



**Figure S1.** Mean power (top) and false-discovery rate (bottom) for QTL discovery in simulated data for a single trait. Analysis methods were either univariate (BayesR) or multi-variate (BayesMV), where there was either no pleiotropic QTL (pQTL = 0, left) or complete pleiotropy (pQTL = 1, right). Error bars indicate the standard error of the mean for 20 replicates.