



**Fig S3. Performance of BayesR in Meishan.** **A)** Accuracy in predicting genetic merit when 50% of MS from the last generation were removed and predicted with BayesR (neutral architecture). **B)** Idem for the selective architecture. **C)** Fraction of variance explained by SNPs when classified as  $10^{-4}$ ,  $10^{-3}$  and  $10^{-2}$  units of genetic variance, according to different SNP sets (neutral architecture). **D)** Idem for the selective architecture. Models as in Fig 4, except that 'sequence' (SEQ) contains only the 2 million SNPs from MAF01, MAF10 plus the QTNs. Accuracy is defined as squared correlation between true and predicted genetic values. Dots correspond to each of the five replicates, horizontal bars in panels A and B correspond to the mean.