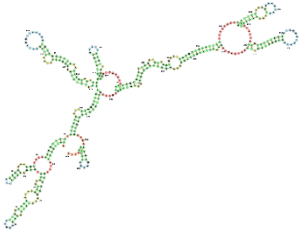
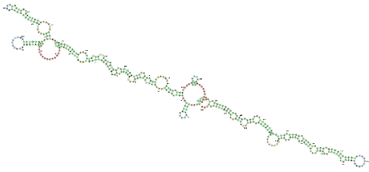
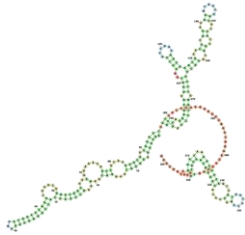
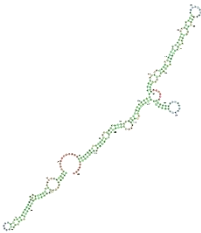
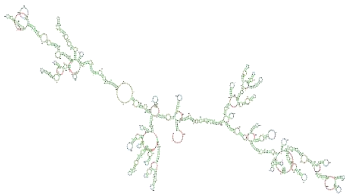
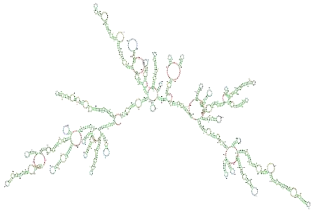
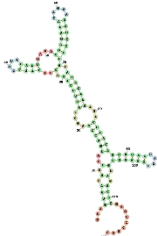
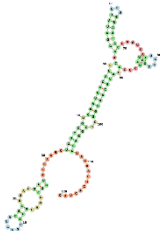


Supplementary Table 1. Target sense strand sequences, including GC content percentage and number of intrinsic Rho-independent terminators/T7 terminator motif sequences found internally , checked using ARNold software (Available at: <http://rssf.i2bc.paris-saclay.fr/toolbox/arnold/>) and sequence alignment.

Sequence name	RNA Sequence	GC Content (%)	Internal Rho-independent/ T7 motif terminator sequences
Dome 11	AUAUCGGACAUCUUGCGGUUUUCUUGUACACGAGGUAGAAGAUGACGCCCAG CACGAGAAUCGCCACGGUCACCUCAAUGGUCUGGUACAUGGCCUUCACGCUGU GCGUGUCCGGUGUACAGAUGAAUCCGUAGAUGCCCCAAUCGGAUCUGUAGAG CCGGUAGGCGGUCAUGUUGGCAGCGUAGGCCUCGAACUGCAGCCGCUCCUCU UCGCCGAGCGCAUCGGUGCGUGCCUCGCAUCCCUUGCCGUUGGUCGACAUAA GCAAAACGGCACCUUCCGUGCAUCCGCUCGCUUCAAACUGCGGAUGCUGCUC CACGUUGAUGGCACGCACCGCUAGCUGGAAGGGAUUGUGGCUGGUGCAGCGC GGCGUGGCCAUACAUAAGGAUAGGUUCCUGCCCC	59	0
GFP	GACAUGGUGAGCAAGGGCGAGGAGCUGUUCACCGGGGUGGUGCCCAUCCUGG UCGAGCUGGACGGCGACGUAAACGGCCACAAGUUCAGCGUGUCCGGCGAGGG CGAGGGCGAUGCCACCUACGGCAAGCUGACCCUGAAGUUCAUCUGCACCACCG GCAAGCUGCCCGUGCCUGGCCACCCUCGUGACCACCCUGACCUACGGCGU GCAGUGCUUCAGCCGCUACCCCGACCACAUGAAGCAGCACGACUUCUUAAG	64	0
Sec23A	GCUUGUUGCCCCCGAAUGCCUUGAUAGGGUUGAUUACCUUUGGGAAGAUGGU CCAAGUGCACGAACUAGGUACCGAGGGCUGCAGCAAAUCUUACGUUUUCCGAG GGACGAAAGACCUCACAGCUAAGCAAGUUCAAGAGAUGUUGGAAGUGGGCAGA GCCGCAGUAAGUGCUCAACCUUGCUCUCAACAACCAGGACAACCCAUGAGGCC UGGAGCACUCCAGCAAGCUCCUACGCCACCAGGAAGCAGGUUCCUUAACCCA UCUCGAAAUGCGACAUGAACCUCACUGAUCUUUUAUUGGAGAGUUGCAAAGAGAC CCAUGGCCUGUCCACCAAGGCAAAUGCGCCCUUAGAUCGACCGGGACAGCUUU AUCGAUAGCCAUUGGGUUGUUGGAGUGCACAUAACGCCAAUACUGGUGCCAGG GUCAUGCUAUUCGUUGGAGGACCUUGCUCUCAAGGCCCUUGGUCAAGUCUUGA AUGAUGAUCUGAAGCAACCUAUCAGAUCUCACCACGACAUCCAAAAAGACAAUG CCAAUACAUGAAGAAAGCAAUCAAGCACUAUGAUAAUUUAGCGAUGAGAGCAG CAACGAAUGGCCACUGCGUUGACAUAUAUUAUGCGCUUUGGAUCAGACAGGA UUGAUGGAGAUGAAACAGUGUUGUAAUUAACAGGGGGACAUAUGGUCAUGGG CGACUCGUUCAAUUCUCCCUUGUUAAGCAAACGUUCCAGCGCAUAUUUUCGA AAGAUCAGAAAAACGAGCUGAAGAUGGCAUUUAAUGGUACUCUGGAGGUCAAG UGUUCCAGGGAGUUGAAAAUUAAGGCGGUUUGGAUCUUGUGUUUCGUUGA AUGUGAAGAAUCCUUUGGUUUCGACACCGAAAUAGGAAUGGGUAACACGGUC CAGUGGAAAAUGUGUACGGUAACUCCAAGUACUACCAUGGCCUUGUUCUUCGA GGUCGUCAACCAACAUUCGCUCCCAUACCUCUAAAGGGGGAAGGGGCUGCAUAC AGUUCAUCACGCAAUUAUCAGCAUGCUAGUGGCCAGAAAGAGGAUCCGAGUAACG ACAGUUGCUAGAAACUGGGCCGAUGCUUCCGCUAAUAUACAUAUGUCAGUGC UGGAUUCGAUCAGGAGGCAGCCGAGUGAUAAUGGCGAGGAUGGCAGUUUAC AGAGCGGAUUCAGACGAUAGCCUGAUGUUUUGAGAUGGGUCGAUAGGAUGU UGAUACGUCUGUGCCAGAAAUUCGGCGAAUAUAACAAGGACGACCCGAUUCGU UCCGCUUGGGCGAAAACUUCAGCCUCUACCCGCAGUUAUGUACCAUUUGAGA AGGUCACAGUUCUGCAGGUGUUUAACAUAUUCUCCCGACGAAACGUCCUUCUA CAGGCACAUGCUUAUGCGCGAAGACCUCACGCAGUCGCUGAUAUGAUCCAGC CGAUACUCUACAGCUACAGUUUCAUUGGACCACCAGAACCUGUGCUUUUGGAU ACGAGUUCCAUCCAACCCGAUAGU	49	0
120 bp	GUAGUGAGUUCUAUGUCCGAGCCAUUGCAUGCGAGAUCGGUAGAUUGAUAGG GGAUACAGAAUAUCCCUUGGAUGCAAUAGACGGACAGCUUGGUAUCCUAAGCGU AGUCGCGCGUCCGAC	51	0

Supplementary Table 2. Table representing predicated centroid secondary structures for Sense and Antisense sequences for all sequences used in the study. Structures for Dome11, GFP, and 120 bp were generated using Mxfold2 Software available at <https://ws.sato-lab.org/mxfold2/> (Sato et al., 2021). Structures for Sec23A were generated using the ViennaRNA fold package 2.0 (Lorenz et al., 2011). Gibbs Free Energy change for sense, antisense and average for 5 random sequences are displayed. Values were calculated using the RNAeval Webserver (<http://rna.tbi.univie.ac.at/cgi-bin/RNAWebSuite/RNAeval.cgi>). Random sequences were generated with equal GC content (%), and unpaired T-tests were run between target sequence samples and random sequences.

	Predicated Centroid Secondary Structure		ΔG (kcal/mol)			
Sequence	Sense	Antisense	Sense	Antisense	Random Sequence Average	P-Value (T-Test)
Dome11			-121.61	-139	-130.305	0.962
GFP			-98.7	-105	-101.85	0.1656
Sec23A			-277.97	-274.88	-276.425	0.0743
120 bp			-34	-30.3	-32.15	0.5902