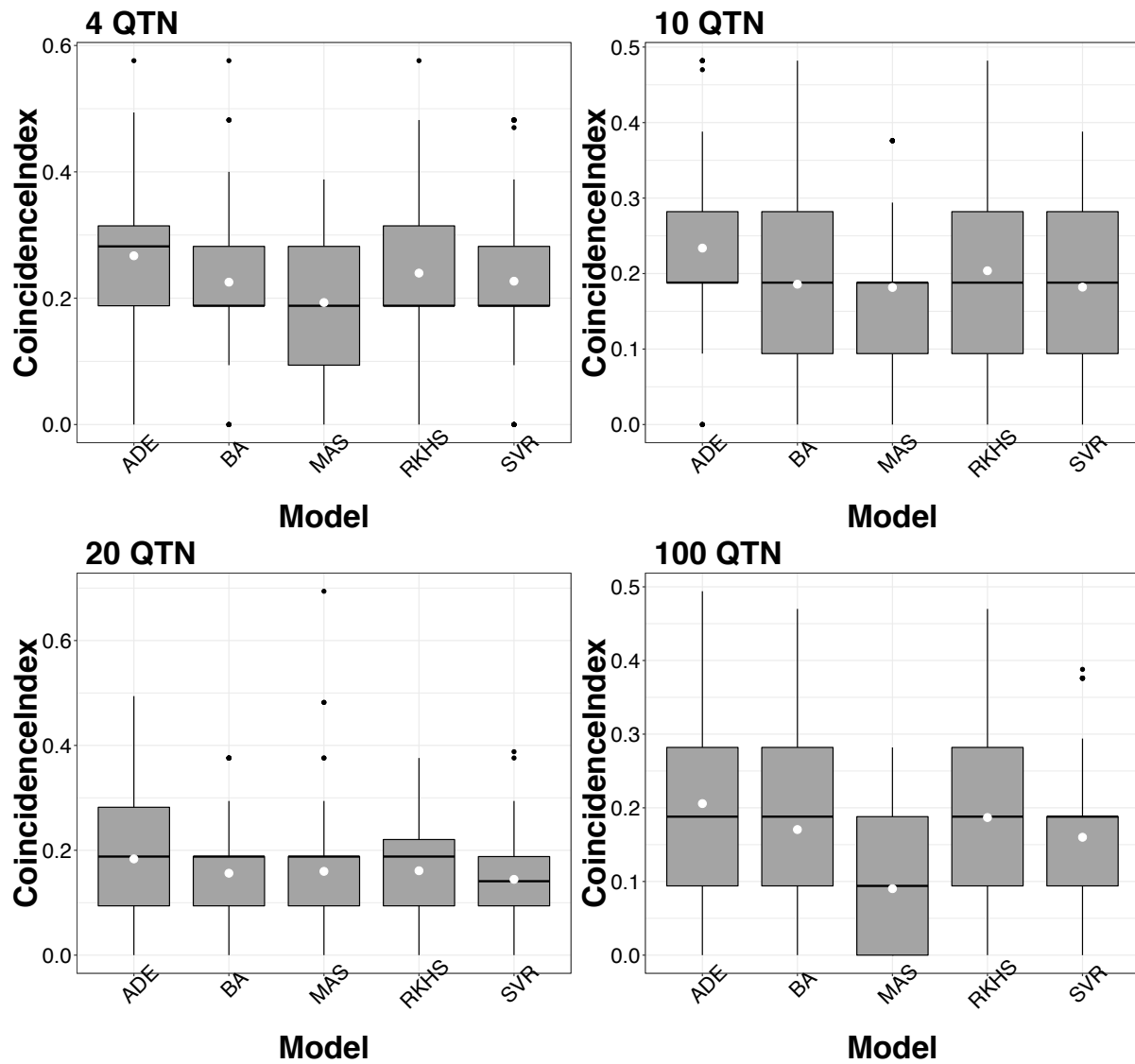
**Figure S17: Comparison of intercept values across GS and MAS models under dominance mechanism and heritability of 0.3 in *Miscanthus* F<sub>1</sub> population for traits simulated with 4, 10, 20, and 100 QTNs.** Slope values for the regression model between simulated trait and GEBVs (Genomic Estimated Breeding Values) for GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] and MAS (Marker Assisted Selection) model for cross validation folds and 100 replicates. The white dots in the boxplots represent the mean of the distribution in each model.



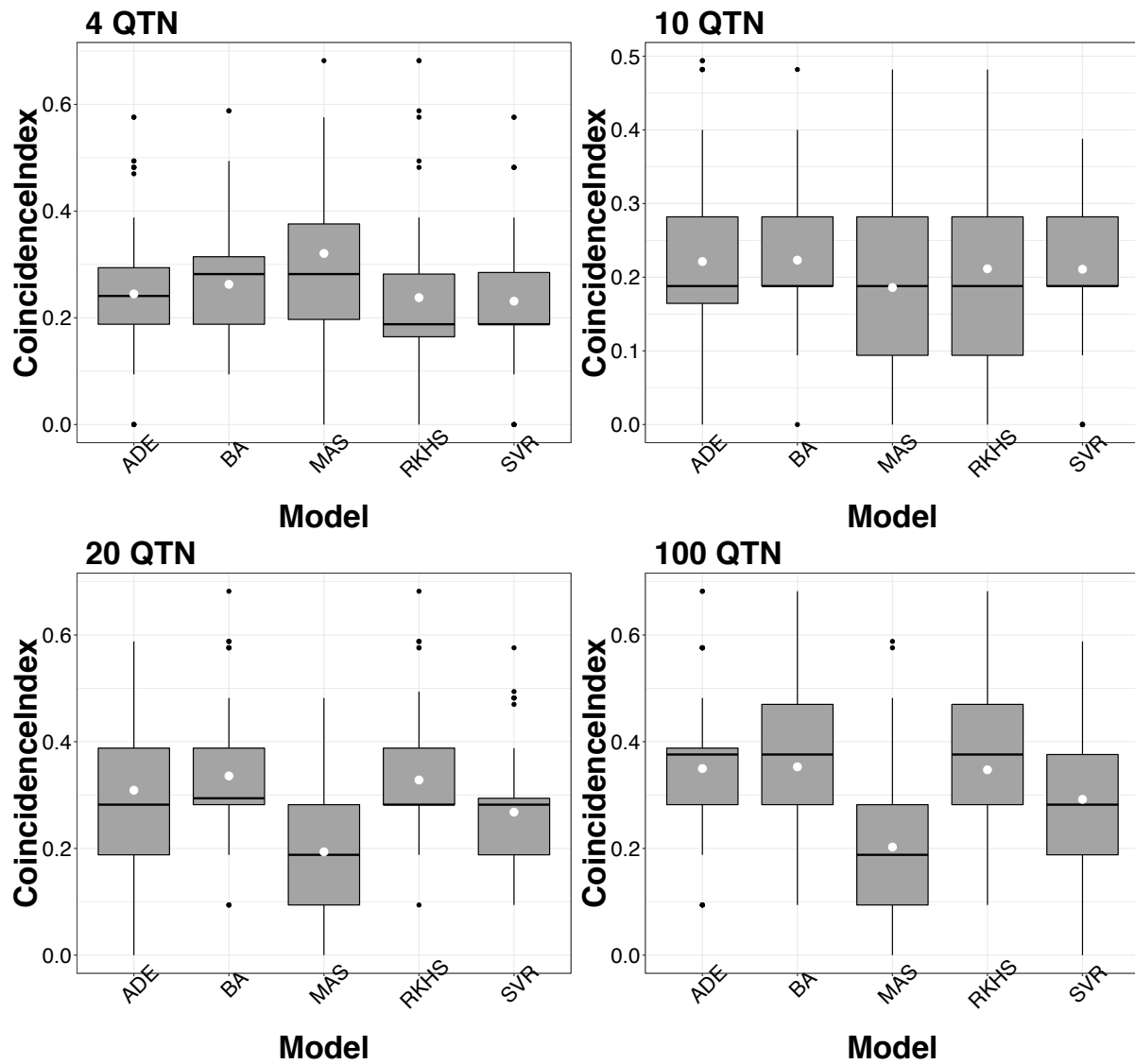
**Figure S18: Comparison of intercept values across GS and MAS models under epistasis mechanism and heritability of 0.3 in *Miscanthus* F<sub>1</sub> population for traits simulated with 4, 10, 20, and 100 QTNs.** Slope values for the regression model between simulated trait and GEBVs (Genomic Estimated Breeding Values) for GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] and MAS (Marker Assisted Selection) model for cross validation folds and 100 replicates. The white dots in the boxplots represent the mean of the distribution in each model.



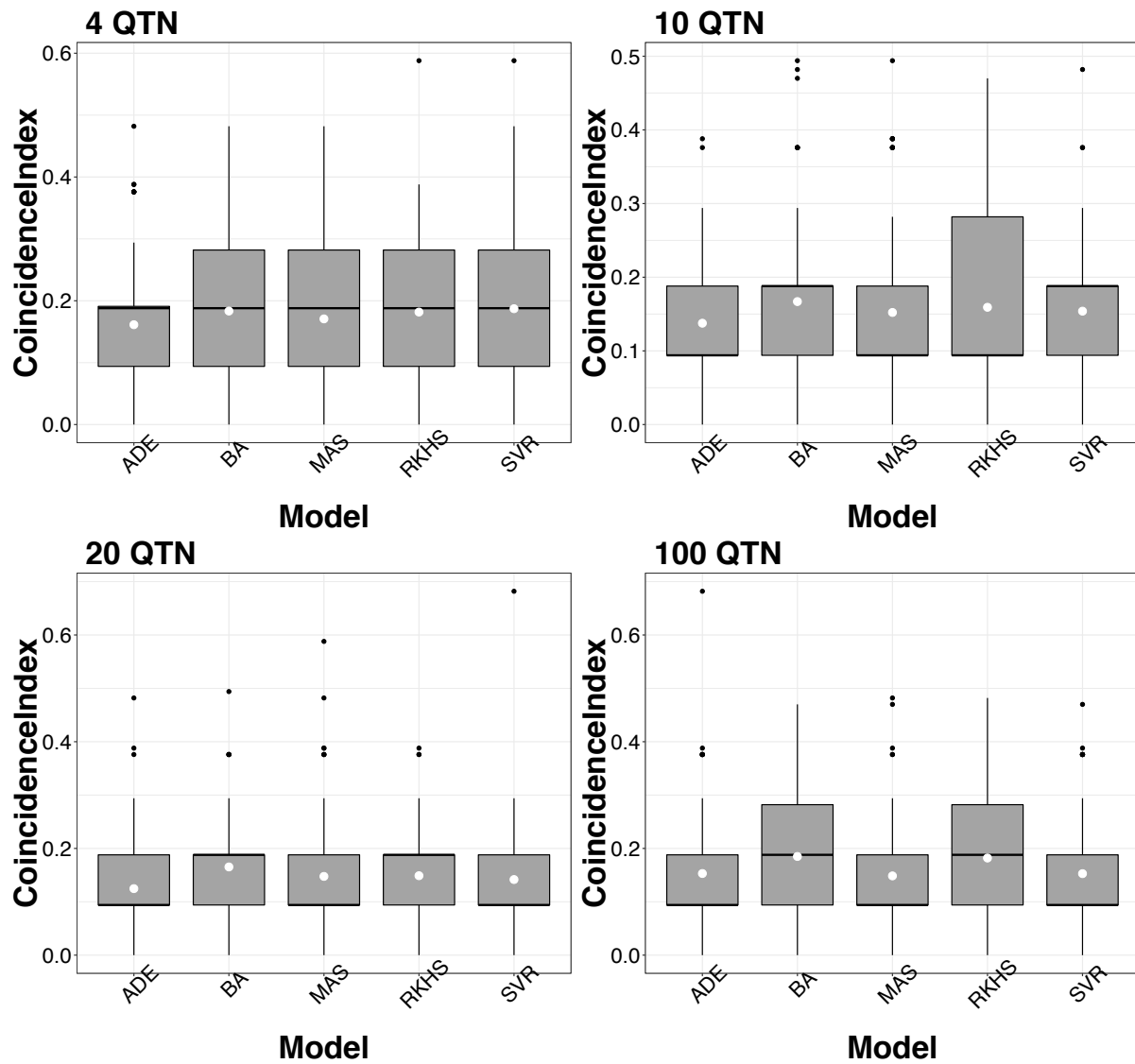
**Figure S19: Comparison of coincidence index among GS and MAS models for traits simulated with 4, 10, 20, and 100 QTNs under the additive mechanism and heritability of 0.7 in *Miscanthus* F<sub>1</sub> population.** Boxplots showing coincidence index distributions for GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] and MAS (Marker Assisted Selection) model for traits simulated with 4, 10, 20, and 100 QTNs. The white dots in the boxplots represent the mean of the distribution.



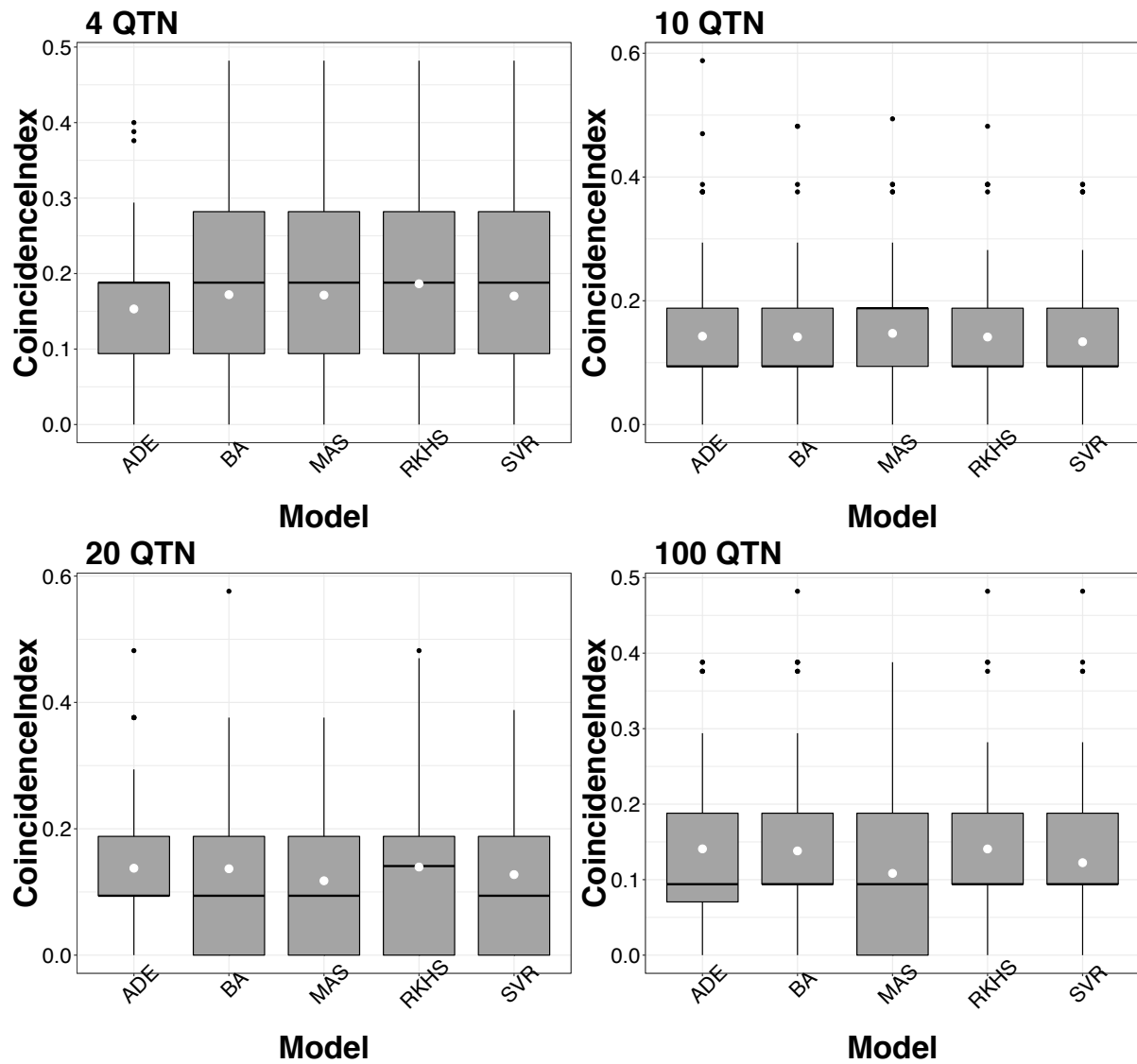
**Figure S20: Comparison of coincidence index among GS and MAS models for traits simulated with 4, 10, 20, and 100 QTNs under the dominance mechanism and heritability of 0.7 in *Miscanthus* F<sub>1</sub> population.** Boxplots showing coincidence index distributions for GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] and MAS (Marker Assisted Selection) model. The white dots in the boxplots represent the mean of the distribution.



**Figure S21: Comparison of coincidence index among GS and MAS models for traits simulated with 4, 10, 20, and 100 QTNs under the epistasis mechanism and heritability of 0.7 in *Miscanthus* F<sub>1</sub> population.** Boxplots showing coincidence index distributions for GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] and MAS (Marker Assisted Selection) model. The white dots in the boxplots represent the mean of the distribution.

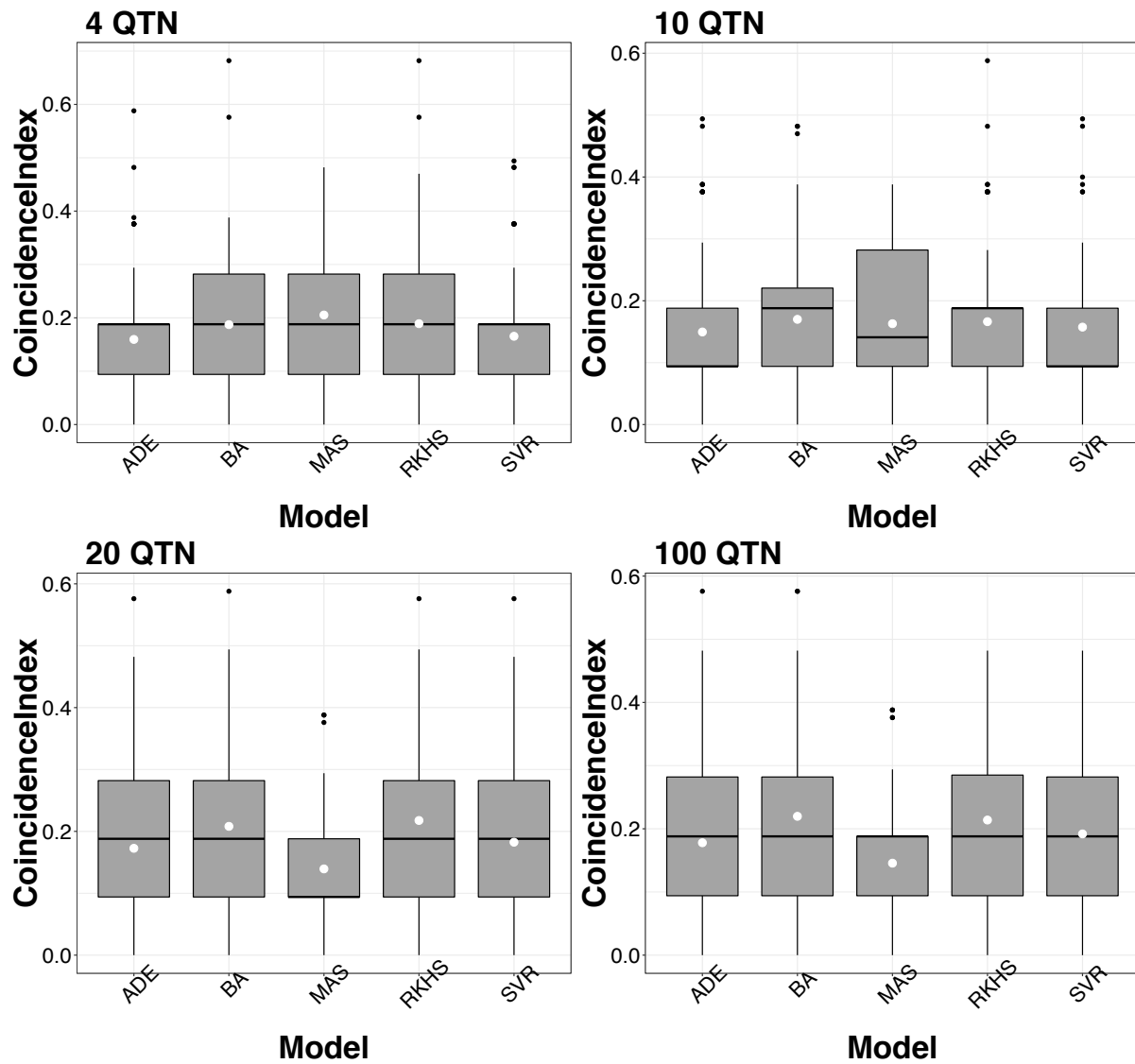


**Figure S22: Comparison of coincidence index among GS and MAS models for traits simulated with 4, 10, 20, and 100 QTNs under the additive mechanism and heritability of 0.3 in *Miscanthus* F<sub>1</sub> population.** Boxplots showing coincidence index distributions for GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] and MAS (Marker Assisted Selection) model. The white dots in the boxplots represent the mean of the distribution.

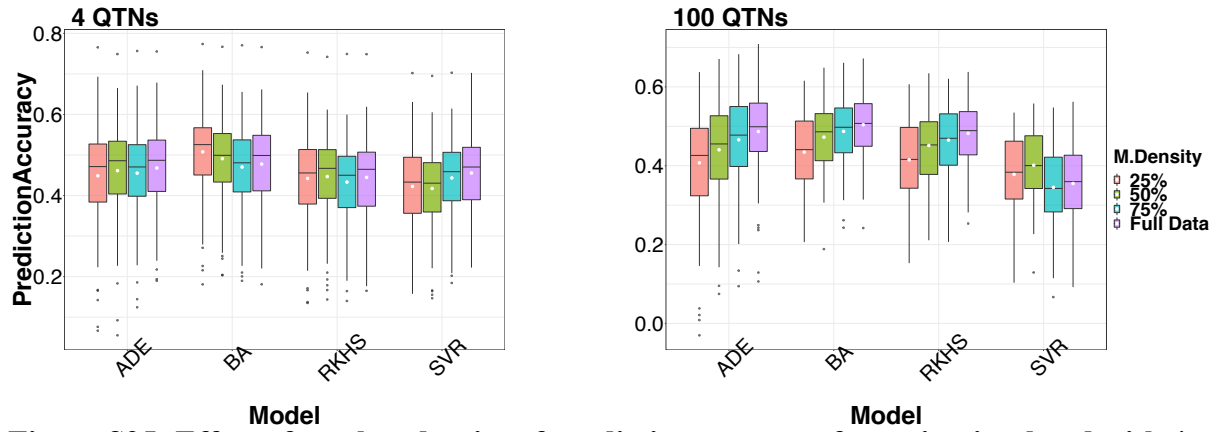


**Figure S23: Comparison of coincidence index among GS and MAS models for traits simulated with 4, 10, 20, and 100 QTNs under the dominance mechanism and heritability of 0.3 in *Miscanthus* F<sub>1</sub> population.** Boxplots showing coincidence index distributions for GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] and MAS (Marker Assisted Selection) model. The white dots in the boxplots represent the mean of the distribution.

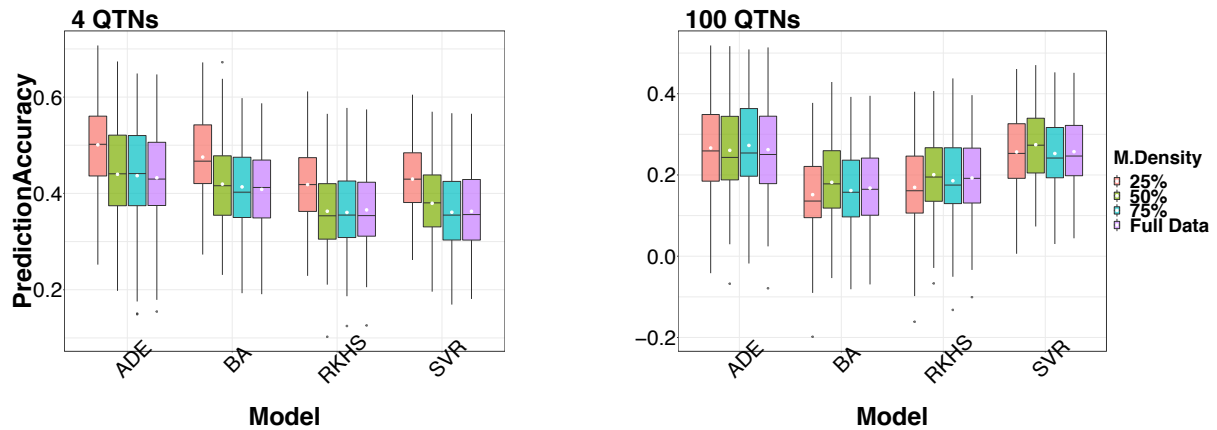




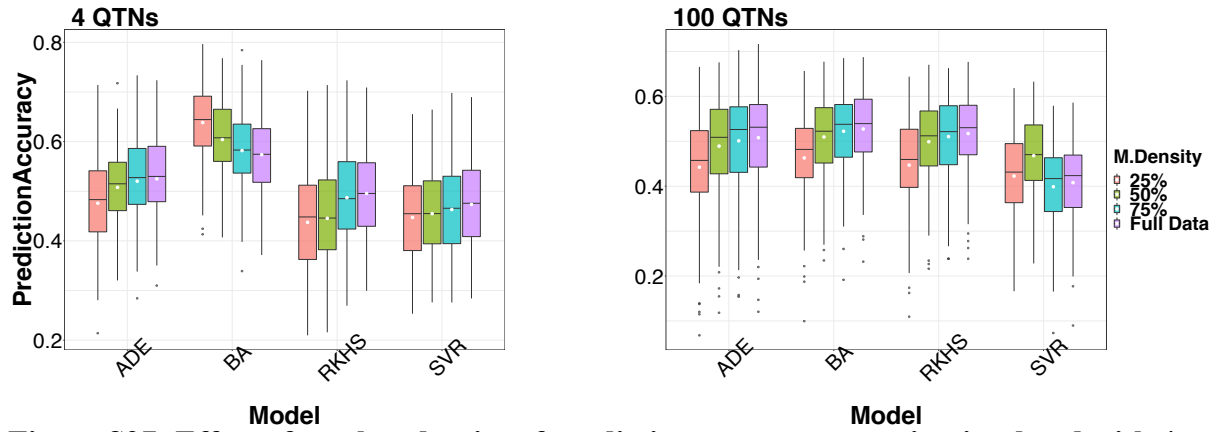
**Figure S24: Comparison of coincidence index among GS and MAS models for traits simulated with 4, 10, 20, and 100 QTNs under the epistasis mechanism and heritability of 0.3 in *Miscanthus* F<sub>1</sub> population.** Boxplots showing coincidence index distributions for GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] and MAS (Marker Assisted Selection) model. The white dots in the boxplots represent the mean of the distribution.



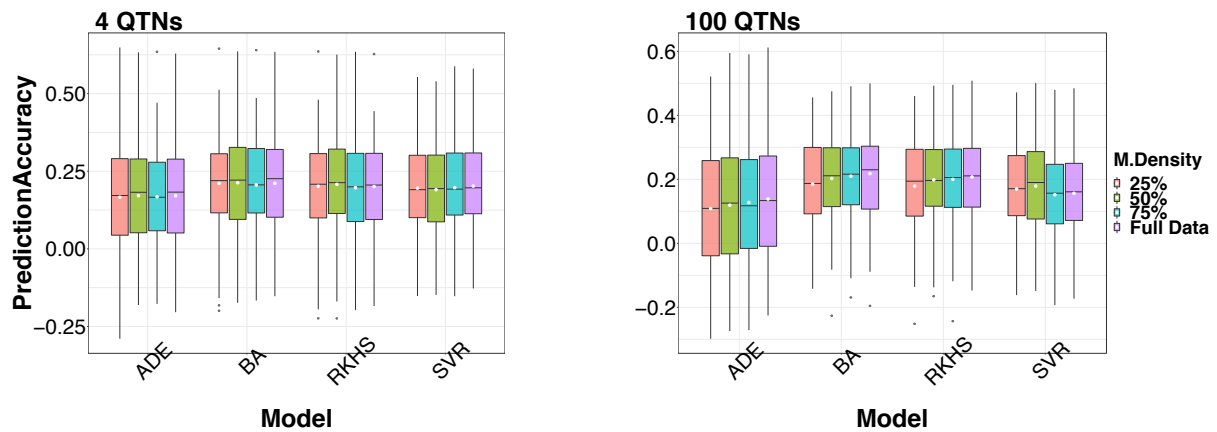
**Figure S25: Effect of marker density of prediction accuracy for traits simulated with 4 and 100 QTNs under the additive mechanism and heritability of 0.7 in *Miscanthus* F<sub>1</sub> population.** Box plots showing the distribution of predicted accuracies across five-folds and 100 replicates for different marker densities GS models [ADE (Additive-Dominance-Epistasis kernels model in *sommer* package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), and Support Vector Machine (SVR)]. The white dots in the middle of the boxplot shows the mean of the distribution.



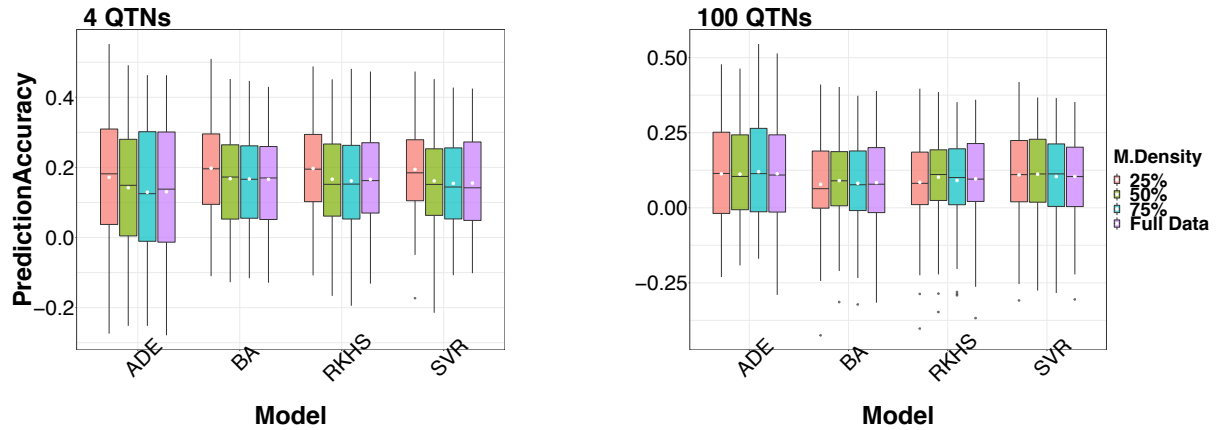
**Figure S26: Effect of marker density of prediction accuracy for traits simulated with 4 and 100 QTNs under the dominance mechanism and heritability of 0.7 in *Miscanthus* F<sub>1</sub> population.** Box plots showing the distribution of predicted accuracies across five-folds and 100 replicates for different marker densities GS models [ADE (Additive-Dominance-Epistasis kernels model in *sommer* package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space)]. The white dots in the middle of the boxplot shows the mean of the distribution.



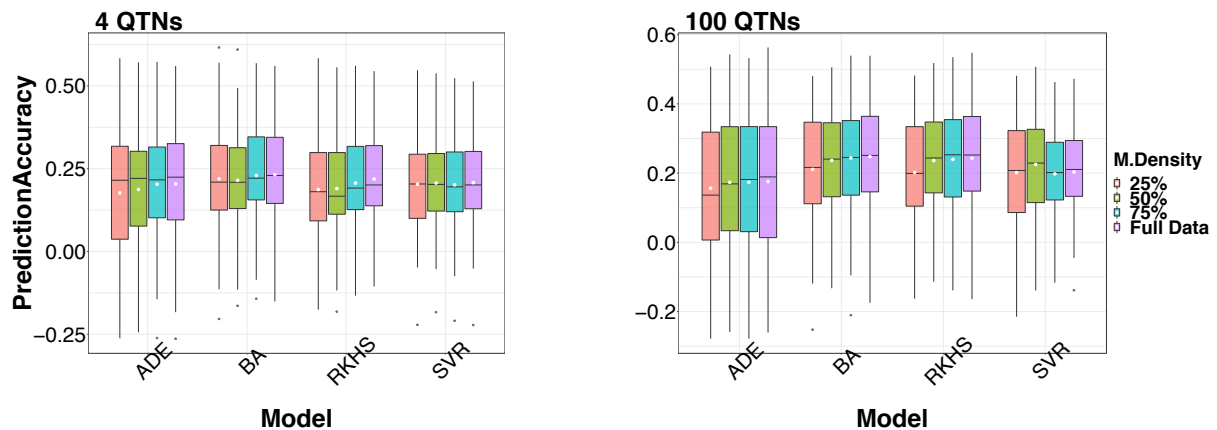
**Figure S27: Effect of marker density of prediction accuracy or traits simulated with 4 and 100 QTNs under the epistasis mechanism and heritability of 0.7 in *Miscanthus* F<sub>1</sub> population.** Box plots showing the distribution of predicted accuracies across five-folds and 100 replicates for different marker densities GS models [ADE (Additive-Dominance-Epistasis kernels model in *sommer* package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space)]. The white dots in the middle of the boxplot shows the mean of the distribution.



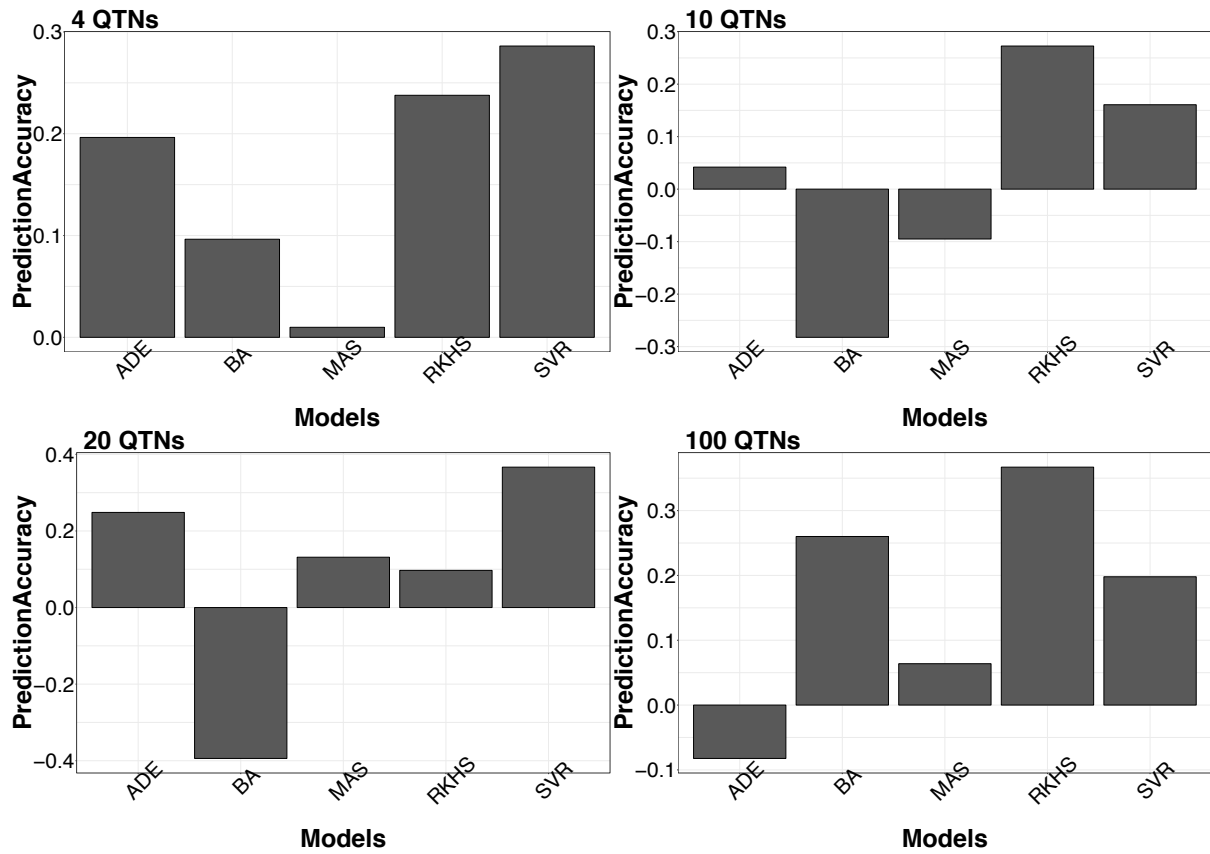
**Figure S28: Effect of marker density of prediction accuracy for traits simulated with 4 and 100 QTNs under the additive mechanism and heritability of 0.3 in *Miscanthus* F<sub>1</sub> population.** Box plots showing the distribution of predicted accuracies across five-folds and 100 replicates for different marker densities GS models [ADE (Additive-Dominance-Epistasis kernels model in *sommer* package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space)]. The white dots in the middle of the boxplot shows the mean of the distribution.



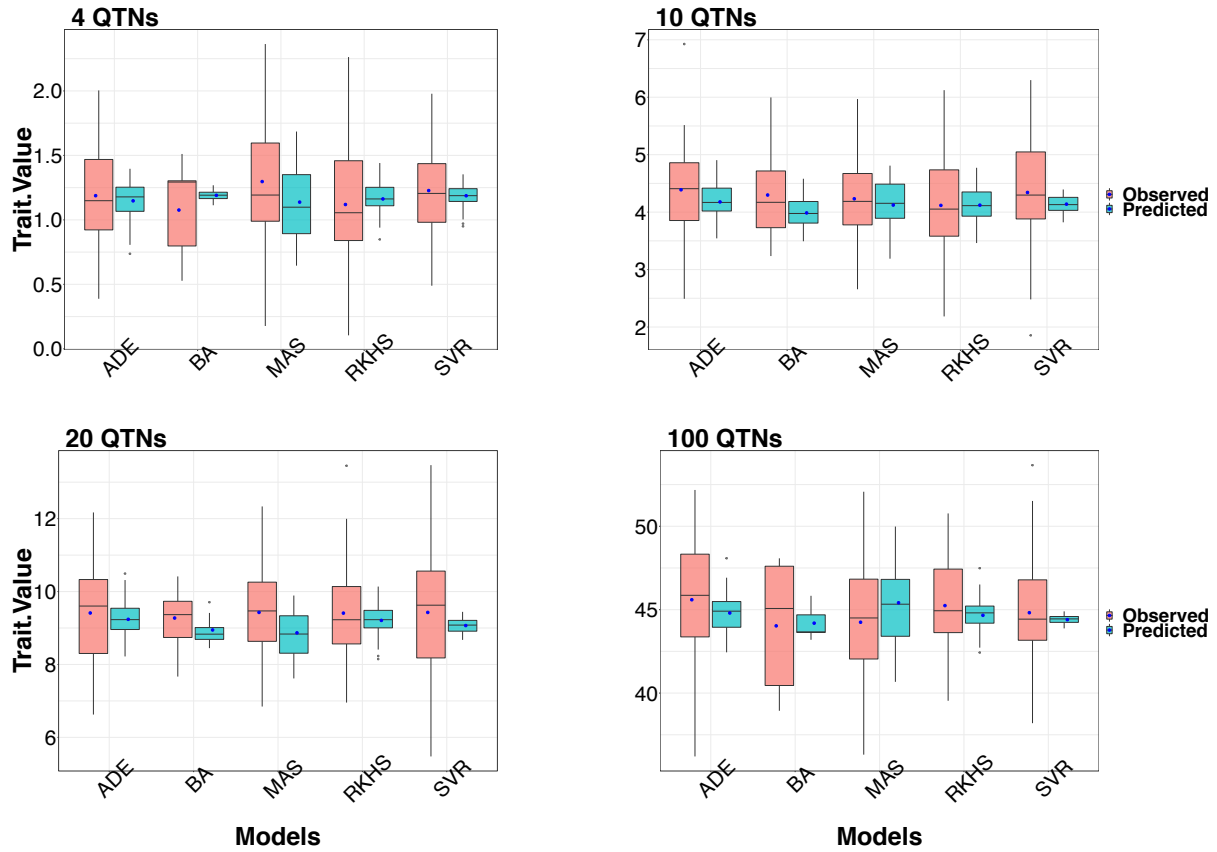
**Figure S29: Effect of marker density of prediction accuracy for traits simulated with 4 and 100 QTNs under the dominance mechanism and heritability of 0.3 in *Miscanthus* F<sub>1</sub> population.** Box plots showing the distribution of predicted accuracies across five-folds and 100 replicates for different marker densities GS models [ADE (Additive-Dominance-Epistasis kernels model in *sommer* package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space)]. The white dots in the middle of the boxplot shows the mean of the distribution.



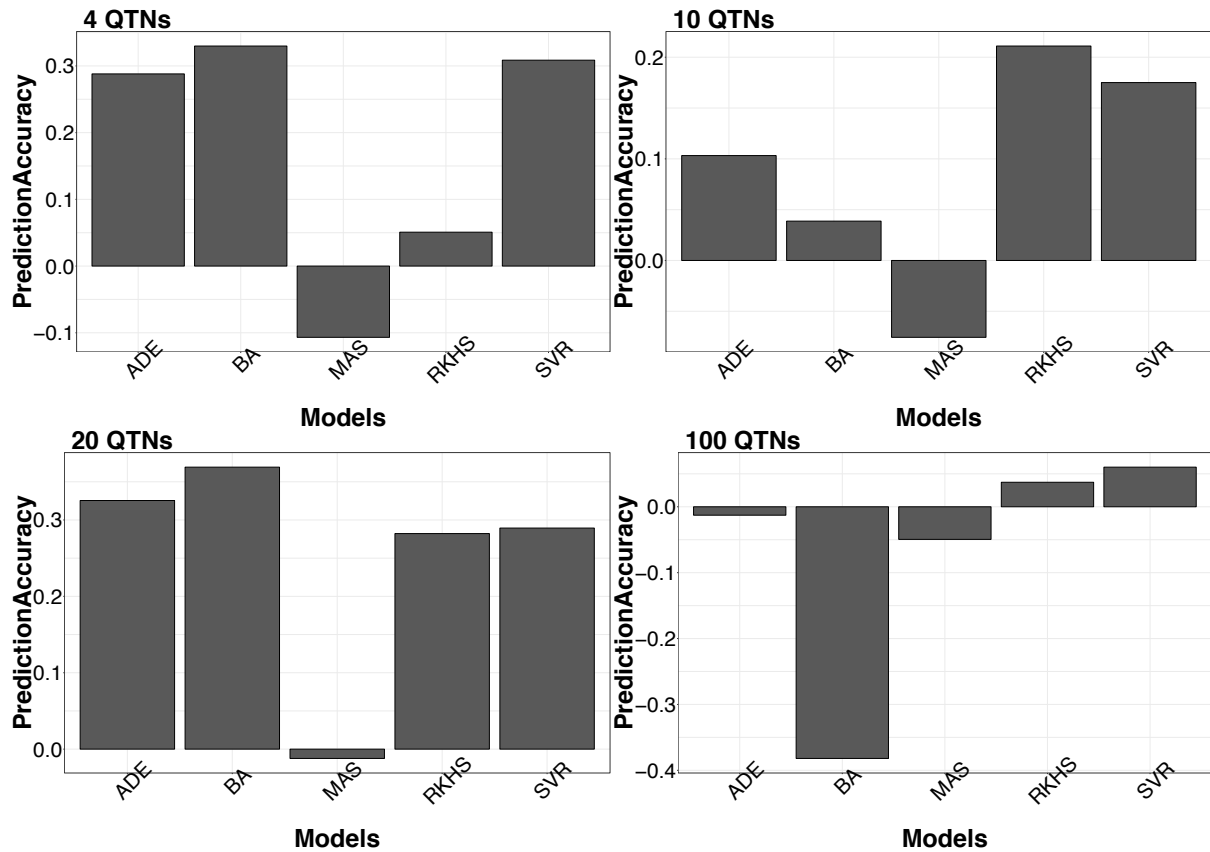
**Figure S30: Effect of marker density of prediction accuracy or traits simulated with 4 and 100 QTNs under the epistasis mechanism and heritability of 0.3 in *Miscanthus* F<sub>1</sub> population.** Box plots showing the distribution of predicted accuracies across five-folds and 100 replicates for different marker densities GS models [ADE (Additive-Dominance-Epistasis kernels model in *sommer* package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space)]. The white dots in the middle of the boxplot shows the mean of the distribution.



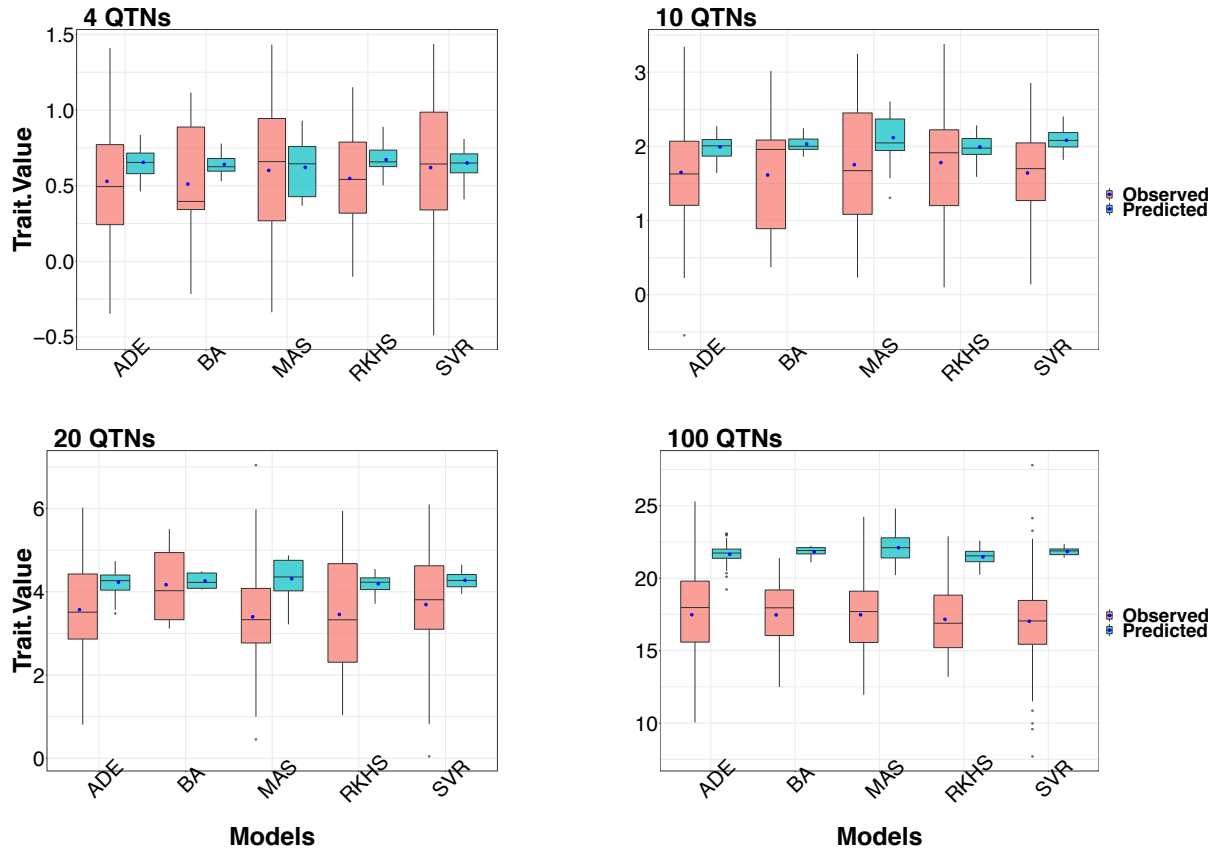
**Figure S31: Comparison among GS and MAS models in GS and MAS derived BC<sub>1</sub> populations in *Miscanthus* for traits simulated with 4, 10, 20, and 100 QTNs under additive mechanism and heritability of 0.7.** Barplots showing prediction accuracy comparison among GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] in GS derived BC<sub>1</sub> and MAS (Marker Assisted Selection) in MAS derived BC<sub>1</sub>.



**Figure S32: Distribution of observed and predicted values in GS and MAS models in GS and MAS derived BC<sub>1</sub> populations in *Miscanthus* for traits simulated with 4, 10, 20, and 100 QTNs under additive mechanism and heritability of 0.7.** Boxplots showing the distributions of observed and predicted trait values in GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] in GS derived BC<sub>1</sub> and MAS (Marker Assisted Selection) in MAS derived BC<sub>1</sub>. The blue dot represents the mean of each distribution.

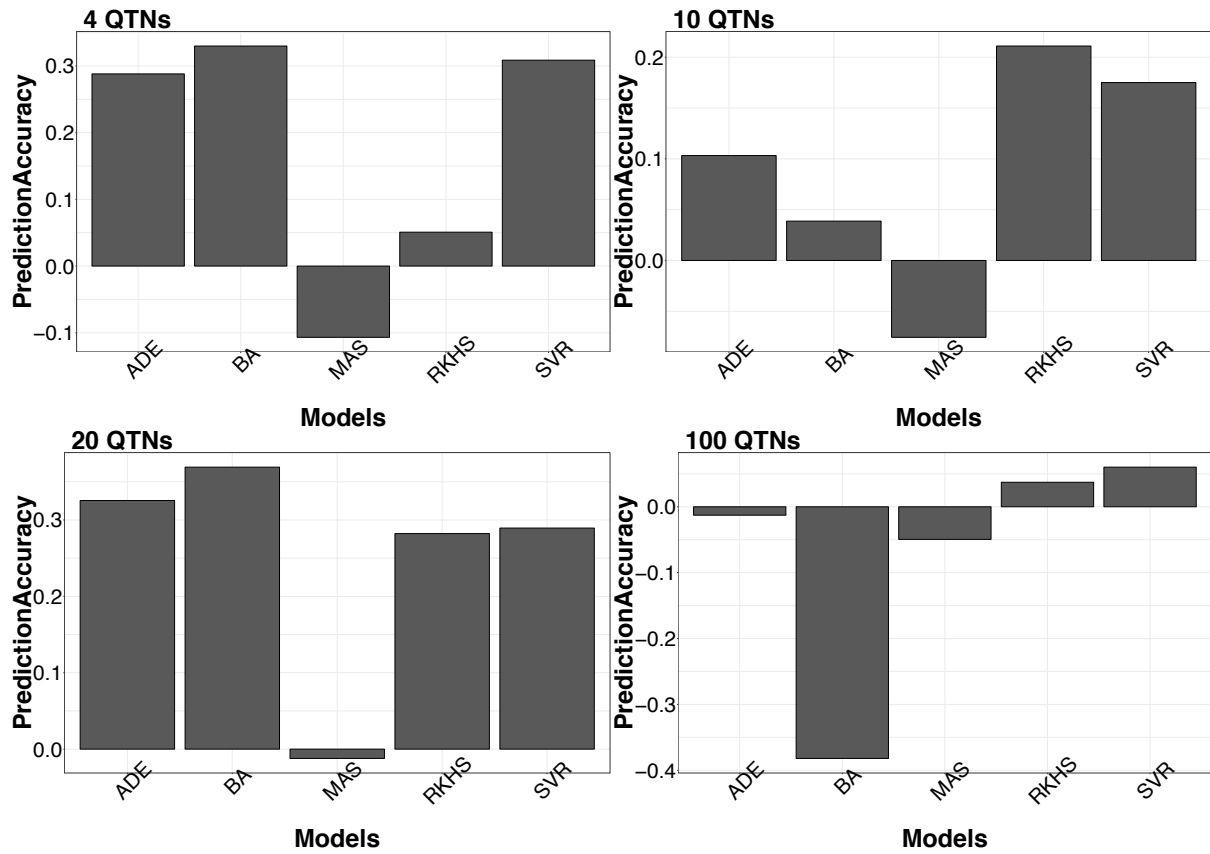


**Figure S33: Comparison among GS and MAS models in GS and MAS derived BC<sub>1</sub> populations in *Miscanthus* for traits simulated with 4, 10, 20, and 100 QTNs under dominance mechanism and heritability of 0.7.** Barplots showing prediction accuracy comparison among GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] in GS derived BC<sub>1</sub> and MAS (Marker Assisted Selection) in MAS derived BC<sub>1</sub>.

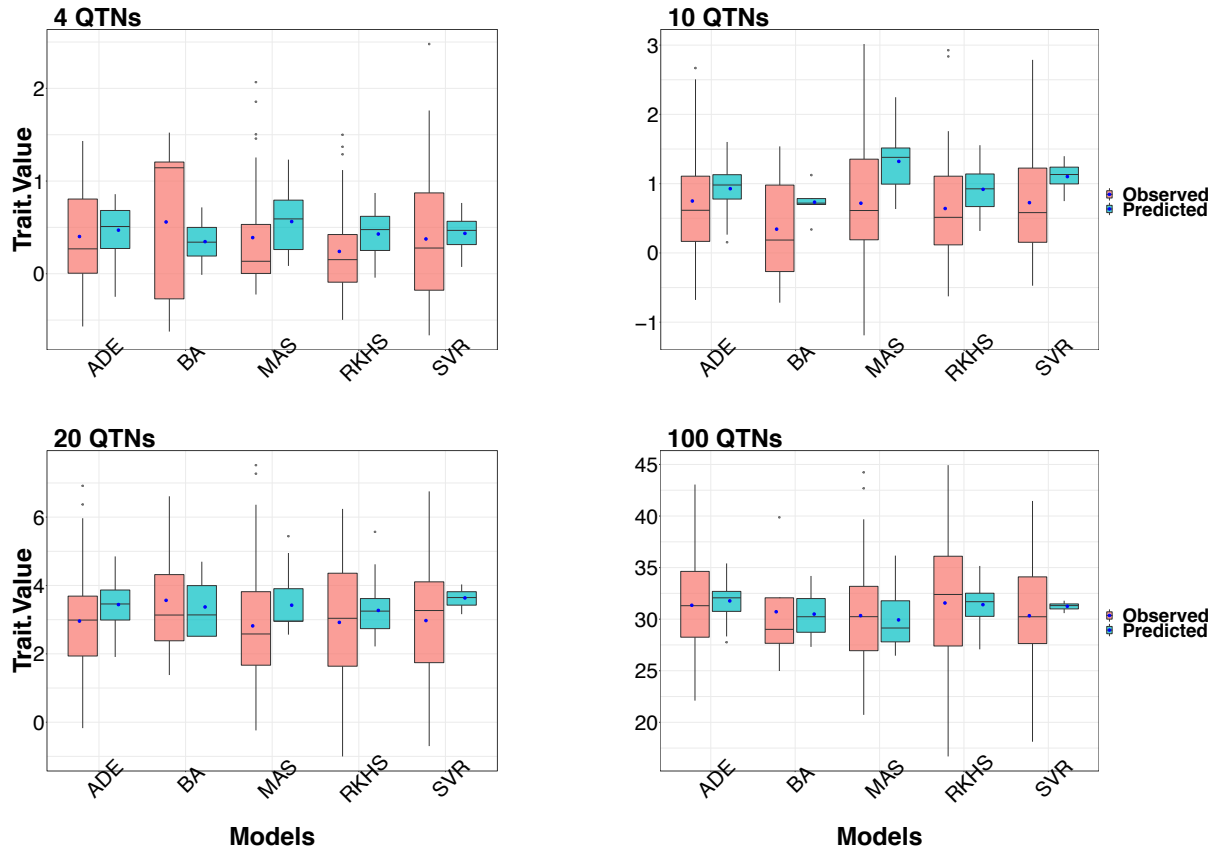


**Figure S34: Distribution of observed and predicted values in GS and MAS models in GS and MAS derived BC<sub>1</sub> populations in *Miscanthus* for traits simulated with 4, 10, 20, and 100 QTNs under dominance mechanism and heritability of 0.7.** Boxplots showing the distributions of observed and predicted trait values in GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] in GS derived BC<sub>1</sub> and MAS (Marker Assisted Selection) in MAS derived BC<sub>1</sub>. The blue dot represents the mean of each distribution.

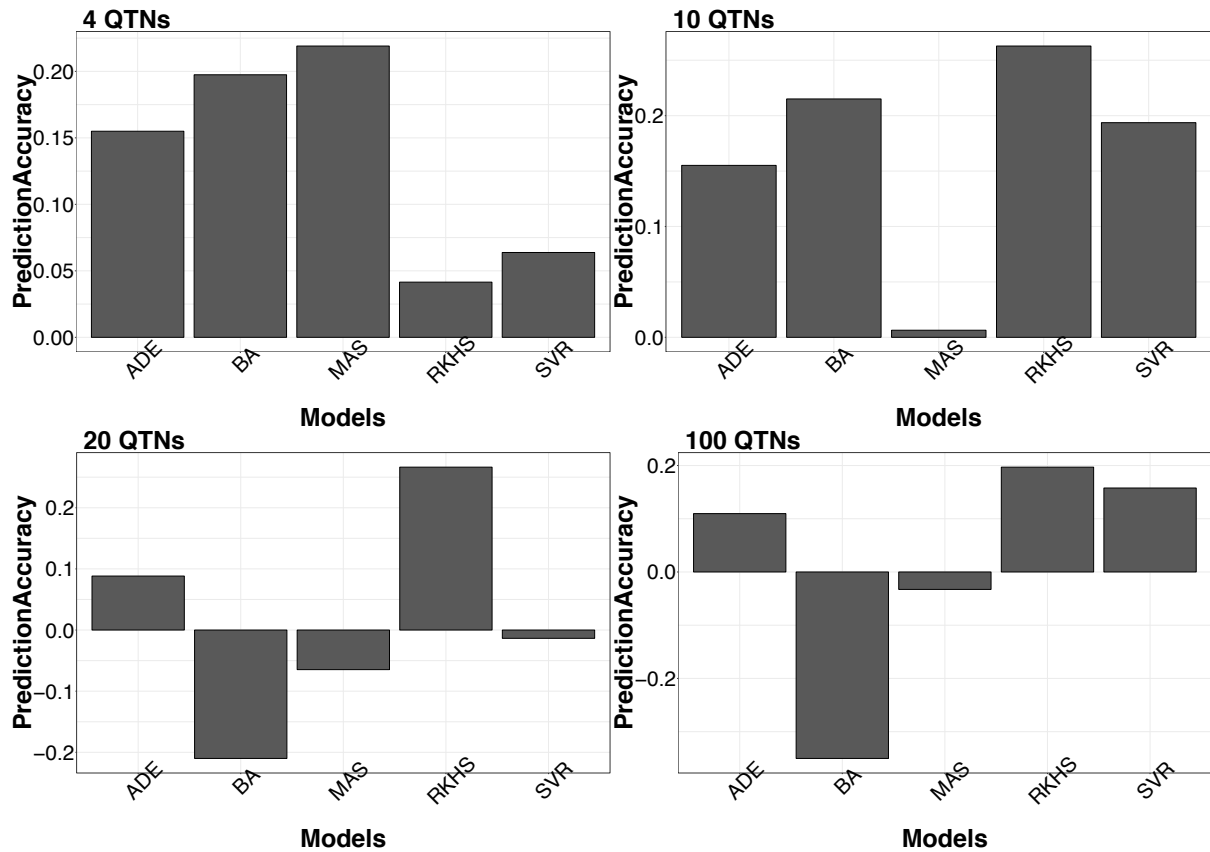




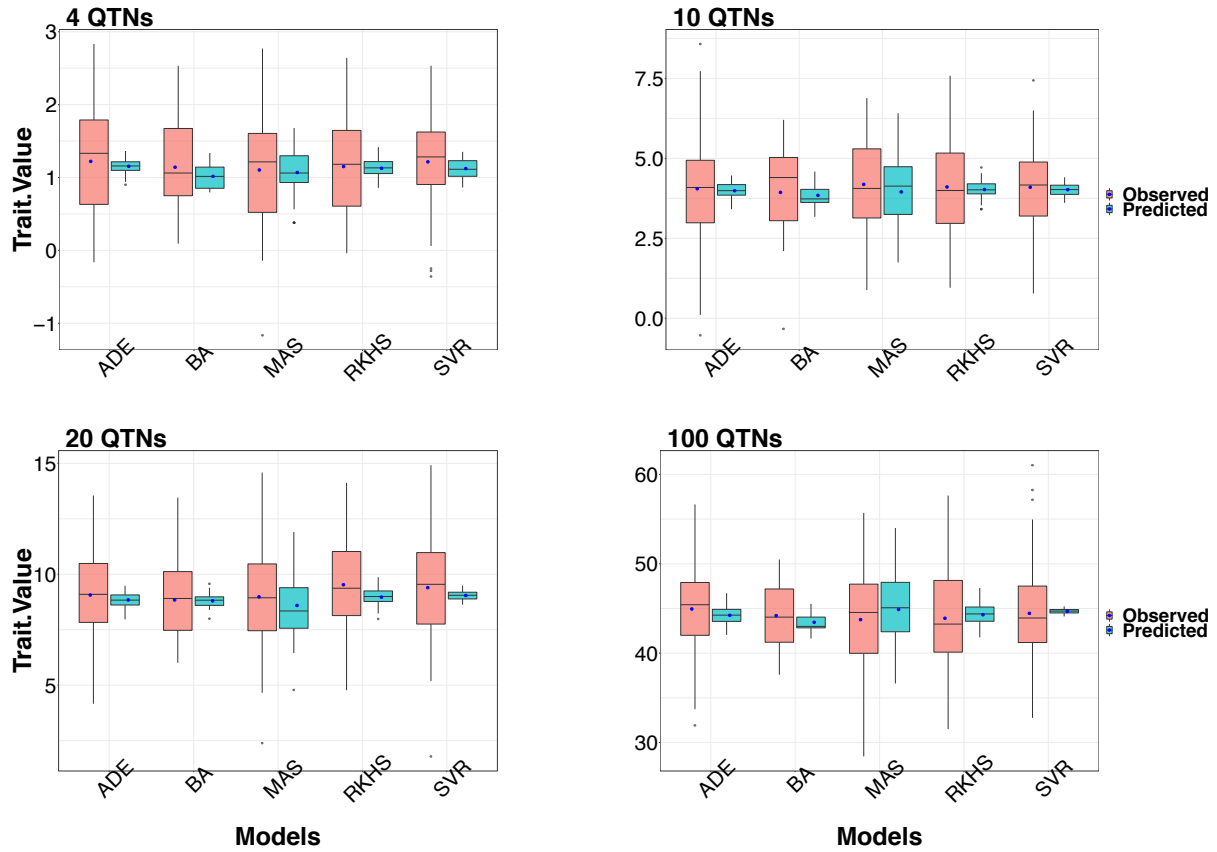
**Figure S35: Comparison among GS and MAS models in GS and MAS derived BC<sub>1</sub> populations in *Miscanthus* for traits simulated with 4, 10, 20, and 100 QTNs under epistasis mechanism and heritability of 0.7.** Barplots showing prediction accuracy comparison among GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] in GS derived BC<sub>1</sub> and MAS (Marker Assisted Selection) in MAS derived BC<sub>1</sub>.



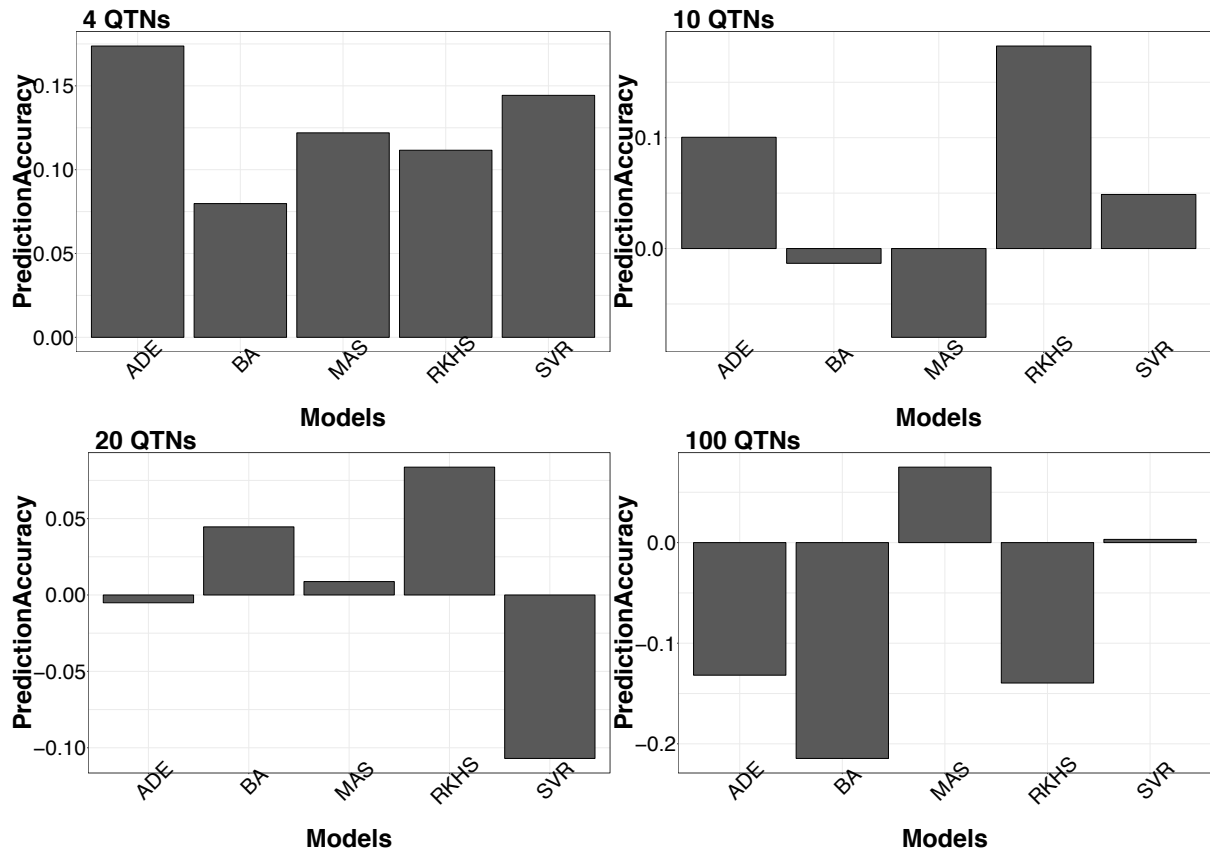
**Figure S36: Distribution of observed and predicted values in GS and MAS models in GS and MAS derived BC<sub>1</sub> populations in *Miscanthus* for traits simulated with 4, 10, 20, and 100 QTNs under epistasis mechanism and heritability of 0.7.** Boxplots showing the distributions of observed and predicted trait values in GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] in GS derived BC<sub>1</sub> and MAS (Marker Assisted Selection) in MAS derived BC<sub>1</sub>. The blue dot represents the mean of each distribution.



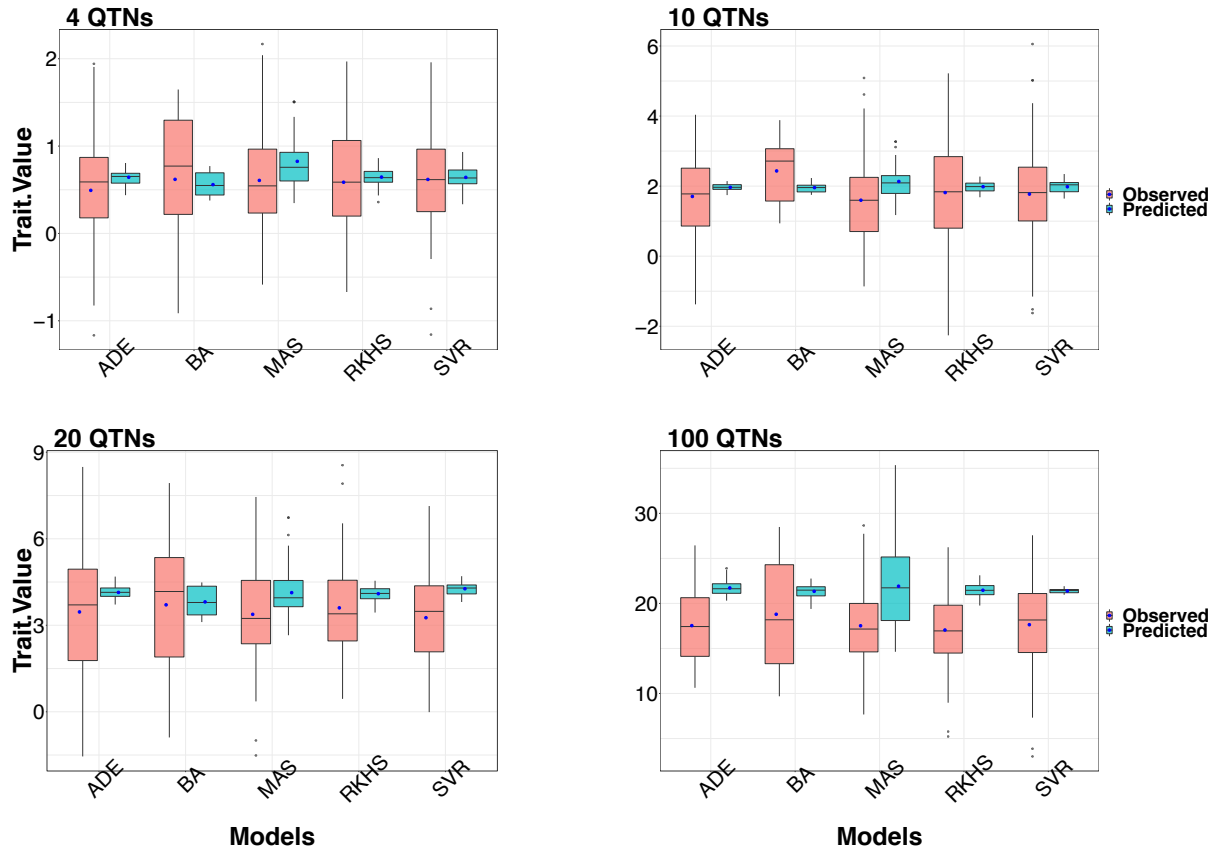
**Figure S37: Comparison among GS and MAS models in GS and MAS derived BC<sub>1</sub> populations in *Miscanthus* for traits simulated with 4, 10, 20, and 100 QTNs under additive mechanism and heritability of 0.3.** Barplots showing prediction accuracy comparison among GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] in GS derived BC<sub>1</sub> and MAS (Marker Assisted Selection) in MAS derived BC<sub>1</sub>.



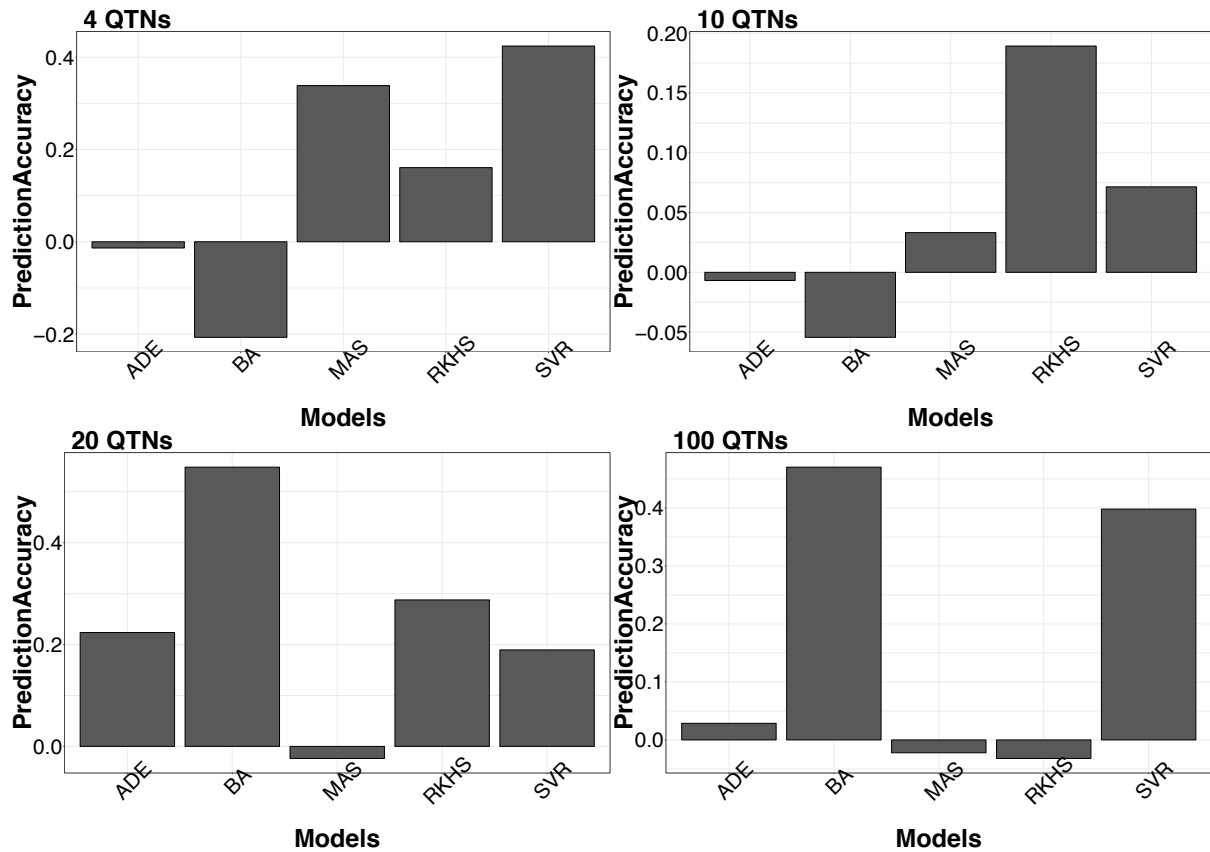
**Figure S38: Distribution of observed and predicted values in GS and MAS models in GS and MAS derived BC<sub>1</sub> populations in *Miscanthus* for traits simulated with 4, 10, 20, and 100 QTNs under additive mechanism and heritability of 0.3.** Boxplots showing the distributions of observed and predicted trait values in GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] in GS derived BC<sub>1</sub> and MAS (Marker Assisted Selection) in MAS derived BC<sub>1</sub>. The blue dot represents the mean of each distribution.



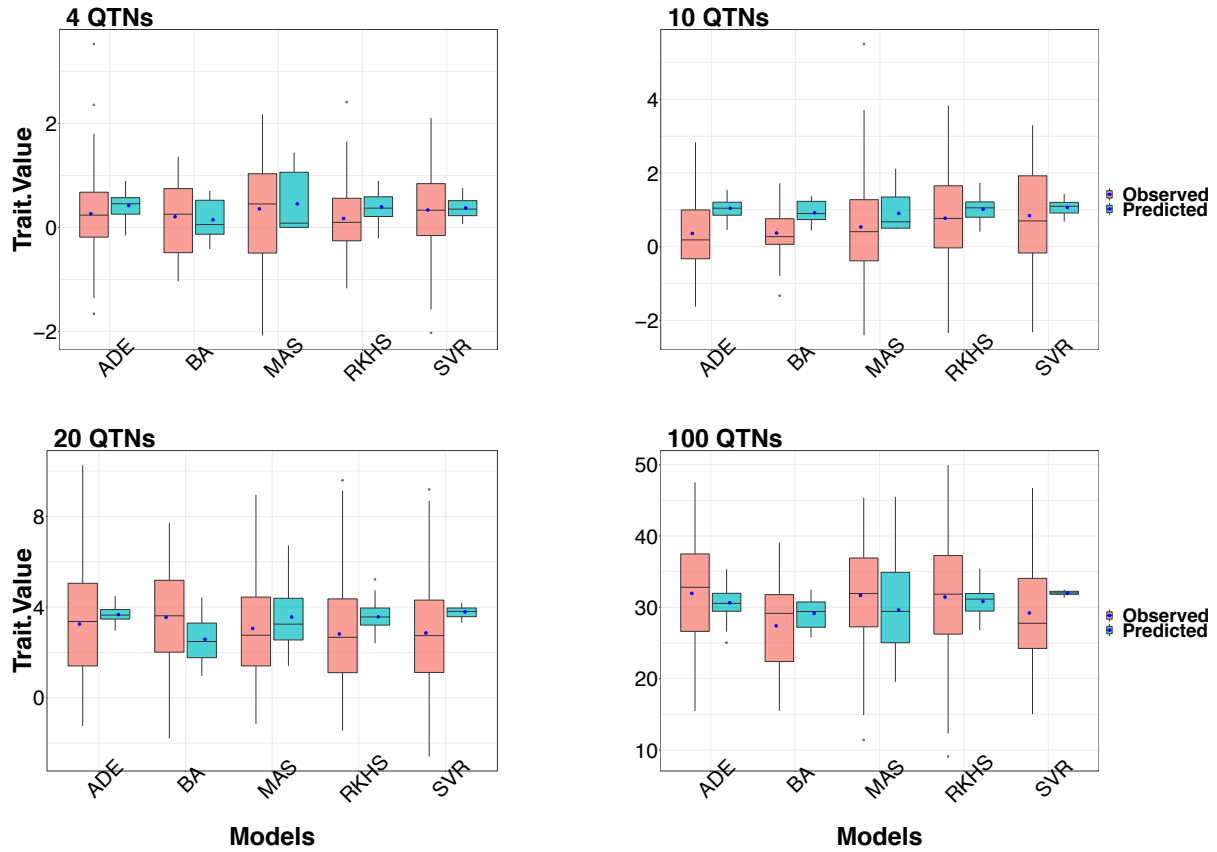
**Figure S39: Comparison among GS and MAS models in GS and MAS derived BC<sub>1</sub> populations in *Miscanthus* for traits simulated with 4, 10, 20, and 100 QTNs under dominance mechanism and heritability of 0.3.** Barplots showing prediction accuracy comparison among GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] in GS derived BC<sub>1</sub> and MAS (Marker Assisted Selection) in MAS derived BC<sub>1</sub>.



**Figure S40: Distribution of observed and predicted values in GS and MAS models in GS and MAS derived BC<sub>1</sub> populations in *Miscanthus* for traits simulated with 4, 10, 20, and 100 QTNs under dominance mechanism and heritability of 0.3.** Boxplots showing the distributions of observed and predicted trait values in GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] in GS derived BC<sub>1</sub> and MAS (Marker Assisted Selection) in MAS derived BC<sub>1</sub>. The blue dot represents the mean of each distribution.

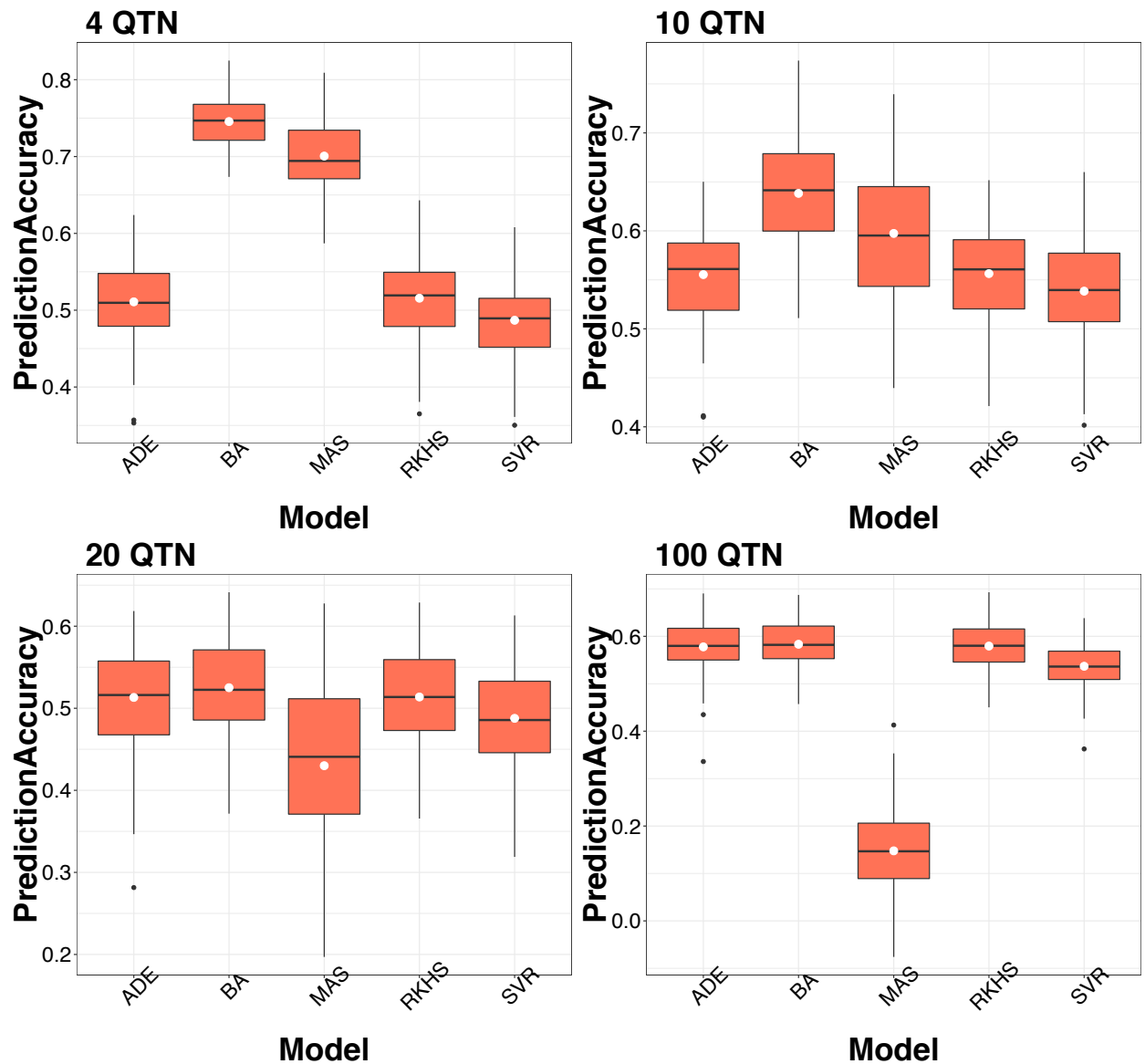


**Figure S41: Comparison among GS and MAS models in GS and MAS derived BC<sub>1</sub> populations in *Miscanthus* for traits simulated with 4, 10, 20, and 100 QTNs under epistasis mechanism and heritability of 0.3.** Barplots showing prediction accuracy comparison among GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] in GS derived BC<sub>1</sub> and MAS (Marker Assisted Selection) in MAS derived BC<sub>1</sub>.

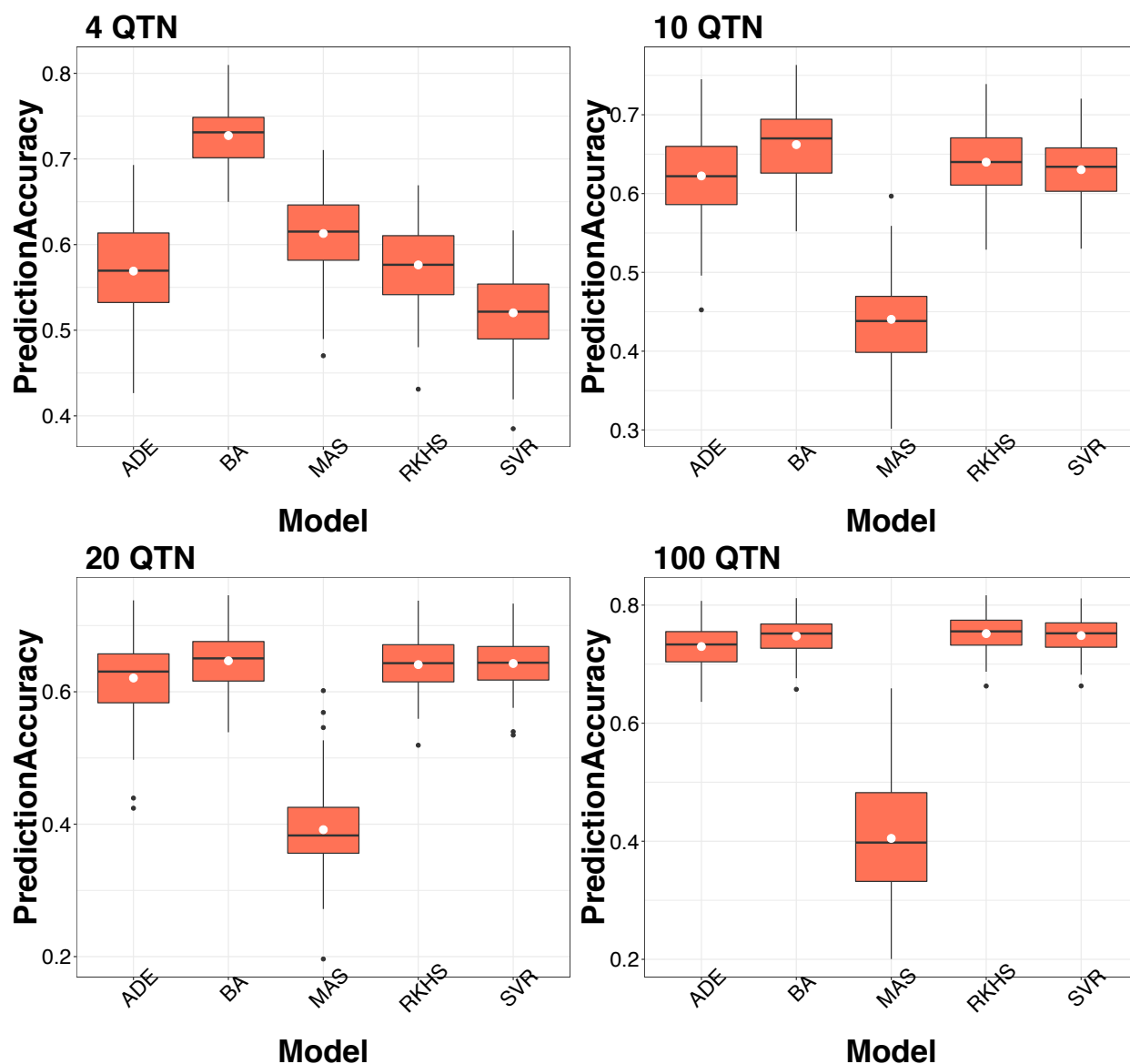


**Figure S42: Distribution of observed and predicted values in GS and MAS models in GS and MAS derived BC<sub>1</sub> populations in *Miscanthus* for traits simulated with 4, 10, 20, and 100 QTNs under epistasis mechanism and heritability of 0.3.** Boxplots showing the distributions of observed and predicted trait values in GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] in GS derived BC<sub>1</sub> and MAS (Marker Assisted Selection) in MAS derived BC<sub>1</sub>. The blue dot represents the mean of each distribution.

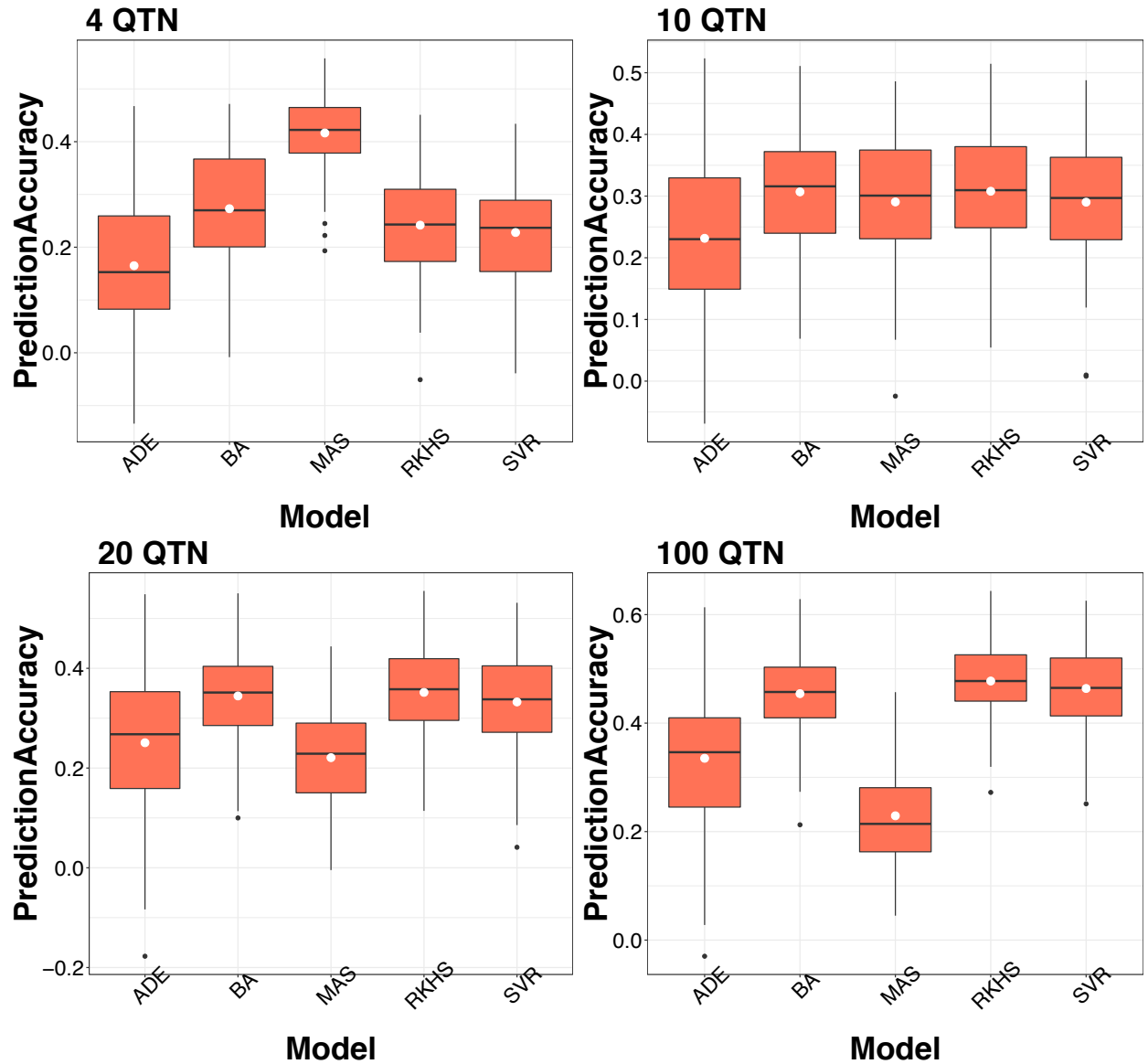




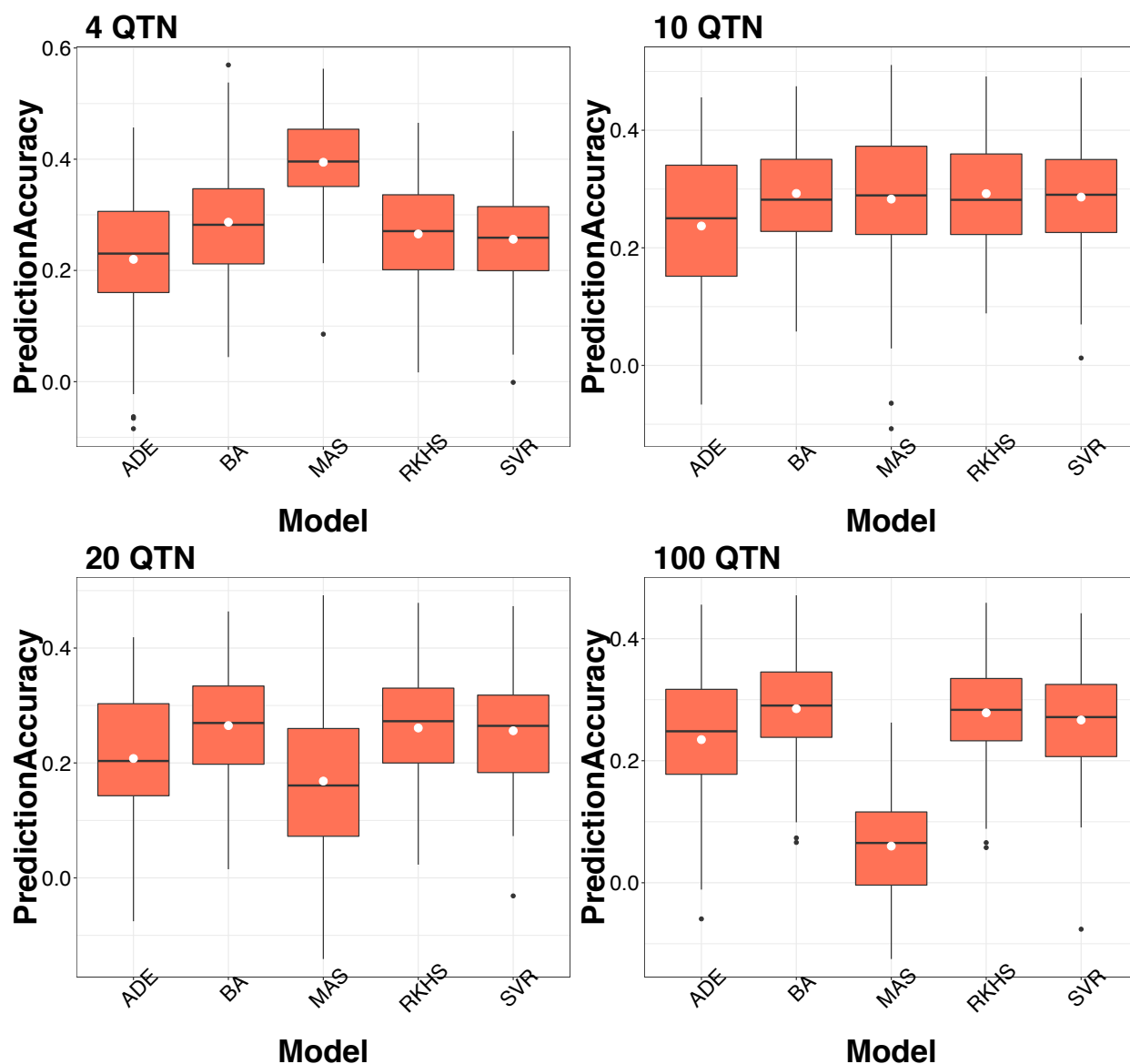
**Figure S43: Comparison among GS models and MAS for traits simulated with 4, 10, 20, and 100 QTNs under dominance mechanism and heritability of 0.7 in sugarcane  $F_1$  population.** On x-axis are the GS models [Additive-Dominance-Epistasis (ADE), Bayes A (BA), Reproducing Kernel Hilbert Space (RKHS), and Support Vector Regression (SVR)] and Marker-Assisted Selection model (MAS). On the y-axis is the prediction accuracy. The white dot in the middle each boxplot represents the position of the mean of the distribution of prediction accuracies across 100 replicates using five-fold cross validation approach.



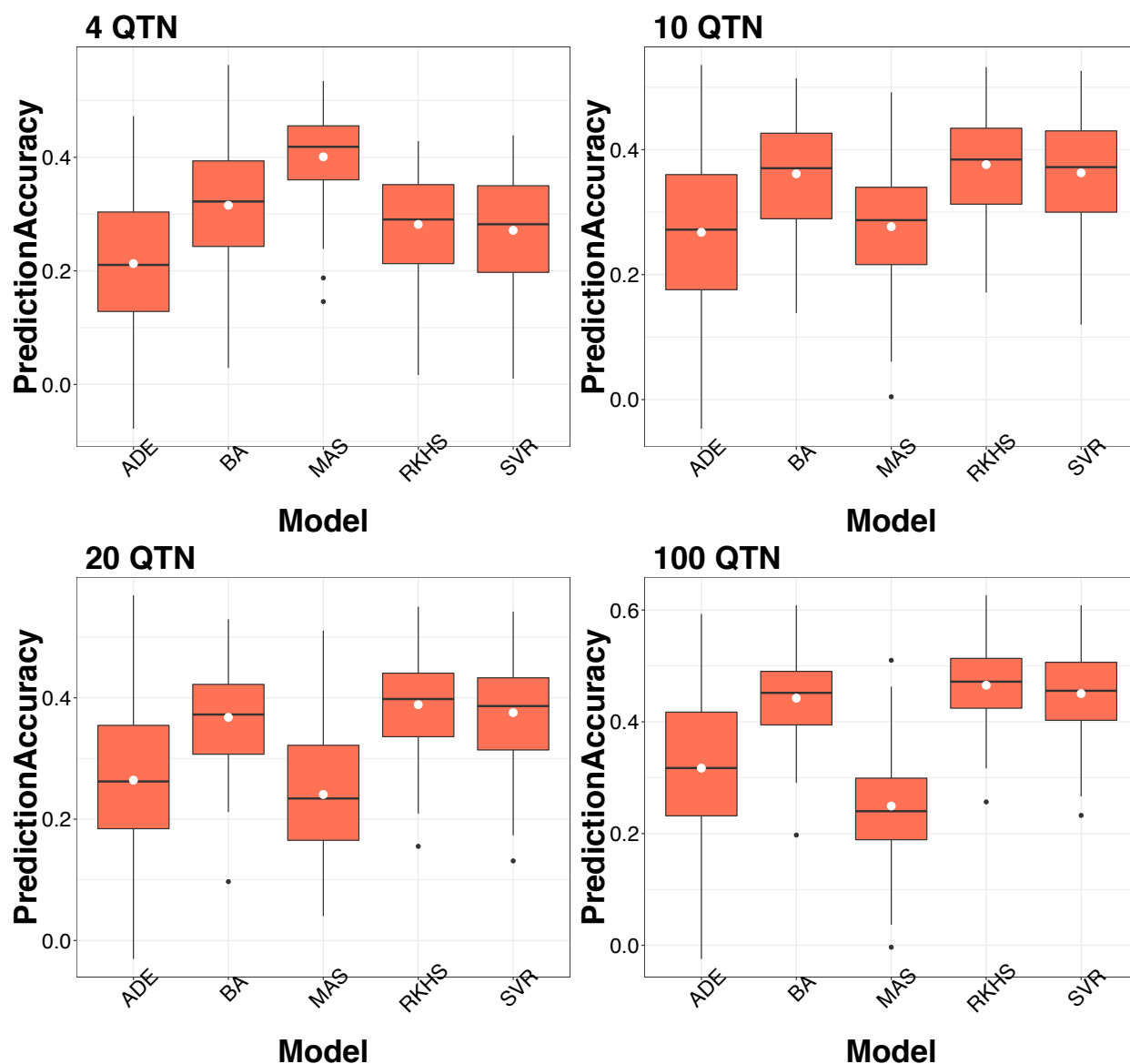
**Figure S44: Comparison among GS models and MAS for traits simulated with 4, 10, 20, and 100 QTNs under epistasis mechanism and heritability of 0.7 in sugarcane  $F_1$  population.** On x-axis are the GS models [Additive-Dominance-Epistasis (ADE), Bayes A (BA), Reproducing Kernel Hilbert Space (RKHS), and Support Vector Regression (SVR)] and Marker-Assisted Selection model (MAS). On the y-axis is the prediction accuracy. The white dot in the middle each boxplot represents the position of the mean of the distribution of prediction accuracies across 100 replicates using five-fold cross validation approach.



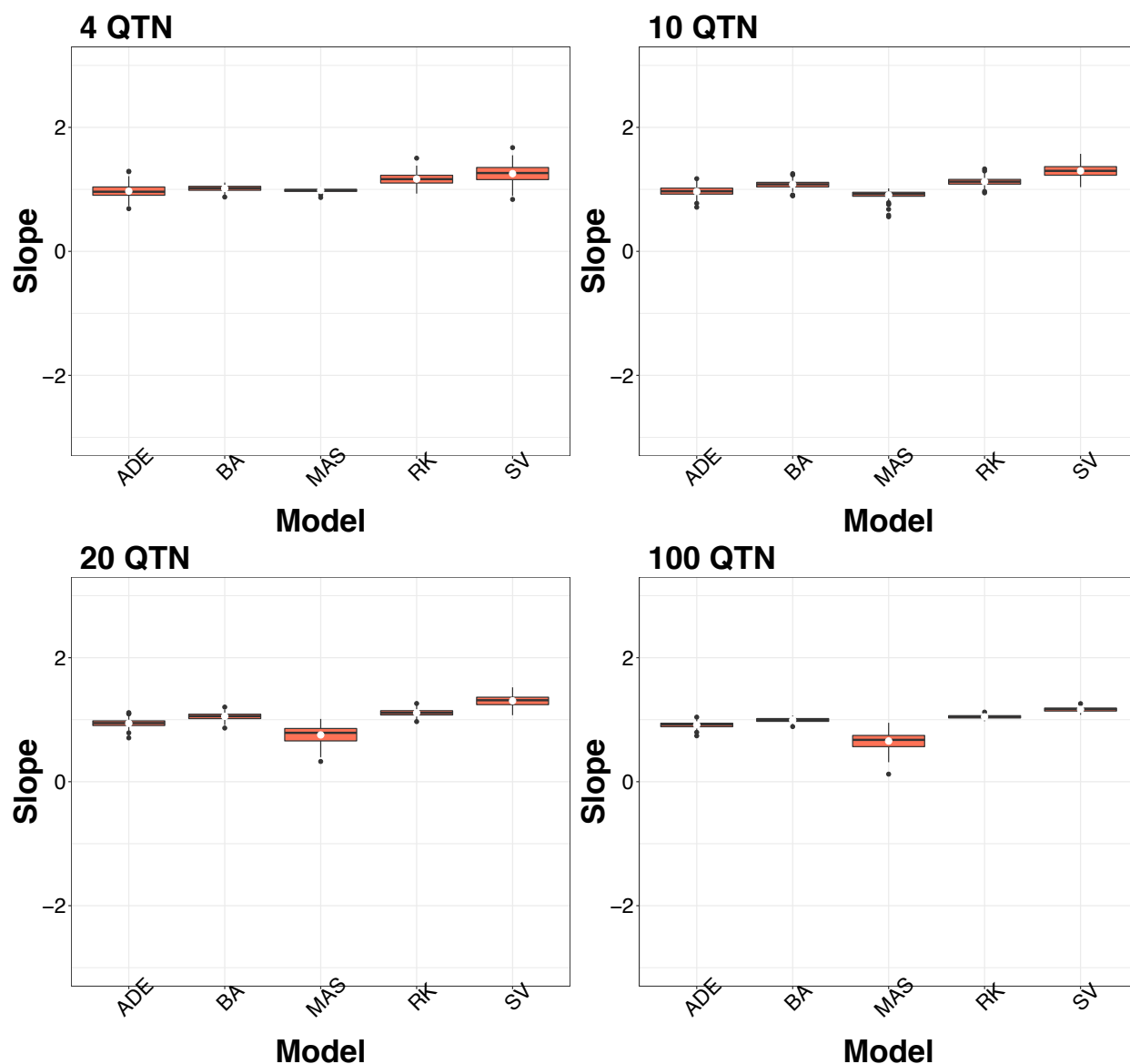
**Figure S45: Comparison among GS models and MAS for traits simulated with 4, 10, 20, and 100 QTNs under additive mechanism and heritability of 0.3 in sugarcane F<sub>1</sub> population.** On x-axis are the GS models [Additive-Dominance-Epistasis (ADE), Bayes A (BA), Reproducing Kernel Hilbert Space (RKHS), and Support Vector Regression (SVR)] and Marker-Assisted Selection model (MAS). On the y-axis is the prediction accuracy. The white dot in the middle each boxplot represents the position of the mean of the distribution of prediction accuracies across 100 replicates using five-fold cross validation approach.



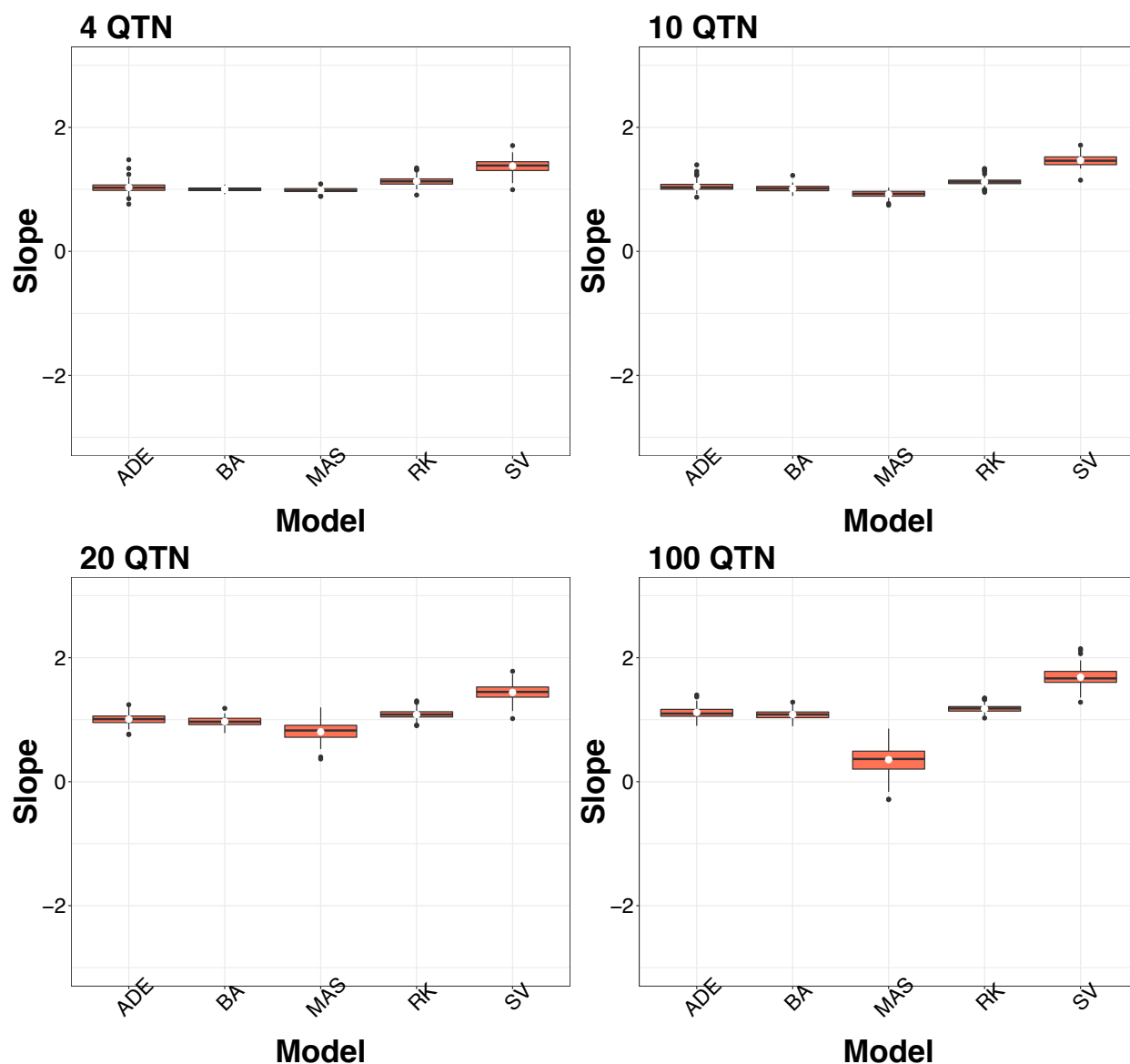
**Figure S46: Comparison among GS models and MAS for traits simulated with 4, 10, 20, and 100 QTNs under dominance mechanism and heritability of 0.3 in sugarcane  $F_1$  population.** On x-axis are the GS models [Additive-Dominance-Epistasis (ADE), Bayes A (BA), Reproducing Kernel Hilbert Space (RKHS), and Support Vector Regression (SVR)] and Marker-Assisted Selection model (MAS). On the y-axis is the prediction accuracy. The white dot in the middle each boxplot represents the position of the mean of the distribution of prediction accuracies across 100 replicates using five-fold cross validation approach.



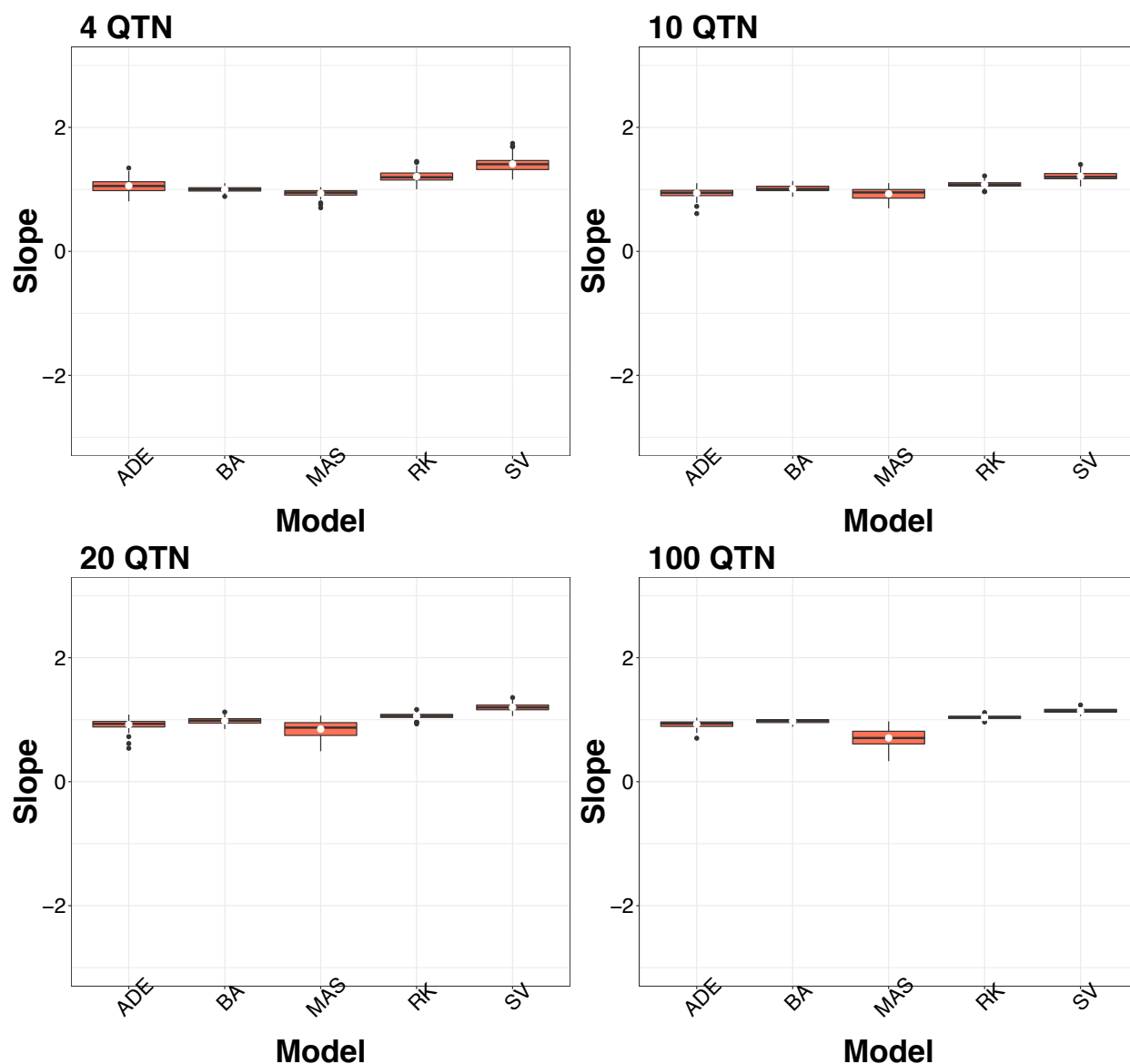
**Figure S47: Comparison among GS models and MAS for traits simulated with 4, 10, 20, and 100 QTNs under epistasis mechanism and heritability of 0.3 in sugarcane  $F_1$  population.** On x-axis are the GS models [Additive-Dominance-Epistasis (ADE), Bayes A (BA), Reproducing Kernel Hilbert Space (RKHS), and Support Vector Regression (SVR)] and Marker-Assisted Selection model (MAS). On the y-axis is the prediction accuracy. The white dot in the middle each boxplot represents the position of the mean of the distribution of prediction accuracies across 100 replicates using five-fold cross validation approach.



**Figure S48: Comparison of slope values across GS and MAS models under additive mechanism and heritability of 0.7 in sugarcane  $F_1$  population for traits simulated with 4, 10, 20, and 100 QTNs.** Slope values for the regression model between simulated trait and GEBVs (Genomic Estimated Breeding Values) for GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] and MAS (Marker Assisted Selection) model for cross validation folds and 100 replicates. The white dots in the boxplots represent the mean of the distribution in each model.

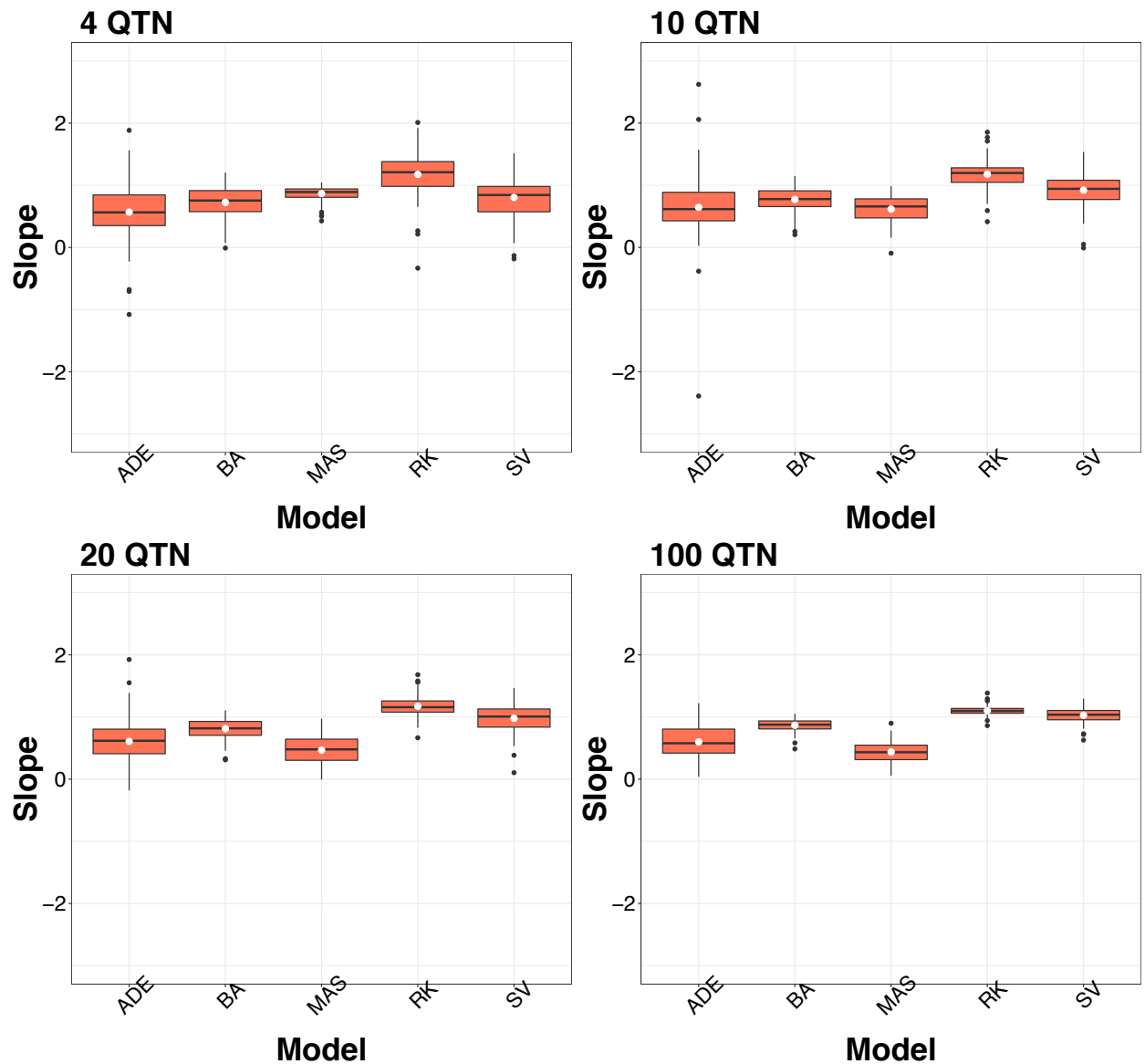


**Figure S49: Comparison of slope values across GS and MAS models under dominance mechanism and heritability of 0.7 in sugarcane  $F_1$  population for traits simulated with 4, 10, 20, and 100 QTNs.** Slope values for the regression model between simulated trait and GEBVs (Genomic Estimated Breeding Values) for GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] and MAS (Marker Assisted Selection) model for cross validation folds and 100 replicates. The white dots in the boxplots represent the mean of the distribution in each model.

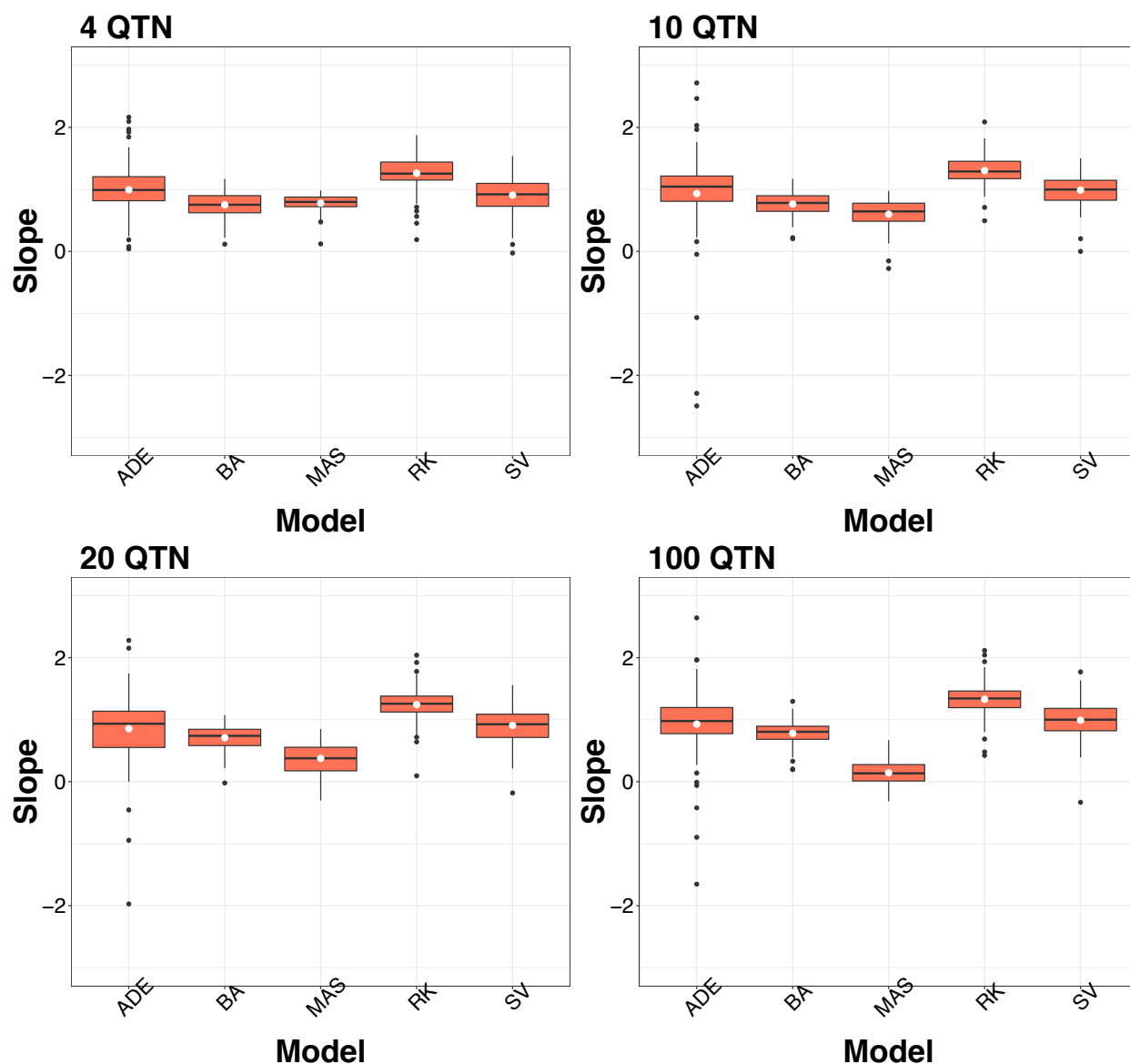


**Figure S50: Comparison of slope values across GS and MAS models under epistasis mechanism and heritability of 0.7 in sugarcane  $F_1$  population for traits simulated with 4, 10, 20, and 100 QTNs.** Slope values for the regression model between simulated trait and GEBVs (Genomic Estimated Breeding Values) for GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] and MAS (Marker Assisted Selection) model for cross validation folds and 100 replicates. The white dots in the boxplots represent the mean of the distribution in each model.

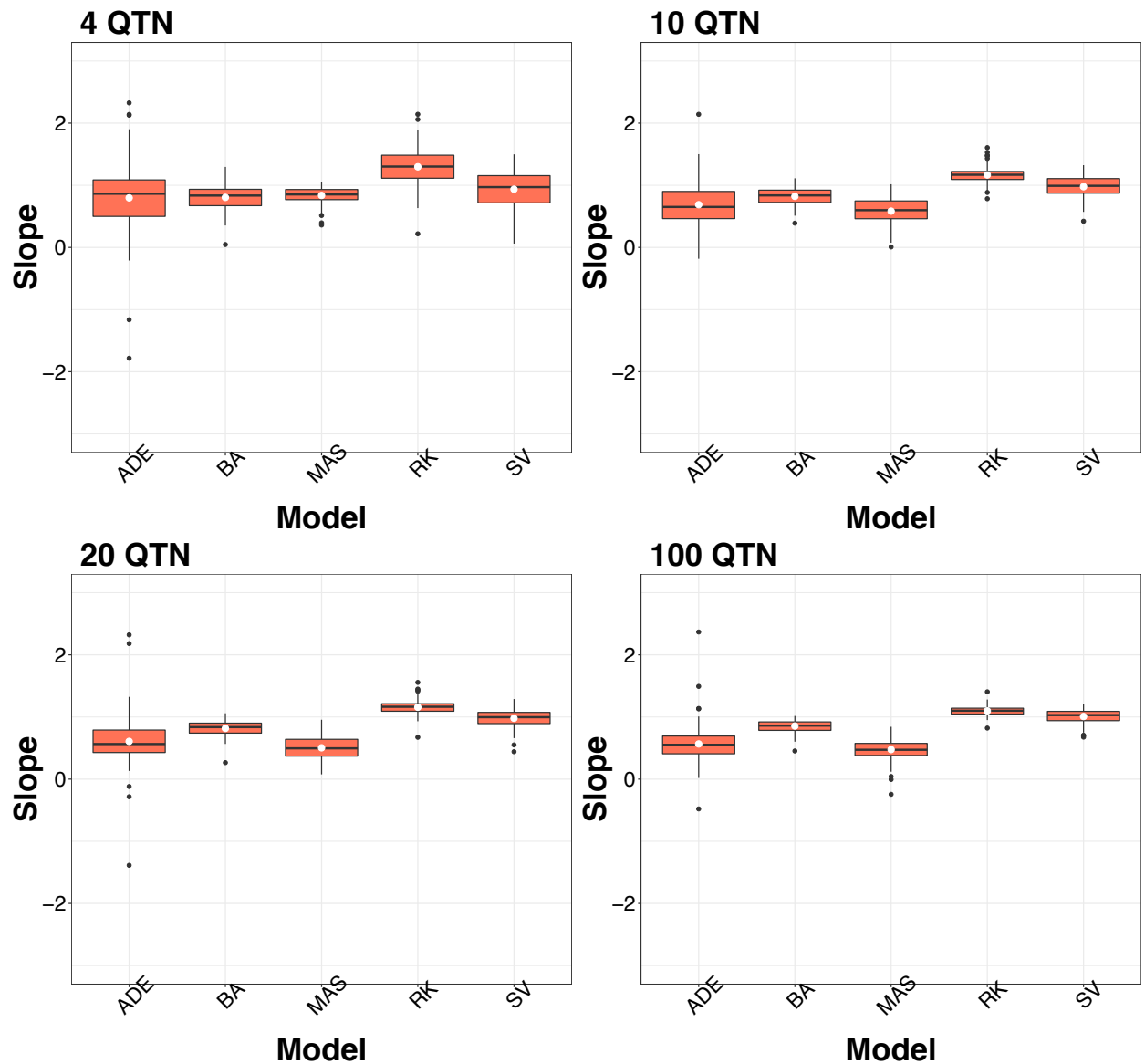




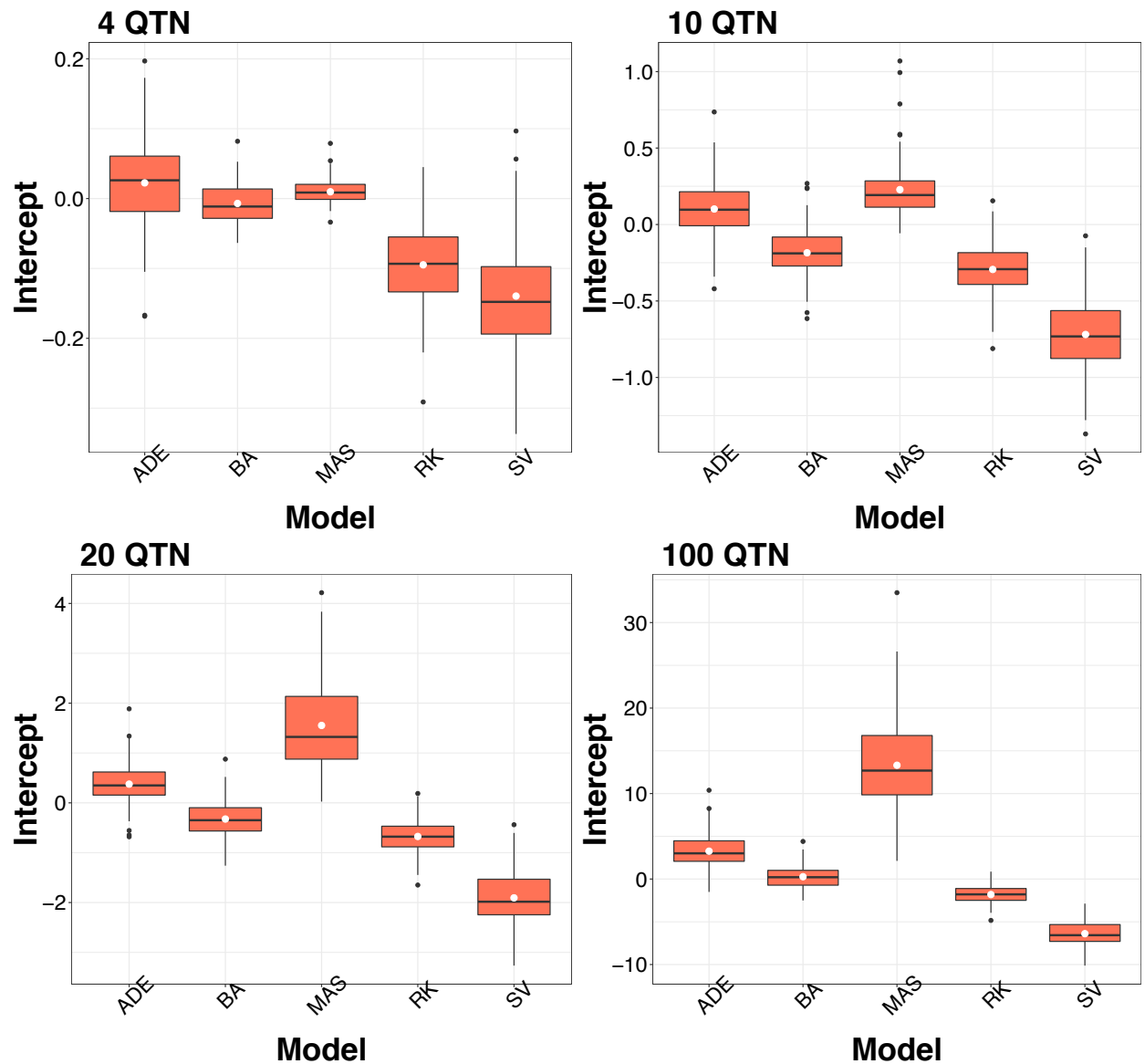
**Figure S51: Comparison of slope values across GS and MAS models under additive mechanism and heritability of 0.3 in sugarcane  $F_1$  population for traits simulated with 4, 10, 20, and 100 QTNs.** Slope values for the regression model between simulated trait and GEBVs (Genomic Estimated Breeding Values) for GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] and MAS (Marker Assisted Selection) model for cross validation folds and 100 replicates. The white dots in the boxplots represent the mean of the distribution in each model.



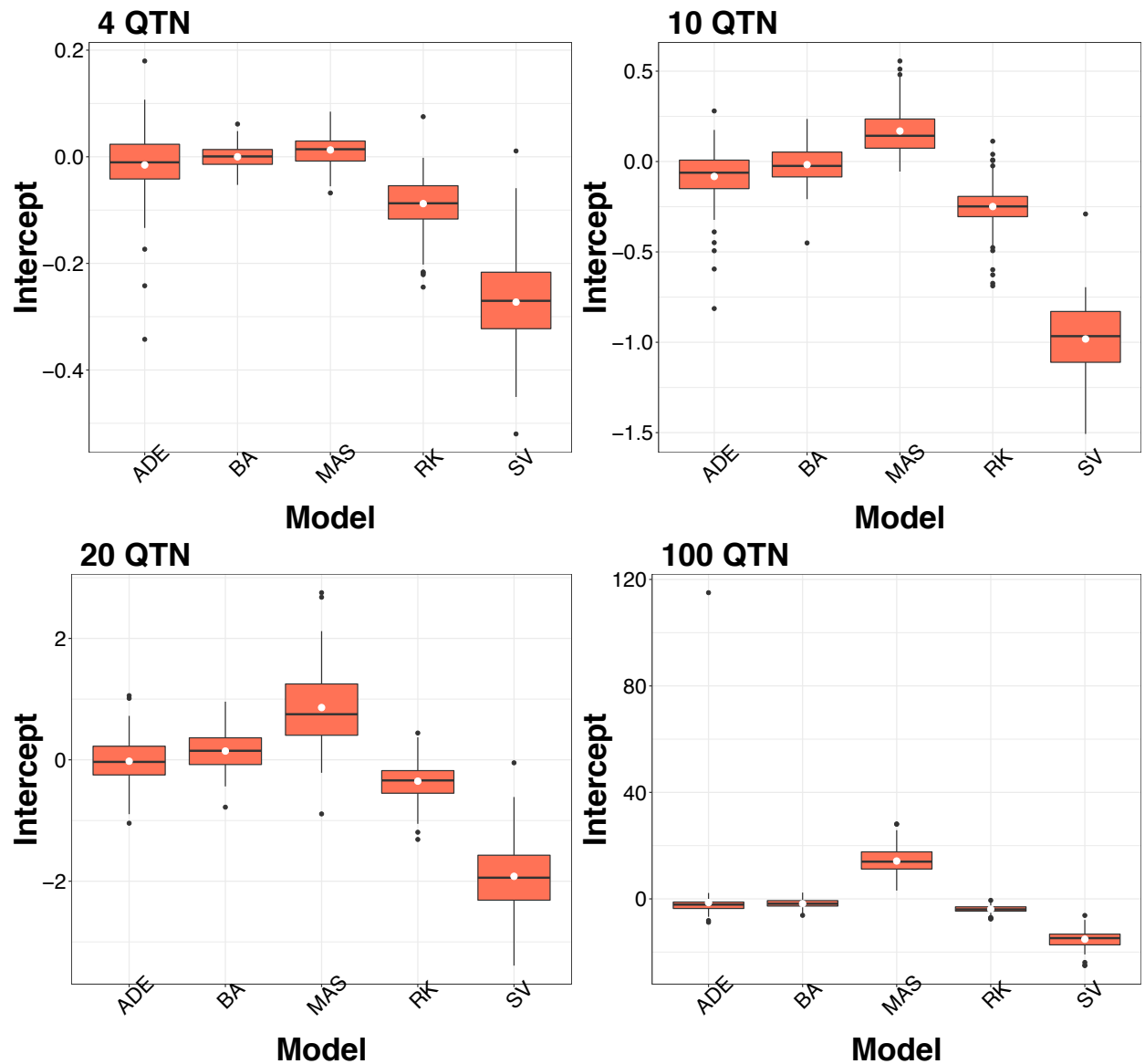
**Figure S52: Comparison of slope values across GS and MAS models under dominance mechanism and heritability of 0.3 in sugarcane  $F_1$  population for traits simulated with 4, 10, 20, and 100 QTNs.** Slope values for the regression model between simulated trait and GEBVs (Genomic Estimated Breeding Values) for GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] and MAS (Marker Assisted Selection) model for cross validation folds and 100 replicates. The white dots in the boxplots represent the mean of the distribution in each model.



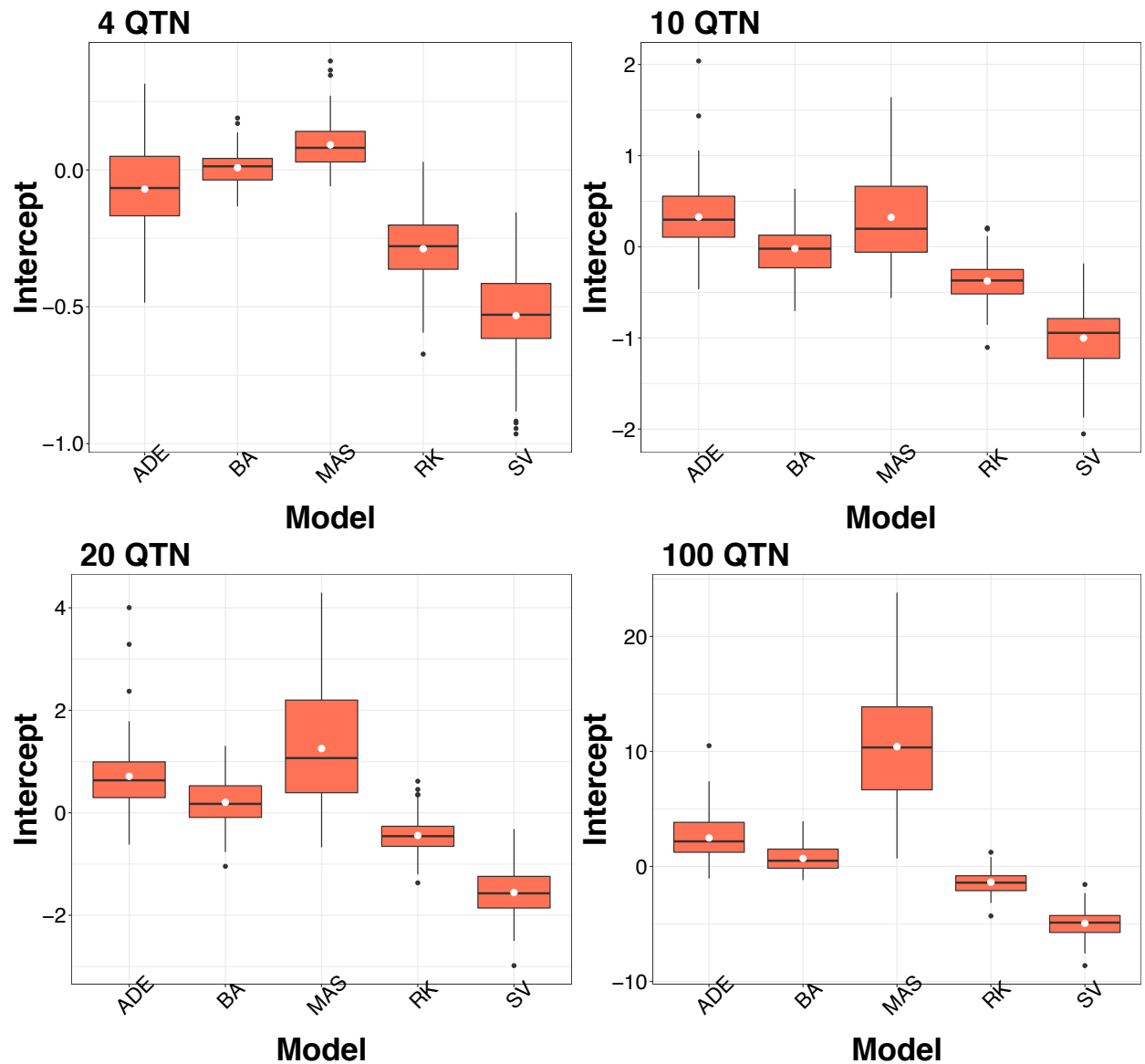
**Figure S53: Comparison of slope values across GS and MAS models under epistasis mechanism and heritability of 0.3 in sugarcane  $F_1$  population for traits simulated with 4, 10, 20, and 100 QTNs.** Slope values for the regression model between simulated trait and GEBVs (Genomic Estimated Breeding Values) for GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] and MAS (Marker Assisted Selection) model for cross validation folds and 100 replicates. The white dots in the boxplots represent the mean of the distribution in each model.



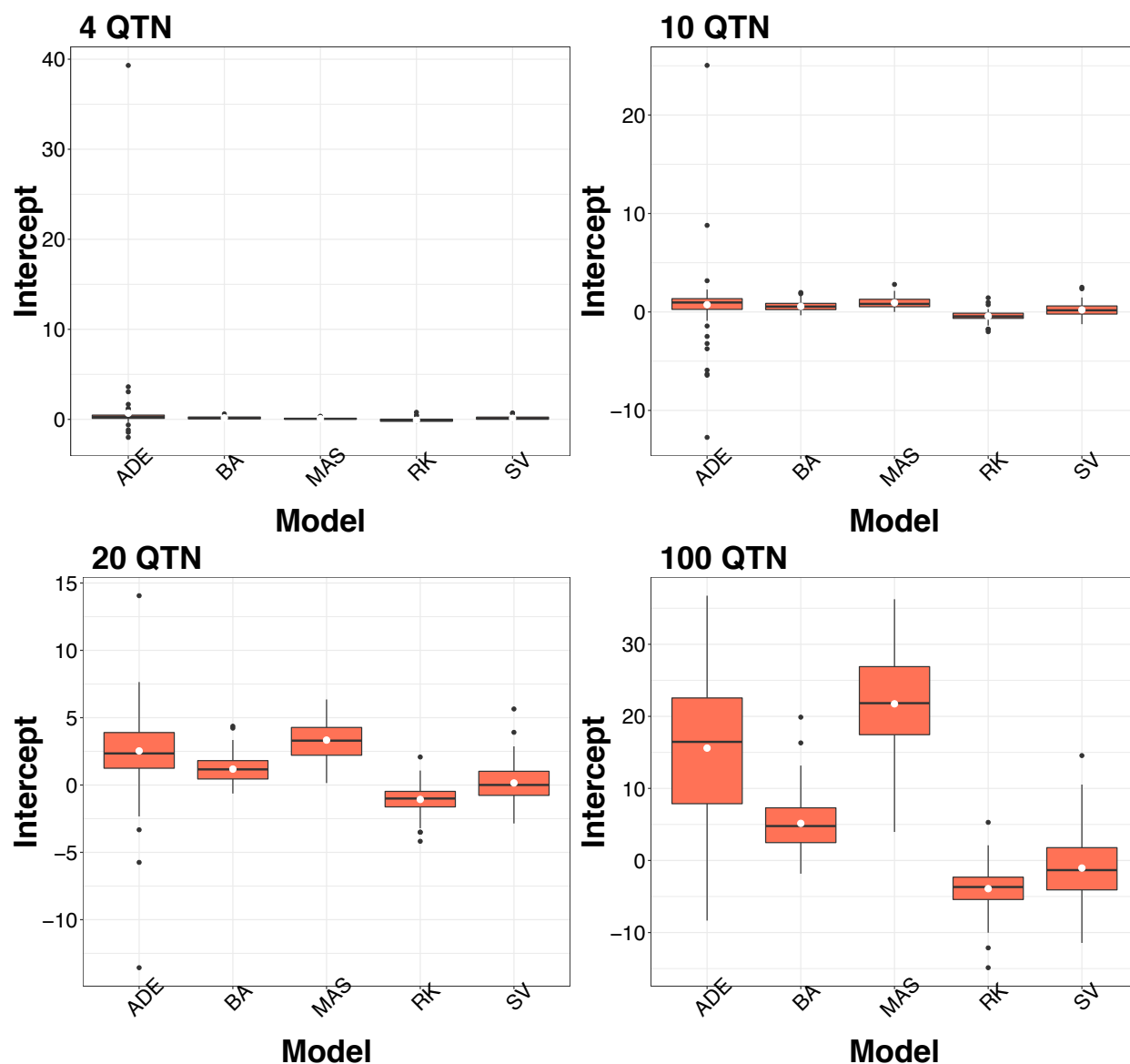
**Figure S54: Comparison of intercept values across GS and MAS models under additive mechanism and heritability of 0.7 in sugarcane  $F_1$  population for traits simulated with 4, 10, 20, and 100 QTNs.** Slope values for the regression model between simulated trait and GEBVs (Genomic Estimated Breeding Values) for GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] and MAS (Marker Assisted Selection) model for cross validation folds and 100 replicates. The white dots in the boxplots represent the mean of the distribution in each model.



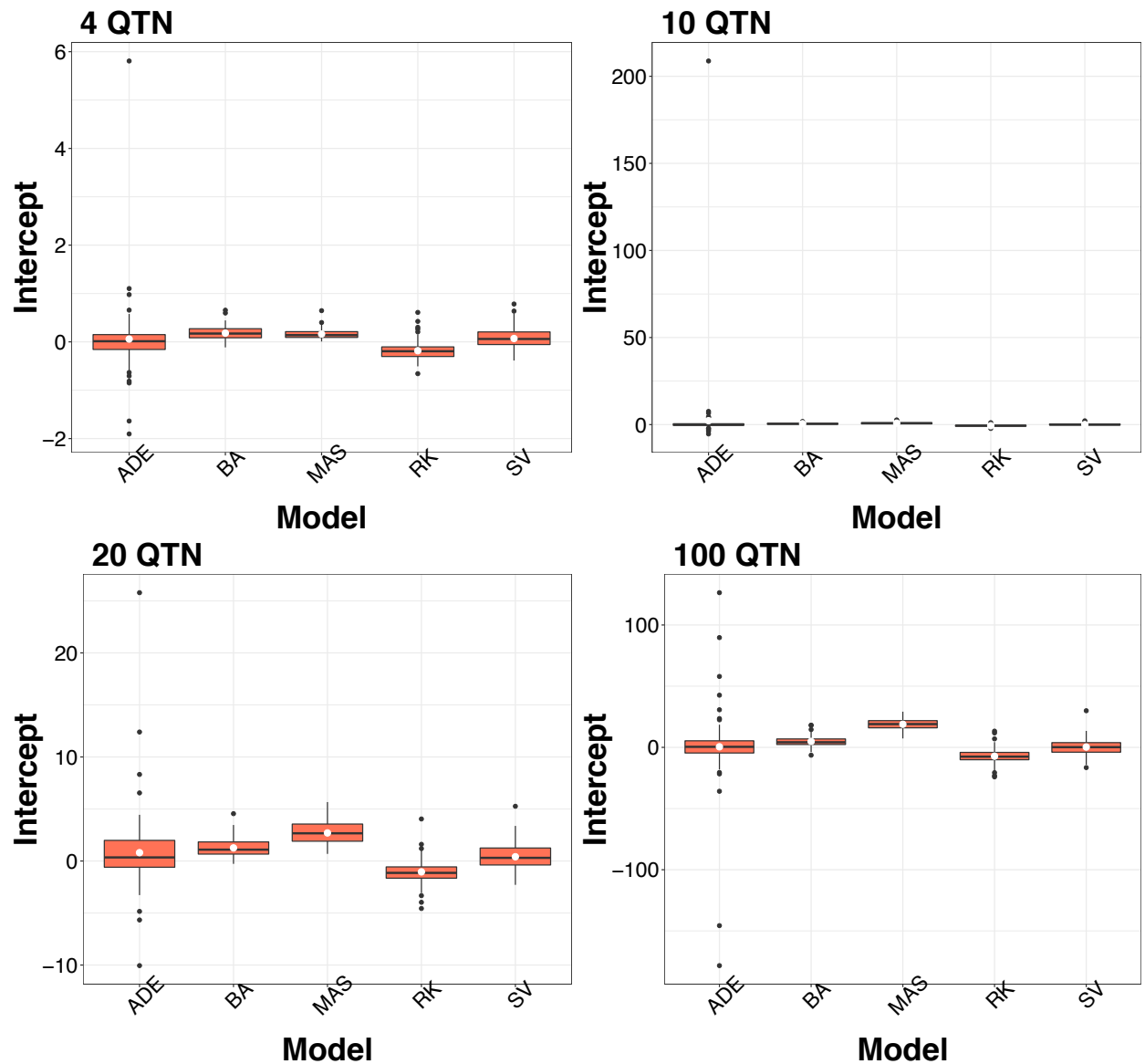
**Figure S55: Comparison of intercept values across GS and MAS models under dominance mechanism and heritability of 0.7 in sugarcane  $F_1$  population for traits simulated with 4, 10, 20, and 100 QTNs.** Slope values for the regression model between simulated trait and GEBVs (Genomic Estimated Breeding Values) for GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] and MAS (Marker Assisted Selection) model for cross validation folds and 100 replicates. The white dots in the boxplots represent the mean of the distribution in each model.



**Figure S56: Comparison of intercept values across GS and MAS models under epistasis mechanism and heritability of 0.7 in sugarcane  $F_1$  population for traits simulated with 4, 10, 20, and 100 QTNs.** Slope values for the regression model between simulated trait and GEBVs (Genomic Estimated Breeding Values) for GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] and MAS (Marker Assisted Selection) model for cross validation folds and 100 replicates. The white dots in the boxplots represent the mean of the distribution in each model.

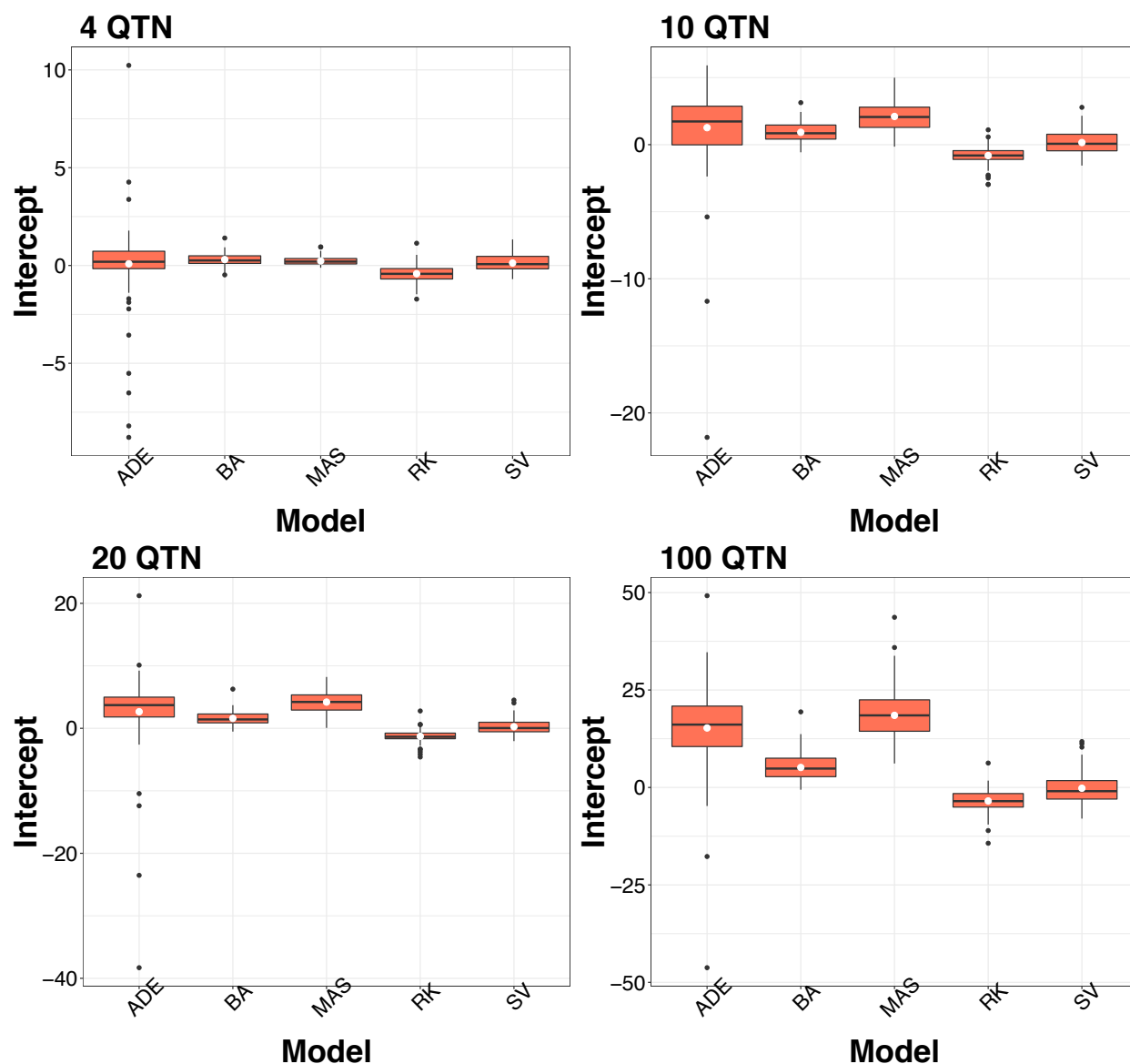


**Figure S57: Comparison of intercept values across GS and MAS models under additive mechanism and heritability of 0.3 in sugarcane  $F_1$  population for traits simulated with 4, 10, 20, and 100 QTNs.** Slope values for the regression model between simulated trait and GEBVs (Genomic Estimated Breeding Values) for GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] and MAS (Marker Assisted Selection) model for cross validation folds and 100 replicates. The white dots in the boxplots represent the mean of the distribution in each model.

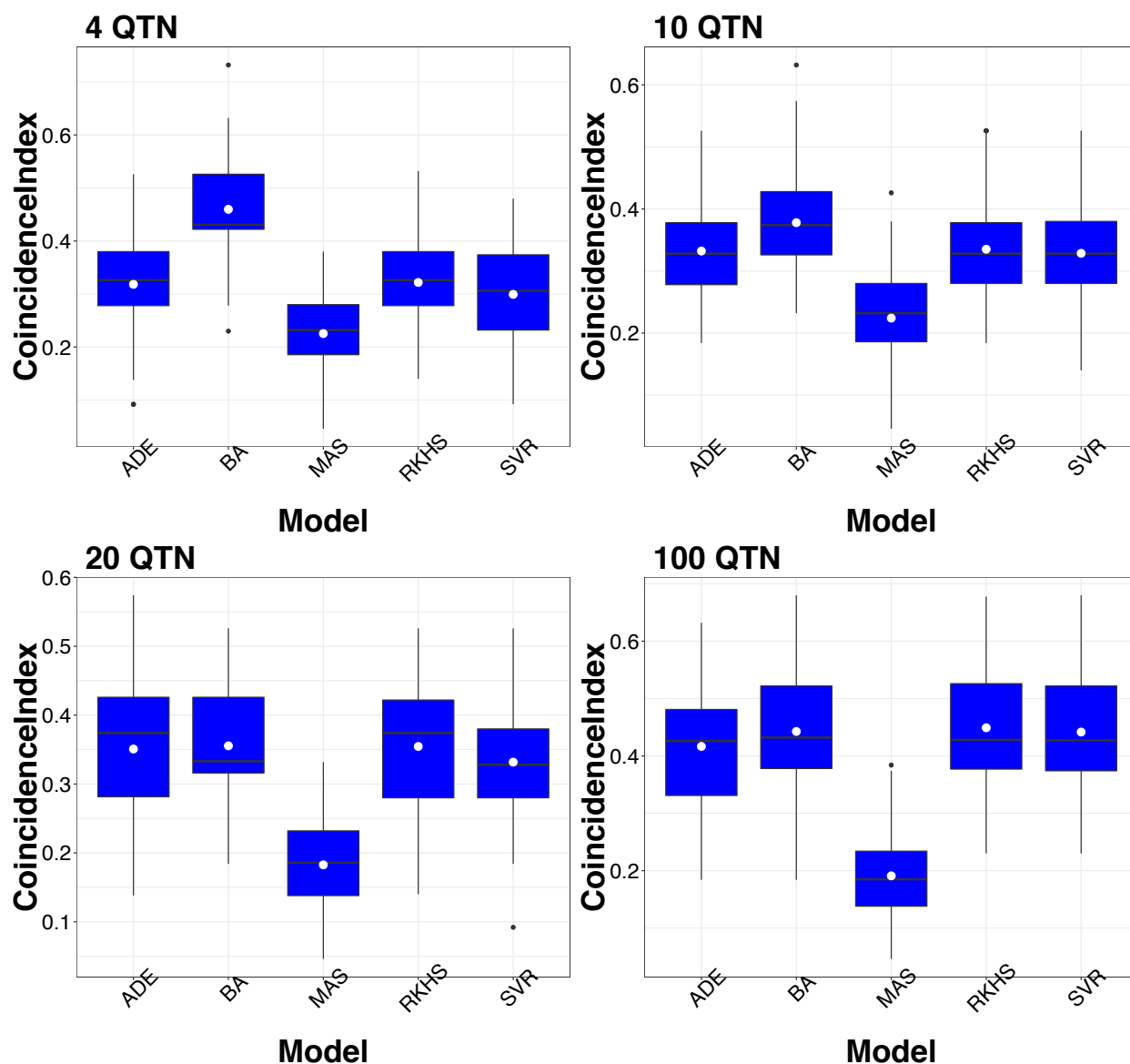


**Figure S58: Comparison of intercept values across GS and MAS models under dominance mechanism and heritability of 0.3 in sugarcane  $F_1$  population for traits simulated with 4, 10, 20, and 100 QTNs.** Slope values for the regression model between simulated trait and GEBVs (Genomic Estimated Breeding Values) for GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] and MAS (Marker Assisted Selection) model for cross validation folds and 100 replicates. The white dots in the boxplots represent the mean of the distribution in each model.

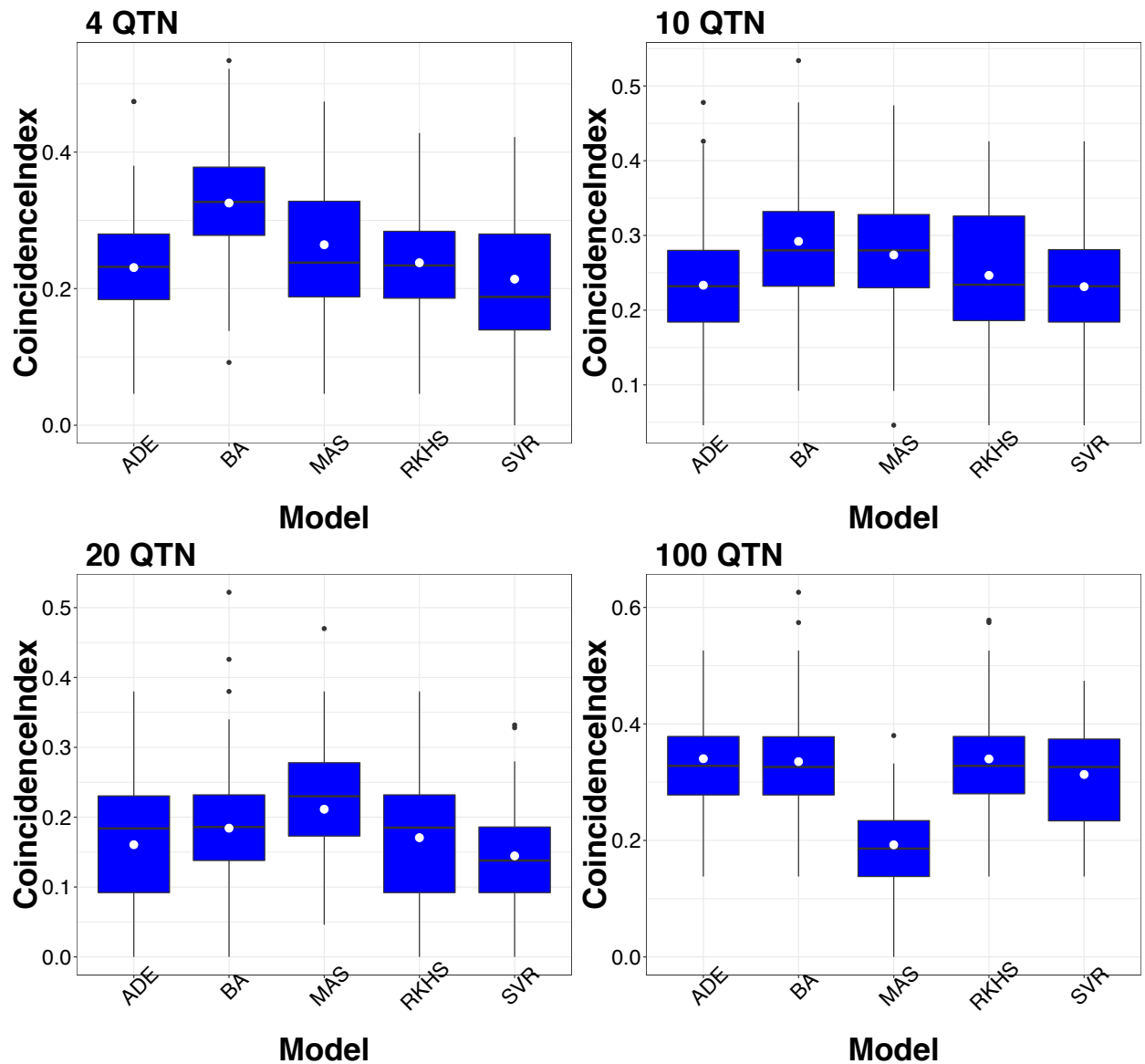




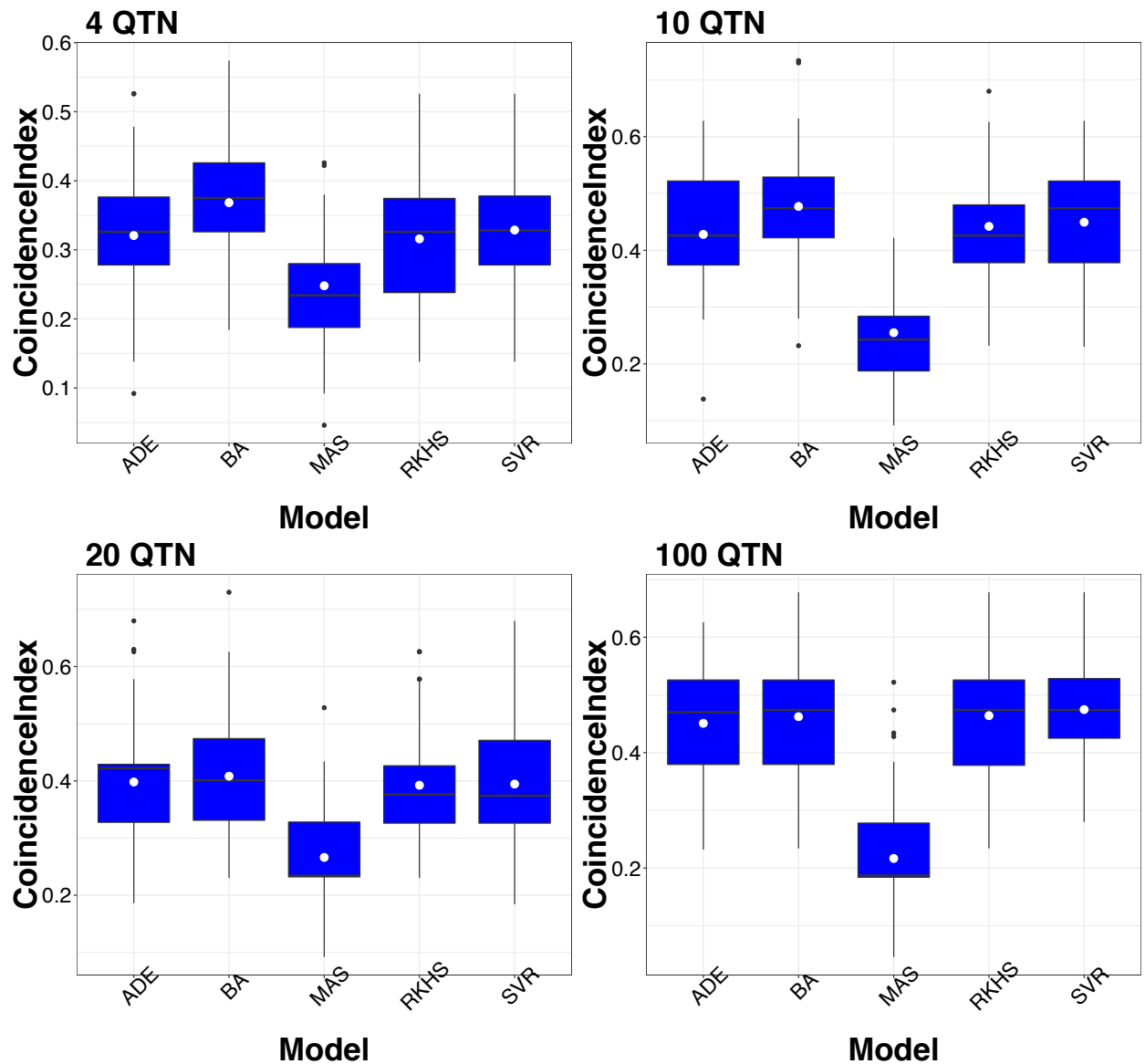
**Figure S58: Comparison of intercept values across GS and MAS models under epistasis mechanism and heritability of 0.3 in sugarcane  $F_1$  population for traits simulated with 4, 10, 20, and 100 QTNs.** Slope values for the regression model between simulated trait and GEBVs (Genomic Estimated Breeding Values) for GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] and MAS (Marker Assisted Selection) model for cross validation folds and 100 replicates. The white dots in the boxplots represent the mean of the distribution in each model.



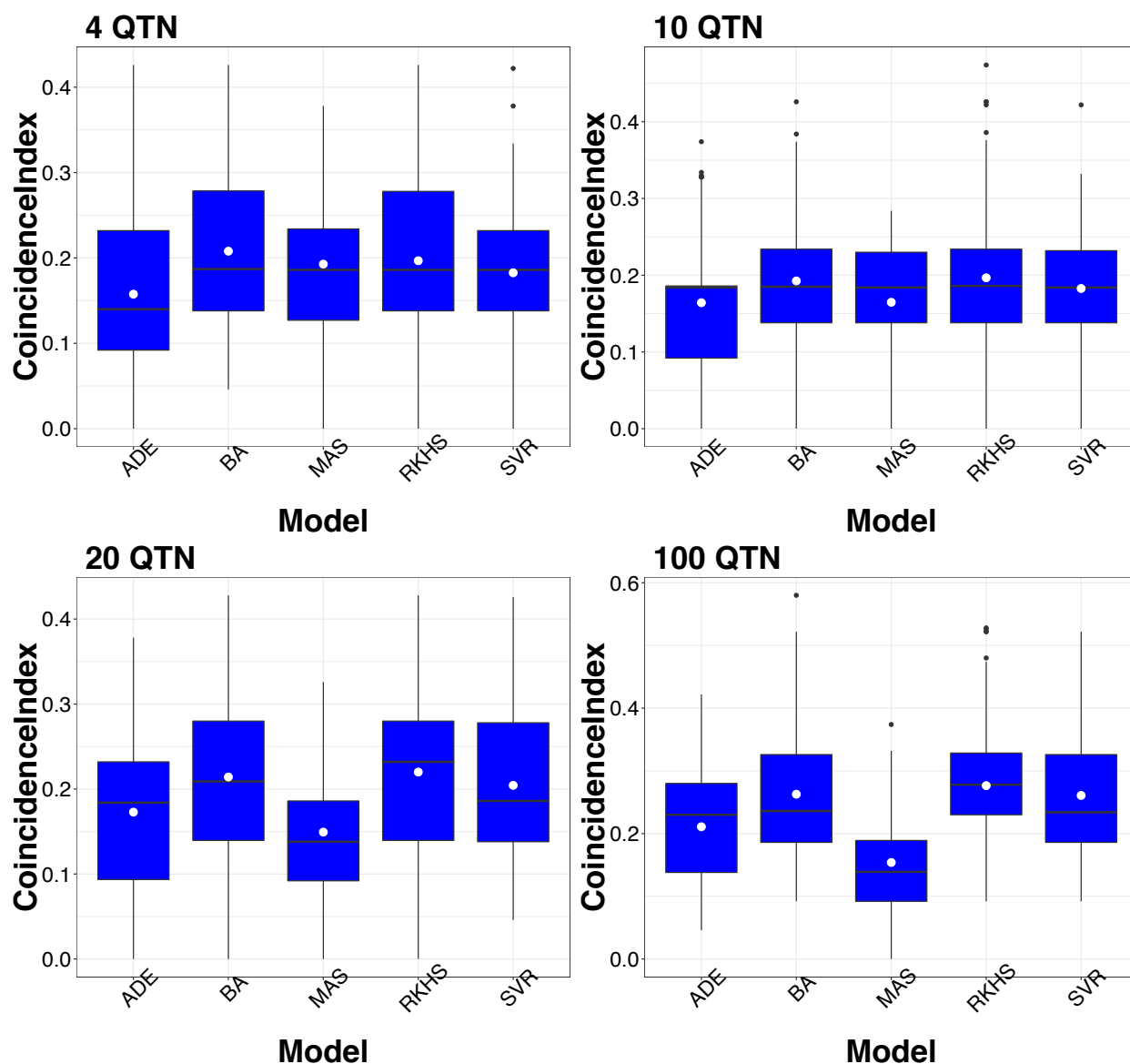
**Figure S59: Comparison of coincidence index among GS and MAS models for traits simulated with 4, 10, 20, and 100 QTNs under the additive mechanism and heritability of 0.7 in sugarcane.** Boxplots showing coincidence index distributions for GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] and MAS (Marker Assisted Selection) model. The white dots in the boxplots represent the mean of the distribution.



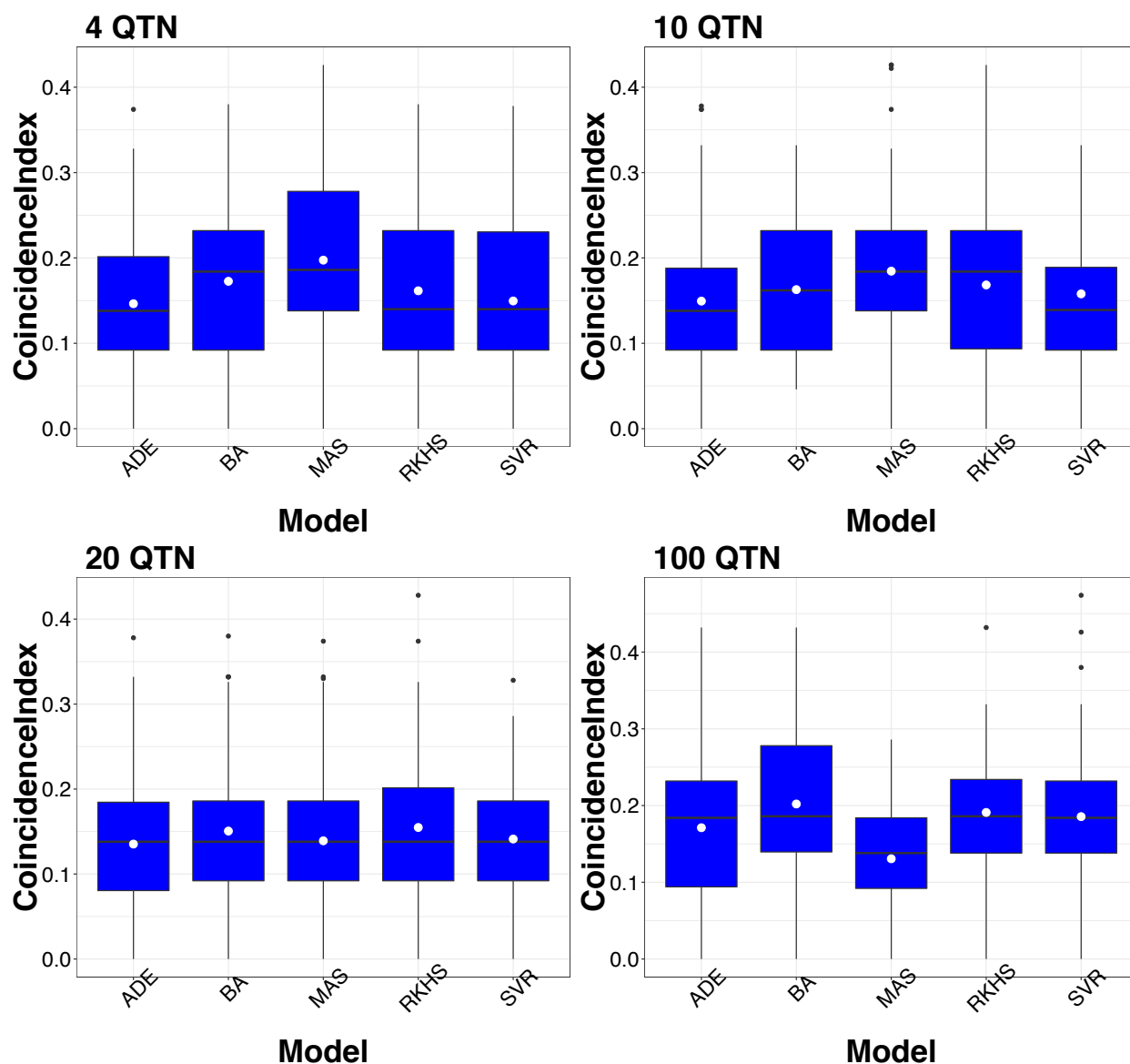
**Figure S60: Comparison of coincidence index among GS and MAS models for traits simulated with 4, 10, 20, and 100 QTNs under the dominance mechanism and heritability of 0.7 in sugarcane.** Boxplots showing coincidence index distributions for GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] and MAS (Marker Assisted Selection) model. The white dots in the boxplots represent the mean of the distribution.



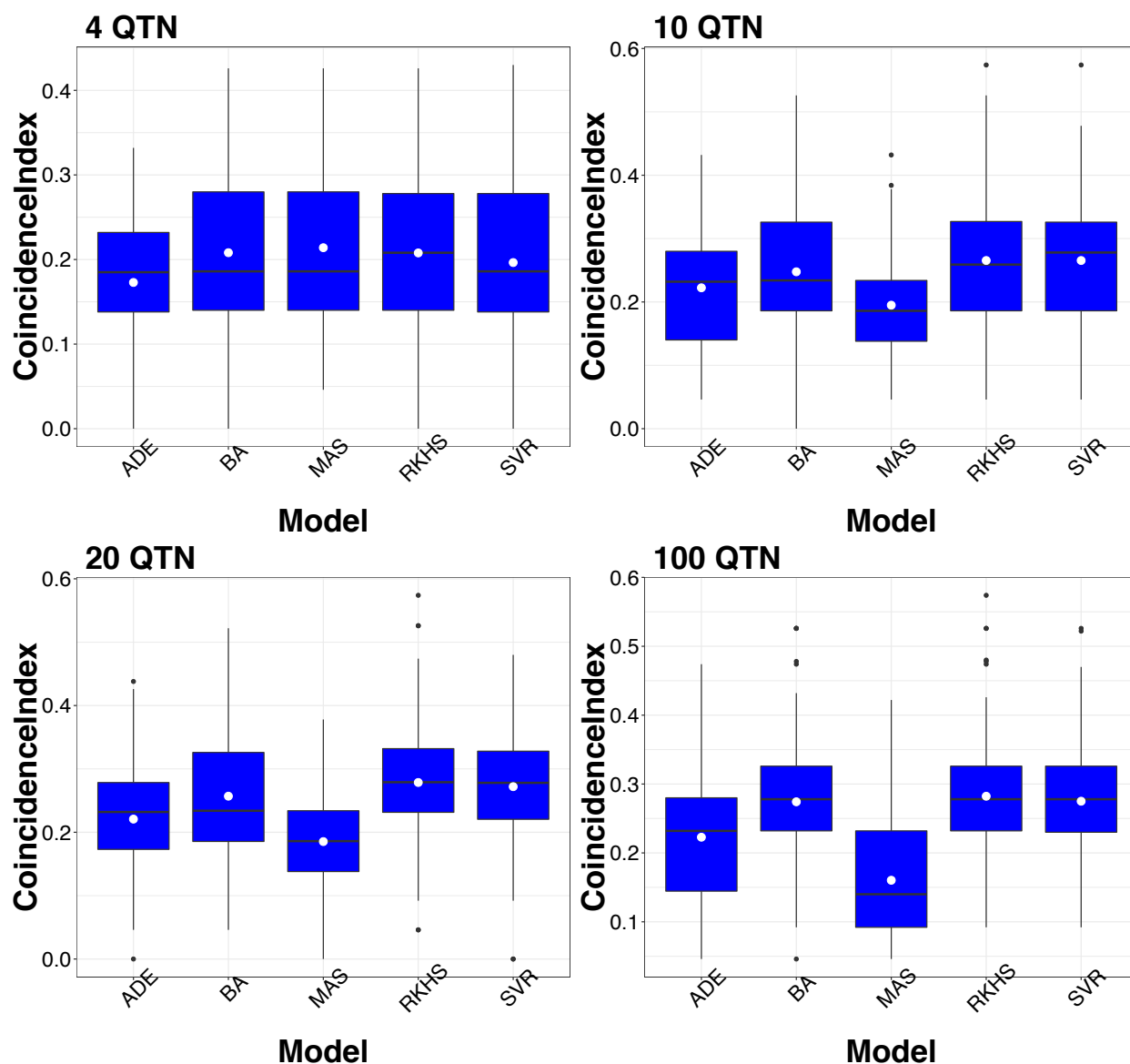
**Figure S61: Comparison of coincidence index among GS and MAS models for traits simulated with 4, 10, 20, and 100 QTNs under the epistasis mechanism and heritability of 0.7 in sugarcane.** Boxplots showing coincidence index distributions for GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] and MAS (Marker Assisted Selection) model. The white dots in the boxplots represent the mean of the distribution.



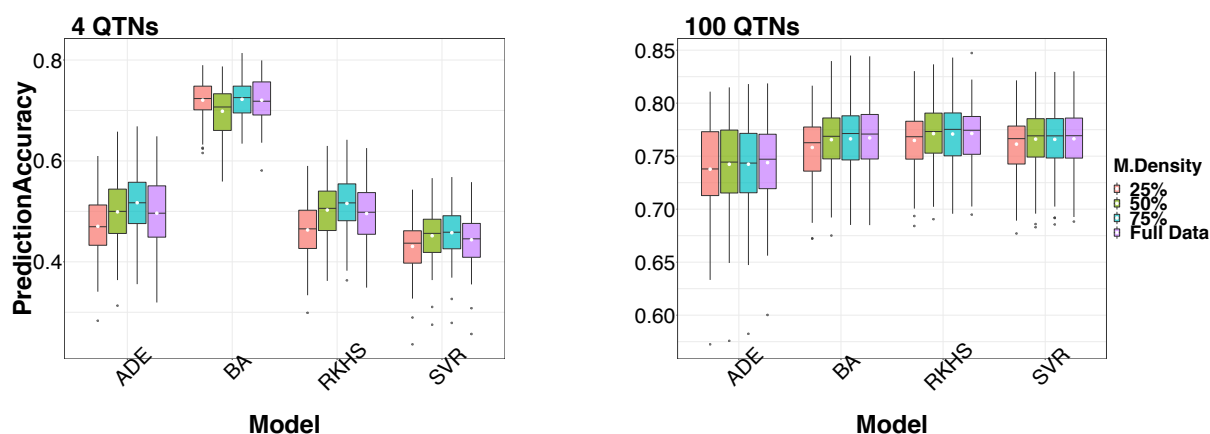
**Figure S62: Comparison of coincidence index among GS and MAS models for traits simulated with 4, 10, 20, and 100 QTNs under the additive mechanism and heritability of 0.3 in sugarcane.** Boxplots showing coincidence index distributions for GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] and MAS (Marker Assisted Selection) model. The white dots in the boxplots represent the mean of the distribution.



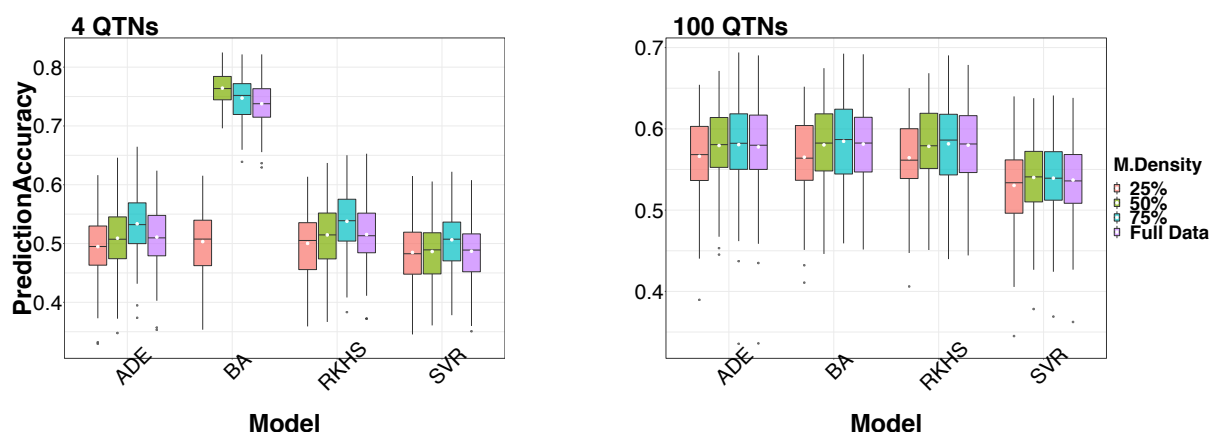
**Figure S63: Comparison of coincidence index among GS and MAS models for traits simulated with 4, 10, 20, and 100 QTNs under the dominance mechanism and heritability of 0.3 in sugarcane.** Boxplots showing coincidence index distributions for GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] and MAS (Marker Assisted Selection) model. The white dots in the boxplots represent the mean of the distribution.



**Figure S64: Comparison of coincidence index among GS and MAS models for traits simulated with 4, 10, 20, and 100 QTNs under the epistasis mechanism and heritability of 0.3 in sugarcane.** Boxplots showing coincidence index distributions for GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] and MAS (Marker Assisted Selection) model. The white dots in the boxplots represent the mean of the distribution.

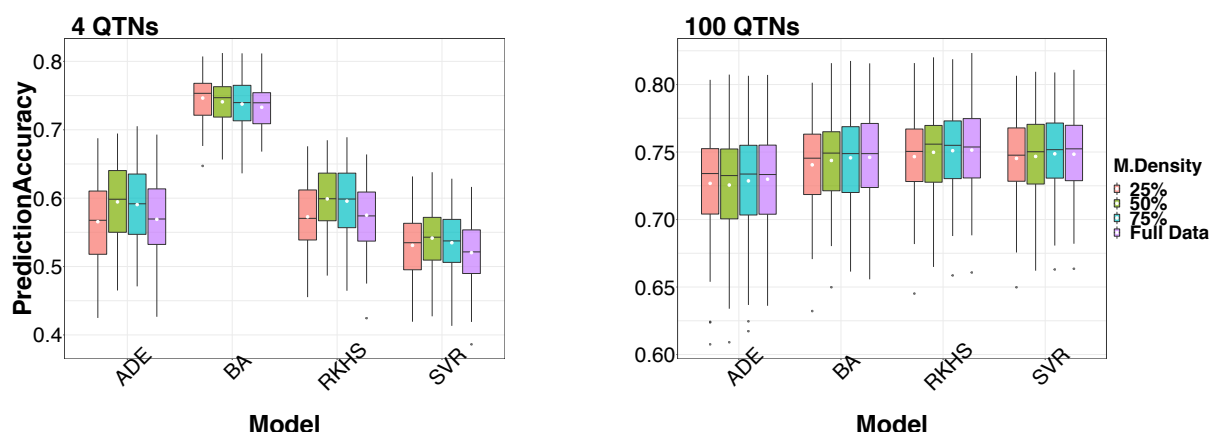


**Figure S65: Effect of marker density of prediction accuracy for traits simulated with 4 and 100 QTNs under the additive mechanism and heritability of 0.7 in sugarcane.** Box plots showing the distribution of predicted accuracies across five-folds and 100 replicates for different marker densities GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space)]. The white dots in the middle of the boxplot shows the mean of the distribution.

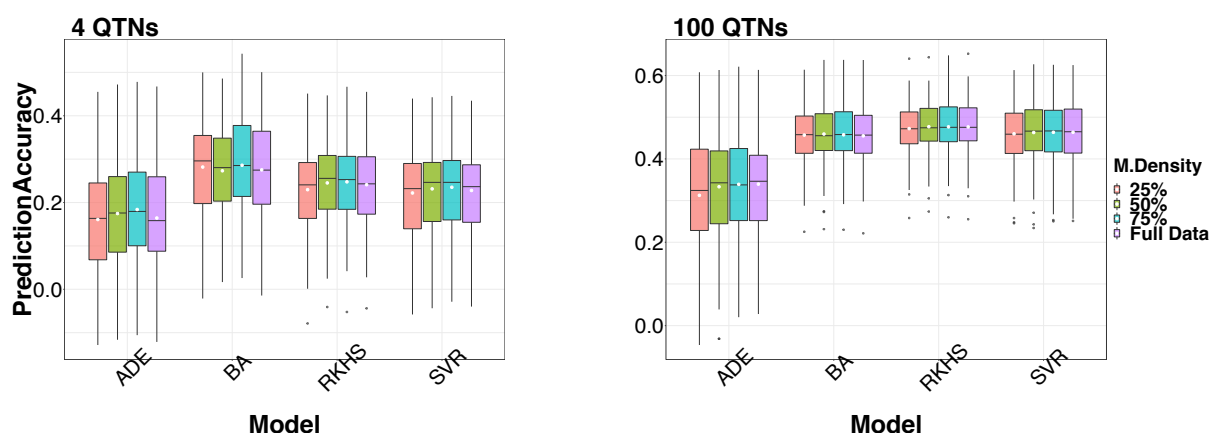


**Figure S66: Effect of marker density of prediction accuracy for traits simulated with 4 and 100 QTNs under the dominance mechanism and heritability of 0.7 in sugarcane.** Box plots showing the distribution of predicted accuracies across five-folds and 100 replicates for different marker densities GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space)]. The white dots in the middle of the boxplot shows the mean of the distribution.

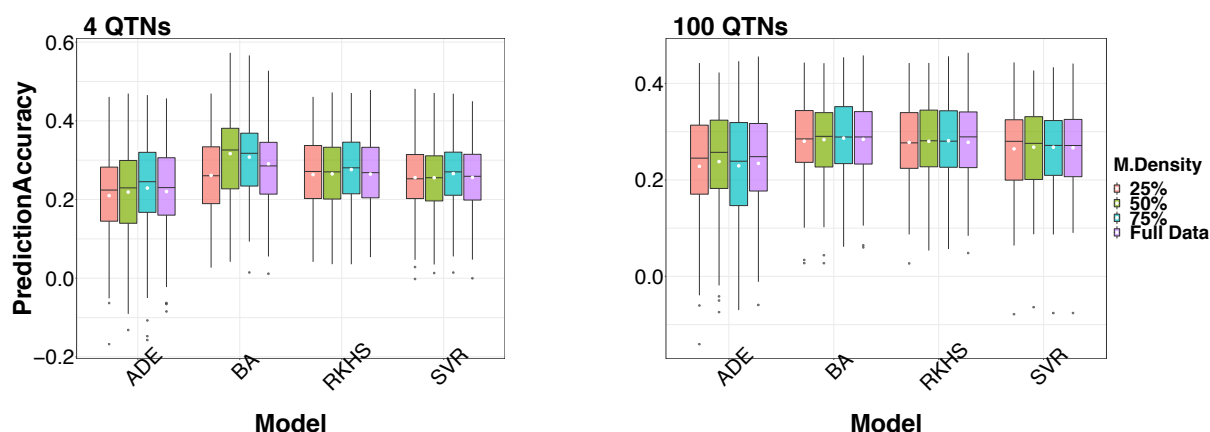




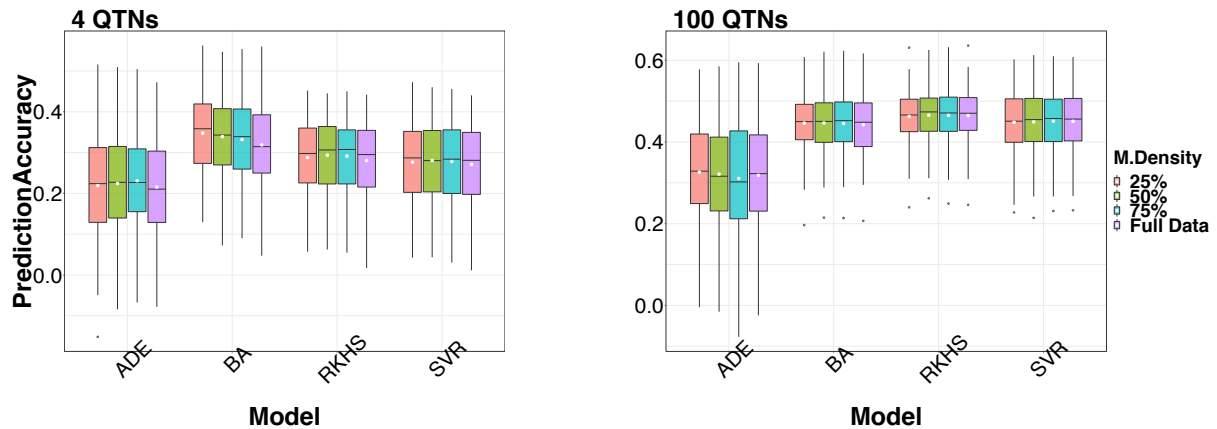
**Figure S67: Effect of marker density of prediction accuracy for traits simulated with 4 and 100 QTNs under the epistasis mechanism and heritability of 0.7 in sugarcane.** Box plots showing the distribution of predicted accuracies across five-folds and 100 replicates for different marker densities GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space)]. The white dots in the middle of the boxplot shows the mean of the distribution.



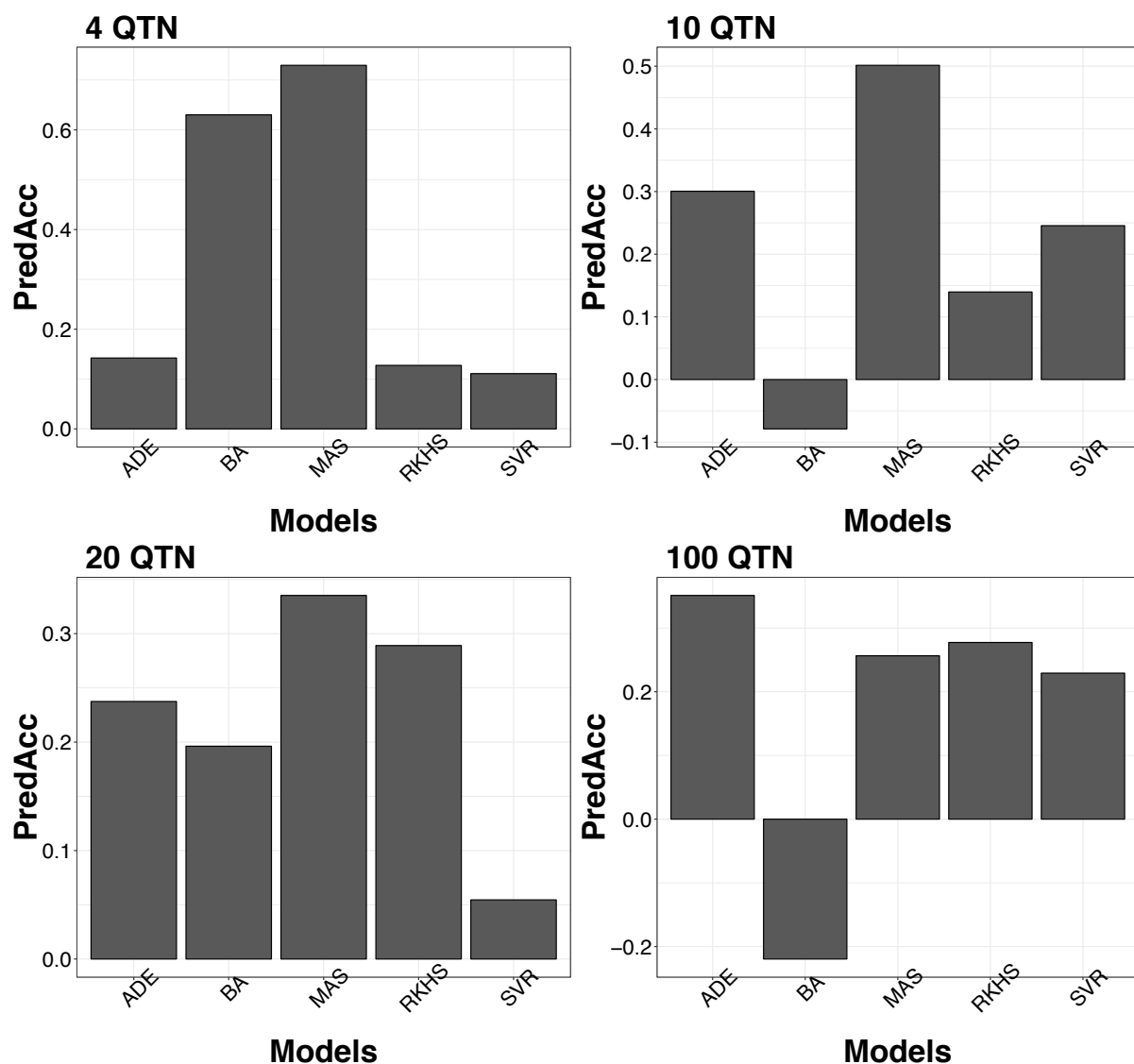
**Figure S68: Effect of marker density of prediction accuracy for traits simulated with 4 and 100 QTNs under the additive mechanism and heritability of 0.3 in sugarcane.** Box plots showing the distribution of predicted accuracies across five-folds and 100 replicates for different marker densities GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space)]. The white dots in the middle of the boxplot shows the mean of the



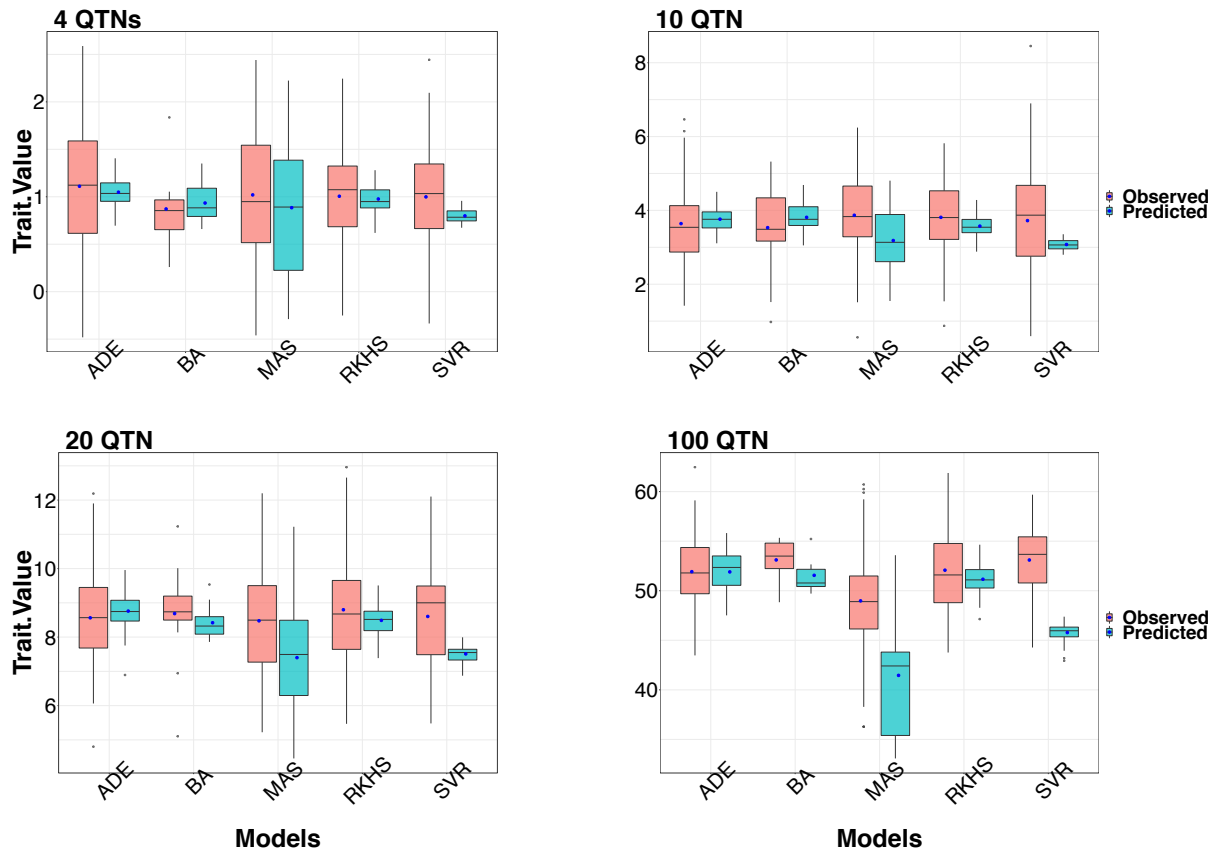
**Figure S69: Effect of marker density of prediction accuracy for traits simulated with 4 and 100 QTNs under the dominance mechanism and heritability of 0.3 in sugarcane.** Box plots showing the distribution of predicted accuracies across five-folds and 100 replicates for different marker densities GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space)]. The white dots in the middle of the boxplot shows the mean of the



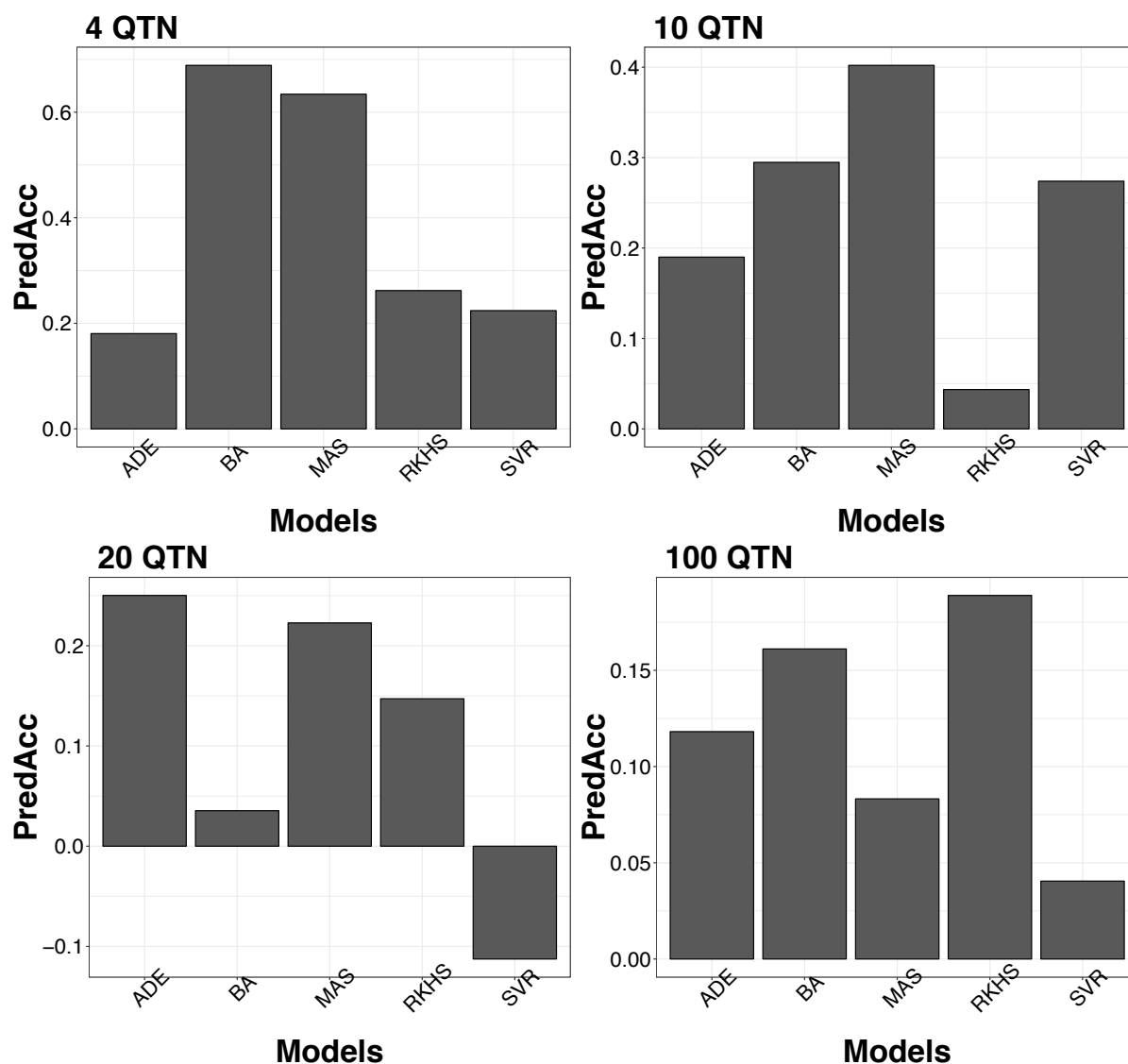
**Figure S70: Effect of marker density of prediction accuracy for traits simulated with 4 and 100 QTNs under the epistasis mechanism and heritability of 0.3 in sugarcane.** Box plots showing the distribution of predicted accuracies across five-folds and 100 replicates for different marker densities GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space)]. The white dots in the middle of the boxplot shows the mean of the



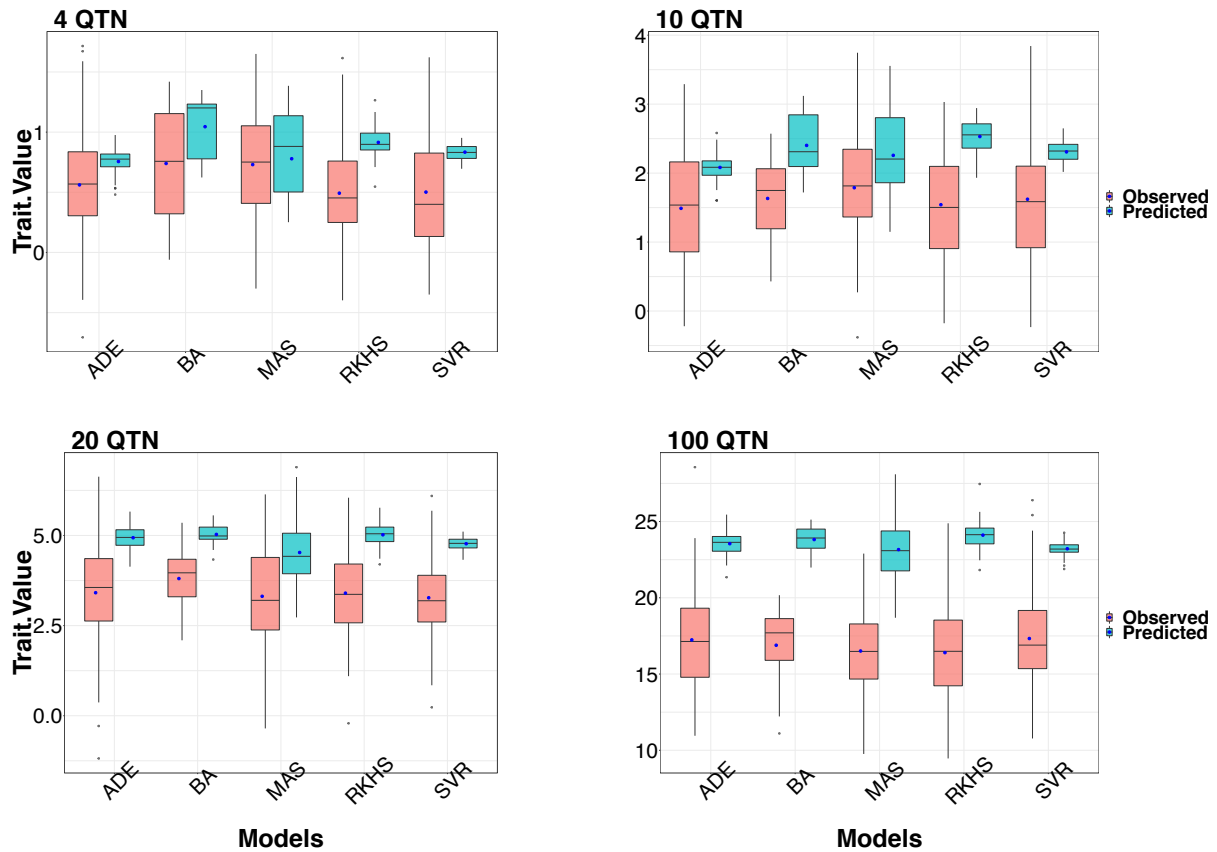
**Figure S71: Comparison among GS and MAS models in GS and MAS derived BC<sub>1</sub> populations in sugarcane for traits simulated with 4, 10, 20, and 100 QTNs under additive mechanism and heritability of 0.7.** Barplots showing prediction accuracy comparison among GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] in GS derived BC<sub>1</sub> and MAS (Marker Assisted Selection) in MAS derived BC<sub>1</sub>.



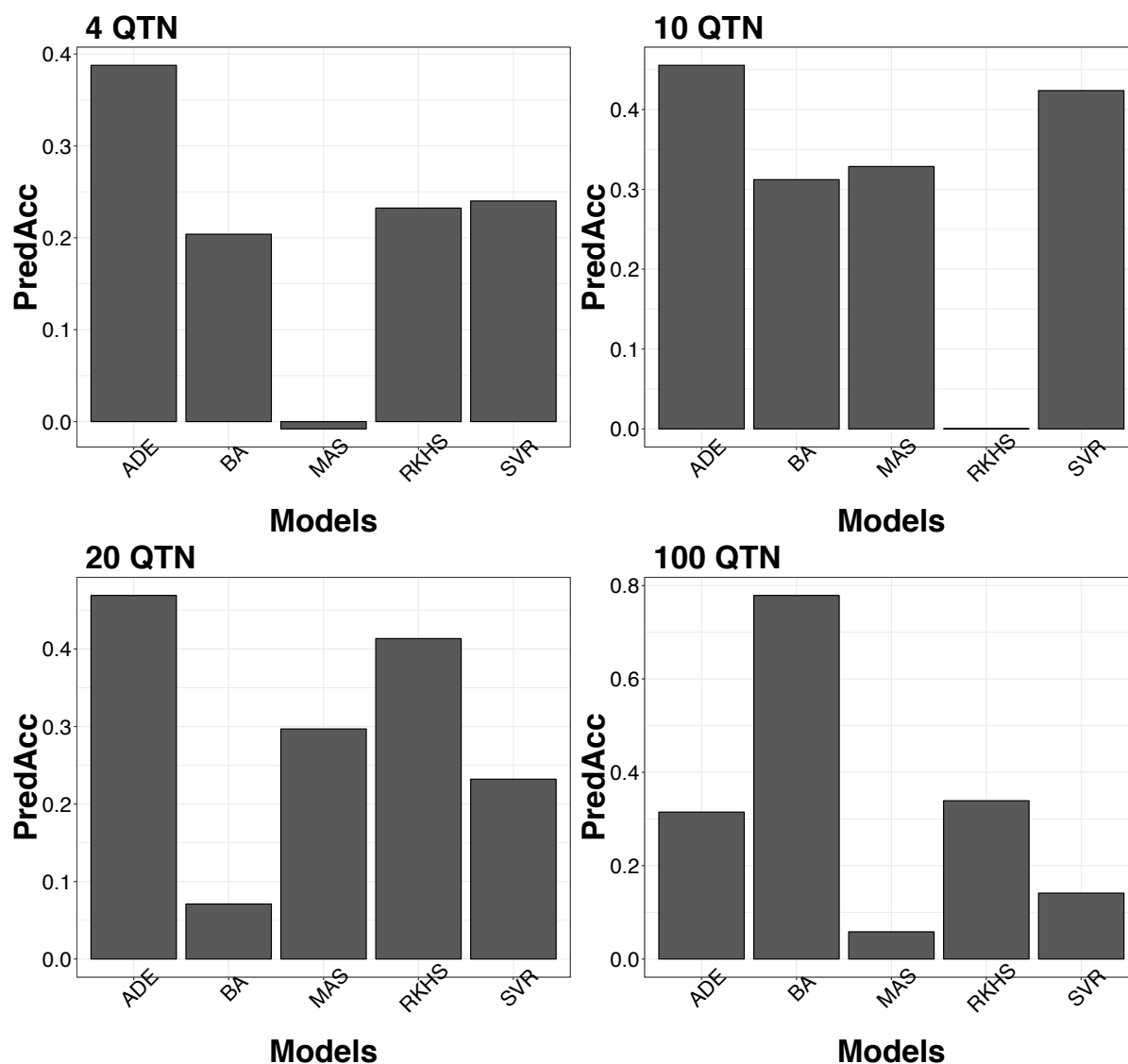
**Figure S72: Distribution of observed and predicted values in GS and MAS models in GS and MAS derived BC<sub>1</sub> populations in sugarcane for traits simulated with 4, 10, 20, and 100 QTNs under additive mechanism and heritability of 0.7.** Boxplots showing the distributions of observed and predicted trait values in GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] in GS derived BC<sub>1</sub> and MAS (Marker Assisted Selection) in MAS derived BC<sub>1</sub>. The blue dot represents the mean of each distribution.



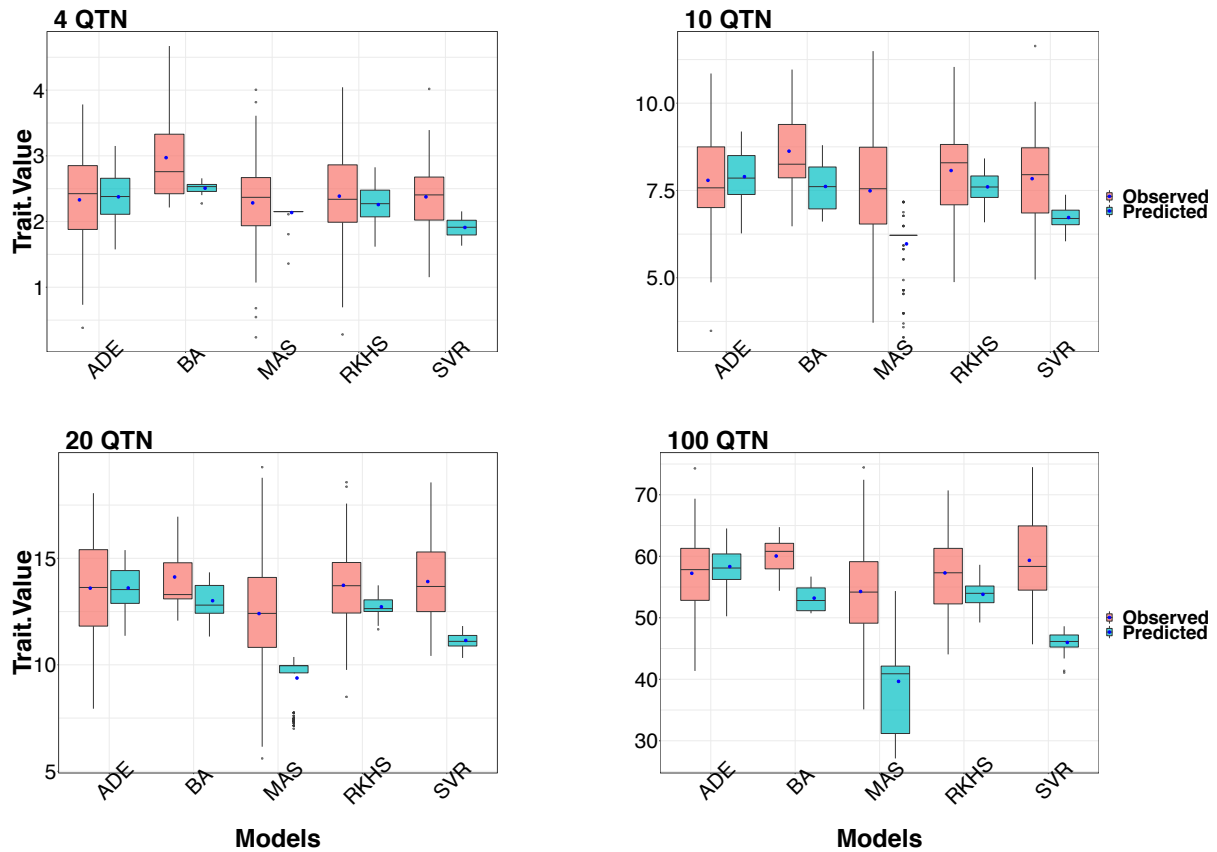
**Figure S73: Comparison among GS and MAS models in GS and MAS derived BC<sub>1</sub> populations in sugarcane for traits simulated with 4, 10, 20, and 100 QTNs under dominance mechanism and heritability of 0.7.** Barplots showing prediction accuracy comparison among GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] in GS derived BC<sub>1</sub> and MAS (Marker Assisted Selection) in MAS derived BC<sub>1</sub>.



**Figure S74: Distribution of observed and predicted values in GS and MAS models in GS and MAS derived BC<sub>1</sub> populations in sugarcane for traits simulated with 4, 10, 20, and 100 QTNs under dominance mechanism and heritability of 0.7.** Boxplots showing the distributions of observed and predicted trait values in GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] in GS derived BC<sub>1</sub> and MAS (Marker Assisted Selection) in MAS derived BC<sub>1</sub>. The blue dot represents the mean of each distribution.

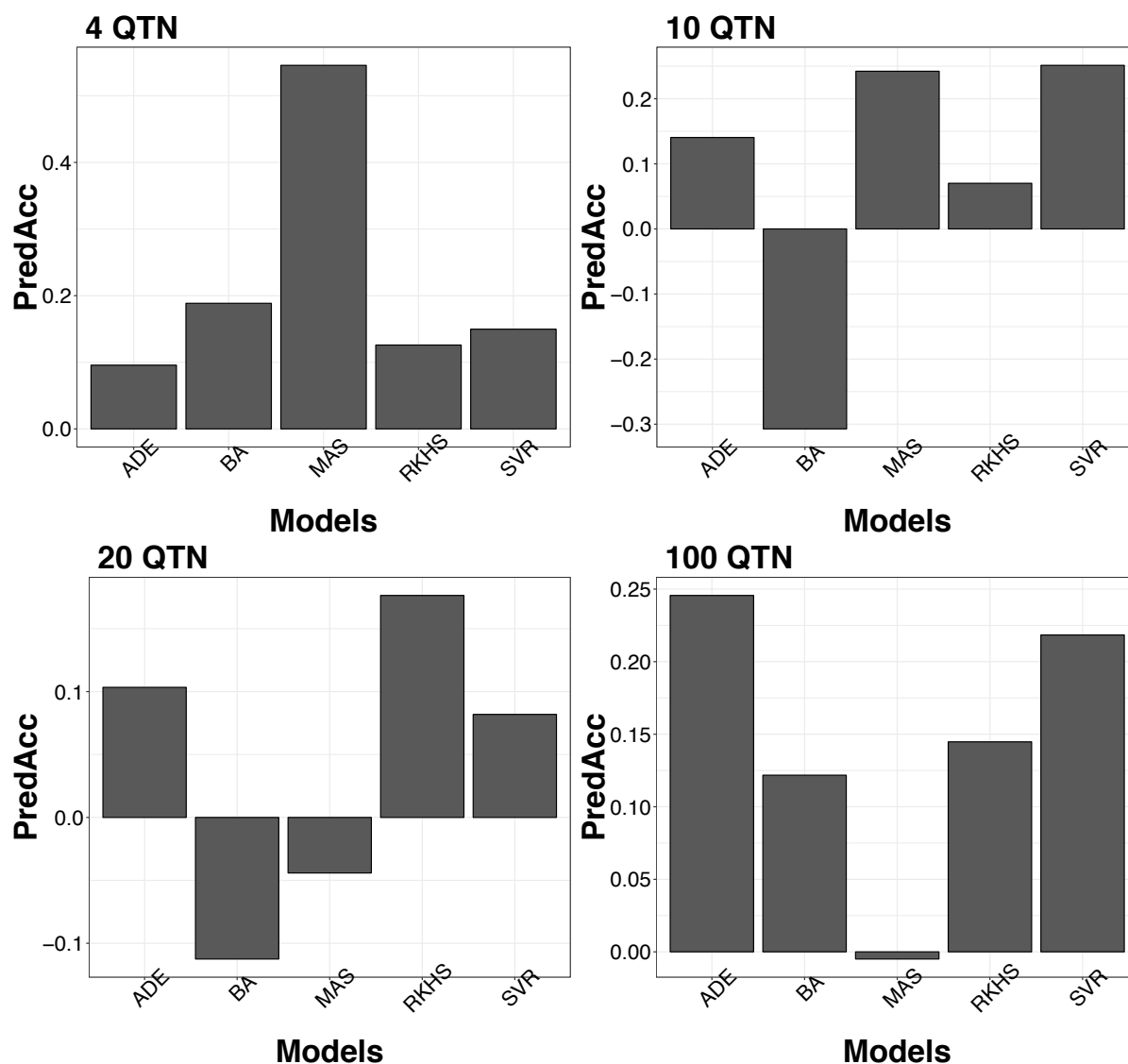


**Figure S75: Comparison among GS and MAS models in GS and MAS derived BC<sub>1</sub> populations in sugarcane for traits simulated with 4, 10, 20, and 100 QTNs under epistasis mechanism and heritability of 0.7.** Barplots showing prediction accuracy comparison among GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] in GS derived BC<sub>1</sub> and MAS (Marker Assisted Selection) in MAS derived BC<sub>1</sub>.

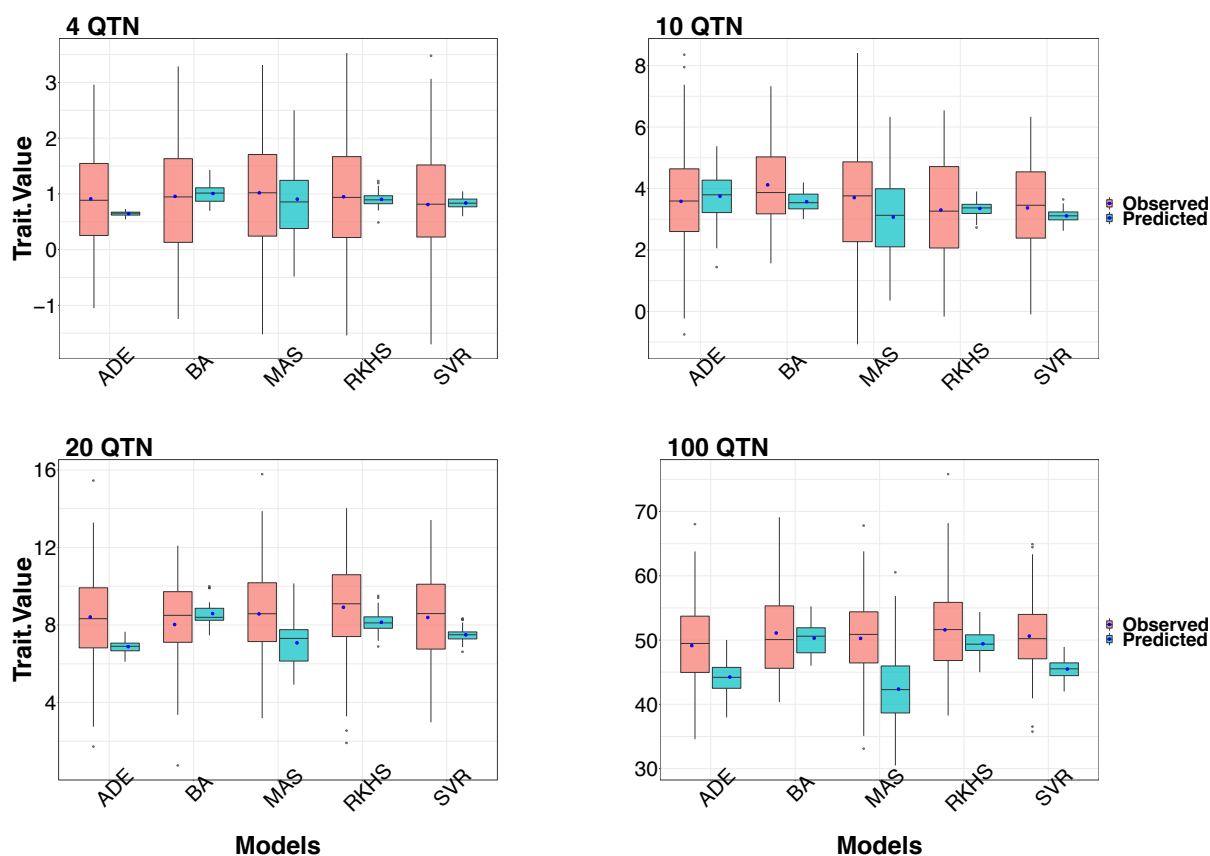


**Figure S76: Distribution of observed and predicted values in GS and MAS models in GS and MAS derived BC<sub>1</sub> populations in sugarcane for traits simulated with 4, 10, 20, and 100 QTNs under epistasis mechanism and heritability of 0.7.** Boxplots showing the distributions of observed and predicted trait values in GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] in GS derived BC<sub>1</sub> and MAS (Marker Assisted Selection) in MAS derived BC<sub>1</sub>. The blue dot represents the mean of each distribution.

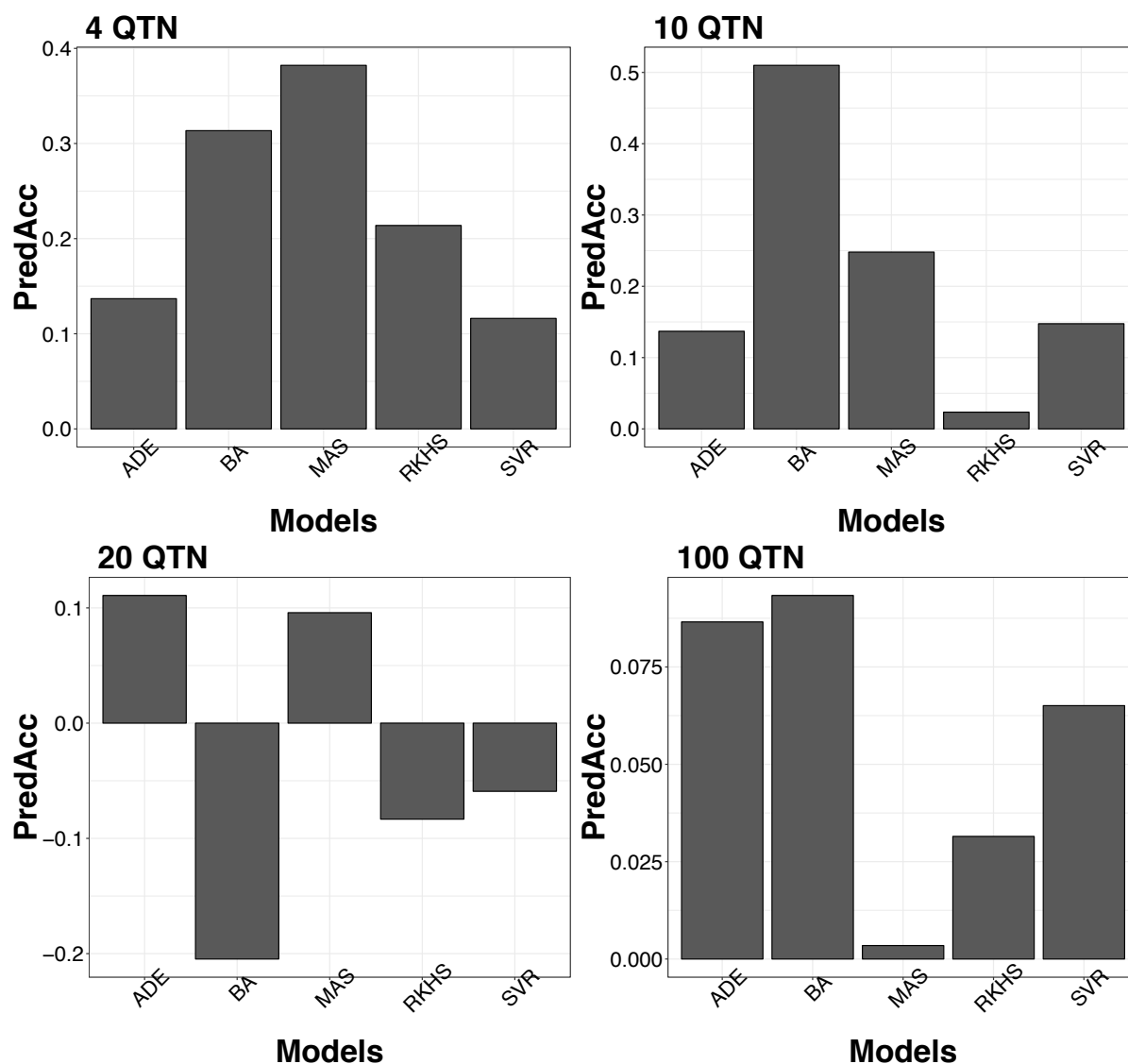




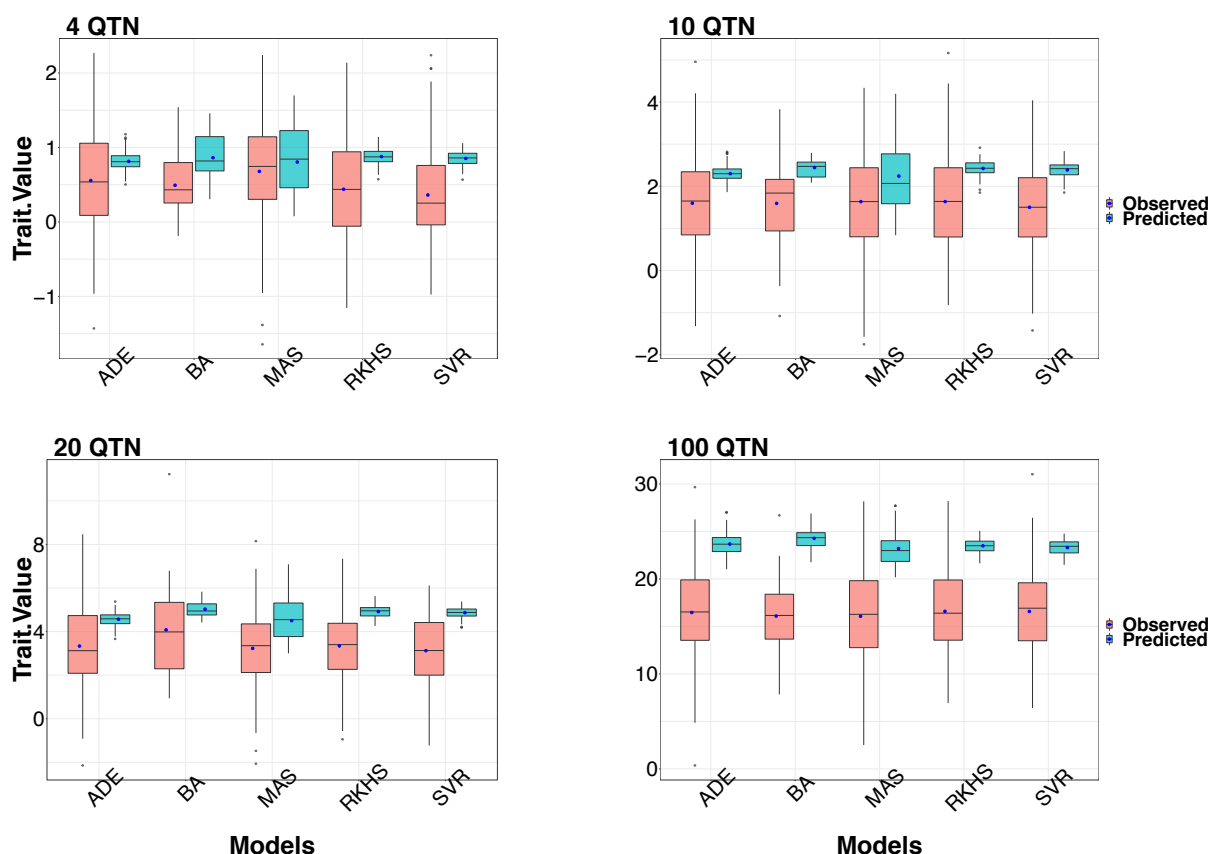
**Figure S77: Comparison among GS and MAS models in GS and MAS derived BC<sub>1</sub> populations in sugarcane for traits simulated with 4, 10, 20, and 100 QTNs under additive mechanism and heritability of 0.3.** Barplots showing prediction accuracy comparison among GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] in GS derived BC<sub>1</sub> and MAS (Marker Assisted Selection) in MAS derived BC<sub>1</sub>.



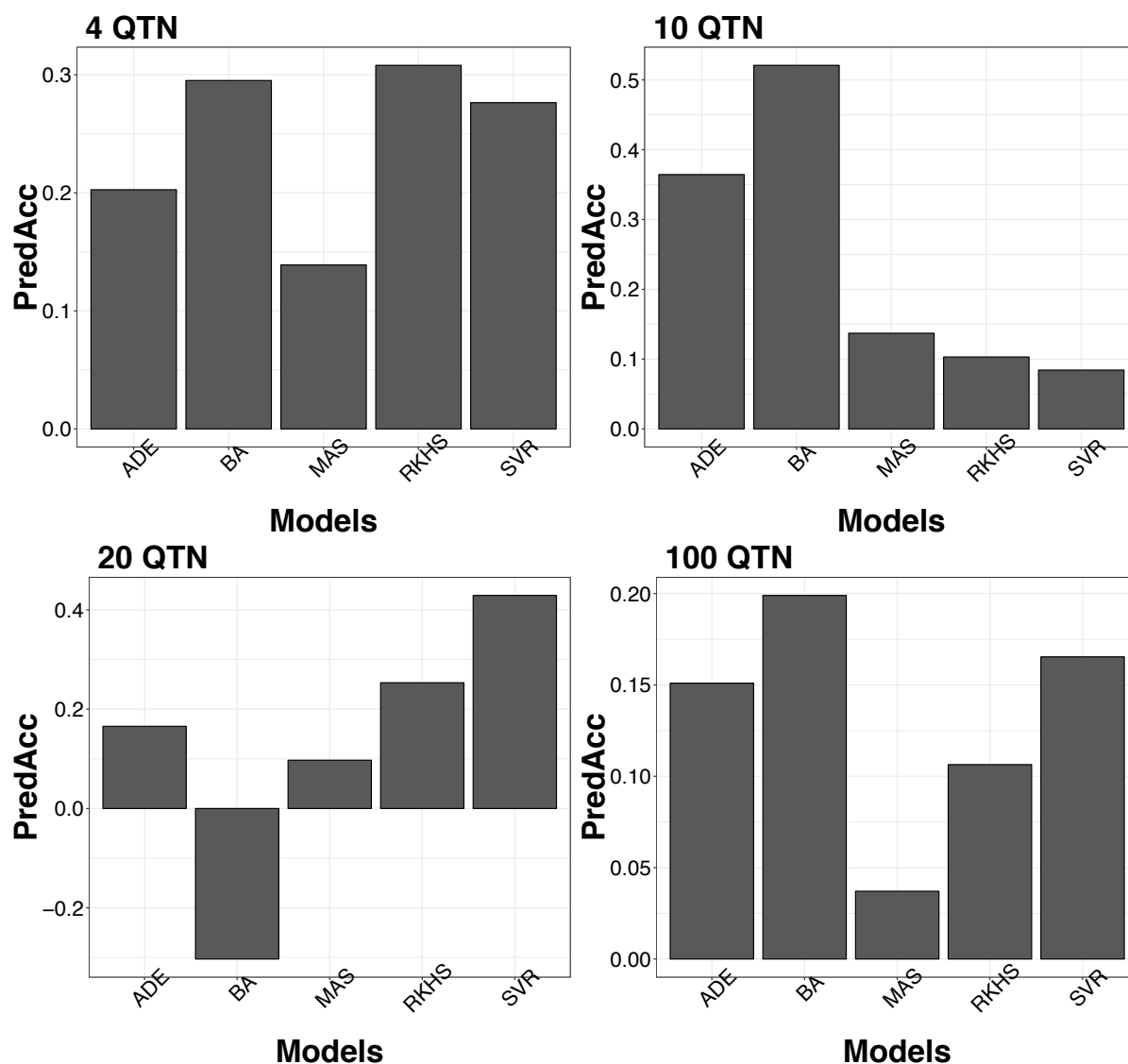
**Figure S78: Distribution of observed and predicted values in GS and MAS models in GS and MAS derived BC<sub>1</sub> populations in sugarcane for traits simulated with 4, 10, 20, and 100 QTNs under additive mechanism and heritability of 0.3.** Boxplots showing the distributions of observed and predicted trait values in GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] in GS derived BC<sub>1</sub> and MAS (Marker Assisted Selection) in MAS derived BC<sub>1</sub>. The blue dot represents the mean of each distribution.



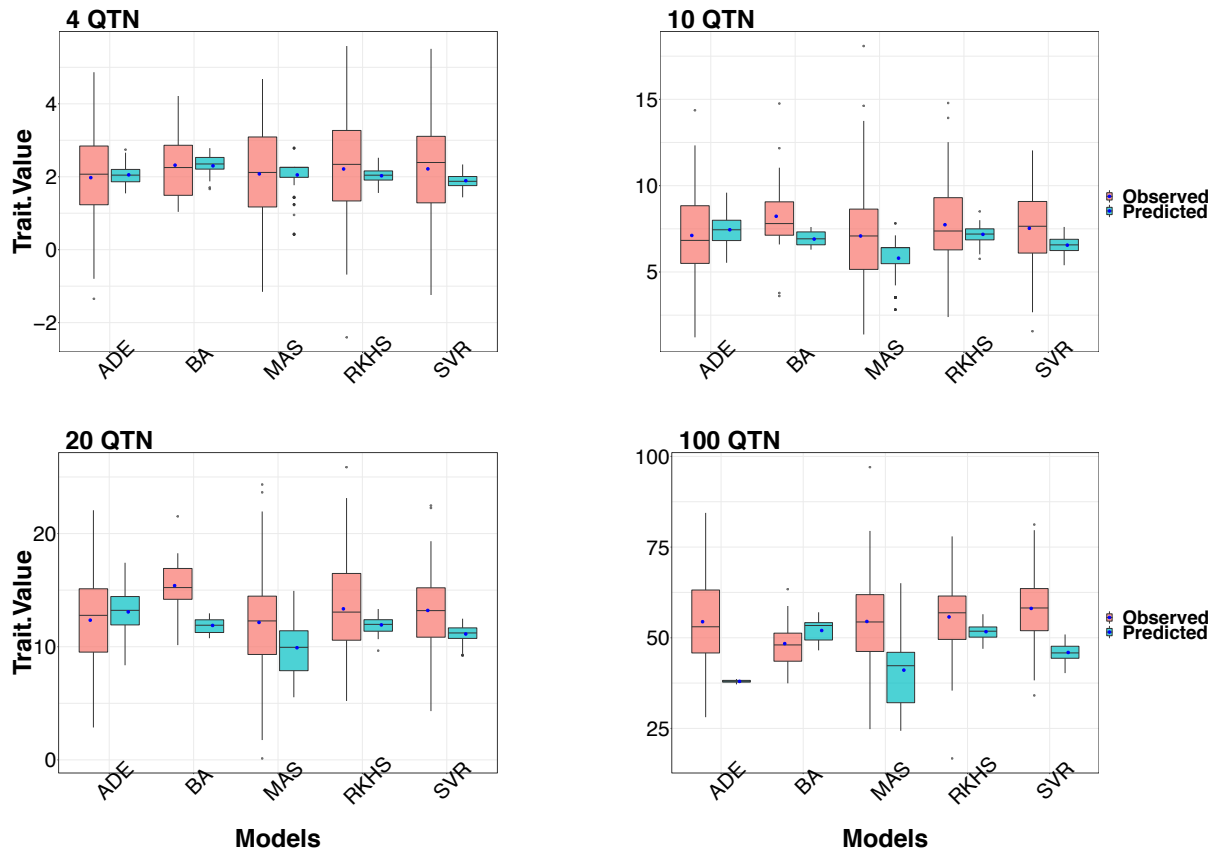
**Figure S79: Comparison among GS and MAS models in GS and MAS derived BC<sub>1</sub> populations in sugarcane for traits simulated with 4, 10, 20, and 100 QTNs under dominance mechanism and heritability of 0.3.** Barplots showing prediction accuracy comparison among GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] in GS derived BC<sub>1</sub> and MAS (Marker Assisted Selection) in MAS derived BC<sub>1</sub>.



**Figure S80: Distribution of observed and predicted values in GS and MAS models in GS and MAS derived BC<sub>1</sub> populations in sugarcane for traits simulated with 4, 10, 20, and 100 QTNs under dominance mechanism and heritability of 0.3.** Boxplots showing the distributions of observed and predicted trait values in GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] in GS derived BC<sub>1</sub> and MAS (Marker Assisted Selection) in MAS derived BC<sub>1</sub>. The blue dot represents the mean of each distribution.



**Figure S81: Comparison among GS and MAS models in GS and MAS derived BC<sub>1</sub> populations in sugarcane for traits simulated with 4, 10, 20, and 100 QTNs under epistasis mechanism and heritability of 0.3.** Barplots showing prediction accuracy comparison among GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] in GS derived BC<sub>1</sub> and MAS (Marker Assisted Selection) in MAS derived BC<sub>1</sub>.



**Figure S82: Distribution of observed and predicted values in GS and MAS models in GS and MAS derived BC<sub>1</sub> populations in sugarcane for traits simulated with 4, 10, 20, and 100 QTNs under epistasis mechanism and heritability of 0.3.** Boxplots showing the distributions of observed and predicted trait values in GS models [ADE (Additive-Dominance-Epistasis kernels model in sommer package), BA (Bayes A), RKHS (Reproducing kernel Hilbert space), SVR (Support Vector Regression)] in GS derived BC<sub>1</sub> and MAS (Marker Assisted Selection) in MAS derived BC<sub>1</sub>. The blue dot represents the mean of each distribution.