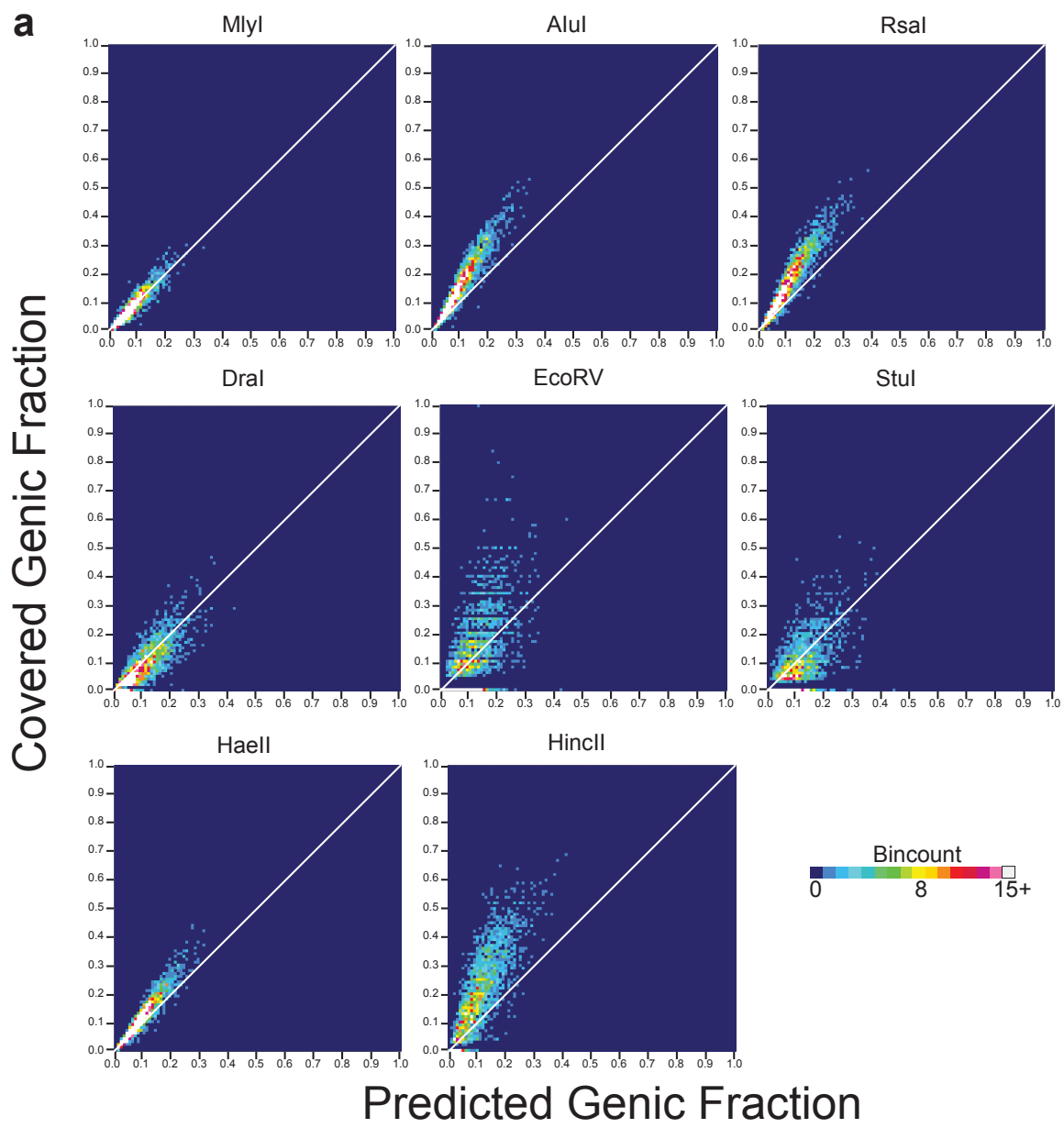
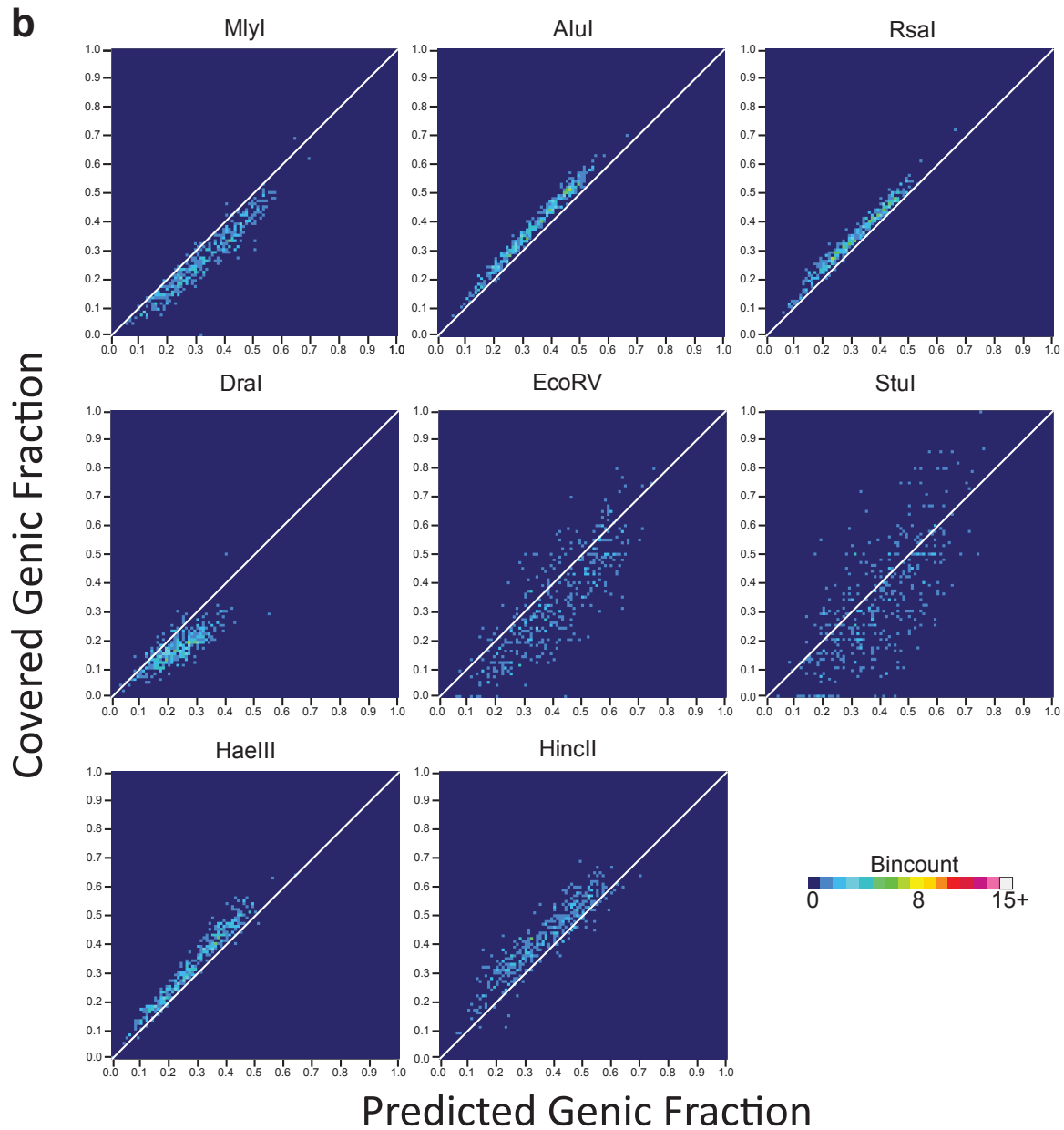






Additional File 3 Supplementary Figure 3: Fraction of predicted sites with aligned reads versus total predicted sites in genic regions.

The A) maize and B) rice genomes were binned into 1 Mbp intervals, then within each bin the fraction of covered sites in genic regions was compared to the fraction of predicted sites in genic regions. Bins were then plotted based on the two ratios and the number of bins in a given point indicated via heatmap. The white lines are present to indicate the predicted values at which the covered and predicted genic fractions would be identical. Points above this line represent bins with a greater fraction of sequenced sites in genic regions than predicted.