

Supplementary Materials to Harnessing Machine Learning to Identify Antimicrobial Peptides in *Drosophila melanogaster*

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Figure S1: Error rate in the Random forest model

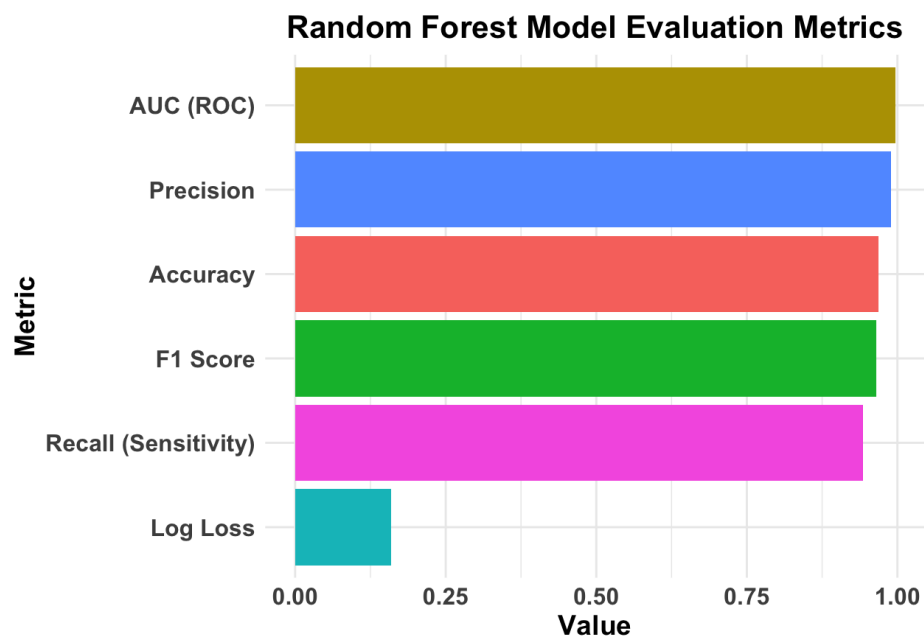


Figure S2: Different evaluation matrices of the Random forest model

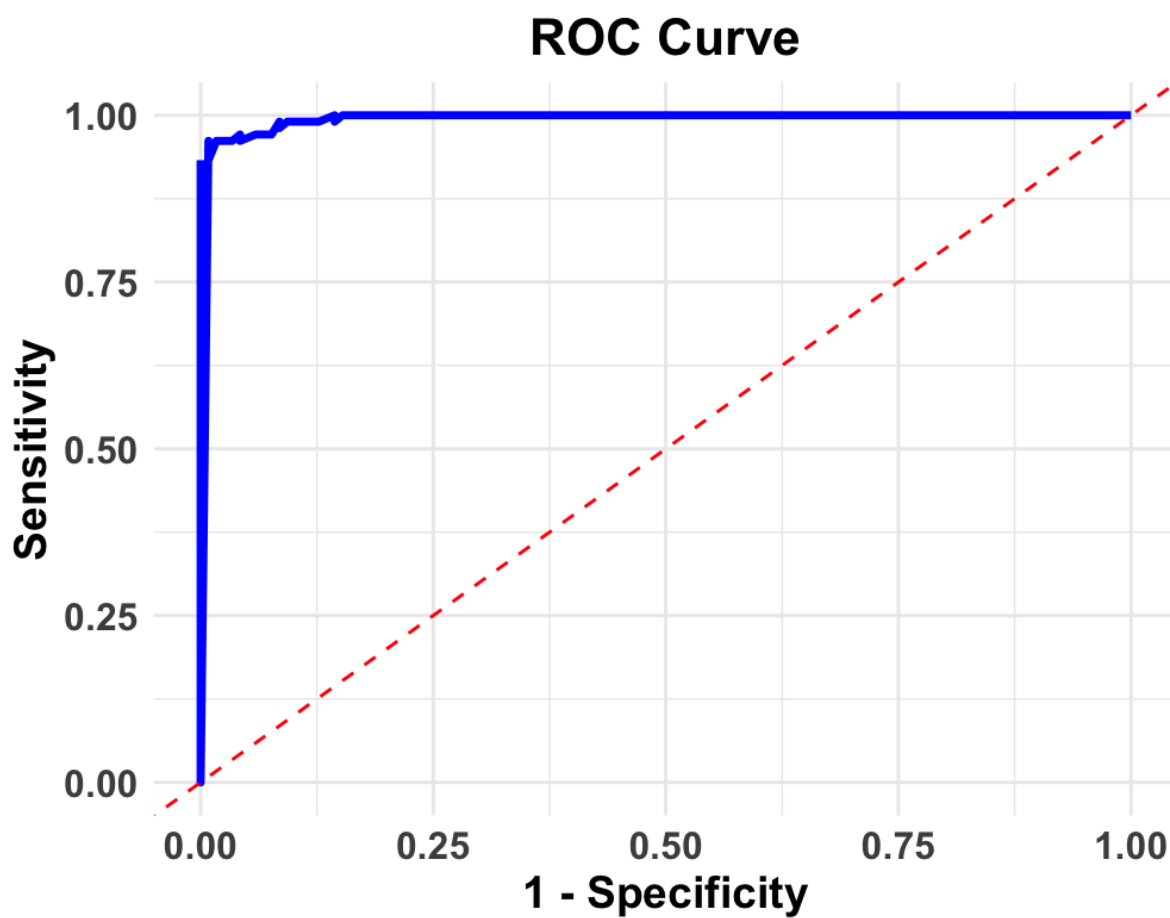


Figure S3: ROC curve of the Random forest model

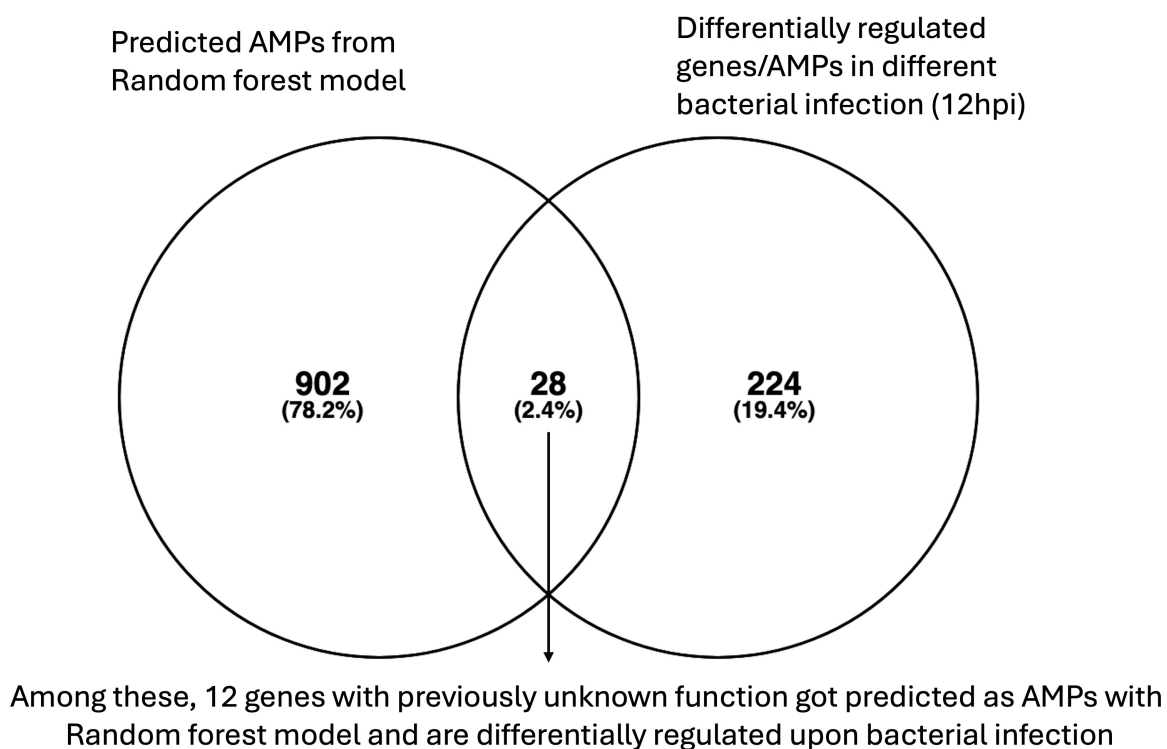


Figure S4: Screening the predicted AMPs with expression data in different bacterial infections

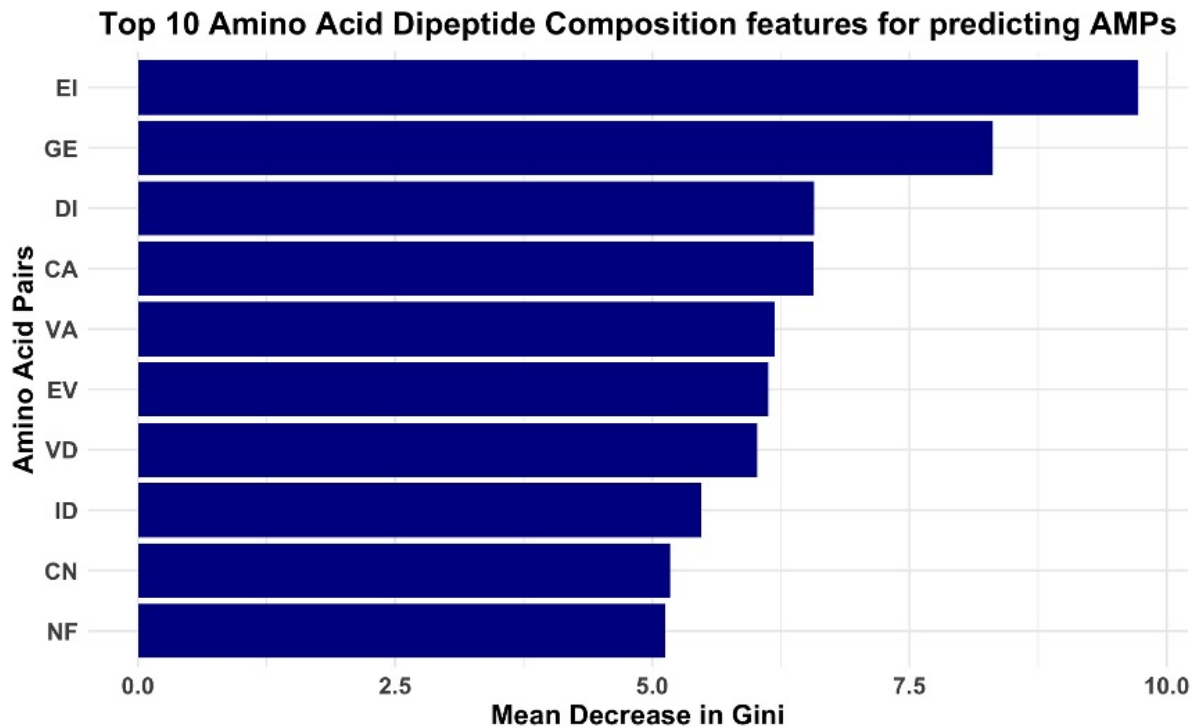


Figure S5: Top 10 amino acid dipeptide composition features for predicting AMPs