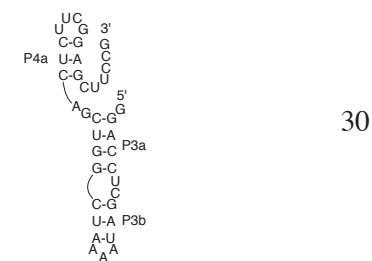
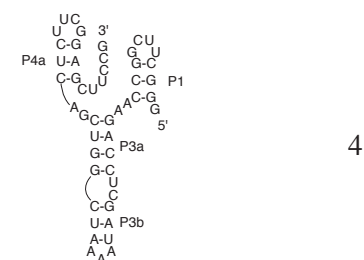
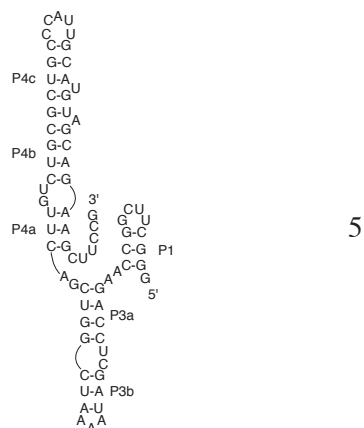
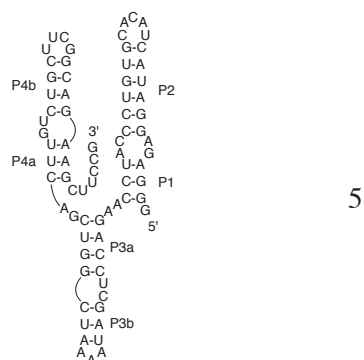
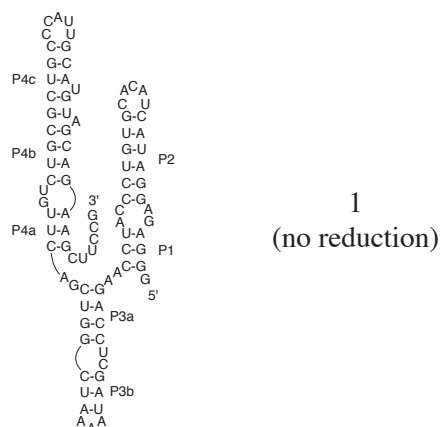


Supplementary Figure 1

a

Ribozyme	Fold reduction in initial rate
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b

Helix	Base pair	Sequence	Fold reduction in initial rate
P1	3-27	G-C	1 (no reduction)
		C C	6
		G G	5
		C-G	3
P2	8-22 9-21	G-C	1
		A-U	7
		C C	5
		U U	1
		G G A A	1
P3	31-49	G-C	1
		C C	> 10
		G G	> 10
		C-G	2
P4	53-90	U-A	1
		U U	40
		A A	> 160
		A-U	1

Supplementary Figure 1 Testing the secondary structure model of the parent ribozyme by site-directed mutagenesis. **(a)** Identification of the minimized catalytic core of the parent ribozyme by deletion analysis. Initial rates were measured in 100 μ M adenylylated phenylalanine. Time points were taken within the first minute of the reaction, and analyzed using either a streptavidin gel-shift assay or a TLC-based assay. **(b)** Testing proposed base pairs with compensatory mutations. Initial rates were measured as described above. Mutations in P3a and P4a were tested in the context of the full length ribozyme, while mutations in P3a and P4a were tested in the context of the ribozyme's minimized catalytic core. Numbering of base pairs is according to the alignment in **Fig. 3**.