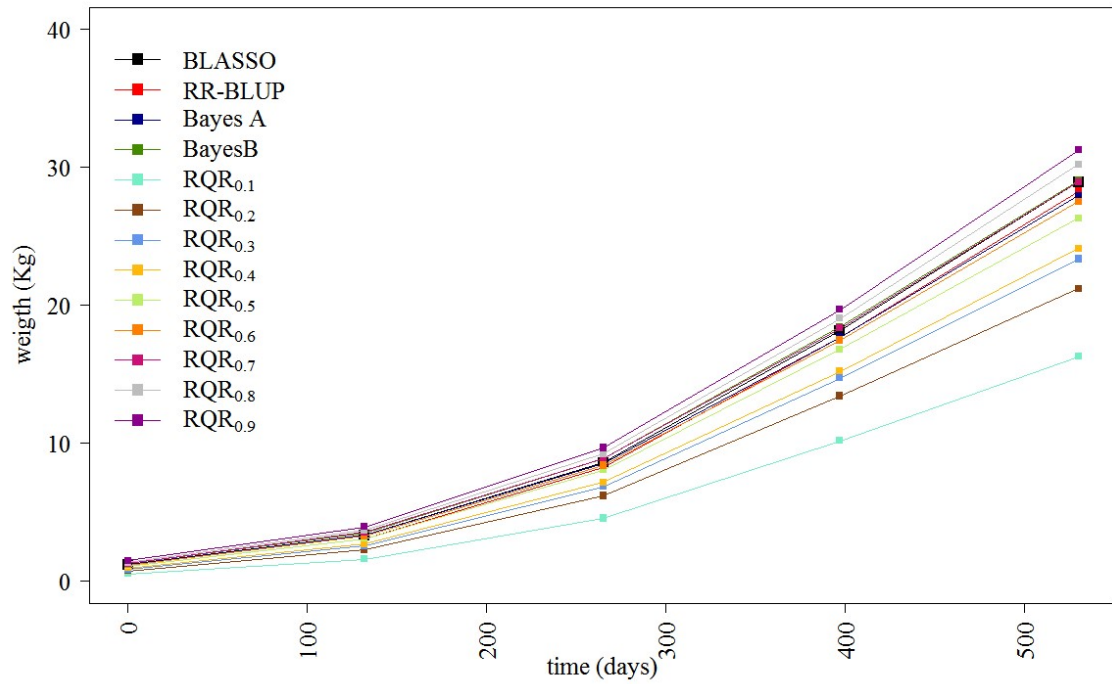
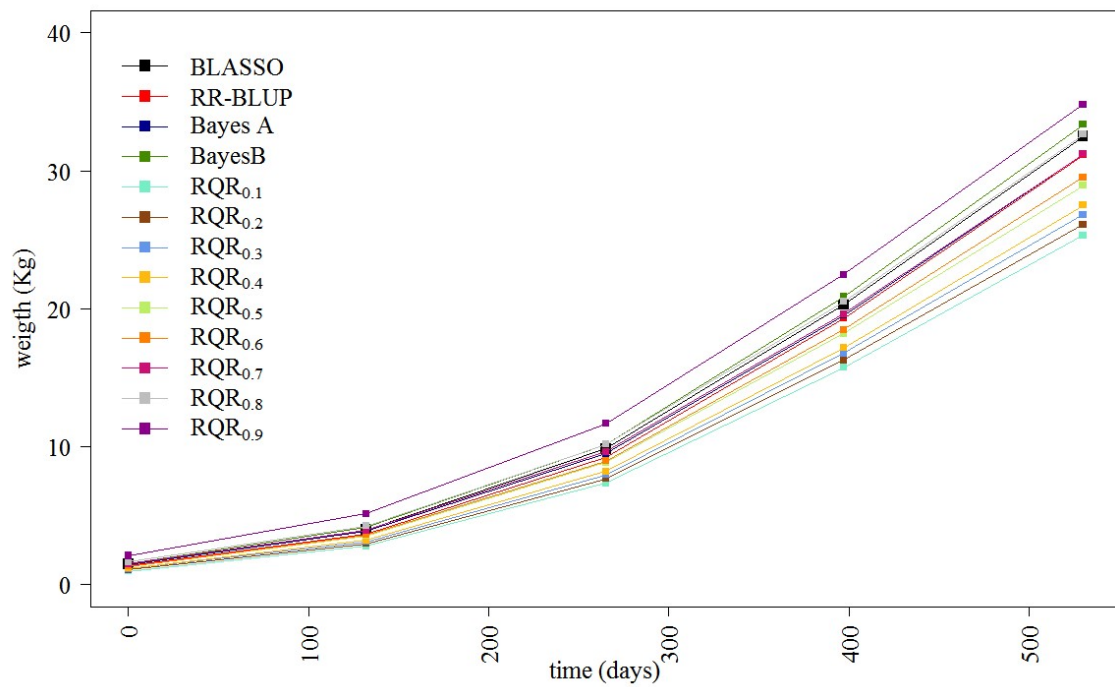


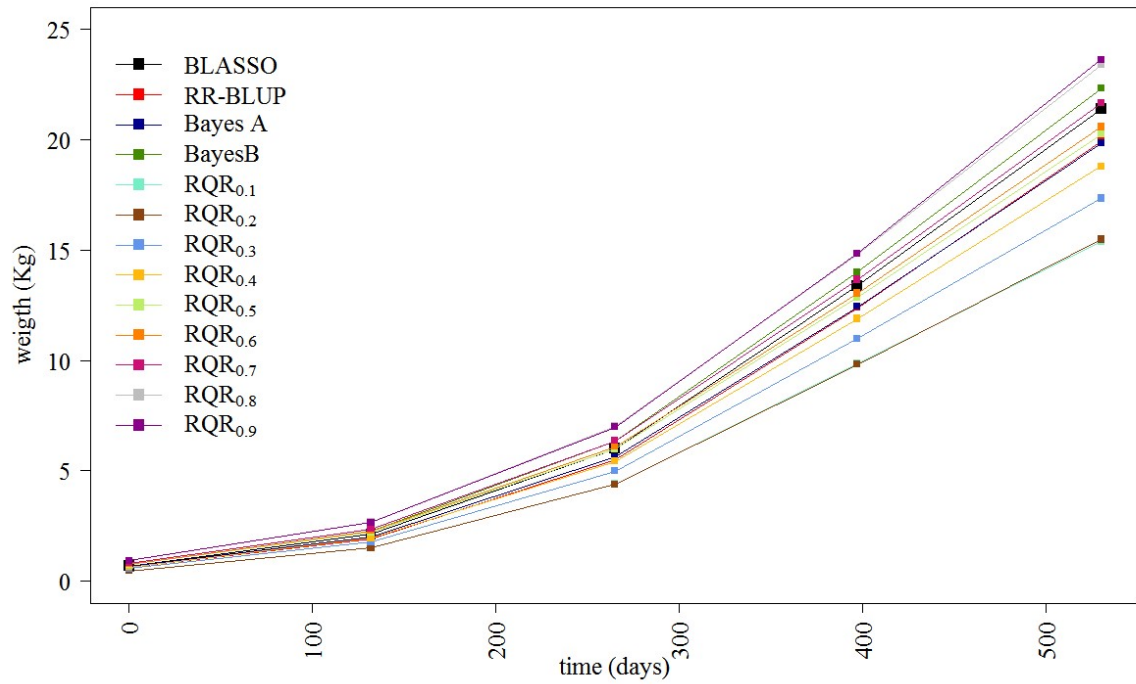
**S1 Figure.** Subsamples obtained using Ward hierarchical clustering analysis.



**S2 Figure.** Mean genomic growth curves using the genomic estimated breeding values (GEBVs) obtained by thirteen (BLASSO, RR-BLUP, Bayes A, Bayes B, RQR<sub>0.1</sub>, RQR<sub>0.2</sub>, ..., RQR<sub>0.9</sub>) different genomic selection models for each parameter of a logistic growth curve considering the symmetric scenario.



**S3 Figure.** Mean genomic growth curves using the genomic estimated breeding values (GEBVs) obtained by thirteen (BLASSO, RR-BLUP, Bayes A, Bayes B, RQR<sub>0.1</sub>, RQR<sub>0.2</sub>, ..., RQR<sub>0.9</sub>) different genomic selection models for each parameter of a logistic growth curve considering the positive skewness scenario.



**S4 Figure.** Mean genomic growth curves using the genomic estimated breeding values (GEBVs) obtained by thirteen (BLASSO, RR-BLUP, Bayes A, Bayes B, RQR<sub>0.1</sub>, RQR<sub>0.2</sub>, ..., RQR<sub>0.9</sub>) different genomic selection models for each parameter of a logistic growth curve considering the negative skewness scenario.