Table S1. The download links of datasets we used

Datasets	Download Links of Protein-coding transcript sequences	Download Links of Long non-coding RNA transcript sequences
human (Homo sapiens) data (Release 29, GRCh38.p12)	ftp://ftp.ebi.ac.uk/pub/databases/gencode/Gencode_human/release_29/gencode.v29.pc_transcripts.fa.gz	ftp://ftp.ebi.ac.uk/pub/databases/gencode/Gencode_human/release_29/gencode.v29.lncRNA_transcripts.fa.gz
mouse (Mus musculus) data (Release M20, GRCm38.p6)	ftp://ftp.ebi.ac.uk/pub/databases/gencode/Gencode_mouse/release_M20/gencode.vM20.pc_transcripts.fa.gz	ftp://ftp.ebi.ac.uk/pub/databases/gencode/Gencode_mouse/release_M20/gencode.vM20.lncRNA_transcripts.fa.gz

Table S2. The intersections of optimal feature subsets for human and mouse

Species	Intersections of optimal feature subsets	Descriptions	Types
Human	A_pos_fickett, G_pos_fickett,	nucleotide position frequencies	codon-related features
	fickett_score	Fickett TESTCODE score	
	longest_orf_Rlen	the longest ORF coverage	ORF-related features
	integrity	whether the longest ORF starts with a start codon and ends with a stop codon	
	EDP_ORF_k_mer_GA, EDP_ORF_k_mer_CG, EDP_ORF_k_mer_CT, EDP_ORF_k_mer_TC	The EDP (entropy density profiles) of ORF	
	transcript_GC	GC content of transcript	GC-related features
	GC1_frame_score, GC3_frame_score	The variance of GC content among three reading frames	
	C1, G1, G2	CTD features	transcript-related features
	transcript_length	The length of transcript	
	hexamer_score	Features calculated based on in-frame hexamer frequency	
	snr	Signal to noise ratio (SNR)	
	EDP_fea_W, EDP_fea_Y	The EDP (entropy density profiles) of transcript	
	ACC, C, GCC, GCT, CTG, AAT, GAA, TT, GGA, GTC, CTC, ORF_k_mer_AGT,	k-mer (the frequencies of different matches of	

	ORF_k_mer_CTA, ORF_k_mer_GA, ORF_k_mer_CGA, ORF_k_mer_GAT, ORF_k_mer_TCG, ORF_k_mer_AAT, ORF_k_mer_TAT, ORF_k_mer_AA, ORF_k_mer_CAC, ORF_k_mer_CGT, ORF_k_mer_AAC, ORF_k_mer_TAC, ORF_k_mer_CC, ORF_k_mer_GGG, ORF_k_mer_GTC, ORF_k_mer_ATC, ORF_k_mer_TAA	the k adjacent bases) on transcript and ORF	
	pI	The theoretical isoelectric point of the predicted peptide	
	PI/Mw	The log 10 transformed ratio of pI and Mw (molecular weight)	structure-related features
	pI/Mw_frame_score	pI/Mw value of ORF	
	Gravy	the grand average of hydropathicity	
	G_pos_fickett	nucleotide position frequencies	codon-related features
	STOP_Codon_Count	the number of stop codons in a transcript	
	integrity	whether the longest ORF starts with a start codon and ends with a stop codon	
	EDP_ORF_k_mer_AG, EDP_ORF_k_mer_TC	The EDP (entropy density profiles) of ORF	ORF-related features
	ORF_frame_score	the variance of ORF length among ORFs	
Mouse	GC1_frame_score	The variance of GC content among three reading frames	GC-related features
	UTR5_GC_content	the GC content of untranslated regions (UTR)	
	txCdsPredict_score	coding potential of the transcripts are calculated by the program txCdsPredict	coding sequence-related features
	transcript_length	The length of transcript	

	TAT, TGT, TAG, CTG, ATG, TA, GC, AC, CGC, GAT, TG, TTG, AA, TAA, ORF_k_mer_GTG, ORF_k_mer_CG, ORF_k_mer_GAT, ORF_k_mer_CT, ORF_k_mer_AGA, ORF_k_mer_CCA,	k-mer (the frequencies of different matches of the k adjacent bases) on transcript and ORF	transcript-related features
	snr	Signal to noise ratio (SNR)	
	EDP_fea_A, EDP_fea_W, EDP_fea_L, EDP_fea_C	The EDP (entropy density profiles) of transcript	
	pI	The theoretical isoelectric point of the predicted peptide	structure-related features
	PI/Mw	The log 10 transformed ratio of pI and Mw (molecular weight)	
	G_pos_fickett	nucleotide position frequencies	codon-related features
	integrity	whether the longest ORF starts with a start codon and ends with a stop codon	ORF-related features
	EDP_ORF_k_mer_TC	The EDP (entropy density profiles) of ORF	
	GC1_frame_score	The variance of GC content among three reading frames	GC-related features
Human and Mouse	transcript_length	The length of transcript	
	snr	Signal to noise ratio (SNR)	
	CTG, ORF_k_mer_GAT	k-mer (the frequencies of different matches of the k adjacent bases) on transcript and ORF	transcript-related features
	EDP_fea_W	The EDP (entropy density profiles) of transcript	
	pI	The theoretical isoelectric point of the predicted peptide	structure-related features

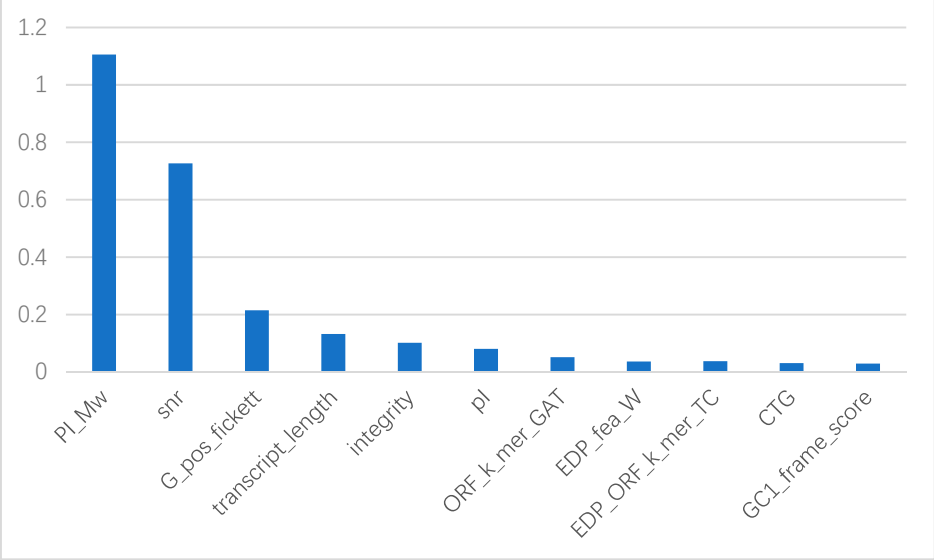
	PI/Mw	The log 10 transformed ratio of pI and Mw (molecular weight)

Table S3. The performance of PredLnc-GFStack on the list of well-known lncRNAs

LncRNA ID	LncRNA Name	References	Prediction results
NR_130791.1	lncRNA-JADE	[1]	lncRNA
NR_144384.1	DINOL	[2]	lncRNA
NR_036469.2	Linc p21	[3]	lncRNA
KT318134.1	DDSR1	[4]	lncRNA
NR_027451.1	NORAD	[5]	lncRNA
NR_038366.1	HOTAIRM1	[6]	lncRNA
NR_024582.1	Xist	[7]	lncRNA
JF519002.1	Tsix	[8]	lncRNA
KX036209.1	NEAT1	[9]	lncRNA
NR_028261.1	Rian	[10]	lncRNA
NR_047517.1	HOTAIR	[11]	lncRNA
NR_045680.1	HEIH	[12]	lncRNA
NR_036484.1	FEZF1-AS1	[13]	lncRNA
NR_046466.1	MEG3	[14]	lncRNA
NR_015379.3	UCA1	[15]	lncRNA
NR_110375.1	THRIL	[16]	lncRNA

NR_045420.2	Bvht	[17]	lncRNA
NR_045471.2	Fendrr	[18]	lncRNA
NR_148381.1	PNKY	[19]	lncRNA
NR_131221.1	SPRY4-IT1	[20]	lncRNA

Figure S1. The importance scores of features in the intersection of optimal subsets for both human. The x-axis means the features in the intersection of optimal subsets for both human and mouse, and y-axis means the importance scores of corresponding features, which is calculated using Sklearn package in Python.



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