

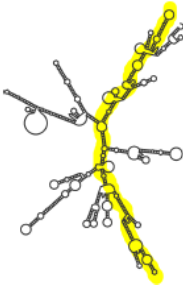
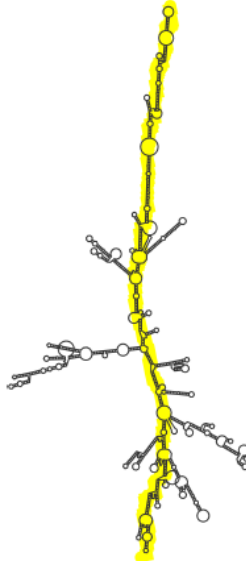
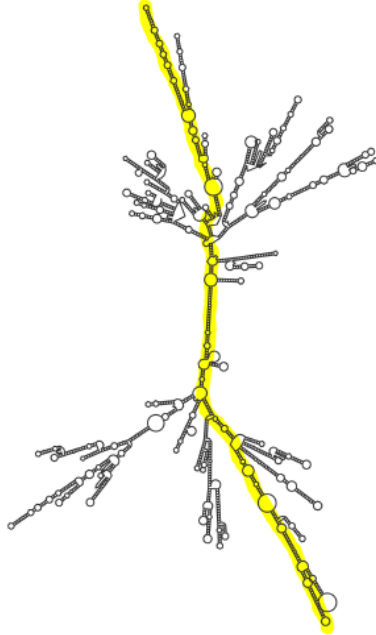
RNA Length		975nt	1523nt	2777nt
%GC		43.3	41.4	42.5
Avg. Duplex Length including single-base bubbles.		<4.85>	<4.92>	<4.98>
T R E E	Total Vertices in Tree Graph	48 <58.8>	77 <92.3>	149 <176.7>
	Terminal Vertices (i.e. stem loops)	20 <19.5>	29 <29.9>	48 <50.0>
G R A P H S	2-fold Junctions	13 <24.7>	22 <38.0>	64 <87.2>
	3-fold Junctions	12 <12.2>	25 <22.1>	30 <33.6>
	4-fold Junctions	3 <2.2>	1 <2.0>	5 <4.6>
	5-fold Junctions	0 <0.2>	0 <0.2>	2 <1.1>
	6-fold Junctions	0 <0>	0 <0>	0 <0.2>
Minimum Free Energy Secondary Structure (longest path highlighted)				

Table ST2: Secondary Structure Properties for 975, 1523 and 2777 nt RNAs. The average duplex length calculation and tree graph calculations are for the minimum free energy (MFE) secondary structures shown in the bottom row and for ensembles of 1000 Boltzmann-sampled secondary structures (ensemble averages values in <>). All secondary structures are predicted using the RNAFold/RNAsubopt programs within the Vienna package (see Methods). Branching analysis is conducted using the RNAs-As-Graphs web application (http://www.biomath.nyu.edu/rna/analysis/rna_matrix.php). Diagonal elements of the output Laplacian matrix are used to calculate branching statistics.