

Supporting Information for:

**SHAPE probing reveals human ribosomal RNAs are largely unfolded in solution**

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Two supporting figures, plus supporting datasets.

**A** Geometric Mean of sensitivity and ppv as a function of low SS regions

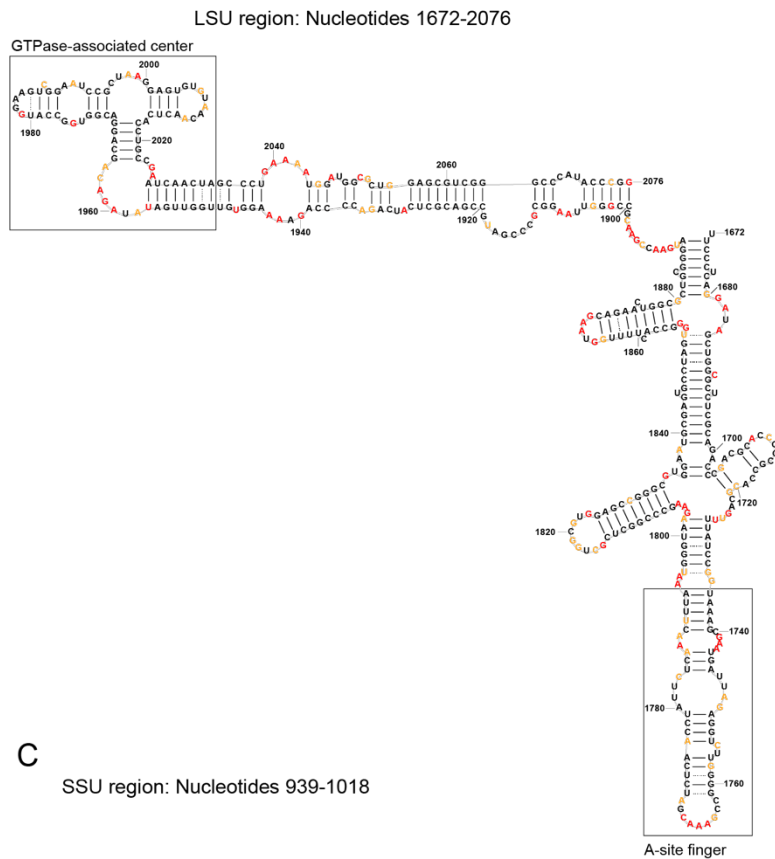
		Entropy										
		0.0001	0.001	0.005	0.01	0.02	0.04	0.08	0.1	0.2	0.5	1
SHAPE	0.13		83%	81%	81%	81%	81%	81%	81%	81%	81%	81%
	0.14	72%	85%	82%	82%	69%	69%	66%	66%	66%	66%	66%
	0.15	68%	81%	84%	84%	73%	73%	71%	71%	69%	69%	69%
	0.2	57%	66%	69%	70%	72%	67%	66%	62%	60%	59%	59%
	0.3	62%	69%	69%	67%	68%	69%	69%	63%	59%	56%	56%
	0.4	60%	67%	69%	67%	68%	69%	67%	63%	53%	51%	51%
	0.5	60%	67%	70%	64%	65%	65%	63%	60%	51%	46%	46%
	0.6	60%	67%	70%	64%	65%	66%	62%	59%	50%	45%	45%
	0.8	60%	67%	70%	64%	65%	66%	62%	59%	50%	44%	44%

**B** Total nucleotide count within lowSS regions

		Entropy										
		0.0001	0.001	0.005	0.01	0.02	0.04	0.08	0.1	0.2	0.5	1
SHAPE	0.13		87	191	191	191	191	191	191	191	191	191
	0.14	57	94	198	198	264	264	291	291	291	291	291
	0.15	83	120	298	298	399	399	426	465	490	490	490
	0.2	227	307	800	968	1136	1217	1241	1411	1533	1599	1599
	0.3	448	638	1095	1345	1586	1746	2181	2532	3095	3442	3442
	0.4	537	766	1095	1345	1633	1829	2361	2737	3441	4086	4086
	0.5	537	766	1119	1542	1873	2079	2577	2936	3951	4739	4739
	0.6	537	766	1119	1542	1873	2105	2584	2971	4139	4906	4906
	0.8	537	766	1119	1542	1873	2105	2584	2971	4139	4920	4920

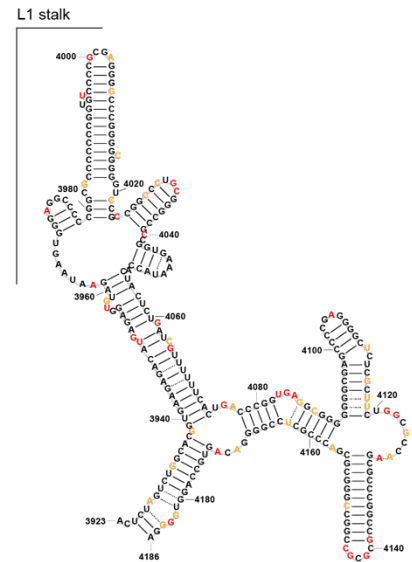
**Figure S1. SHAPE and Shannon entropy thresholds for low SHAPE/low Shannon entropy (lowSS) region modeling.** (A) Structure modeling accuracy (geometric mean of sens and ppv) for lowSS region models in human 18S and 28S rRNAs. Percentages are colored from low (red) to high (green). (B) Number of nucleotides in lowSS regions (including both human 18S and 28S rRNAs). Boxes highlight thresholds used in this work.

A



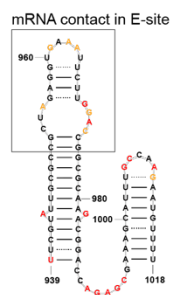
B

LSU region: Nucleotides 3923-4186



C

SSU region: Nucleotides 939-1018



**Figure S2. Models of selected lowSS regions in human rRNAs.** (A) Model of human 28S rRNA region spanning the GTPase-associated center and A-site finger regions. (B) Model of 28S rRNA region containing the L1 stalk. (C) Model of lowSS 18S rRNA region that forms a site of direct mRNA contact.