

576 **A Appendix**

Table A1. Classification Report for Human Specific Light Weight Model)

-	Precision	Recall	F1-Score
Coding	0.92	0.88	0.90
Noncoding	0.88	0.91	0.89
accuracy			0.90
macro avg	0.90	0.90	0.90
weighted avg	0.90	0.90	0.90

Table A2. Confusion Matrix for Human Specific Light Weight Model)

-	Positive	Negative
Positive	885	117
Negative	81	819

Positive class: lncRNA,
Negative class: other RNA

Table A3. Classification Report for Human Specific Full Model)

-	Precision	Recall	F1-Score
Coding	0.92	0.89	0.90
Noncoding	0.88	0.91	0.90
accuracy			0.90
macro avg	0.90	0.90	0.90
weighted avg	0.90	0.90	0.90

Table A4. Confusion Matrix for Human Specific Full Model)

-	Positive	Negative
Positive	890	112
Negative	77	823

Positive class: lncRNA,
Negative class: other RNA

Table A5. Classification Report for Species Agnostic Light Weight Model)

-	Precision	Recall	F1-Score
Coding	0.91	0.89	0.90
Noncoding	0.88	0.91	0.89
accuracy			0.89
macro avg	0.89	0.90	0.89
weighted avg	0.90	0.89	0.89

Table A6. Confusion Matrix for Species Agnostic Light Weight Model)

-	Positive	Negative
Positive	887	115
Negative	85	815

Positive class: lncRNA,
Negative class: other RNA

Table A7. Classification Report for Species Agnostic Full Model)

-	Precision	Recall	F1-Score
Coding	0.91	0.88	0.89
Noncoding	0.87	0.90	0.89
accuracy			0.89
macro avg	0.89	0.89	0.89
weighted avg	0.90	0.89	0.89

Table A8. Confusion Matrix for Species Agnostic Full Model)

-	Positive	Negative
Positive	887	115
Negative	85	815

Positive class: lncRNA,
Negative class: other RNA

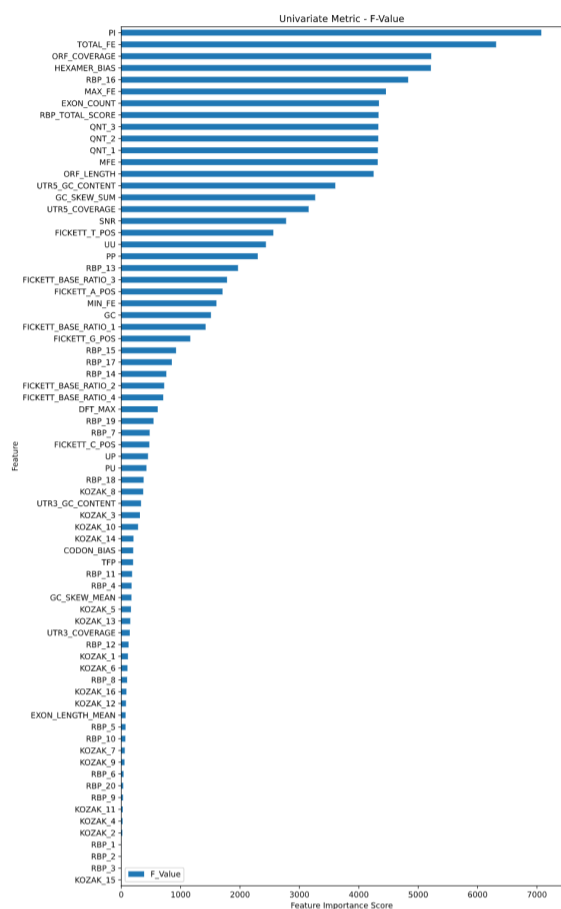


Fig. A1. Feature importance measures using F-Value.

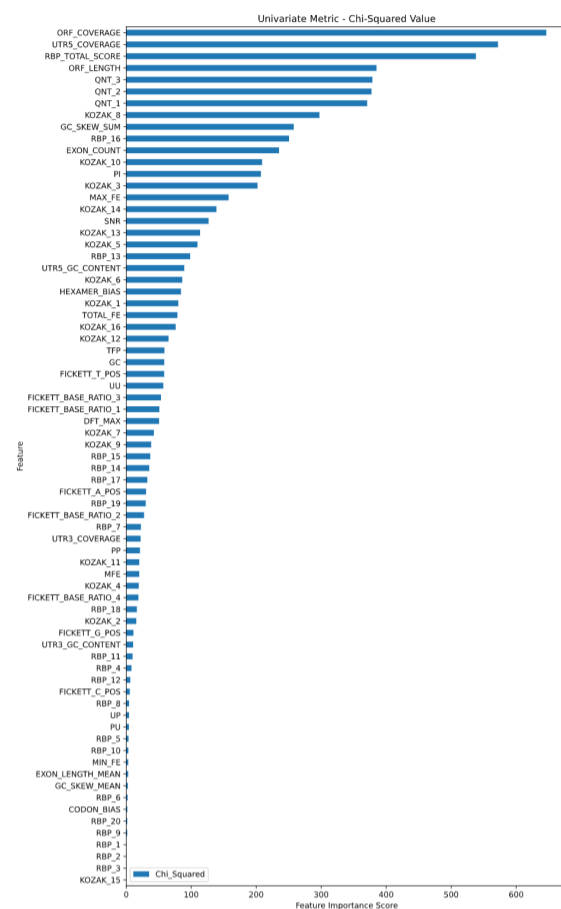


Fig. A2. Feature importance measures using Chi-Squared.

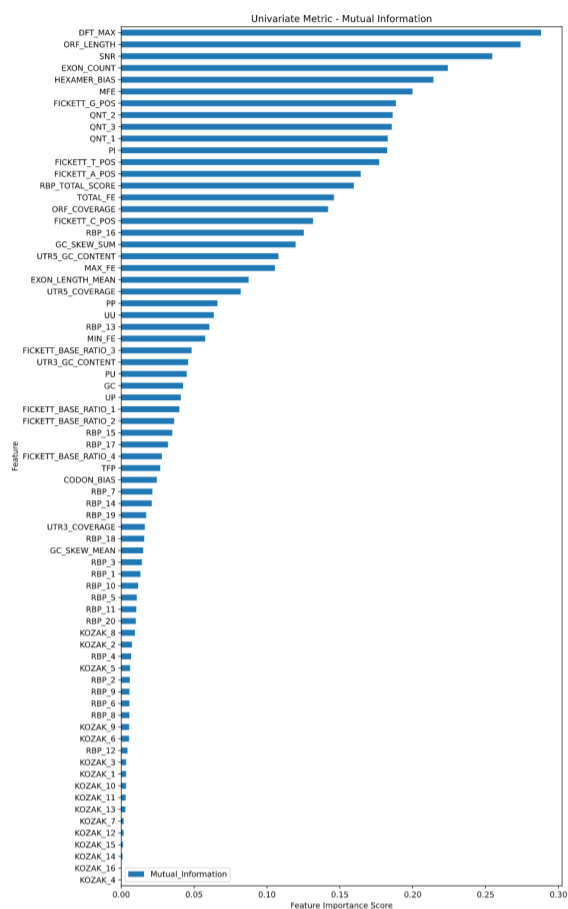


Fig. A3. Feature importance measures using Mutual Information.

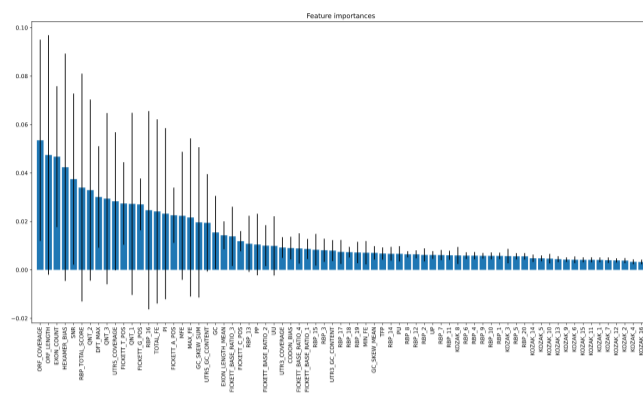


Fig. A4. Feature importance measures using tree based models.