# Supplementary materials

- **Figure S1** Context scoring matrix measures the similarity of Kozak sequence (human)
- Figure S2 Distribution of all feature scores in human
- Figure S3 Distribution of all feature scores in mouse
- Figure S4 Correlations (r) of features indicates redundant features in mouse
- **Figure S5** Feature selection by using  $\mathcal{L}1$ -logistic regression in mouse
- **Figure S6** Training *L*1-logistic regression model on the dataset of **a** ribo-lncRNAs and mRNAs; **b** noribo-lncRNAs and mRNAs in human
- **Figure S7** Training *L*1-logistic regression model on the dataset of **a** ribo-lncRNAs and mRNAs; **b** noribo-lncRNAs and mRNAs in mouse
- **Table S1.** Sequence features were considered to influence the ribosomal association
- **Table S2.** Low-redundant features in human and mouse



**Figure S1** Context scoring matrix measures the similarity of Kozak sequence (human). We calculated the context scoring matrix from 5,000 CDSs (see "Method"). This indicates a Kozak sequence motif (gcc[a/g]ccATGg) surrounding the start codon.





**Figure S2** Distribution of all feature scores in human. Each feature was ranked by -log(KS p-value), in which KS represents two samples Kolmogorov-Smirnov test between ribo-lncRNAs (red) and noribo-lncRNAs (blue).



Figure S2 Distribution of all feature scores in human (continued).



**Figure S3** Distribution of all feature scores in mouse. Each feature was ranked by -log(KS p-value), in which KS represents two samples Kolmogorov-Smirnov test between ribo-IncRNAs (red) and noribo-IncRNAs (blue).





Figure S3 Distribution of all feature scores in mouse (continued).



**Figure S4** Correlations (r) of features indicates redundant features in mouse. **a** Correlations of all extracted features shows that features of several sub-regions are highly correlated (redundant). **b** After removing high redundant (|r| > 0.8) features, we obtained a low redundant feature set for further analysis in this study.



**Figure S5** Feature selection by using  $\pounds$ 1-logistic regression in mouse. Total data was separated into 80% for training the model and 20% for the calculation of accuracy (blue dashed line, left y-axis). On the x-axis, C indicates the inverse of regularization strength. As C is increased, the number of features with non-zero coefficients (right y-axis) is increased and the model becomes more complicated. The black dashed line shows the final model chosen in this study, and outputs 9 features with non-zero coefficients. These features were ranked by the absolute value of coefficient, which represents the importance for prediction, and shown in the upper left.



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**Figure S6** Training  $\bot$ 1-logistic regression model on the dataset of **a** ribo-lncRNAs and mRNAs; **b** noribo-lncRNAs and mRNAs in human.





**Figure S7** Training  $\perp$ 1-logistic regression model on the dataset of **a** ribo-lncRNAs and mRNAs; **b** noribo-lncRNAs and mRNAs in mouse.

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No.	Feature	Description		
Basic				
1	fLen	$Log_{10}(length+1)$ of the mature IncRNA		
2	gc	G+C content of the mature IncRNA		
RNA sj	plicing			
3	nE	Number of exons		
4	fELen	$Log_{10}(length+1)$ of the first exon		
5	minELen	Log <sub>10</sub> (length+1) of the shortest exon		
6	maxELen	$Log_{10}(length+1)$ of the longest exon		
7	avgELen	$Log_{10}(averaged\_length+1)$ of exons		
8	fEgc	G+C content of the first exon		
9	minEgc	G+C content of the shortest exon		
10	ma×Egc	G+C content of the longest exon		
11	avgEgc	Averaged G+C content of exons		
12	flLen	$Log_{10}(length+1)$ of the first intron		
13	minILen	$Log_{10}(length+1)$ of the shortest intron		
14	maxILen	$Log_{10}(length+1)$ of the longest intron		
15	avglLen	$Log_{10}(averaged\_length+1)$ of introns		
16	flgc	G+C content of the first intron		
17	minlgc	G+C content of the shortest intron		
18	maxlgc	G+C content of the longest intron		
19	avglgc	Averaged G+C content of introns		

## Table S1. Sequence features were considered to influence the ribosomal association.

20-22	p/f/uOrfLen	$Log_{10}(length + 1)$ of ORF
23-25	p/f/uOrfCov	Percentage of ORF length compared to that of IncRNA
26-28	p/f/uOrf5utrLen	$Log_{10}(length+1)$ of the upstream region of ORF (5' UTR)
29-31	p/f/uOrf5utrCov	Percentage of the 5 $^\prime$ UTR length compared to that of IncRNA
32-34	p/f/uOrf3utrLen	$Log_{10}(length+1)$ of the downstream region of ORF (3' UTR)
35-37	p/f/uOrf3utrCov	Percentage of the 3' UTR length compared to that of IncRNA

#### K-mer frequency

38-40	p/f/uOrfStartContext	Context sore of ORF start
41-43	p/f/uOrfSeqTrimer	Trimer score of ORF

# Table S1. Sequence features (continued).

44-46         p/f/uOrfSeqHexamer         Hexamer score of ORF           RNA secondary structure           47-49         p/f/uOrfSp         Averaged RNA stem probability of ORF           50-52         p/f/uOrfSutSp         Averaged RNA stem probability of 5' UTR           53-55         p/f/uOrfSutSpFC         Ratio of RNA stem probability of 3' UTR to that of ORF           56-58         p/f/uOrfJutSpFC         Ratio of RNA stem probability of 3' UTR to that of ORF           62         g4NearTIS_log         Log10(minimum distance) from G4 to transcription initiation           63         g4NearTIS_log         Log10(minimum distance) from G4 to ORF start           67-69         g4Near(p/f/u)ORFstart.log         Log10(minimum distance) from G4 to ORF end           70         g4Near(p/f/u)ORFstart.%         Minimum distance from G4 to TIS divided by length of IncRNA           71         g4Near(p/f/u)ORFstart.%         Minimum distance from G4 to ORF start divided by length of IncRNA           72-77         g4Near(p/f/u)ORFstart.%         Minimum distance from G4 to CRF end divided by length of IncRNA           75-77         g4Near(p/f/u)ORFstart.gg         Log10(minimum distance) from m <sup>6</sup> A to transcription initiation           79         m6aNearTIS_log         Log10(minimum distance) from m <sup>6</sup> A to ORF start           82-85         m6aNearTIS_log         Log10(minimum distance) from m <sup>6</sup> A t	No.	Feature	Description			
RNA secondary structure         47.49       p/f/uOrf5p       Averaged RNA stem probability of ORF         50-52       p/f/uOrf5utr5p       Averaged RNA stem probability of 5' UTR         53-55       p/f/uOrf5utr5p       Averaged RNA stem probability of 5' UTR         55-56       p/f/uOrf3utr5pFC       Ratio of RNA stem probability of 3' UTR         59-61       p/f/uOrf3utr5pFC       Ratio of RNA stem probability of 3' UTR         59-61       p/f/uOrf3utr5pFC       Ratio of RNA stem probability of 3' UTR         62       g4NearTIS_log       Log10(minimum distance) from G4 to transcription initiation         63       g4NearTIS_log       Log10(minimum distance) from G4 to ORF start         67-69       g4NearTIS_%       Minimum distance from G4 to TIS divided by length of IncRNA         71       g4NearTIS_%       Minimum distance from G4 to ORF start divided by length of IncRNA         72-74       g4Near(p/f/u)ORFstart_%       Minimum distance from G4 to ORF end divided by length of IncRNA         75-77       g4Near(p/f/u)ORFstart_g       Log10(minimum distance) from m <sup>6</sup> A to transcription initiation         79       m6aNear(p/f/u)ORFstart_g       Log10(minimum distance) from m <sup>6</sup> A to CRF start         83-85       m6aNear(p/f/u)ORFstart_g       Log10(minimum distance) from m <sup>6</sup> A to ORF start         83-85       m6aNear(p/f/u)ORFstart_g	44-46	p/f/uOrfSeqHexamer	Hexamer score of ORF			
47-49       p/fuOrfSp       Averaged RNA stem probability of ORF         50-52       p/fuOrfSutrSp       Averaged RNA stem probability of 5' UTR         53-55       p/fuOrfSutrSpFC       Ratio of RNA stem probability of 5' UTR         56-58       p/fuOrfSutrSpFC       Ratio of RNA stem probability of 3' UTR         59-61       p/fuOrfSutrSpFC       Ratio of RNA stem probability of 3' UTR         59-61       p/fuOrfSutrSp       Averaged RNA stem probability of 3' UTR         62       g4NearTIS_log       Log10(minimum distance) from G4 to transcription initiation         63       g4NearTIS_log       Log10(minimum distance) from G4 to ORF statt         67-69       g4Near(p/fu)ORFstart_log       Log10(minimum distance) from G4 to ORF end         70       g4Near(p/fu)ORFstart_%       Minimum distance from G4 to TIS divided by length of IncRNA         71       g4Near(p/fu)ORFstart_%       Minimum distance from G4 to ORF end         72-74       g4Near(p/fu)ORFstart_%       Minimum distance from G4 to TARScription initiation         79       m6aNearTIS_log       Log10(minimum distance) from m <sup>6</sup> A to transcription termination         80-82       m6aNearTIS_log       Log10(minimum distance) from m <sup>6</sup> A to TARScription termination         80-82       m6aNearTIS_M       Minimum distance from m <sup>6</sup> A to ORF end         81       m6aNearTIS_M	RNA se	RNA secondary structure				
50-52       p/f/uOrfSutrSp       Averaged RNA stem probability of 5' UTR         53-55       p/f/uOrfSutrSpFC       Ratio of RNA stem probability of 5' UTR         56-58       p/f/uOrfSutrSpFC       Ratio of RNA stem probability of 3' UTR         59-61       p/f/uOrfSutrSpFC       Ratio of RNA stem probability of 3' UTR         59-61       p/f/uOrfSutrSpFC       Ratio of RNA stem probability of 3' UTR         62       g4NearTIS_log       Log10(minimum distance) from G4 to transcription initiation         63       g4NearTIS_log       Log10(minimum distance) from G4 to transcription termination         64-66       g4Near(p/f/u)ORFstart_log       Log10(minimum distance) from G4 to ORF start         67-69       g4Near(p/f/u)ORFstart_log       Log10(minimum distance) from G4 to ORF start         71       g4Near(p/f/u)ORFstart_%       Minimum distance from G4 to TIS divided by length of IncRNA         72       rd4Near(p/f/u)ORFstart_%       Minimum distance from G4 to ORF start divided by length of IncRNA         75-77       g4Near(p/f/u)ORFstart_%       Minimum distance) from m <sup>6</sup> A to CRF start         80-82       m6aNearTIS_log       Log10(minimum distance) from m <sup>6</sup> A to ORF start         83-85       m6aNearTIS_M       Minimum distance from m <sup>6</sup> A to ORF start         83-85       m6aNearTIS_M       Minimum distance from m <sup>6</sup> A to ORF start <t< th=""><th>47-49</th><th>p/f/uOrfSp</th><th>Averaged RNA stem probability of ORF</th></t<>	47-49	p/f/uOrfSp	Averaged RNA stem probability of ORF			
53-55       p/f/uOrf5utrSpFC       Ratio of RNA stem probability of 5'UTR to that of ORF         56-58       p/f/uOrf3utrSp       Averaged RNA stem probability of 3'UTR         59-61       p/f/uOrf3utrSpFC       Ratio of RNA stem probability of 3'UTR to that of ORF         62       g4NearTIS_log       Log10(minimum distance) from G4 to transcription initiation         63       g4NearTIS_log       Log10(minimum distance) from G4 to transcription termination         64-66       g4Near(p/f/u)ORFstart_log       Log10(minimum distance) from G4 to ORF start         67-69       g4Near(p/f/u)ORFstart_log       Log10(minimum distance) from G4 to ORF start         70       g4NearTIS_%       Minimum distance from G4 to TIS divided by length of IncRNA         71       g4Near(p/f/u)ORFstart_%       Minimum distance from G4 to ORF start divided by length of IncRNA         72-74       g4Near(p/f/u)ORFstart_%       Minimum distance) from m <sup>6</sup> A to transcription initiation         78       m6aNearTIS_log       Log10(minimum distance) from m <sup>6</sup> A to transcription initiation         79       m6aNearTIS_log       Log10(minimum distance) from m <sup>6</sup> A to TRA to transcription initiation         80-80       m6aNearTIS_%       Minimum distance) from m <sup>6</sup> A to TRA to transcription initiation         79       m6aNearTIS_log       Log10(minimum distance) from m <sup>6</sup> A to TRA to transcription initiation         8	50-52	p/f/uOrf5utrSp	Averaged RNA stem probability of 5 $'$ UTR			
56-58       p/f/uOrf3utrSp       Averaged RNA stem probability of 3' UTR         59-61       p/f/uOrf3utrSpFC       Ratio of RNA stem probability of 3' UTR to that of ORF         62       g4NearTIS_log       Log10 (minimum distance) from G4 to transcription initiation         63       g4NearTIS_log       Log10 (minimum distance) from G4 to transcription termination         64-66       g4Near(p/f/u)ORFstart_log       Log10 (minimum distance) from G4 to ORF start         67-69       g4Near(p/f/u)ORFend_log       Log10 (minimum distance) from G4 to ORF end         70       g4NearTIS_%       Minimum distance from G4 to TIS divided by length of IncRNA         71       g4Near(p/f/u)ORFstart_%       Minimum distance from G4 to ORF end         72-74       g4Near(p/f/u)ORFstart_%       Minimum distance from G4 to ORF end divided by length of IncRNA         75-77       g4Near(p/f/u)ORFstart_%       Minimum distance) from m <sup>6</sup> A to transcription initiation         78       m6aNearTIS_log       Log10 (minimum distance) from m <sup>6</sup> A to transcription initiation         79       m6aNearTIS_log       Log10 (minimum distance) from m <sup>6</sup> A to transcription initiation         80-82       m6aNear(p/f/u)ORFstart_0g       Log10 (minimum distance) from m <sup>6</sup> A to TIS divided by length of IncRNA         81-85       m6aNear(D/f/u)ORFstart_0g       Log10 (minimum distance) from m <sup>6</sup> A to TIS divided by length of IncRNA	53-55	p/f/uOrf5utrSpFC	Ratio of RNA stem probability of $5'$ UTR to that of ORF			
59-61       p/f/uOrf3utrSpFC       Ratio of RNA stem probability of 3'UTR to that of ORF         62       g4NearTIS_log       Log10 (minimum distance) from G4 to transcription initiation         63       g4NearTTS_log       Log10 (minimum distance) from G4 to transcription termination         64-66       g4Near(p/f/u)ORFstart_log       Log10 (minimum distance) from G4 to ORF start         67-69       g4Near(p/f/u)ORFend_log       Log10 (minimum distance) from G4 to ORF end         70       g4NearTIS_%       Minimum distance from G4 to TIS divided by length of IncRNA         71       g4NearTIS_%       Minimum distance from G4 to TIS divided by length of IncRNA         72-74       g4Near(p/f/u)ORFstart_%       Minimum distance from G4 to ORF end         75-77       g4Near(p/f/u)ORFend_%       Minimum distance from G4 to ORF end divided by length of IncRNA         78       m6aNearTIS_log       Log10 (minimum distance) from m <sup>6</sup> A to transcription initiation         79       m6aNearTIS_log       Log10 (minimum distance) from m <sup>6</sup> A to ORF start         83-85       m6aNear(p/f/u)ORFend_log       Log10 (minimum distance) from m <sup>6</sup> A to ORF end         86       m6aNearTIS_%       Minimum distance from m <sup>6</sup> A to TIS divided by length of IncRNA         87       m6aNearTIS_%       Minimum distance from m <sup>6</sup> A to TIS divided by length of IncRNA         88       m6aNearTIS_%	56-58	p/f/uOrf3utrSp	Averaged RNA stem probability of 3 $'$ UTR			
62       g4NearTIS_log       Log10 (minimum distance) from G4 to transcription initiation         63       g4NearTTS_log       Log10 (minimum distance) from G4 to transcription termination         64-66       g4Near(p/f/u)ORFstart_log       Log10 (minimum distance) from G4 to ORF start         67-69       g4Near(p/f/u)ORFend_log       Log10 (minimum distance) from G4 to ORF end         70       g4NearTIS_%       Minimum distance from G4 to TIS divided by length of IncRNA         71       g4NearTIS_%       Minimum distance from G4 to ORF start divided by length of IncRNA         72-74       g4Near(p/f/u)ORFstart_%       Minimum distance from G4 to ORF end divided by length of IncRNA         75-77       g4Near(p/f/u)ORFend_%       Minimum distance) from m <sup>6</sup> A to transcription initiation         79       m6aNearTIS_log       Log10 (minimum distance) from m <sup>6</sup> A to transcription initiation         79       m6aNearTIS_log       Log10 (minimum distance) from m <sup>6</sup> A to Tanscription initiation         80-82       m6aNear[p/f/u)ORFstart_log       Log10 (minimum distance) from m <sup>6</sup> A to ORF start         83-85       m6aNearTIS_%       Minimum distance from m <sup>6</sup> A to TIS divided by length of IncRNA         87       m6aNearTIS_%       Minimum distance from m <sup>6</sup> A to ORF start         88-90       m6aNearTIS_%       Minimum distance from m <sup>6</sup> A to ORF start divided by length of IncRNA         88-	59-61	p/f/uOrf3utrSpFC	Ratio of RNA stem probability of $3'$ UTR to that of ORF			
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67-69       g4Near(p/f/u)ORFend.log       Log10 (minimum distance) from G4 to ORF end         70       g4NearTIS_%       Minimum distance from G4 to TIS divided by length of IncRNA         71       g4NearTTS_%       Minimum distance from G4 to ORF start divided by length of IncRNA         72-74       g4Near(p/f/u)ORFstart_%       Minimum distance from G4 to ORF start divided by length of IncRNA         75-77       g4Near(p/f/u)ORFend_%       Minimum distance from G4 to ORF end divided by length of IncRNA         RNA modification         78       m6aNearTTS_log       Log10 (minimum distance) from m <sup>6</sup> A to transcription initiation         79       m6aNearTTS_log       Log10 (minimum distance) from m <sup>6</sup> A to ORF start         83-85       m6aNear(p/f/u)ORFstart_log       Log10 (minimum distance) from m <sup>6</sup> A to ORF end         86       m6aNearTIS_%       Minimum distance from m <sup>6</sup> A to TIS divided by length of IncRNA         87       m6aNearTIS_%       Minimum distance from m <sup>6</sup> A to TIS divided by length of IncRNA         87       m6aNearTIS_%       Minimum distance from m <sup>6</sup> A to ORF end         88-90       m6aNear(p/f/u)ORFstart_%       Minimum distance from m <sup>6</sup> A to ORF end divided by length of IncRNA         91-93       m6aNear(p/f/u)ORFstart_%       Minimum distance from m <sup>6</sup> A to ORF end divided by length of IncRNA         91-93       m6aNear(p/f/u)ORFend_%       Minim	64-66	g4Near(p/f/u)ORFstart_log	$Log_{10}$ (minimum distance) from G4 to ORF start			
70g4NearTIS_%Minimum distance from G4 to TIS divided by length of IncRNA71g4NearTTS_%Minimum distance from G4 to TTS divided by length of IncRNA72-74g4Near(p/f/u)ORFstart_%Minimum distance from G4 to ORF start divided by length of IncRNA75-77g4Near(p/f/u)ORFend_%Minimum distance from G4 to ORF end divided by length of IncRNARNA modification78m6aNearTIS_logLog10(minimum distance) from m <sup>6</sup> A to transcription initiation79m6aNearTIS_logLog10(minimum distance) from m <sup>6</sup> A to ORF start80-82m6aNear(p/f/u)ORFstart_logLog10(minimum distance) from m <sup>6</sup> A to ORF start83-85m6aNear(p/f/u)ORFend_logLog10(minimum distance) from m <sup>6</sup> A to ORF end86m6aNearTIS_%Minimum distance from m <sup>6</sup> A to TIS divided by length of IncRNA87m6aNearTIS_%Minimum distance from m <sup>6</sup> A to ORF start80m6aNear(p/f/u)ORFstart_logLog10(minimum distance from m <sup>6</sup> A to ORF end86m6aNearTIS_%Minimum distance from m <sup>6</sup> A to ORF start divided by length of IncRNA87m6aNearTIS_%Minimum distance from m <sup>6</sup> A to ORF start divided by length of IncRNA88-90m6aNear(p/f/u)ORFstart_%Minimum distance from m <sup>6</sup> A to ORF start divided by length of IncRNA91-93m6aNear(p/f/u)ORFend_%Minimum distance from m <sup>6</sup> A to ORF end divided by length of IncRNA91-93m6aNear(p/f/u)ORFstart_%Minimum distance from m <sup>6</sup> A to ORF end divided by length of IncRNA91SINEContaining DNA transposon or not95LINEContaining SINE element or not	67-69	g4Near(p/f/u)ORFend_log	$Log_{10}$ (minimum distance) from G4 to ORF end			
71g4NearTTS_%Minimum distance from G4 to TTS divided by length of lncRNA72-74g4Near(p/f/u)ORFstart_%Minimum distance from G4 to ORF start divided by length of lncRNA75-77g4Near(p/f/u)ORFend_%Minimum distance from G4 to ORF end divided by length of lncRNARNA modification78m6aNearTIS_logLog10(minimum distance) from m <sup>6</sup> A to transcription initiation79m6aNearTIS_logLog10(minimum distance) from m <sup>6</sup> A to transcription termination80-82m6aNear(p/f/u)ORFstart_logLog10(minimum distance) from m <sup>6</sup> A to ORF start83-85m6aNear(p/f/u)ORFstart_logLog10(minimum distance) from m <sup>6</sup> A to ORF end86m6aNearTIS_%Minimum distance from m <sup>6</sup> A to TIS divided by length of lncRNA87m6aNearTTS_%Minimum distance from m <sup>6</sup> A to ORF start divided by length of lncRNA88-90m6aNear(p/f/u)ORFstart_%Minimum distance from m <sup>6</sup> A to ORF start divided by length of lncRNA91-93m6aNear(p/f/u)ORFstart_%Minimum distance from m <sup>6</sup> A to ORF start divided by length of lncRNA92DNAContaining DNA transposon or not95LINEContaining LINE element or not96LTRContaining SINE element or not97SINEContaining Retroposon element or not98RetroposonContaining Satellite element or not99SatelliteContaining Satellite element or not	70	g4NearTIS_%	Minimum distance from G4 to TIS divided by length of IncRNA			
72-74       g4Near(p/f/u)ORFstart.%       Minimum distance from G4 to ORF start divided by length of IncRNA         75-77       g4Near(p/f/u)ORFend.%       Minimum distance from G4 to ORF end divided by length of IncRNA         RNA modification         78       m6aNearTIS_log       Log10(minimum distance) from m <sup>6</sup> A to transcription initiation         79       m6aNearTTS_log       Log10(minimum distance) from m <sup>6</sup> A to transcription termination         80-82       m6aNear(p/f/u)ORFstart_log       Log10(minimum distance) from m <sup>6</sup> A to ORF start         83-85       m6aNear(p/f/u)ORFstart_log       Log10(minimum distance) from m <sup>6</sup> A to ORF end         86       m6aNearTIS_%       Minimum distance from m <sup>6</sup> A to TIS divided by length of IncRNA         87       m6aNearTIS_%       Minimum distance from m <sup>6</sup> A to ORF start divided by length of IncRNA         88-90       m6aNear(p/f/u)ORFstart_%       Minimum distance from m <sup>6</sup> A to ORF end divided by length of IncRNA         91-93       m6aNear(p/f/u)ORFend_%       Minimum distance from m <sup>6</sup> A to ORF end divided by length of IncRNA         91-93       m6aNear(p/f/u)ORFend_%       Minimum distance from m <sup>6</sup> A to ORF end divided by length of IncRNA         94       DNA       Containing DNA transposon or not       10c         95       LINE       Containing LINE element or not       10c         96       LTR       C	71	g4NearTTS_%	Minimum distance from G4 to TTS divided by length of IncRNA			
75-77       g4Near(p/f/u)ORFend_%       Minimum distance from G4 to ORF end divided by length of IncRNA         RNA modification       Image: Containing DNA transposed or provided or pro	72-74	g4Near(p/f/u)ORFstart_%	Minimum distance from G4 to ORF start divided by length of IncRNA			
RNA modification78m6aNearTIS_logLog10 (minimum distance) from m <sup>6</sup> A to transcription initiation79m6aNearTTS_logLog10 (minimum distance) from m <sup>6</sup> A to transcription termination80-82m6aNear(p/f/u)ORFstart_logLog10 (minimum distance) from m <sup>6</sup> A to ORF start83-85m6aNear(p/f/u)ORFend_logLog10 (minimum distance) from m <sup>6</sup> A to ORF end86m6aNearTIS_%Minimum distance from m <sup>6</sup> A to TIS divided by length of IncRNA87m6aNearTTS_%Minimum distance from m <sup>6</sup> A to ORF start divided by length of IncRNA88-90m6aNear(p/f/u)ORFstart_%Minimum distance from m <sup>6</sup> A to ORF end divided by length of IncRNA91-93m6aNear(p/f/u)ORFend_%Minimum distance from m <sup>6</sup> A to ORF end divided by length of IncRNA91-93m6aNear(p/f/u)ORFend_%Minimum distance from m <sup>6</sup> A to ORF end divided by length of IncRNA94DNAContaining DNA transposon or not95LINEContaining LINE element or not96LTRContaining SINE element or not97SINEContaining Retroposon element or not98RetroposonContaining Retroposon element or not99SatelliteContaining Satellite element or not	75-77	g4Near(p/f/u)ORFend_%	Minimum distance from G4 to ORF end divided by length of IncRNA			
78       m6aNearTIS_log       Log10 (minimum distance) from m <sup>6</sup> A to transcription initiation         79       m6aNearTTS_log       Log10 (minimum distance) from m <sup>6</sup> A to transcription termination         80-82       m6aNear(p/f/u)ORFstart_log       Log10 (minimum distance) from m <sup>6</sup> A to ORF start         83-85       m6aNear(p/f/u)ORFend_log       Log10 (minimum distance) from m <sup>6</sup> A to ORF end         86       m6aNearTIS_%       Minimum distance from m <sup>6</sup> A to TIS divided by length of IncRNA         87       m6aNearTTS_%       Minimum distance from m <sup>6</sup> A to TTS divided by length of IncRNA         88-90       m6aNear(p/f/u)ORFstart_%       Minimum distance from m <sup>6</sup> A to ORF start divided by length of IncRNA         91-93       m6aNear(p/f/u)ORFend_%       Minimum distance from m <sup>6</sup> A to ORF end divided by length of IncRNA         91-93       m6aNear(p/f/u)ORFend_%       Minimum distance from m <sup>6</sup> A to ORF end divided by length of IncRNA         91-93       m6aNear(p/f/u)ORFend_%       Minimum distance from m <sup>6</sup> A to ORF end divided by length of IncRNA         94       DNA       Containing DNA transposon or not       05         95       LINE       Containing LINE element or not       07         96       LTR       Containing SINE element or not       07         97       SINE       Containing Retroposon element or not       08         98	RNA m	odification				
79m6aNearTTS_logLog10 (minimum distance) from m6A to transcription termination80-82m6aNear(p/f/u)ORFstart_logLog10 (minimum distance) from m6A to ORF start83-85m6aNear(p/f/u)ORFend_logLog10 (minimum distance) from m6A to ORF end86m6aNearTIS_%Minimum distance from m6A to TIS divided by length of IncRNA87m6aNearTTS_%Minimum distance from m6A to ORF start divided by length of IncRNA88-90m6aNear(p/f/u)ORFstart_%Minimum distance from m6A to ORF start divided by length of IncRNA91-93m6aNear(p/f/u)ORFend_%Minimum distance from m6A to ORF end divided by length of IncRNA91-93m6aNear(p/f/u)ORFend_%Minimum distance from m6A to ORF end divided by length of IncRNA91-93m6aNear(p/f/u)ORFend_%Minimum distance from m6A to ORF end divided by length of IncRNA91-93m6aNear(p/f/u)ORFend_%Minimum distance from m6A to ORF end divided by length of IncRNA91-93m6aNear(p/f/u)ORFend_%Minimum distance from m6A to ORF end divided by length of IncRNA91-93m6aNear(p/f/u)ORFend_%Minimum distance from m6A to ORF end divided by length of IncRNA91-93m6aNear(p/f/u)ORFend_%Minimum distance from m6A to ORF end divided by length of IncRNA91-93m6aNear(p/f/u)ORFend_%Minimum distance from m6A to ORF end divided by length of IncRNA91-93m6aNear(p/f/u)ORFend_%Containing DNA transposon or not95LINEContaining LINE element or not96LTRContaining SINE element or not97SINEContaining Retroposon element or not98 <th>78</th> <td>m6aNearTIS_log</td> <td><math>Log_{10}</math> (minimum distance) from m<sup>6</sup>A to transcription initiation</td>	78	m6aNearTIS_log	$Log_{10}$ (minimum distance) from m <sup>6</sup> A to transcription initiation			
80-82m6aNear(p/f/u)ORFstart_logLog10 (minimum distance) from m6 A to ORF start83-85m6aNear(p/f/u)ORFend_logLog10 (minimum distance) from m6 A to ORF end86m6aNearTIS_%Minimum distance from m6 A to TIS divided by length of lncRNA87m6aNearTTS_%Minimum distance from m6 A to TTS divided by length of lncRNA88-90m6aNear(p/f/u)ORFstart_%Minimum distance from m6 A to ORF start divided by length of lncRNA91-93m6aNear(p/f/u)ORFstart_%Minimum distance from m6 A to ORF start divided by length of lncRNA91-93m6aNear(p/f/u)ORFend_%Minimum distance from m6 A to ORF end divided by length of lncRNA91-93m6aNear(p/f/u)ORFend_%Minimum distance from m6 A to ORF end divided by length of lncRNA91-93m6aNear(p/f/u)ORFend_%Minimum distance from m6 A to ORF end divided by length of lncRNA91-93m6aNear(p/f/u)ORFend_%Minimum distance from m6 A to ORF end divided by length of lncRNA91-93m6aNear(p/f/u)ORFend_%Minimum distance from m6 A to ORF end divided by length of lncRNA91-93m6aNear(p/f/u)ORFend_%Minimum distance from m6 A to ORF end divided by length of lncRNA94DNAContaining DNA transposon or not95LINEContaining LINE element or not96LTRContaining SINE element or not97SINEContaining Retroposon element or not98RetroposonContaining Satellite element or not99SatelliteContaining Satellite element or not	79	m6aNearTTS_log	$Log_{10}$ (minimum distance) from m <sup>6</sup> A to transcription termination			
83-85m6aNear(p/f/u)ORFend_logLog10 (minimum distance) from m6A to ORF end86m6aNearTIS_%Minimum distance from m6A to TIS divided by length of IncRNA87m6aNearTTS_%Minimum distance from m6A to TTS divided by length of IncRNA88-90m6aNear(p/f/u)ORFstart_%Minimum distance from m6A to ORF start divided by length of IncRNA91-93m6aNear(p/f/u)ORFend_%Minimum distance from m6A to ORF end divided by length of IncRNAMinimum distance from m6A to ORF end divided by length of IncRNA91-93m6aNear(p/f/u)ORFend_%Minimum distance from m6A to ORF end divided by length of IncRNAMinimum distance from m6A to ORF end divided by length of IncRNA91-93m6aNear(p/f/u)ORFend_%Minimum distance from m6A to ORF end divided by length of IncRNAMinimum distance from m6A to ORF end divided by length of IncRNA91-93m6aNear(p/f/u)ORFend_%Minimum distance from m6A to ORF end divided by length of IncRNAMinimum distance from m6A to ORF end divided by length of IncRNAMinimum distance from m6A to ORF end divided by length of IncRNAMinimum distance from m6A to ORF end divided by length of IncRNAMinimum distance from m6A to ORF end divided by length of IncRNAORF end_information of ORF end_information of IncRNA94DNAContaining DNA transposon or not95LINEContaining LINE element or not96LTRContaining SINE element or not98RetroposonContaining Retroposon element or not99Satellite </th <th>80-82</th> <th>m6aNear(p/f/u)ORFstart_log</th> <th><math>Log_{10}</math>(minimum distance) from m<sup>6</sup>A to ORF start</th>	80-82	m6aNear(p/f/u)ORFstart_log	$Log_{10}$ (minimum distance) from m <sup>6</sup> A to ORF start			
86m6aNearTIS_%Minimum distance from m6A to TIS divided by length of IncRNA87m6aNearTTS_%Minimum distance from m6A to TTS divided by length of IncRNA88-90m6aNear(p/f/u)ORFstart_%Minimum distance from m6A to ORF start divided by length of IncRNA91-93m6aNear(p/f/u)ORFend_%Minimum distance from m6A to ORF end divided by length of IncRNARepeat element94DNAContaining DNA transposon or not95LINEContaining LINE element or not96LTRContaining SINE element or not97SINEContaining Retroposon element or not98RetroposonContaining Retroposon element or not99SatelliteContaining Satellite element or not	83-85	m6aNear(p/f/u)ORFend_log	$Log_{10}$ (minimum distance) from m <sup>6</sup> A to ORF end			
87m6aNearTTS_%Minimum distance from m <sup>6</sup> A to TTS divided by length of IncRNA88-90m6aNear(p/f/u)ORFstart_%Minimum distance from m <sup>6</sup> A to ORF start divided by length of IncRNA91-93m6aNear(p/f/u)ORFend_%Minimum distance from m <sup>6</sup> A to ORF end divided by length of IncRNARepeat element94DNAContaining DNA transposon or not95LINEContaining LINE element or not96LTRContaining SINE element or not97SINEContaining SINE element or not98RetroposonContaining Retroposon element or not99SatelliteContaining Satellite element or not	86	m6aNearTIS₋%	Minimum distance from $m^6A$ to TIS divided by length of IncRNA			
88-90m6aNear(p/f/u)ORFstart_%Minimum distance from m6A to ORF start divided by length of IncRNA91-93m6aNear(p/f/u)ORFend_%Minimum distance from m6A to ORF end divided by length of IncRNARepeat element94DNAContaining DNA transposon or not95LINEContaining LINE element or not96LTRContaining LTR element or not97SINEContaining SINE element or not98RetroposonContaining Retroposon element or not99SatelliteContaining Satellite element or not	87	m6aNearTTS_%	Minimum distance from $m^6A$ to TTS divided by length of IncRNA			
91-93m6aNear(p/f/u)ORFend_%Minimum distance from m <sup>6</sup> A to ORF end divided by length of IncRNARepeat element94DNAContaining DNA transposon or not95LINEContaining LINE element or not96LTRContaining LTR element or not97SINEContaining SINE element or not98RetroposonContaining Retroposon element or not99SatelliteContaining Satellite element or not	88-90	m6aNear(p/f/u)ORFstart_%	Minimum distance from $m^6A$ to ORF start divided by length of IncRNA			
Repeat element94DNAContaining DNA transposon or not95LINEContaining LINE element or not96LTRContaining LTR element or not97SINEContaining SINE element or not98RetroposonContaining Retroposon element or not99SatelliteContaining Satellite element or not	91-93	m6aNear(p/f/u)ORFend_%	Minimum distance from m <sup>6</sup> A to ORF end divided by length of lncRNA			
94DNAContaining DNA transposon or not95LINEContaining LINE element or not96LTRContaining LTR element or not97SINEContaining SINE element or not98RetroposonContaining Retroposon element or not99SatelliteContaining Satellite element or not	Repeat	Repeat element				
95LINEContaining LINE element or not96LTRContaining LTR element or not97SINEContaining SINE element or not98RetroposonContaining Retroposon element or not99SatelliteContaining Satellite element or not	94	DNA	Containing DNA transposon or not			
96LTRContaining LTR element or not97SINEContaining SINE element or not98RetroposonContaining Retroposon element or not99SatelliteContaining Satellite element or not	95	LINE	Containing LINE element or not			
97SINEContaining SINE element or not98RetroposonContaining Retroposon element or not99SatelliteContaining Satellite element or not	96	LTR	Containing LTR element or not			
98RetroposonContaining Retroposon element or not99SatelliteContaining Satellite element or not	97	SINE	Containing SINE element or not			
99 Satellite Containing Satellite element or not	98	Retroposon	Containing Retroposon element or not			
	99	Satellite	Containing Satellite element or not			

### Table S2. Low-redundant features in human and mouse.

No.	Human	Mouse	No.	Human	Mouse
1	fLen	fLen	31	DNA	DNA
2	gc	gc	32	LINE	LINE
3	nE	nE	33	LTR	LTR
4	fELen	fELen	34	Retroposon	SINE
5	fEgc	fEgc	35	SINE	m6aNearTIS_log
6	flLen	minEgc	36	Satellite	m6aNearTTS_log
7	pOrfCov	flLen	37	m6aNearTIS_log	m6aNearpORFstart_log
8	pOrfSp	pOrfCov	38	m6aNearTTS_log	m6aNearuORFstart_log
9	pOrf5utrCov	pOrfSp	39	m6aNearpORFstart_log	g4NearTIS_log
10	pOrf5utrSp	pOrf5utrCov	40	m6aNearuORFstart_log	g4NearTTS_log
11	pOrf5utrSpFC	pOrf5utrSp	41	g4NearTIS_log	g4NearpORFstart_log
12	pOrf3utrLen	pOrf5utrSpFC	42	g4NearTTS_log	m6aNearTIS_%
13	pOrf3utrCov	pOrf3utrLen	43	g4NearpORFstart_log	m6aNearTTS_%
14	pOrf3utrSp	pOrf3utrCov	44	g4NearfORFend_log	m6aNearpORFstart_%
15	fOrfLen	pOrf3utrSp	45	m6aNearTIS_%	g4NearTIS_%
16	fOrfCov	fOrfLen	46	m6aNearTTS_%	g4NearTTS_%
17	fOrfSp	fOrfCov	47	m6aNearpORFstart_%	g4NearpORFstart_%
18	fOrf5utrLen	fOrfSp	48	g4NearTIS_%	pOrfStartContext
19	fOrf5utrCov	fOrf5utrLen	49	g4NearTTS_%	fOrfStartContext
20	fOrf5utrSp	fOrf5utrCov	50	g4NearpORFstart_%	uOrfStartContext
21	fOrf5utrSpFC	fOrf5utrSp	51	pOrfStartContext	pOrfSeqTrimer
22	fOrf3utrCov	fOrf5utrSpFC	52	fOrfStartContext	fOrfSeqTrimer
23	fOrf3utrSp	fOrf3utrCov	53	uOrfStartContext	fOrfSeqHexamer
24	uOrfCov	fOrf3utrSp	54	pOrfSeqTrimer	uOrfSeqTrimer
25	uOrfSp	uOrfCov	55	pOrfSeqHexamer	uOrfSeqHexamer
26	uOrf5utrLen	uOrfSp	56	fOrfSeqTrimer	
27	uOrf5utrCov	uOrf5utrLen	57	fOrfSeqHexamer	
28	uOrf5utrSp	uOrf5utrCov	58	uOrfSeqTrimer	
29	uOrf5utrSpFC	uOrf5utrSp	59	uOrfSeqHexamer	
30	uOrf3utrSpFC	uOrf3utrSpFC			