Supplementary Figures and Tables to:

Analysis of Nucleosome Positioning Landscapes Enables Gene Discovery in the Human Malaria Parasite *Plasmodium falciparum*

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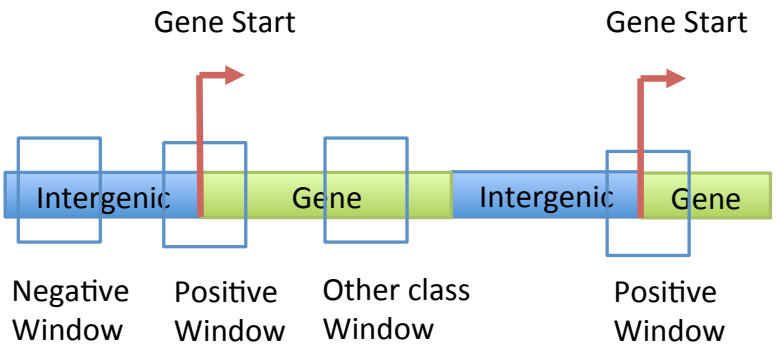
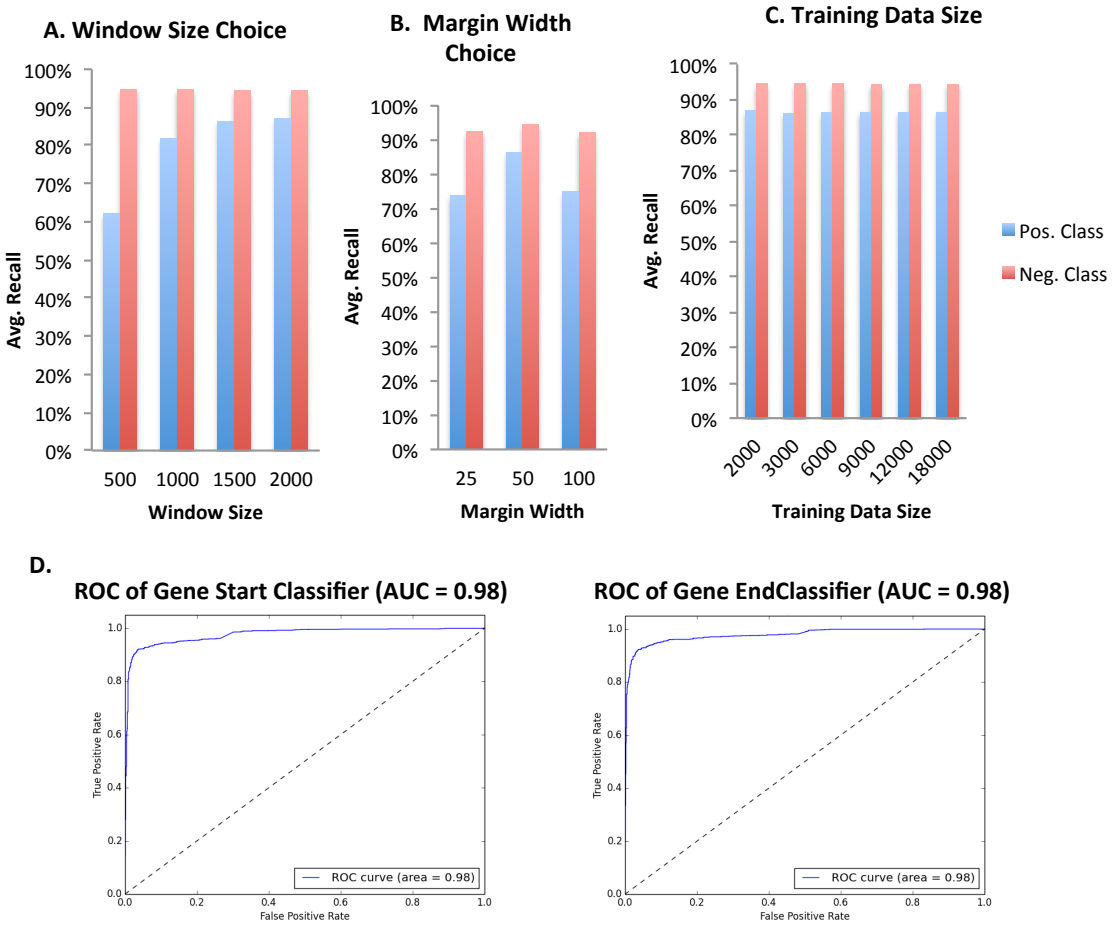


Supplementary Figure 1. **Supervised machine learning approach for novel gene detection.** Using a sliding window method, the genome-wide nucleosome positioning data set was converted into a set of subsequences ("windows"), where each window is a vector of length w, and each position is a numeric value representing the summed number of mapped reads. A label was then assigned to each of the windows based on the presence of a gene start. A binary classifier for gene start recognition was trained on gene start-containing windows (positive class) and intergenic windows (negative class) with support vector machine (SVM), RBF kernel. A similar approach was used to train a classifier for the detection of gene ends.

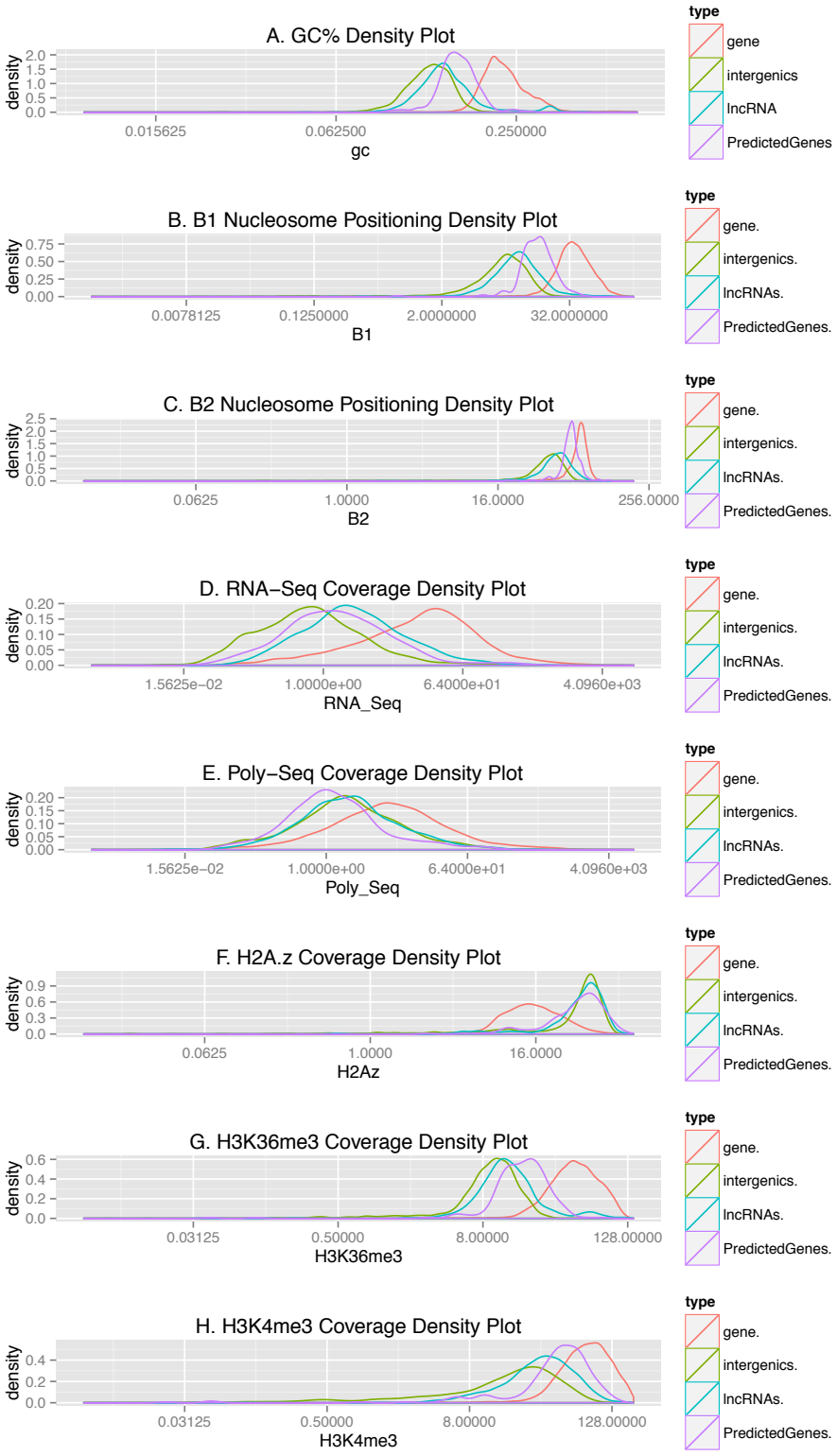


Supplementary Figure 2. Optimization of classifier parameters trained on the positive strand of data set B1. Average recall rates for gene start detection from 10 cross-validation experiments for window size **(A)**, margin width **(B)**, and training data size **(C)**. After comparing the recall rate for each parameter, the optimized classifier was trained using 6,000 windows of 1,500 bp with 50 bp margin width drawn in equal quantities from both positive and negative class. The ROC curves for optimized gene start and gene end classifiers are reported in (**D**). Results of optimization experiments for classifiers trained on the negative strand of data set B1 and classifiers trained on data set B2 were very similar and are therefore not shown. A detailed explanation of classifier optimization is presented in the Material and Methods section.

B1 dataset							
Gene Start				Gene End			
	Class	Recall	AUC		Class	Recall	AUC
Positive Strand Classifier	Intergenic (0)	0.97	0.98	Positive Strand Classifier	Intergenic (0)	0.94	0.98
	Gene(1)	0.91			Gene(1)	0.92	
	total	0.94			total	0.93	
	Class	Recall	AUC		Class	Recall	AUC
Negative Strand Classifier	Intergenic (0)	0.94	0.98	Negative Strand Classifier	Intergenic (0)	0.96	0.98
	Gene(1)	0.94			Gene(1)	0.94	
	total	0.94			total	0.95	

B2 dataset							
Gene Start				Gene End			
	Class	Recall	AUC		Class	Recall	AUC
Positive Strand Classifier	Intergenic (0)	0.92	0.96	Positive Strand Classifier	Intergenic (0)	0.92	0.97
	Gene(1)	0.90			Gene(1)	0.92	
	total	0.91			total	0.92	
	Class	Recall	AUC		Class	Recall	AUC
Negative Strand Classifier	Intergenic (0)	0.92	0.97	Negative Strand Classifier	Intergenic (0)	0.93	0.98
	Gene(1)	0.93			Gene(1)	0.94	
	total	0.92			total	0.93	

Supplementary Table 1: Classifier performance records.



Supplementary Figure 3. Density plots of various characteristics of predicted gene regions versus intergenic regions and annotated coding and non-coding genes in *P. falciparum*.

Supplementary Figure 4: Coverage profiles of histone variants around gene boundaries.