A. Figure S9a: Power in simulations ($h^2 = 0.2$), for single trait mapping (red), bivariate ETM with the most correlated environmental variable (black), bivariate ETM with 4 different prediction methods (LM, EN, RF, CCA; respectively green, blue, brown and purple solid lines), and single trait mapping with the 4 predicted traits (same colors, dashed lines). Bivariate ETM was performed by testing for a common marker effect (top) and by testing whether there is any effect on environment or trait (bottom). The causal SNP explained 2% of the variance of the simulated trait, while polygenic background and residual variance explained respectively 18% and 80%. Correlations between true and observed environmental variables were 0.89.
Figure S9b: Power in simulations ($h^2 = 0.2$), for single trait mapping (red), bivariate ETM with the most correlated environmental variable (black), bivariate ETM with 4 different prediction methods (LM, EN, RF, CCA; respectively green, blue, brown and purple solid lines), and single trait mapping with the 4 predicted traits (same colors, dashed lines). Bivariate ETM was performed by testing for a common marker effect (top) and by testing whether there is any effect on environment or trait (bottom). The causal SNP explained 5% of the variance of the simulated trait, while polygenic background and residual variance explained respectively 15% and 80%. Correlations between true and observed environmental variables were 0.8.
Figure S9c: Power in simulations ($h^2=0.2$), for single trait mapping (red), bivariate ETM with the most correlated environmental variable (black), bivariate ETM with 4 different prediction methods (LM, EN, RF, CCA; respectively green, blue, brown and purple solid lines), and single trait mapping with the 4 predicted traits (same colors, dashed lines). Bivariate ETM was performed by testing for a common marker effect (top) and by testing whether there is any effect on environment or trait (bottom). The causal SNP explained 10% of the variance of the simulated trait, while polygenic background and residual variance explained respectively 10% and 80%. Correlations between true and observed environmental variables were 0.8.
Figure S9d: Power in simulations ($h^2 = 0.5$), for single trait mapping (red), bivariate ETM with the most correlated environmental variable (black), bivariate ETM with 4 different prediction methods (LM, EN, RF, CCA; respectively green, blue, brown and purple solid lines), and single trait mapping with the 4 predicted traits (same colors, dashed lines). Bivariate ETM was performed by testing for a common marker effect (top) and by testing whether there is any effect on environment or trait (bottom). The causal SNP explained 2% of the variance of the simulated trait, while polygenic background and residual variance explained respectively 48% and 50%. Correlations between true and observed environmental variables were 0.812.
Figure S9e: Power in simulations ($h^2 = 0.5$), for single trait mapping (red), bivariate ETM with the most correlated environmental variable (black), bivariate ETM with 4 different prediction methods (LM, EN, RF, CCA; respectively green, blue, brown and purple solid lines), and single trait mapping with the 4 predicted traits (same colors, dashed lines). Bivariate ETM was performed by testing for a common marker effect (top) and by testing whether there is any effect on environment or trait (bottom). The causal SNP explained 5% of the variance of the simulated trait, while polygenic background and residual variance explained respectively 45% and 50%. Correlations between true and observed environmental variables were 0.8.
Figure S9f: Power in simulations ($h^2 = 0.5$), for single trait mapping (red), bivariate ETM with the most correlated environmental variable (black), bivariate ETM with 4 different prediction methods (LM, EN, RF, CCA; respectively green, blue, brown and purple solid lines), and single trait mapping with the 4 predicted traits (same colors, dashed lines). Bivariate ETM was performed by testing for a common marker effect (top) and by testing whether there is any effect on environment or trait (bottom). The causal SNP explained 10% of the variance of the simulated trait, while polygenic background and residual variance explained respectively 40% and 50%. Correlations between true and observed environmental variables were 0.8.
Figure S9g: Power in simulations ($h^2=0.8$), for single trait mapping (red), bivariate ETM with the most correlated environmental variable (black), bivariate ETM with 4 different prediction methods (LM, EN, RF, CCA; respectively green, blue, brown and purple solid lines), and single trait mapping with the 4 predicted traits (same colors, dashed lines). Bivariate ETM was performed by testing for a common marker effect (top) and by testing whether there is any effect on environment or trait (bottom). The causal SNP explained 2% of the variance of the simulated trait, while polygenic background and residual variance explained respectively 78% and 20%. Correlations between true and observed environmental variables were 0.815.
Figure S9h: Power in simulations ($\hat{h}^2 = 0.8$), for single trait mapping (red), bivariate ETM with the most correlated environmental variable (black), bivariate ETM with 4 different prediction methods (LM, EN, RF, CCA; respectively green, blue, brown and purple solid lines), and single trait mapping with the 4 predicted traits (same colors, dashed lines). Bivariate ETM was performed by testing for a common marker effect (top) and by testing whether there is any effect on environment or trait (bottom). The causal SNP explained 5% of the variance of the simulated trait, while polygenic background and residual variance explained respectively 75% and 20%. Correlations between true and observed environmental variables were 0.8.
Figure S9i: Power in simulations ($h^2 = 0.8$), for single trait mapping (red), bivariate ETM with the most correlated environmental variable (black), bivariate ETM with 4 different prediction methods (LM, EN, RF, CCA; respectively green, blue, brown and purple solid lines), and single trait mapping with the 4 predicted traits (same colors, dashed lines). Bivariate ETM was performed by testing for a common marker effect (top) and by testing whether there is any effect on environment or trait (bottom). The causal SNP explained 10% of the variance of the simulated trait, while polygenic background and residual variance explained respectively 70% and 20%. Correlations between true and observed environmental variables were 0.817.