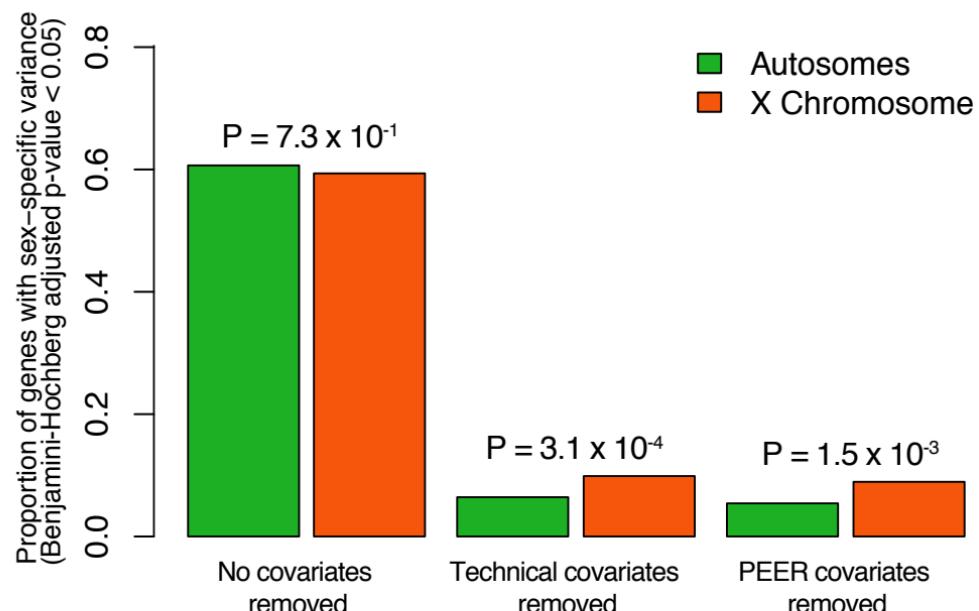
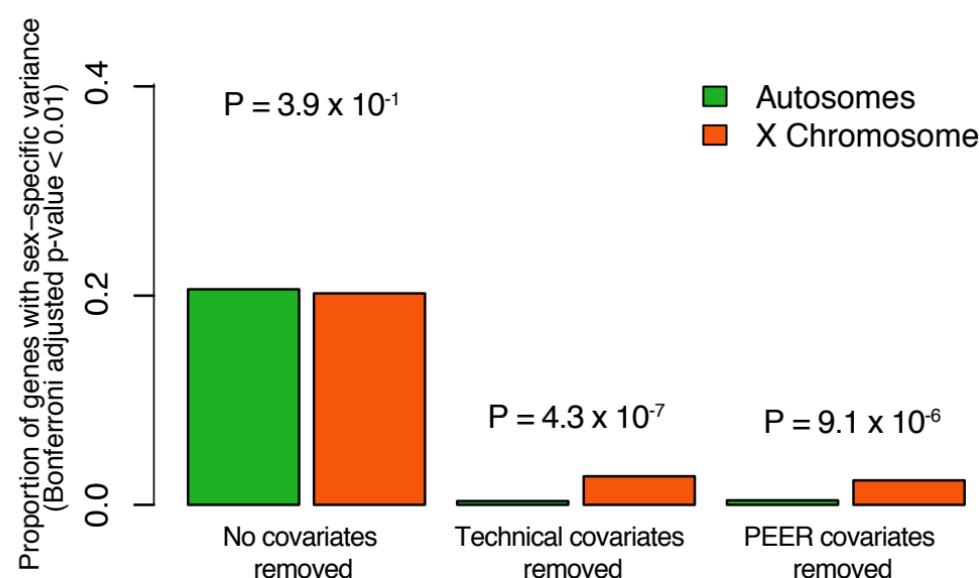


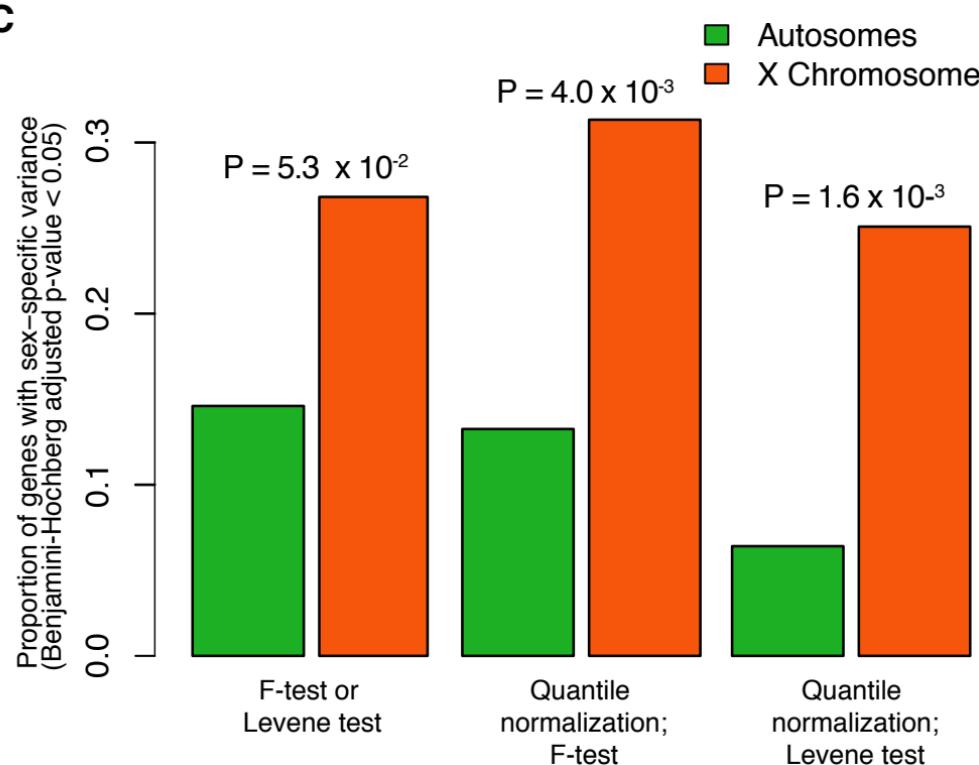
A



B



C



**Figure S2. Effect of normalization on differential expression variance analysis.**

We compared the effect of different normalization methods on the differential expression variance analysis (Figure 1A) to determine if technical or environmental factors were influencing the analysis. We investigated the effect of three different normalization methods, including the effect of removing no covariates, removing the technical covariates, and removing the hidden PEER covariates. **A.** If we consider genes to have differential variance if they fall below the Benjamini-Hochberg adjusted p-value < 0.05 (FDR 5%), we observe that the X Chromosome has a greater proportion of DV genes than the autosomes for each normalization method. **B.** Similarly, if we consider genes to have differential variance if they fall below the more conservative Bonferroni adjusted p-value < 0.01, we also observe that the X Chromosome has a greater proportion of DV genes than autosomes. **C.** We investigated the effect of two different normalization methods, i.e. effect of removing PEER covariates followed or not by quantile normalization, and two different variance tests, F-tests or Levene test. We consider genes to have differential variance if they fall below the Benjamini-Hochberg adjusted p-value < 0.05 (FDR 5%). We observe that the X Chromosome has a greater proportion of DV genes than the autosomes for each normalization method and testing strategy.