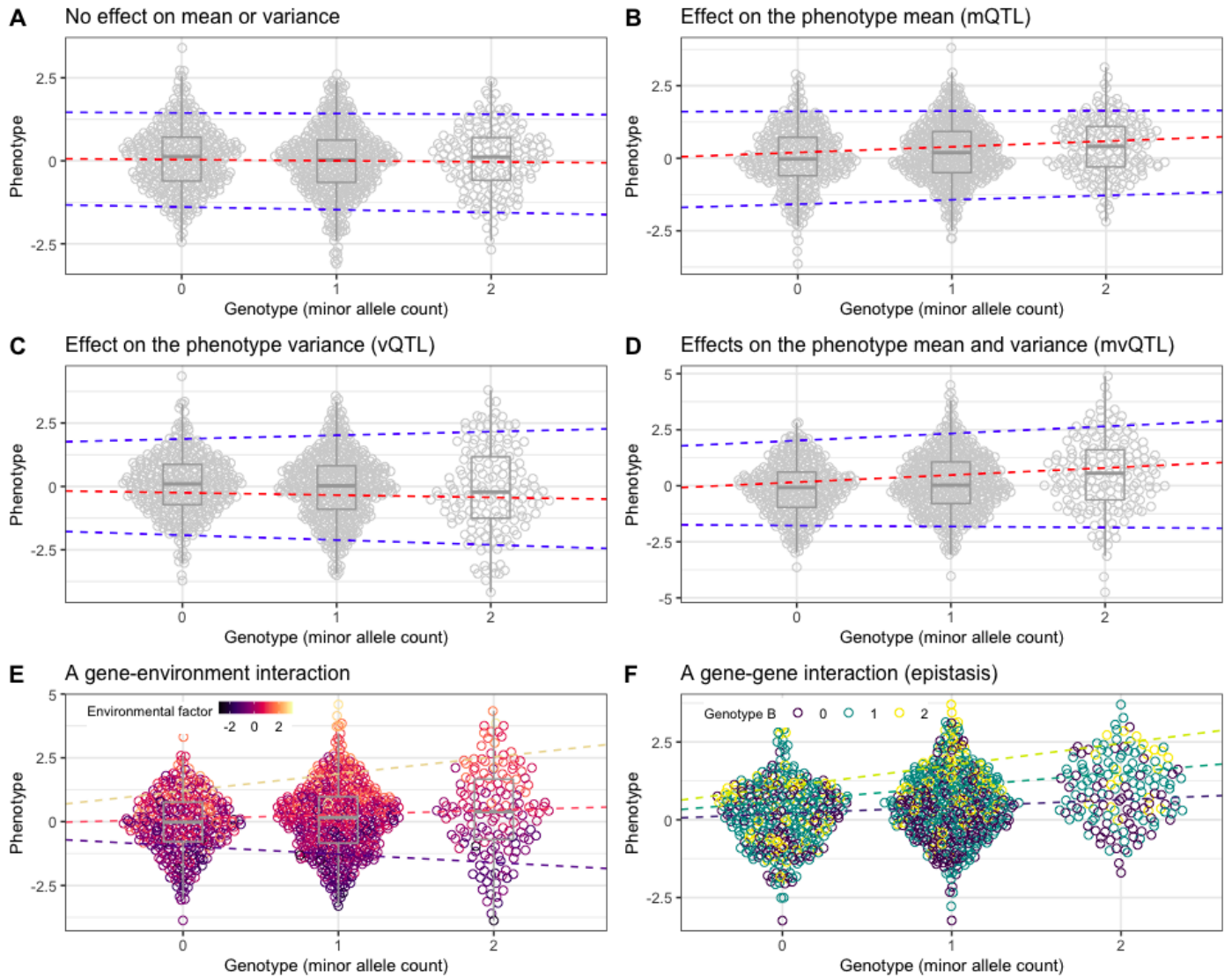## S.Figure 1. Plots of simulated SNP effects on phenotype mean and variance.

Violin plots display the distribution of a phenotype by minor allele count, at genotypes with different effects on the mean and variance of the phenotype. (A-D) The red dotted lines represent the regression of phenotype on genotype. Blue lines represent regression of phenotype on genotype, restricted to individuals in the upper and lower quintiles of the phenotype distribution - this helps to visualise the heteroscedasticity across genotype levels. All genotypes were simulated with minor allele frequency equal to 0.4 and environments had a normal distribution (n=1000). All phenotypes were simulated as a function of genetic and/or environmental effects with random normal error distribution. (A) For the null model the phenotype was simulated without any effect from genotype or environment. (B) the mQTL model was simulated with genetic effect β=.2. (C) the vQTL model was simulated with genetic effect β=0, an environmental effect β=.5 and a GxE interaction effect β=.4. (D) the mvQTL model was simulated with genetic effect β=.2, an environmental effect β=.5 and a GxE interaction effect β=.4. (E-F) Points are coloured based on a second variable. Lines represent regression of phenotype on genotype stratified by (E) tertiles of environmental exposure and (F) a genotype at a second locus. This illustrates how the interaction between a genotype and a second factor (an environmental exposure or a second genetic locus) contributes to increased variance across the genotype levels. (E) the GxE model was simulated with genetic effect β=.2, an environmental effect β=.5 and a GxE interaction effect β=.4. (F) the GxG model was simulated with genotype 1 effect β=.2, genotype 2 effect β=.2 and a GxG interaction effect β=.2.