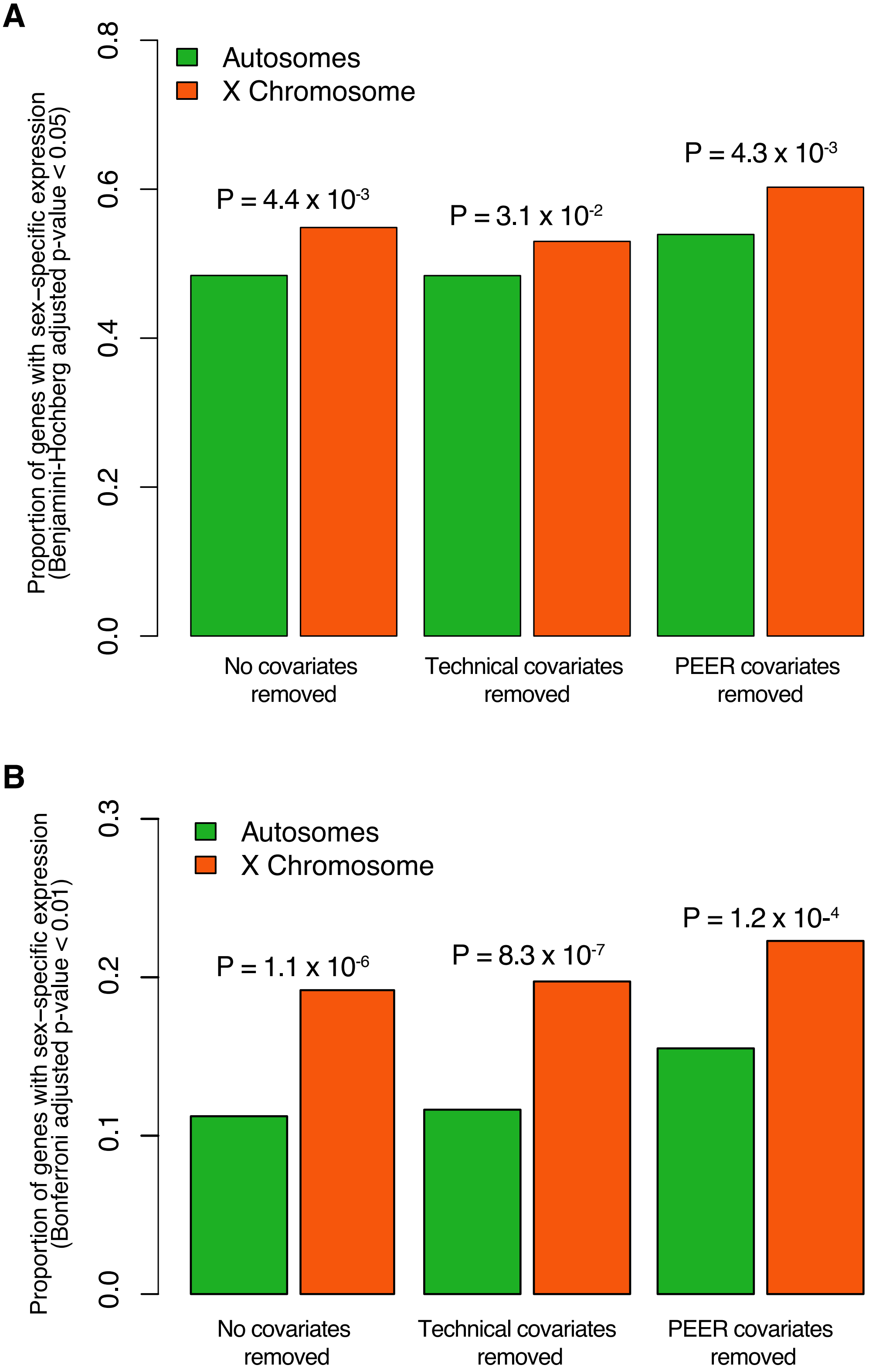

Figure S1. Effect of normalization on differential expression analysis. We compared the effect of different normalization methods on the differential expression analysis (Figure 1A) to determine if technical or environmental factors were influencing the analysis. We investigated the effect of three different normalization methods, including the effect or removing no covariates, removing the technical covariates, and removing the hidden PEER covariates. **A.** If we consider genes differentially expressed 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 DE genes than the autosomes for each normalization method. **B.** Similarly, if we consider genes differentially expressed 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 DE genes than autosomes.