

Table S3. Comparisons between different RNA motif identification algorithms.

	RSSVM	RNAz	Dynalign+LIBSVM	QRNA
Structure prediction	RNA Sampler	RNAalifold	Dynalign	N/A
Algorithm	SVM	SVM	SVM	Probabilistic Model
Input	Unaligned sequences	Sequence alignments	Two unaligned sequences	Pairwise sequence alignments
Feature vector	Z, SCI^a, I, MI, id, n	Z, SCI^a, id, n	$\Delta G_{total}, L, f_{seq1}^A, f_{seq1}^U, f_{seq1}^C, f_{seq2}^A, f_{seq2}^U, f_{seq2}^C$	N/A
Training sets	All bacterial RNA motif families from Rfam Sequence identity: 20% -90%	Rfam families from Rfam Sequence identities: > 50%	tRNAs and rRNAs	tRNAs and rRNAs
Output	Common RNA secondary structures, classification P -value	Common RNA secondary structures, classification P -value	Common RNA secondary structures, classification P -value	Classification of RNA, Coding or Null

^a. The SCI score in RNAz is calculated from the common structure predicted by RNAalifold. It also considers covariance between base pairs. The SCI score in RSSVM is calculated from the common structure predicted by RNA Sampler.