Additional file 3 — Known RNA genes in the yeast genome, covered by predicted RNA structures

Known RNA genes in the yeast genome, covered by predicted RNA structures. The annotation was taken from the `Saccharomyces Genome Database`. Structured elements with reported $P^\star_{\text{SVM}}$-values larger than 0.5 and 0.9, resp., are shown. S_E denotes the sensitivity to detect functional classes of known RNAs, **ali** refers to the number of elements in the input alignments, mpi is the mean percent identity of the windows.

Feature class	$P^\star_{\text{SVM}^{0.5}}$	$P^\star_{\text{SVM}^{0.9}}$	ali	S_E	SGD	mpi
snoRNA	32	26	68	0.47	68	74%
tRNAs	200	159	274	0.72	299	85%
rRNA	21	19	27	0.78	27	94%
snRNA	4	4	6	0.66	6	78%
CDS	1309	455	6651	0.20	7050	79%
pseudogene	6	5	22	0.32	22	81%
introns	72	57	332	0.22	365	82%
transposons	50	50	50	1.00	50	78%
telomere region	17	14	22	0.77	32	84%