

Translational control by secondary-structure formation in mRNA in a eukaryotic system

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Figure S1. Mfold predictions of designed mRNA secondary structure.

Table S1. mRNA sequences in this study. Complementary sequence between 5' UTR and 3' UTR indicated in bold and Kozak sequence is underlined. Stop codon is in italics.

Name	Sequence (5' to 3')
ds_Rluc (1007 nt)	GCUAUC<u>AUGUCUGCUCGAAGCGGCCGCUCUAGAAGCCACCAUG</u>ACUUCGAA AGUUUAUGAUCCAGAACAAAGGAAACGGAUGAUACUGGUCCGCAGUGGUGG GCCAGAU<u>GUA</u>AAACAAUGAAUGUUCUUGAUUCAUUUAUUAAUUAAUUAUGAUU CAGAAAAACAUGCAGAAAAUGCUGUUAUUUUUUUACAUGGUAACGCGGCCUC UUCUUAUUUAUGGCGACAUGUUGUGCCACAUAUUGAGCCAGUAGCGCGGUGU AUUAUACCAGACCUUAUUGGUAUGGGCAAUCAGGCAAUCUGGUA<u>AUGGUU</u> CUUAUAGGUUACUUGAUCAUUACAAAUACUUACUGCAUGGUUUGAACUUCU UAAUUUACCAAAGAAGAUCAUUUUUGUCGGCCAUGAUUGGGGUGCUUGUUUG GCAUUUCAUUUAUAGCUAUGAGCAUCAAGAUAAAGAUCAAAGCAAUAGUUCACG CUGAAAGUGUAGUAGAUGUGAUUGAAUCAUGGGAUGAAUGGCCUGAUUUUGA AGAAGAUAAUGCGUUGAUCAAAUCUGAAGAAGGAGAAAAAAUGGUUUUGGAG AAUAACUUCUUCGUGGAAACCAUGUUGCCAUCAAAAUCAUGAGAAAGUUAG AACCAGAAGAAUUUGCAGCAUAUCUUGAACCAUUCAAAGAGAAAGGUGAAGU UCGUCGUCCAACAUAUCAUGGCCUCGUGAAAUCCCGUUAGUAAAAGGUGGU AAACCUGACGUUGUACAAAUUGUUAUGGAAUUAUAAUGCUUAUCUACGUGCAA GUGAUGAUUUACCAAAAAUGUUUAUUGAAUCGGACCCAGGAUUCUUUUCCAA UGCUAUUGUUGAAGGUGCCAAGAAGUUUCCUAAUACUGAAUUUGUCAAAAGUA AAAGGUCUUCAUUUUUCGCAAGAAGAUGCACCUGAUGAAAUGGGAAAAUAUA UCAAAUCGUUCGUUGAGCGAGUUCUCAAAAAUGAACAAUAAUUCUAGAGCGG CCGCUUCGAGCAGACAUGAA
ss_Rluc (1007 nt)	GCUAUC<u>AUGUCUGCUCGAAGCGGCCGCUCUAGAAGCCACCAUG</u>ACUUCGAAAG UUUAUGAUCCAGAACAAAGGAAACGGAUGAUACUGGUCCGCAGUGGUGGGC CAGAU<u>GUA</u>AAACAAUGAAUGUUCUUGAUUCAUUUAUUAAUUAAUUAUGAUUCA GAAAAACAUGCAGAAAAUGCUGUUAUUUUUUUACAUGGUAACGCGGCCUCUU CUUAUUUAUGGCGACAUGUUGUGCCACAUAUUGAGCCAGUAGCGCGGUGUAU UAUACCAGACCUUAUUGGUAUGGGCAAUCAGGCAAUCUGGUA<u>AUGGUUCU</u> UAUAGGUUACUUGAUCAUUACAAAUACUUACUGCAUGGUUUGAACUUCUUA AUUUACCAAAGAAGAUCAUUUUUGUCGGCCAUGAUUGGGGUGCUUGUUUGGC AUUUCAUUUAUAGCUAUGAGCAUCAAGAUAAAGAUCAAAGCAAUAGUUCACGCU GAAAGUGUAGUAGAUGUGAUUGAAUCAUGGGAUGAAUGGCCUGAUUUUGAAG AAGAUAAUGCGUUGAUCAAAUCUGAAGAAGGAGAAAAAAUGGUUUUGGAGAA UAACUUCUUCGUGGAAACCAUGUUGCCAUCAAAAUCAUGAGAAAGUUAGAA CCAGAAGAAUUUGCAGCAUAUCUUGAACCAUUCAAAGAGAAAGGUGAAGUUC

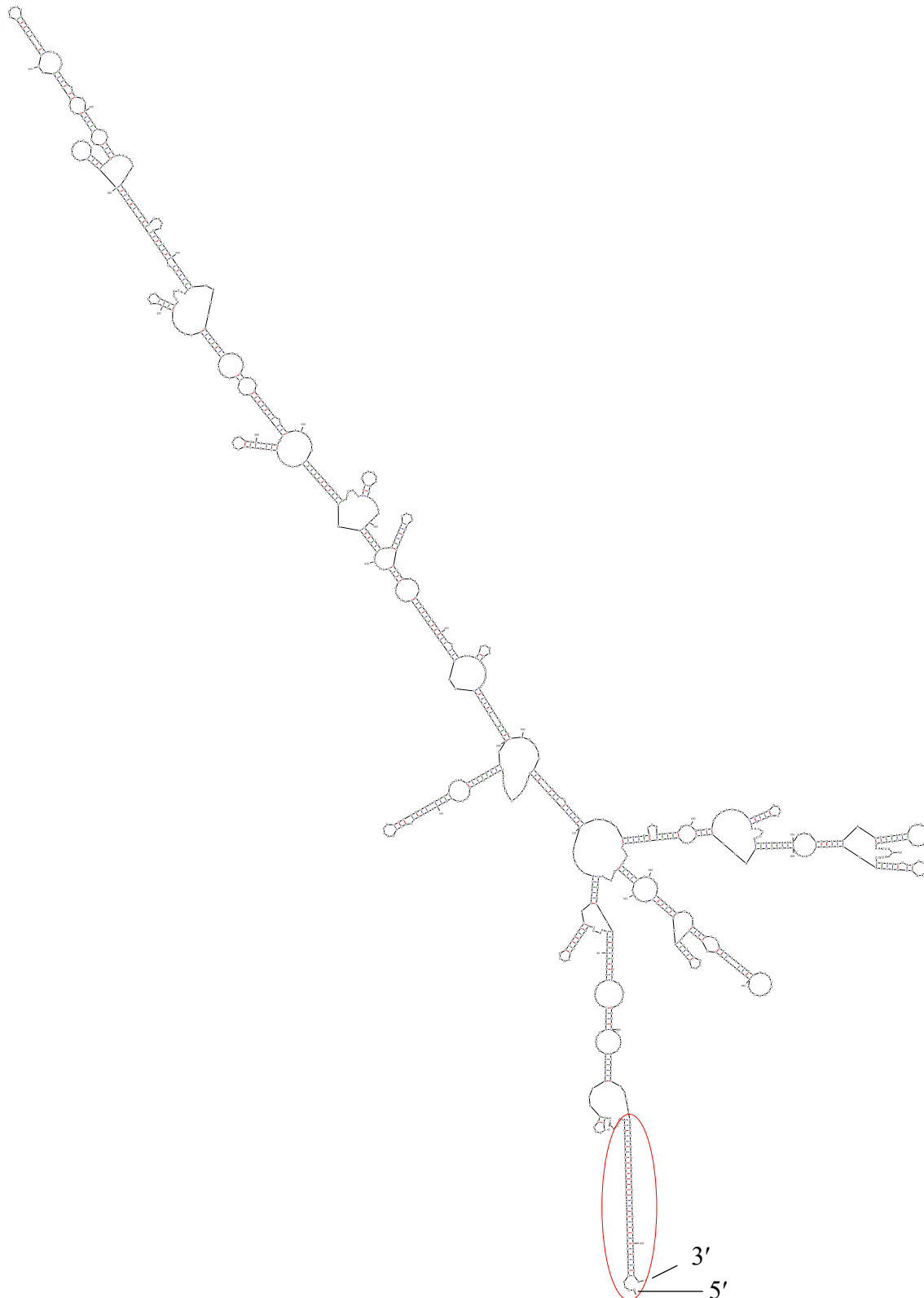
	GUCGUCCAACAUAUCAUGGCCUCGUGAAAUCCCGUUAGUAAAAGGUGGUAA ACCUGACGUUGUACAAAUUGUUAGGAAUUAUAAUGCUUAUCUACGUGCAAGU GAUGAUUUACCAAAAUGUUUAUUGAAUCGGACCCAGGAUUCUUUCCAAUG CUAUUGUUGAAGGUGCCAAGAAGUUUCCUAAUACUGAAUUUGUCAAAAGUAAA AGGUCUUCAUUUUUCGCAAGAAGAUGCACCUGAUGAAAUGGGAAAAUAUAUC AAAUCGUUCGUUGAGCGAGUUCUCAAAAAUGAACAAUAAACAUUUGCUUCUGA CAUAGUUGUGUUGACUA
cap-polyA_Rluc (1014 nt)	m7GpppGCUAUCAUGUCUGCUCGAAGCGGCCGCUCUAGAAGGCCACCAUGACUUC GAAAGUUUAUGAUCCAGAACAAAGGAAACGGAUGAUAAACUGGUCCGCAGUGG UGGGCCAGAUGUAAAACAAUGAAUGUUCUUGAUUCAUUUAUUAAUUAUUAUG AUUCAGAAAAACAUGCAGAAAAUGCUGUUAUUUUUUUACAUGGUAACGCGGC CUCUUCUUAUUUAUGGCGACAUGUUGUGCCACAUAUUGAGCCAGUAGCGCGG UGUAUUUAUACCAGACCUUAUUGGUAUGGGCAAUCAGGCAAUCUGGUAAUG GUUCUUAUAGGUUACUUGAUCAUUACAAUAUCUACUGCAUGGUUUGAACU UCUUAUUUACCAAAGAAGAUCAUUUUUGUCGGCCAUGAUUGGGGUGCUUGU UUGGCAUUUCAUUAUAGCUAUGAGCAUCAAGAUAGAUCAAAGCAAUAGUUC ACGCUGAAAGUGUAGUAGAUGUGAUUGAAUCAUGGGAUGAAUGGCCUGAUAU UGAAGAAGAUUUUGCGUUGAUCAAAUCUGAAGAAGGAGAAAAAUGGUUUUG GAGAAUAACUUCUUCGUGGAAACCAUGUUGCCAUCAAAAAUCAUGAGAAAGU UAGAACCAGAAGAAUUUGCAGCAUAUCUUGAACCAUUCAAAGAGAAAGGUGA AGUUCGUCGUCCAACAUUAUCAUGGCCUCGUGAAAUCCCGUUAGUAAAAGGU GGUAAACCUGACGUUGUACAAAUUGUUAGGAAUUAUAAUGCUUAUCUACGUG CAAGUGAUGAUUUACCAAAAUGUUUAUUGAAUCGGACCCAGGAUUCUUUUC CAAUGCUAUUGUUGAAGGUGCCAAGAAGUUUCCUAAUACUGAAUUUGUCAAA GUAAAAGGUCUUCAUUUUUCGCAAGAAGAUGCACCUGAUGAAUGGGAAAAU AUAUCAAAUCGUUCGUUGAGCGAGUUCUCAAAAAUGAACAAUAAUUCUAGAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

Figure S1. Mfold predictions of designed mRNA secondary structure. Only in ds_Rluc, there was a base pairing between 5' UTR and 3' UTR (red circle).

a. ds_Rluc

Output of sir_graph ©
mfold_util 4.7

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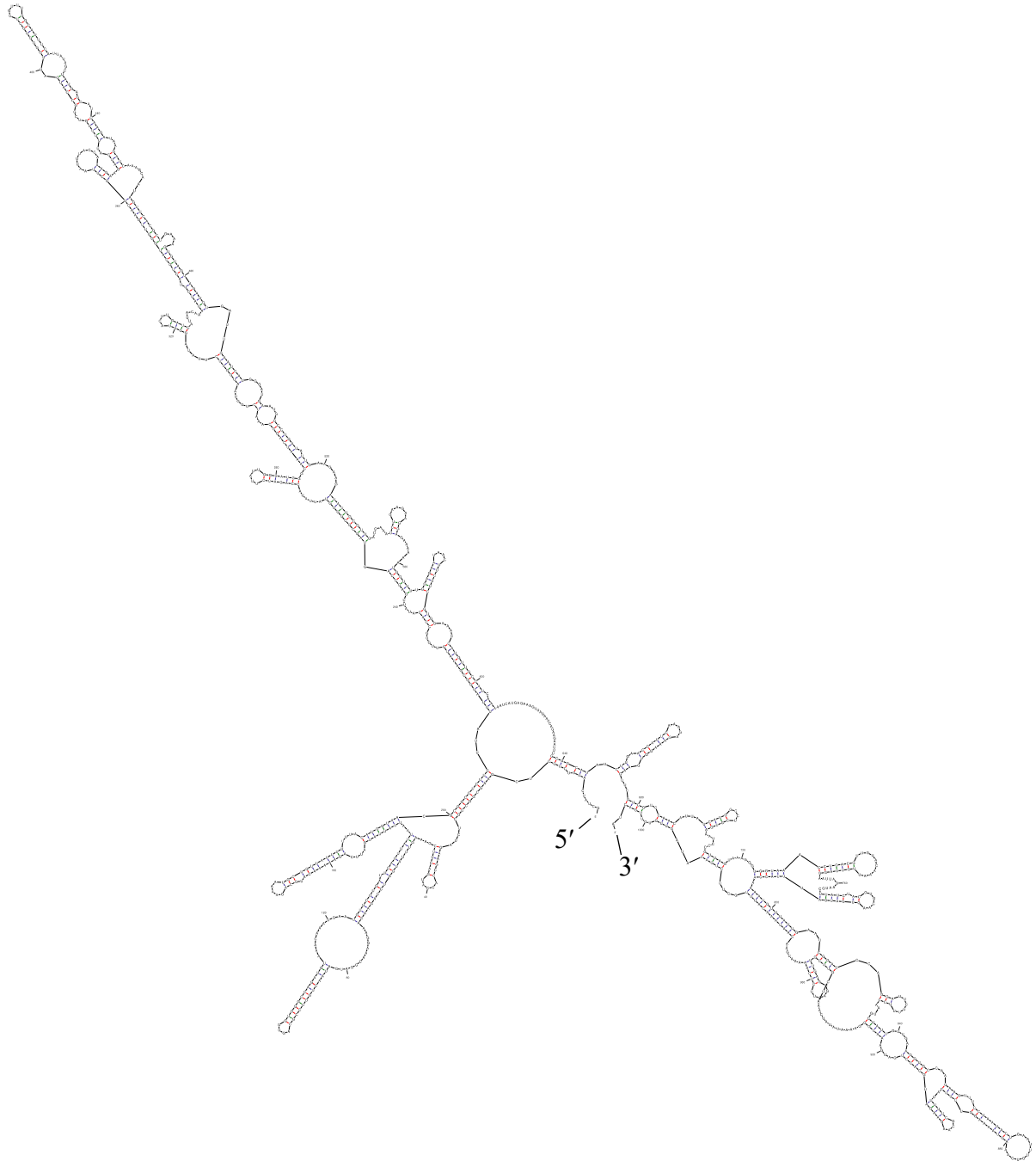


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b. ss_Rluc

Output of sir_graph (©)
mfold_util 4.7

Created Tue Aug 27 03:52:17 2019

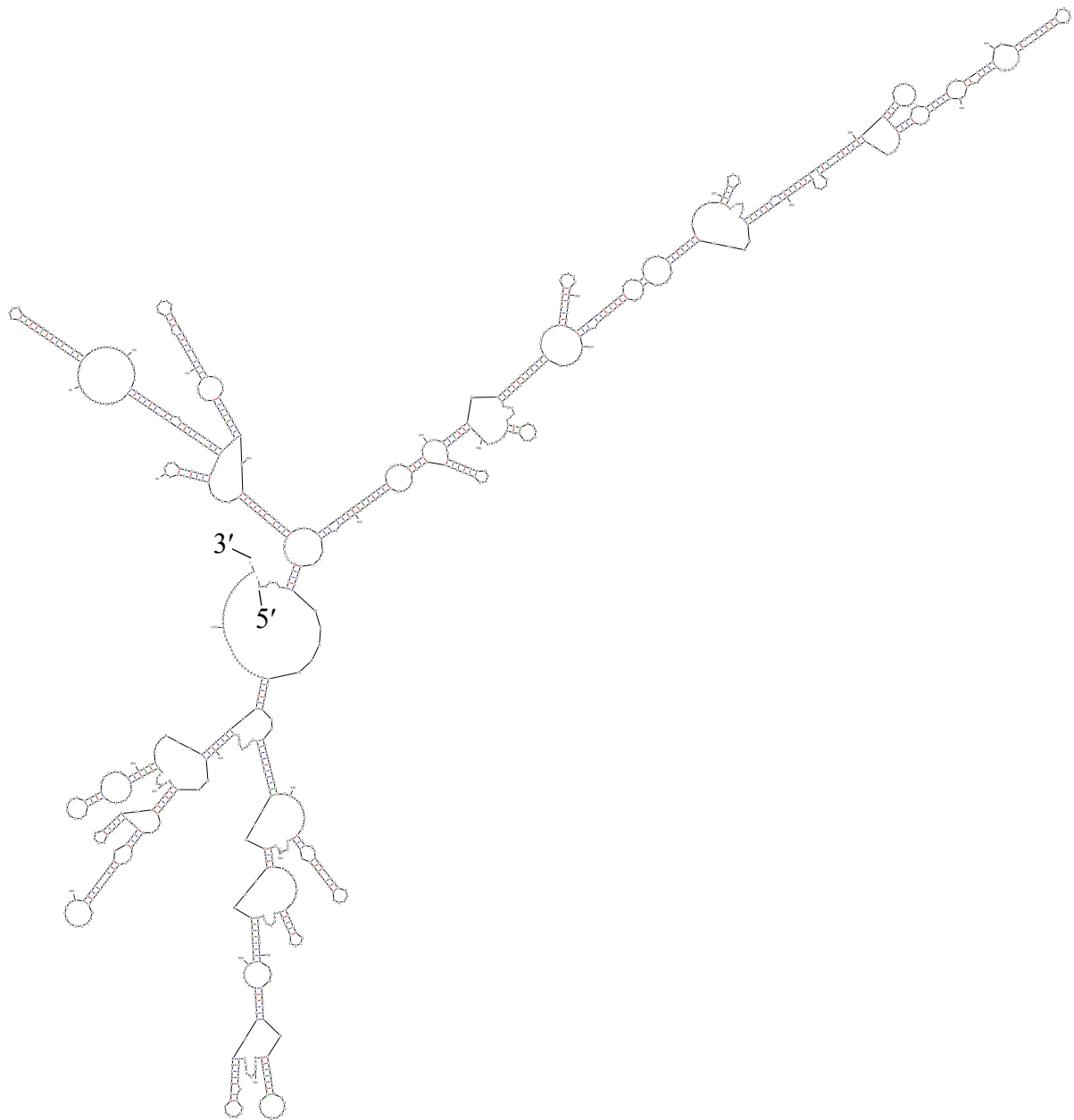


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c. cap-polyA_Rluc

Output of sir_graph ©
mfold_util 4.7

Created Tue Aug 27 03:49:28 2019



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