

Table 1: Prediction of stable quadruplex structures in Rfam seed alignments, version 11.0 [3]. All families without a predicted quadruplex in either the seed alignment or any seed sequence are omitted. The columns 'cons', '#', and 'all' show, if a quadruplex was predicted in the consensus structure, the number of seed sequences where a quadruplex is predicted upon single sequence folding and the total number of seed sequences, respectively. Likely true positives are indicated by a bold Rfam ID and/or followed by a publication reference.

Rfam ID	Description	cons.	#	all	Reference
<i>Structured small RNAs</i>					
RF00024	Telomerase-vert		14	37	
RF00177	SSU bacteria		69	93	[4]
RF01960	SSU_rRNA_eukarya		3	84	[4]
RF01959	SSU_rRNA_archaea		2	19	[4]
RF00001	5S_rRNA		4	712	
RF02001	group-II intron D1D4-3		25	539	
RF00029	group-II intron		4	98	
RF02004	group-II-D1D4-5		3	139	
RF00010	RNase P_bac		21	458	
RF00373	RNaseP_arch		3	70	
RF00009	RNaseP_nuc		2	117	
RF00030	RNase_MRP		3	66	
RF01857	Archaea_SRP		14	53	
RF01502	Fungi_SRP		9	51	
RF00017	Metazoa_SRP		2	91	
RF00012	U3		2	87	
RF01294	snoU89		7	16	
RF01268	SCARNA2		4	20	
RF00441	snoZ242	+	2	5	
RF00023	tmRNA		6	483	
RF02035	IMES-2		5	366	
RF00018	CsrB		4	38	
RF01686	Acido-1		2	4	
RF01528	CC3513		2	2	
<i>MicroRNAs</i>					
RF00978	mir-638	+	5	6	
RF01010	mir-632		4	16	
RF00793	mir-497	+	4	8	
RF02007	mir-1237	+	3	3	
RF01314	mir-1227	+	3	3	
RF00957	mir-663		3	12	
RF00829	mir-149	+	3	3	
RF00981	mir-939	+	2	3	
RF00879	mir-615		2	6	
RF00736	mir-320		2	56	

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Table 1 – *Continued from previous page*

Rfam ID	Description	cons.	#	all	Reference
<i>IRES elements</i>					
RF00261	IRES_L-myc	+	8	11	
RF00461	IRES_VEGF_A		3	7	[6]
RF00224	IRES_FGF2	+	6	6	
RF00226	IRES_n-myc		3	6	
RF00222	IRES_Bag1		2	15	
<i>other eukaryotic mRNA elements</i>					
RF00523	prion ψ knot		142	146	[8, 1]
RF01383	GRIK4_3p_UTR		11	11	[7]
RF01845	enod40		2	35	
<i>other viral elements</i>					
RF00525	Flavivirus_DB		6	111	
RF00468	HCV_SLVII		5	110	
RF01695	C4 (phage)		2	456	
<i>procaryotic cis-regulatory elements</i>					
RF00174	Cobalamin		7	430	
RF00162	SAM		4	433	
RF00059	TPP		2	115	
<i>lncRNAs</i> [5]					
RF02266	XIST_intron	+	18	20	
RF02118	FMR1-AS1_2	+	7	25	[2]
RF02151	MIMT1_1		16	21	
RF02247	Six3os1_2		11	15	
RF02143	HYMAI		11	16	
RF01992	VIS1		11	27	
RF02215	ZNFX1-AS1_1		6	15	
RF02204	WT1-AS_2		5	18	
RF02207	WT1-AS_5	+	4	4	
RF02209	WT1-AS_7		3	21	
RF02127	GNAS-AS1_1		5	21	
RF02176	SMAD5-AS1_4		4	19	
RF02164	PVT1_1		4	17	
RF02165	PVT1_2		3	17	
RF02040	HOTTIP_1	+	4	7	
RF01958	EGOT		4	17	
RF01953	SOX2OT_exon3		4	11	
RF01729	Termite-flg		4	13	
RF02216	ZNFX1-AS1_2		3	18	
RF02201	TTC28-AS1_4		2	18	
RF02197	TP73-AS1	+	2	4	
RF02193	TCL6_3		2	26	
RF02184	ST7-OT3_2	+	2	5	
RF02160	PART1_2		2	29	
RF02158	NPPA-AS1_3R		2	24	
RF02141	HOXA11-AS1_5		2	28	

REFERENCES

- [1] I. Barrette, G. Poisson, P. Gendron, and F. Major. Pseudoknots in prion protein mRNAs confirmed by comparative sequence analysis and pattern searching. *Nucleic Acids Res*, 29:753–758, 2001.
- [2] A. Bugaut and S. Balasubramanian. 5'-UTR RNA G-quadruplexes: translation regulation and targeting. *Nucleic Acids Res.*, 40:4727–4741, 2012.
- [3] S. W. Burge, J. Daub, R. Eberhardt, J. Tate, L. Barquist, E. P. Nawrocki, S. R. Eddy, P. P. Gardner, and A. Bateman. Rfam 11.0: 10 years of RNA families. *Nucleic Acids Res.*, 2012. doi: 10.1093/nar/gks1005.
- [4] J. A. Capra, K. Paeschke, M. Singh, and V. A. Zakian. G-quadruplex DNA sequences are evolutionarily conserved and associated with distinct genomic features in *Saccharomyces cerevisiae*. *PLoS Comput Biol*, 6:e1000861, 2010.
- [5] G. G. Jayaraj, S. Pandey, V. Scaria, and S. Maiti. Potential G-quadruplexes in the human long non-coding transcriptome. *RNA Biolog*, 9:81–86, 2012.
- [6] M. J. Morris, Y. Negishi, C. Papsint, J. D. Schonhoft, and S. Basu. An RNA G-quadruplex is essential for Cap-independent translation initiation in human VEGF IRES. *J. Amer. Chem. Soc.*, 132:17831–17839, 2010.
- [7] M. Subramanian, F. Rage, R. Tabet, E. Flatter, J.-L. Mandel, and H. Moine. G-quadruplex rna structure as a signal for neurite mRNA targeting. *EMBO Reports*, 12, 2011.
- [8] P. R. Wills. Potential pseudoknots in the PrP-encoding mRNA. *J. Theor. Biol.*, 159:523–527, 1992.