Supplementary Data

Novel RNA molecular bioengineering technology efficiently produces functional miRNA agents

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Supplemental Tables S1 to S4

Supplemental Figures 1 to 2

Supplemental Table S1. Sequences of novel BioRNAs bearing target RNAi warheads produced in this study. Underlined, htRNA; Black, hsa-pre-miR-34a; Red and Green, miRNA guide and passenger strand, respectively.

BioRNA	Length (nt)	Sequence (5' to 3')	MW (Da)
BioRNA^{Leu}			
miR-143b-3p	192	ACCAGGAUGGCCGAGUGGUUAAGGCGUUGGACUGGCCAGCUGUGAGUGUUUCU UUGAGAUGAAGCACUGUAGCUCUUGUGAGCAAUAGUAAGGAAGGAGCUGCAUG CAUUCAUCUCUCAGAAGUGCUGCACGUUGUUGGCCCGAUCCAAUGGACAUAUGU CCGCGUGGGUUCGAACCCCACUCCUGGUACCA	62,093
miR-206-3p	192	ACCAGGAUGGCCGAGUGGUUAAGGCGUUGGACUGGCCAGCUGUGAGUGUUUCU UUGGAAUGUAAGGAAGUGUGUGGUGUGAGCAAUAGUAAGGAAUCACACACUCC UGUACAUUCCCUAGAAGUGCUGCACGUUGUUGGCCCGAUCCAAUGGACAUAUGU CCGCGUGGGUUCGAACCCCACUCCUGGUACCA	62,117
miR-375-3p	192	ACCAGGAUGGCCGAGUGGUUAAGGCGUUGGACUGGCCAGCUGUGAGUGUUUCU UUUUGUUCGUUCGGCUCGCGUGAUGUGAGCAAUAGUAAGGAAUCGCGCGAGCG ACACGAACAACUAGAAGUGCUGCACGUUGUUGGCCCGAUCCAAUGGACAUAUGU CCGCGUGGGUUCGAACCCCACUCCUGGUACCA	62,123
miR-497-5p	192	ACCAGGAUGGCCGAGUGGUUAAGGCGUUGGACUGGCCAGCUGUGAGUGUUUCU UCAGCAGCACACUGUGGUUUGUUUGUGAGCAAUAGUAAGGAAGGCAAACCAAG UAGUGCUGUUAUAGAAGUGCUGCACGUUGUUGGCCCGAUCCAAUGGACAUAUG UCCGCGUGGGUUCGAACCCCACUCCUGGUACCA	62,157
miR-125b-5p	192	ACCAGGAUGGCCGAGUGGUUAAGGCGUUGGACUGGCCAGCUGUGAGUGUUUCU UUCCCUGAGACCCUAACUUGUGAUGUGAGCAAUAGUAAGGAAUCACGGGUUGG GCUCUUGGGGCUAGAAGUGCUGCACGUUGUUGGCCCGAUCCAAUGGACAUAUG UCCGCGUGGGUUCGAACCCCACUCCUGGUACCA	62,117
let-7a-5p	192	ACCAGGAUGGCCGAGUGGUUAAGGCGUUGGACUGGCCAGCUGUGAGUGUUUCU UUGAGGUAGUAGGUUGUAUAGUUUGUGAGCAAUAGUAAGGAAAACUGUACACC UGACUACCUUUCAGAAGUGCUGCACGUUGUUGGCCCGAUCCAAUGGACAUAUGU CCGCGUGGGUUCGAACCCCACUCCUGGUACCA	62,080
let-7b-5p	192	ACCAGGAUGGCCGAGUGGUUAAGGCGUUGGACUGGCCAGCUGUGAGUGUUUCU UUGAGGUAGUAGGUUGUGUGGUUUGUGAGCAAUAGUAAGGAAAACUGUACACC UGACUACCUUUCAGAAGUGCUGCACGUUGUUGGCCCGAUCCAAUGGACAUAUGU CCGCGUGGGUUCGAACCCCACUCCUGGUACCA	62,112

let-7c-5p	192	ACCAGGAUGGCCGAGUGGUUAAGGCGUUGGACUGGCCAGCUGUGAGUGUUUCU UUGAGGUAGUAGGUUGUAUGGUUUGUGAGCAAUAGUAAGGAAAACUGUACACC UGACUACCUUUCAGAAGUGCUGCACGUUGUUGGCCCGAUCCAAUGGACAUAUGU CCGCGUGGGUUCGAACCCCACUCCUGGUACCA	62,096
let-7d-5p	192	ACCAGGAUGGCCGAGUGGUUAAGGCGUUGGACUGGCCAGCUGUGAGUGUUUCU UAGAGGUAGUAGGUUGCAUAGUUUGUGAGCAAUAGUAAGGAAAACUGUGCACC UGACUACCUUCCAGAAGUGCUGCACGUUGUUGGCCCGAUCCAAUGGACAUAUGU CCGCGUGGGUUCGAACCCCACUCCUGGUACCA	62,117
let-7e-5p	192	ACCAGGAUGGCCGAGUGGUUAAGGCGUUGGACUGGCCAGCUGUGAGUGUUUCU UUGAGGUAGGAGGUUGUAUAGUUUGUGAGCAAUAGUAAGGAAAACUGUACACC UGCCUACCUUUCAGAAGUGCUGCACGUUGUUGGCCCGAUCCAAUGGACAUAUGU CCGCGUGGGUUCGAACCCCACUCCUGGUACCA	62,095
let-7f-5p	192	ACCAGGAUGGCCGAGUGGUUAAGGCGUUGGACUGGCCAGCUGUGAGUGUUUCU UUGAGGUAGUAGAUUGUAUAGUUUGUGAGCAAUAGUAAGGAAAACUGUACAUC UGACUACCUUUCAGAAGUGCUGCACGUUGUUGGCCCGAUCCAAUGGACAUAUGU CCGCGUGGGUUCGAACCCCACUCCUGGUACCA	62,065
let-7g-5p	192	ACCAGGAUGGCCGAGUGGUUAAGGCGUUGGACUGGCCAGCUGUGAGUGUUUCU UUGAGGUAGUAGUUUGUACAGUUUGUGAGCAAUAGUAAGGAAAACUGUACAAC UGACUACCUUUCAGAAGUGCUGCACGUUGUUGGCCCGAUCCAAUGGACAUAUGU CCGCGUGGGUUCGAACCCCACUCCUGGUACCA	62,064
miR-101-3p	192	ACCAGGAUGGCCGAGUGGUUAAGGCGUUGGACUGGCCAGCUGUGAGUGUUUCU UUACAGUACUGUGAUAACUGAAUUGUGAGCAAUAGUAAGGAAGUUCAGUUACA CUAGUGCUGUCUAGAAGUGCUGCACGUUGUUGGCCCGAUCCAAUGGACAUAUG UCCGCGUGGGUUCGAACCCCACUCCUGGUACCA	62,064
miR-195-5p	192	ACCAGGAUGGCCGAGUGGUUAAGGCGUUGGACUGGCCAGCUGUGAGUGUUUCU UUAGCAGCACAGAAAUAUUGGCUUGUGAGCAAUAGUAAGGAAGGCCAAUAUUC UAGUGCUGCUCCAGAAGUGCUGCACGUUGUUGGCCCGAUCCAAUGGACAUAUGU CCGCGUGGGUUCGAACCCCACUCCUGGUACCA	62,100
miR-370-3p	192	ACCAGGAUGGCCGAGUGGUUAAGGCGUUGGACUGGCCAGCUGUGAGUGUUUCU UGCCUGCUGGGGUGGAACCUGGUUGUGAGCAAUAGUAAGGAAGCCAGGUUCGC CAUCAGCAGGAUAGAAGUGCUGCACGUUGUUGGCCCGAUCCAAUGGACAUAUG UCCGCGUGGGUUCGAACCCCACUCCUGGUACCA	62,257

miR-495-3p	192	ACCAGGAUGGCCGAGUGGUUAAGGCGUUGGACUGGCCAGCUGUGAGUGUUUCUUAAACAAACAUGGUGCACUUCUUUGUGAGCAAUAGUAAGGAAGAGAAGUGCCCACUGUUUGUUCUAGAAGUGCUGCACGUUGUUGGCCCGAUCCAAUGGACAUAUGUCCGCGUGGGUUCGAACCCCACUCCUGGUACCA	62,062
miR-519a-5p	192	ACCAGGAUGGCCGAGUGGUUAAGGCGUUGGACUGGCCAGCUGUGAGUGUUUCUUCUCUAGAGGGAAGCGCUUUCUGUGUGAGCAAUAGUAAGGAAUGGAAAGUGUUCGCUUUUAGACUAGAAGUGCUGCACGUUGUUGGCCCGAUCCAAUGGACAUAUGUCCGCGUGGGUUCGAACCCCACUCCUGGUACCA	62,151
miR-29a-3p	192	ACCAGGAUGGCCGAGUGGUUAAGGCGUUGGACUGGCCAGCUGUGAGUGUUUCUUUAGCACCAUCUGAAAUCGGUUAUGUGAGCAAUAGUAAGGAAUGACUGAUUCAGCAUGGUGUUCUAGAAGUGCUGCACGUUGUUGGCCCGAUCCAAUGGACAUAUGUCCGCGUGGGUUCGAACCCCACUCCUGGUACCA	62,079
miR-99a-5p	192	ACCAGGAUGGCCGAGUGGUUAAGGCGUUGGACUGGCCAGCUGUGAGUGUUUCUUAACCCGUAGAUCCGAUCUUGUGUGUGAGCAAUAGUAAGGAAUACAAGGUCGAUACUAUGGGUCUAGAAGUGCUGCACGUUGUUGGCCCGAUCCAAUGGACAUAUGUCCGCGUGGGUUCGAACCCCACUCCUGGUACCA	62,117
miR-100-5p	192	ACCAGGAUGGCCGAGUGGUUAAGGCGUUGGACUGGCCAGCUGUGAGUGUUUCUUAACCCGUAGAUCCGAACUUGUGUGUGAGCAAUAGUAAGGAAUACAAGUUCGAUACUAUGGGUCUAGAAGUGCUGCACGUUGUUGGCCCGAUCCAAUGGACAUAUGUCCGCGUGGGUUCGAACCCCACUCCUGGUACCA	62,101
miR-146a-5p	194	ACCAGGAUGGCCGAGUGGUUAAGGCGUUGGACUGGCCAGCUGUGAGUGUUUCUUUGAGAACUGAAUUCCAUGGGUUUGUGAGCAAUAGUAAGGAAGACCUGUGGAUUACAGUUCUUCUAGAAGUGCUGCACGUUGUUGGCCCGAUCCAAUGGACAUAUGUCCGCGUGGGUUCGAACCCCACUCCUGGUACCA	62,096
miR-146b-5p	192	ACCAGGAUGGCCGAGUGGUUAAGGCGUUGGACUGGCCAGCUGUGAGUGUUUCUUUGAGAACUGAAUUCCAUAGGCUGGUGAGCAAUAGUAAGGA**U**GGCCUGUGGAUUACAGUUCUCCUAGAAGUGCUGCACGUUGUUGGCCCGAUCCAAUGGACAUAUGUCCGCGUGGGUUCGAACCCCACUCCUGGUACCA	62,110

BioRNA^{Gly}

miR-7-5p	180	GCAUGGGUGGUUCAGUGGUAGAAUUCUCGCCUGGCCAGCUGUGAGUGUUUCUU UGGAAGACUAGUGAUUUUGUUGUGUGAGCAAUAGUAAGGAACAACAAAAUACU CAGUCUUCCCUAGAAGUGCUGCACGUUGUUGGCCCACGCGGGAGGCCCGGGUUC GAUUCCCGGCCCAUGCACCA	58,174
miR-126b-3p	180	GCAUGGGUGGUUCAGUGGUAGAAUUCUCGCCUGGCCAGCUGUGAGUGUUUCUU UCGUACCGUGAGUAAUAAUGCGUGUGAGCAAUAGUAAGGAAUGCAUUAUUCUC UAUGGUACGCUAGAAGUGCUGCACGUUGUUGGCCCACGCGGGAGGCCCGGGUUC GAUUCCCGGCCCAUGCACCA	58,183
miR-133a-3p	180	GCAUGGGUGGUUCAGUGGUAGAAUUCUCGCCUGGCCAGCUGUGAGUGUUUCUU UUUGGUCCCCUUCAACCAGCUGUGUGAGCAAUAGUAAGGAAGCAGCUGGUUAA GUGGGACCAACUAGAAGUGCUGCACGUUGUUGGCCCACGCGGGAGGCCCGGGUU CGAUUCCCGGCCCAUGCACCA	58,540
miR-200b-3p	180	GCAUGGGUGGUUCAGUGGUAGAAUUCUCGCCUGGCCAGCUGUGAGUGUUUCUU UAAUACUGCCUGGUAAUGAUGAUGUGAGCAAUAGUAAGGAAUCAUCAUUAUAG UGCAGUAUUCUAGAAGUGCUGCACGUUGUUGGCCCACGCGGGAGGCCCGGGUUC GAUUCCCGGCCCAUGCACCA	58,176
miR-143b-3p	180	GCAUGGGUGGUUCAGUGGUAGAAUUCUCGCCUGGCCAGCUGUGAGUGUUUCUU UGAGAUGAAGCACUGUAGCUCUUGUGAGCAAUAGUAAGGAAGGAGCUGCAUGC AUUCAUCUCUCAGAAGUGCUGCACGUUGUUGGCCCACGCGGGAGGCCCGGGUUC GAUUCCCGGCCCAUGCACCA	58,220
miR-206-3p	180	GCAUGGGUGGUUCAGUGGUAGAAUUCUCGCCUGGCCAGCUGUGAGUGUUUCUU UGGAAUGUAAGGAAGUGUGUGGUGUGAGCAAUAGUAAGGAAUCACACACUCCU GUACAUUCCCUAGAAGUGCUGCACGUUGUUGGCCCACGCGGGAGGCCCGGGUUC GAUUCCCGGCCCAUGCACCA	58,244
miR-375-3p	180	GCAUGGGUGGUUCAGUGGUAGAAUUCUCGCCUGGCCAGCUGUGAGUGUUUCUU UUUGUUCGUUCGGCUCGCGUGAUGUGAGCAAUAGUAAGGAAUCGCGCGAGCGA CACGAACAACUAGAAGUGCUGCACGUUGUUGGCCCACGCGGGAGGCCCGGGUUC GAUUCCCGGCCCAUGCACCA	58,250
miR-497-5p	180	GCAUGGGUGGUUCAGUGGUAGAAUUCUCGCCUGGCCAGCUGUGAGUGUUUCUU CAGCAGCACACUGUGGUUUGUUUGUGAGCAAUAGUAAGGAAGGCAAACCAAGU AGUGCUGUUAUAGAAGUGCUGCACGUUGUUGGCCCACGCGGGAGGCCCGGGUUC GAUUCCCGGCCCAUGCACCA	58,284

miR-125b-5p	180	GCAUGGGUGGUUCAGUGGUAGAAUUCUCGCCUGGCCAGCUGUGAGUGUUUCUUUCCCUGAGACCCUAACUUGUGAUGUGAGCAAUAGUAAGGAAUCACGGGUUGGGCUCUUGGGGCUAGAAGUGCUGCACGUUGUUGGCCCACGCGGGAGGCCCGGGUUCGAUUCCCGGCCCAUGCACCA	58,244
let-7a-5p	180	GCAUGGGUGGUUCAGUGGUAGAAUUCUCGCCUGGCCAGCUGUGAGUGUUUCUUUGAGGUAGUAGGUUGUAUAGUUUGUGAGCAAUAGUAAGGAAAACUGUACACCUGACUACCUUUCAGAAGUGCUGCACGUUGUUGGCCCACGCGGGAGGCCCGGGUUCGAUUCCCGGCCCAUGCACCA	58,207
let-7b-5p	180	GCAUGGGUGGUUCAGUGGUAGAAUUCUCGCCUGGCCAGCUGUGAGUGUUUCUUUGAGGUAGUAGGUUGUGUGGUUUGUGAGCAAUAGUAAGGAAAACUGUACACCUGACUACCUUUCAGAAGUGCUGCACGUUGUUGGCCCACGCGGGAGGCCCGGGUUCGAUUCCCGGCCCAUGCACCA	58,239
let-7c-5p	180	GCAUGGGUGGUUCAGUGGUAGAAUUCUCGCCUGGCCAGCUGUGAGUGUUUCUUUGAGGUAGUAGGUUGUGUGGUUUGUGAGCAAUAGUAAGGAAAACUGUACACCUGACUACCUUUCAGAAGUGCUGCACGUUGUUGGCCCACGCGGGAGGCCCGGGUUCGAUUCCCGGCCCAUGCACCA	58,239
let-7d-5p	180	GCAUGGGUGGUUCAGUGGUAGAAUUCUCGCCUGGCCAGCUGUGAGUGUUUCUUAGAGGUAGUAGGUUGCAUAGUUUGUGAGCAAUAGUAAGGAAAACUGUGCACCUGACUACCUUCCAGAAGUGCUGCACGUUGUUGGCCCACGCGGGAGGCCCGGGUUCGAUUCCCGGCCCAUGCACCA	58,244
let-7e-5p	180	GCAUGGGUGGUUCAGUGGUAGAAUUCUCGCCUGGCCAGCUGUGAGUGUUUCUUUGAGGUAGGAGGUUGUAUAGUUUGUGAGCAAUAGUAAGGAAAACUGUACACCUGCCUACCUUUCAGAAGUGCUGCACGUUGUUGGCCCACGCGGGAGGCCCGGGUUCGAUUCCCGGCCCAUGCACCA	58,222
let-7f-5p	180	GCAUGGGUGGUUCAGUGGUAGAAUUCUCGCCUGGCCAGCUGUGAGUGUUUCUUUGAGGUAGUAGAUUGUAUAGUUUGUGAGCAAUAGUAAGGAAAACUGUACAUCUGACUACCUUUCAGAAGUGCUGCACGUUGUUGGCCCACGCGGGAGGCCCGGGUUCGAUUCCCGGCCCAUGCACCA	58,19
let-7g-5p	180	GCAUGGGUGGUUCAGUGGUAGAAUUCUCGCCUGGCCAGCUGUGAGUGUUUCUUUGAGGUAGUAGUUUGUACAGUUUGUGAGCAAUAGUAAGGAAAACUGUACAACUGACUACCUUUCAGAAGUGCUGCACGUUGUUGGCCCACGCGGGAGGCCCGGGUUCGAUUCCCGGCCCAUGCACCA	58,191

miR-370-3p	180	GCAUGGGUGGUUCAGUGGUAGAAUUCUCGCCUGGCCAGCUGUGAGUGUUUCUU GCCUGCUGGGGUGGAACCUGGUUGUGAGCAAUAGUAAGGAAGCCAGGUUCGCC AUCAGCAGGAUAGAAGUGCUGCACGUUGUUGGCCCACGCGGGAGGCCCGGGUUC GAUUCCCGGCCCAUGCACCA	58,384
miR-495-3p	180	GCAUGGGUGGUUCAGUGGUAGAAUUCUCGCCUGGCCAGCUGUGAGUGUUUCUU AAACAAACAUGGUGCACUUCUUUGUGAGCAAUAGUAAGGAAGAGAAGUGCCCA CUGUUUGUUCUAGAAGUGCUGCACGUUGUUGGCCCACGCGGGAGGCCCGGGUUC GAUUCCCGGCCCAUGCACCA	58,189
miR-519a-5p	180	GCAUGGGUGGUUCAGUGGUAGAAUUCUCGCCUGGCCAGCUGUGAGUGUUUCUU CUCUAGAGGGAAGCGCUUUCUGUGUGAGCAAUAGUAAGGAAUGGAAAGUGUUC GCUUUUAGACUAGAAGUGCUGCACGUUGUUGGCCCACGCGGGAGGCCCGGGUUC GAUUCCCGGCCCAUGCACCA	58,278
miR-29a-3p	180	GCAUGGGUGGUUCAGUGGUAGAAUUCUCGCCUGGCCAGCUGUGAGUGUUUCUU UAGCACCAUCUGAAAUCGGUUAUGUGAGCAAUAGUAAGGAAUGACUGAUUCAG CAUGGUGUUCUAGAAGUGCUGCACGUUGUUGGCCCACGCGGGAGGCCCGGGUUC GAUUCCCGGCCCAUGCACCA	58,206
miR-101-3p	180	GCAUGGGUGGUUCAGUGGUAGAAUUCUCGCCUGGCCAGCUGUGAGUGUUUCUU UACAGUACUGUGAUAACUGAAUUGUGAGCAAUAGUAAGGAAGUUCAGUUACAC UAGUGCUGUCUAGAAGUGCUGCACGUUGUUGGCCCACGCGGGAGGCCCGGGUUC GAUUCCCGGCCCAUGCACCA	58,191
miR-195-5p	180	GCAUGGGUGGUUCAGUGGUAGAAUUCUCGCCUGGCCAGCUGUGAGUGUUUCUU UAGCAGCACAGAAAUAUUGGCUUGUGAGCAAUAGUAAGGAAGGCCAAUAUUCU AGUGCUGCUCCAGAAGUGCUGCACGUUGUUGGCCCACGCGGGAGGCCCGGGUUC GAUUCCCGGCCCAUGCACCA	58,227
miR-99-5p	180	GCAUGGGUGGUUCAGUGGUAGAAUUCUCGCCUGGCCAGCUGUGAGUGUUUCUU AACCCGUAGAUCCGAUCUUGUGUGUGAGCAAUAGUAAGGAAUACAAGGUCGAU ACUAUGGGUCUAGAAGUGCUGCACGUUGUUGGCCCACGCGGGAGGCCCGGGUUC GAUUCCCGGCCCAUGCACCA	58,244
miR-100-5p	180	GCAUGGGUGGUUCAGUGGUAGAAUUCUCGCCUGGCCAGCUGUGAGUGUUUCUU AACCCGUAGAUCCGAACUUGUGUGUGAGCAAUAGUAAGGAAUACAAGUUCGAU ACUAUGGGUCUAGAAGUGCUGCACGUUGUUGGCCCACGCGGGAGGCCCGGGUUC GAUUCCCGGCCCAUGCACCA	58,228

miR-146a-5p	180	GCAUGGGUGGUUCAGUGGUAGAAUUCUCGCCUGGCCAGCUGUGAGUGUUUCUU UGAGAACUGAAUUCCAUGGGUUUGUGAGCAAUAGUAAGGAAGACCUGUGGAUU ACAGUUCUUCUAGAAGUGCUGCACGUUGUUGGCCCACGCGGGAGGCCCGGGUUC GAUUCCCGGCCCAUGCACCA	58,223
miR-146b-5p	180	GCAUGGGUGGUUCAGUGGUAGAAUUCUCGCCUGGCCAGCUGUGAGUGUUUCUU UGAGAACUGAAUUCCAUAGGCUGGUGAGCAAUAGUAAGGA**U**GGCCUGUGGAUU ACAGUUCUCCUAGAAGUGCUGCACGUUGUUGGCCCACGCGGGAGGCCCGGGUUC GAUUCCCGGCCCAUGCACCA	58,237

Supplemental Table S2. Primers used for the construction of RNA expression plasmids in this study. Black, BioRNA; Orange, *EcoRI* restriction site overhang; Blue, *PstI* restriction site overhang; F, forward primer; R, reverse primer.

BioRNA		**Cloning Primers (5' to 3')**
BioRNA^{Leu}		
miR-143b-3p	F	TTGTAACGCTGAATTCACCAGGATGGCCGAGTGGTTAAGGCGTTGGACTGGCCAGCTGTGAGTGTTTCTTTGAGATGAAGCACTGTAGCTCTTGTGAGCAATAGTAAGGAAGGAGCTGCATGC
	R	CTTTCGCTAAGGATCTGCAGTGGTACCAGGAGTGGGGTTCGAACCCACGCGGACATATGTCCATTGGATCGGGCCAACAACGTGCAGCACTTCTGAGAGATGAATGCATGCAGCTCCTTCC
miR-206-3p	F	TTGTAACGCTGAATTCACCAGGATGGCCGAGTGGTTAAGGCGTTGGACTGGCCAGCTGTGAGTGTTTCTTTGGAATGTAAGGAAGTGTGTGGTGTGAGCAATAGTAAGGAATCACACACTCC
	R	CTTTCGCTAAGGATCTGCAGTGGTACCAGGAGTGGGGTTCGAACCCACGCGGACATATGTCCATTGGATCGGGCCAACAACGTGCAGCACTTCTAGGGAATGTACAGGAGTGTGTGATTC
miR-375-3p	F	TTGTAACGCTGAATTCACCAGGATGGCCGAGTGGTTAAGGCGTTGGACTGGCCAGCTGTGAGTGTTTCTTTTTGTTCGTTCGGCTCGCGTGATGTGAGCAATAGTAAGGAATCGCGCGAGCG
	R	CTTTCGCTAAGGATCTGCAGTGGTACCAGGAGTGGGGTTCGAACCCACGCGGACATATGTCCATTGGATCGGGCCAACAACGTGCAGCACTTCTAGTTGTTCGTGTCGCTCGCGCGATTCC
miR-497-5p	F	TTGTAACGCTGAATTCACCAGGATGGCCGAGTGGTTAAGGCGTTGGACTGGCCAGCTGTGAGTGTTTCTTCAGCAGCACACTGTGGTTTGTTTGTGAGCAATAGTAAGGAAGGCAAACCAAG
	R	CTTTCGCTAAGGATCTGCAGTGGTACCAGGAGTGGGGTTCGAACCCACGCGGACATATGTCCATTGGATCGGGCCAACAACGTGCAGCACTTCTATAACAGCACTACTTGGTTTGCCTTC
miR-125b-5p	F	TTGTAACGCTGAATTCACCAGGATGGCCGAGTGGTTAAGGCGTTGGACTGGCCAGCTGTGAGTGTTTCTTTCCCTGAGACCCTAACTTGTGATGTGAGCAATAGTAAGGAATCACGGGTTGG
	R	CTTTCGCTAAGGATCTGCAGTGGTACCAGGAGTGGGGTTCGAACCCACGCGGACATATGTCCATTGGATCGGGCCAACAACGTGCAGCACTTCTAGCCCCAAGAGCCCAACCCGTGATTC
let-7a-5p	F	TTGTAACGCTGAATTCACCAGGATGGCCGAGTGGTTAAGGCGTTGGACTGGCCAGCTGTGAGTGTTTCTTTGAGGTAGTAGGTTGTATAGTTTGTGAGCAATAGTAAGGAAAACTGTACAC
	R	CTTTCGCTAAGGATCTGCAGGTGGTACCAGGAGTGGGGTTCGAACCCACGCGGACATATGTCCATTGGATCGGGCCAACAACGTGCAGCACTTCTGAAAGGTAGTCAGGTGTACAGTTTTCCT
let-7b-5p	F	TTGTAACGCTGAATTCACCAGGATGGCCGAGTGGTTAAGGCGTTGGACTGGCCAGCTGTGAGTGTTTCTTTGAGGTAGTAGGTTGTGTGGTTTGTGAGCAATAGTAAGGAAAACTGTACAC
	R	CTTTCGCTAAGGATCTGCAGGTGGTACCAGGAGTGGGGTTCGAACCCACGCGGACATATGTCCATTGGATCGGGCCAACAACGTGCAGCACTTCTGAAAGGTAGTCAGGTGTACAGTTTTCCT
let-7c-5p	F	TTGTAACGCTGAATTCACCAGGATGGCCGAGTGGTtAAGGCGTTGGACTGGCCAGCTGTGAGTGTTTCTTTGAGGTAGTAGGTTGTATGGTTTGTGAGCAATAGTAAGGAAAACTGTACA

	R	CTTTCGCTAAGGATCTGCAGTGGTACCAGGAGTGGGGTTCGAACCCACGCGGACATATGTCCATTGGATCGGGCCAACAACGTGCAGCACTTCTGAAAGGTAGTcAGGTGTACAGTTTTCCTTA
let-7d-5p	F	TTGTAACGCTGAATTCACCAGGATGGCCGAGTGGTTAAGGCGTTGGACTGGCCAGCTGTGAGTGTTTCTTAGAGGTAGTAGGTTGCATAGTTTGTGAGCAATAGTAAGGAAAACTGTGCAC
	R	CTTTCGCTAAGGATCTGCAGGTGGTACCAGGAGTGGGGTTCGAACCCACGCGGACATATGTCCATTGGATCGGGCCAACAACGTGCAGCACTTCTGGAAGGTAGTCAGGTGCACAGTTTTCCT
let-7e-5p	F	TTGTAACGCTGAATTCACCAGGATGGCCGAGTGGTTAAGGCGTTGGACTGGCCAGCTGTGAGTGTTTCTTTGAGGTAGGAGGTTGTATAGTTTGTGAGCAATAGTAAGGAAAACTGTACAC
	R	CTTTCGCTAAGGATCTGCAGGTGGTACCAGGAGTGGGGTTCGAACCCACGCGGACATATGTCCATTGGATCGGGCCAACAACGTGCAGCACTTCTGAAAGGTAGGCAGGTGTACAGTTTTCCT
let-7f-5p	F	TTGTAACGCTGAATTCACCAGGATGGCCGAGTGGTTAAGGCGTTGGACTGGCCAGCTGTGAGTGTTTCTTTGAGGTAGTAGATTGTATAGTTTGTGAGCAATAGTAAGGAAAACTGTACAT
	R	CTTTCGCTAAGGATCTGCAGGTGGTACCAGGAGTGGGGTTCGAACCCACGCGGACATATGTCCATTGGATCGGGCCAACAACGTGCAGCACTTCTGAAAGGTAGTCAGATGTACAGTTTTCCT
let-7g-5p	F	TTGTAACGCTGAATTCACCAGGATGGCCGAGTGGTTAAGGCGTTGGACTGGCCAGCTGTGAGTGTTTCTTTGAGGTAGTAGTTTGTACAGTTTGTGAGCAATAGTAAGGAAAACTGTACA
	R	CTTTCGCTAAGGATCTGCAGTGGTACCAGGAGTGGGGTTCGAACCCACGCGGACATATGTCCATTGGATCGGGCCAACAACGTGCAGCACTTCTGAAAGGTAGTCAGTTGTACAGTTTTCCTT
miR-370-3p	F	TTGTAACGCTGAATTCACCAGGATGGCCGAGTGGTTAAGGCGTTGGACTGGCCAGCTGTGAGTGTTTCTTTACAGTACTGTGATAACTGAATTGTGAGCAATAGTAAGGAAGTTCAGTTACAC
	R	CTTTCGCTAAGGATCTGCAGTGGTACCAGGAGTGGGGTTCGAACCCACGCGGACATATGTCCATTGGATCGGGCCAACAACGTGCAGCACTTCTAGACAGCACTAGTGTAACTGAACTTC
miR-495-3p	F	TTGTAACGCTGAATTCACCAGGATGGCCGAGTGGTTAAGGCGTTGGACTGGCCAGCTGTGAGTGTTTCTTTAGCAGCACAGAAATATTGGCTTGTGAGCAATAGTAAGGAAGGCCAATATTCT
	R	CTTTCGCTAAGGATCTGCAGTGGTACCAGGAGTGGGGTTCGAACCCACGCGGACATATGTCCATTGGATCGGGCCAACAACGTGCAGCACTTCTGGAGCAGCACTAGAATATTGGCCTTC
miR-519a-5p	F	TTGTAACGCTGAATTCACCAGGATGGCCGAGTGGTTAAGGCGTTGGACTGGCCAGCTGTGAGTGTTTCTTGCCTGCTGGGGTGGAACCTGGTTGTGAGCAATAGTAAGGAAGCCAGGTTCGC
	R	CTTTCGCTAAGGATCTGCAGTGGTACCAGGAGTGGGGTTCGAACCCACGCGGACATATGTCCATTGGATCGGGCCAACAACGTGCAGCACTTCTATCCTGCTGATGGCGAACCTGGCTTCC
miR-29a-3p	F	TTGTAACGCTGAATTCACCAGGATGGCCGAGTGGTTAAGGCGTTGGACTGGCCAGCTGTGAGTGTTTCTTAAACAAACATGGTGCACTTCTTTGTGAGCAATAGTAAGGAAGAGAAGTGCCC
	R	CTTTCGCTAAGGATCTGCAGTGGTACCAGGAGTGGGGTTCGAACCCACGCGGACATATGTCCATTGGATCGGGCCAACAACGTGCAGCACTTCTAGAACAAACAGTGGGCACTTCTCTTCC
miR-101-3p	F	TTGTAACGCTGAATTCACCAGGATGGCCGAGTGGTTAAGGCGTTGGACTGGCCAGCTGTGAGTGTTTCTTCTCTAGAGGGAAGCGCTTTCTGTGTGAGCAATAGTAAGGAATGGAAAGTGTT

	R	CTTTCGCTAAGGATCTGCAGTGGTACCAGGAGTGGGGTTCGAACCCACGCGGACATATGTCCATTGGATCGGGC CAACAACGTGCAGCACTTCTAGTCTAAAAGCGAACACTTTCCATTCC
miR-195-5p	F	TTGTAACGCTGAATTCACCAGGATGGCCGAGTGGTTAAGGCGTTGGACTGGCCAGCTGTGAGTGTTTCTTTAGCA CCATCTGAAATCGGTTATGTGAGCAATAGTAAGGAATGACTGATTC
	R	CTTTCGCTAAGGATCTGCAGTGGTACCAGGAGTGGGGTTCGAACCCACGCGGACATATGTCCATTGGATCGGGC CAACAACGTGCAGCACTTCTAGAACACCATGCTGAATCAGTCATTCCT
miR-99-5p	F	TTGTAACGCTGAATTCACCAGGATGGCCGAGTGGTTAAGGCGTTGGACTGGCCAGCTGTGAGTGTTTCTTAACCC GTAGATCCGATCTTGTGTGTGAGCAATAGTAAGGAATACAAGGTCG
	R	CTTTCGCTAAGGATCTGCAGTGGTACCAGGAGTGGGGTTCGAACCCACGCGGACATATGTCCATTGGATCGGGC CAACAACGTGCAGCACTTCTAGACCCATAGTATCGACCTTGTATTCCT
miR-100-5p	F	TTGTAACGCTGAATTCACCAGGATGGCCGAGTGGTTAAGGCGTTGGACTGGCCAGCTGTGAGTGTTTCTTAACCC GTAGATCCGAACTTGTGTGTGAGCAATAGTAAGGAATACAAGTTCG
	R	CTTTCGCTAAGGATCTGCAGTGGTACCAGGAGTGGGGTTCGAACCCACGCGGACATATGTCCATTGGATCGGGC CAACAACGTGCAGCACTTCTAGACCCATAGTATCGAACTTGTATTCCT
miR-146a-5p	F	TTGTAACGCTGAATTCACCAGGATGGCCGAGTGGTTAAGGCGTTGGACTGGCCAGCTGTGAGTGTTTCTTTGAG AACTGAATTCCATGGGTTTGTGAGCAATAGTAAGGAAGACCTGTGGA
	R	CTTTCGCTAAGGATCTGCAGTGGTACCAGGAGTGGGGTTCGAACCCACGCGGACATATGTCCATTGGATCGGGC CAACAACGTGCAGCACTTCTAGAAGAACTGTAATCCACAGGTCTTCCT
miR-146b-5p	F	TTGTAACGCTGAATTCACCAGGATGGCCGAGTGGTTAAGGCGTTGGACTGGCCAGCTGTGAGTGTTTCTTTGAG AACTGAATTCCATAGGCTGGTGAGCAATAGTAAGGA**T**GGCCTGTGGA
	R	CTTTCGCTAAGGATCTGCAGTGGTACCAGGAGTGGGGTTCGAACCCACGCGGACATATGTCCATTGGATCGGGC CAACAACGTGCAGCACTTCTAGGAGAACTGTAATCCACAGGCCATCCT
BioRNA^{Gly}		
miR-126b-3p	F	TTGTAACGCTGAATTCGCATGGGTGGTTCAGTGGTAGAATTCTCGCCTGGCCAGCTGTGAGTG
	R	CTTTCGCTAAGGATCTGCAGTGGTGCATGGGCCGGGAATCGAACCCGGGCCTCCCGCGTGGGCCAACAACGTGC
miR-133a-3p	F	TTGTAACGCTGAATTCGCATGGGTGGTTCAGTGGTAGAATTCTCGCCTGGCCAGCTGTGAGTG
	R	CTTTCGCTAAGGATCTGCAGTGGTGCATGGGCCGGGAATCGAACCCGGGCCTCCCGCGTGGGCCAACAACGTGC
miR-200b-3p	F	TTGTAACGCTGAATTCGCATGGGTGGTTCAGTGGTAGAATTCTCGCCTGGCCAGCTGTGAGTG
	R	CTTTCGCTAAGGATCTGCAGTGGTGCATGGGCCGGGAATCGAACCCGGGCCTCCCGCGTGGGCCAACAACGTGC
miR-7-5p	F	TTGTAACGCTGAATTCGCATGGGTGGTTCAGTGGTAGAATTCTCGCCTGGCCAGCTGTGAGTG
	R	CTTTCGCTAAGGATCTGCAGTGGTGCATGGGCCGGGAATCGAACCCGGGCCTCCCGCGTGGGCCAACAACGTGC

miR-143b-3p	F	TTGTAACGCTGAATTCGCATGGGTGGTTCAGTGGTAGAATTCTCGCCTGGCCAGCTGTGAGTG
	R	CTTTCGCTAAGGATCTGCAGTGGTGCATGGGCCGGGAATCGAACCCGGGCCTCCCGCGTGGGCCAACAACGTGC
miR-206-3p	F	TTGTAACGCTGAATTCGCATGGGTGGTTCAGTGGTAGAATTCTCGCCTGGCCAGCTGTGAGTG
	R	CTTTCGCTAAGGATCTGCAGTGGTGCATGGGCCGGGAATCGAACCCGGGCCTCCCGCGTGGGCCAACAACGTGC
miR-375-3p	F	TTGTAACGCTGAATTCGCATGGGTGGTTCAGTGGTAGAATTCTCGCCTGGCCAGCTGTGAGTG
	R	CTTTCGCTAAGGATCTGCAGTGGTGCATGGGCCGGGAATCGAACCCGGGCCTCCCGCGTGGGCCAACAACGTGC
miR-497-5p	F	TTGTAACGCTGAATTCGCATGGGTGGTTCAGTGGTAGAATTCTCGCCTGGCCAGCTGTGAGTG
	R	CTTTCGCTAAGGATCTGCAGTGGTGCATGGGCCGGGAATCGAACCCGGGCCTCCCGCGTGGGCCAACAACGTGC
miR-125b-5p	F	TTGTAACGCTGAATTCGCATGGGTGGTTCAGTGGTAGAATTCTCGCCTGGCCAGCTGTGAGTG
	R	CTTTCGCTAAGGATCTGCAGTGGTGCATGGGCCGGGAATCGAACCCGGGCCTCCCGCGTGGGCCAACAACGTGC
let-7a-5p	F	TTGTAACGCTGAATTCGCATGGGTGGTTCAGTGGTAGAATTCTCGCCTGGCCAGCTGTGAGTG
	R	CTTTCGCTAAGGATCTGCAGTGGTGCATGGGCCGGGAATCGAACCCGGGCCTCCCGCGTGGGCCAACAACGTGC
let-7b-5p	F	TTGTAACGCTGAATTCGCATGGGTGGTTCAGTGGTAGAATTCTCGCCTGGCCAGCTGTGAGTG
	R	CTTTCGCTAAGGATCTGCAGTGGTGCATGGGCCGGGAATCGAACCCGGGCCTCCCGCGTGGGCCAACAACGTGC
let-7c-5p	F	TTGTAACGCTGAATTCGCATGGGTGGTTCAGTGGTAGAATTCTCGCCTGGCCAGCTGTGAGTGTTTCTTTGAGGT AGTAGGTTGTATGGTTTGTGAGCAATAGTAAGGAAAACTGTA
	R	CTTTCGCTAAGGATCTGCAGTGGTGCATGGGCCGGGAATCGAACCCGGGCCTCCCGCGTGGGCCAACAACGTGC AGCACTTCTGAAAGGTAGTCAGGTGTACAGTTTTCCTTA
let-7d-5p	F	TTGTAACGCTGAATTCGCATGGGTGGTTCAGTGGTAGAATTCTCGCCTGGCCAGCTGTGAGTG
	R	CTTTCGCTAAGGATCTGCAGTGGTGCATGGGCCGGGAATCGAACCCGGGCCTCCCGCGTGGGCCAACAACGTGC
let-7e-5p	F	TTGTAACGCTGAATTCGCATGGGTGGTTCAGTGGTAGAATTCTCGCCTGGCCAGCTGTGAGTG
	R	CTTTCGCTAAGGATCTGCAGTGGTGCATGGGCCGGGAATCGAACCCGGGCCTCCCGCGTGGGCCAACAACGTGC
let-7f-5p	F	TTGTAACGCTGAATTCGCATGGGTGGTTCAGTGGTAGAATTCTCGCCTGGCCAGCTGTGAGTG
	R	CTTTCGCTAAGGATCTGCAGTGGTGCATGGGCCGGGAATCGAACCCGGGCCTCCCGCGTGGGCCAACAACGTGC
let-7g-5p	F	TTGTAACGCTGAATTCGCATGGGTGGTTCAGTGGTAGAATTCTCGCCTGGCCAGCTGTGAGTG
	R	CTTTCGCTAAGGATCTGCAGTGGTGCATGGGCCGGGAATCGAACCCGGGCCTCCCGCGTGGGCCAACAACGTGC

miR-370-3p	F	TTGTAACGCTGAATTCGCATGGGTGGTTCAGTGGTAGAATTCTCGCCTGGCCAGCTGTGAGTG
	R	CTTTCGCTAAGGATCTGCAGTGGTGCATGGGCCGGGAATCGAACCCGGGCCTCCCGCGTGGGCCAACAACGTGC
miR-495-3p	F	TTGTAACGCTGAATTCGCATGGGTGGTTCAGTGGTAGAATTCTCGCCTGGCCAGCTGTGAGTG
	R	CTTTCGCTAAGGATCTGCAGTGGTGCATGGGCCGGGAATCGAACCCGGGCCTCCCGCGTGGGCCAACAACGTGC
miR-519a-5p	F	TTGTAACGCTGAATTCGCATGGGTGGTTCAGTGGTAGAATTCTCGCCTGGCCAGCTGTGAGTG
	R	CTTTCGCTAAGGATCTGCAGTGGTGCATGGGCCGGGAATCGAACCCGGGCCTCCCGCGTGGGCCAACAACGTGC
miR-29a-3p	F	TTGTAACGCTGAATTCGCATGGGTGGTTCAGTGGTAGAATTCTCGCCTGGCCAGCTGTGAGTG
	R	CTTTCGCTAAGGATCTGCAGTGGTGCATGGGCCGGGAATCGAACCCGGGCCTCCCGCGTGGGCCAACAACGTGC
miR-101-3p	F	TTGTAACGCTGAATTCGCATGGGTGGTTCAGTGGTAGAATTCTCGCCTGGCCAGCTGTGAGTG
	R	CTTTCGCTAAGGATCTGCAGTGGTGCATGGGCCGGGAATCGAACCCGGGCCTCCCGCGTGGGCCAACAACGTGC
miR-195-5p	F	TTGTAACGCTGAATTCGCATGGGTGGTTCAGTGGTAGAATTCTCGCCTGGCCAGCTGTGAGTG
	R	CTTTCGCTAAGGATCTGCAGTGGTGCATGGGCCGGGAATCGAACCCGGGCCTCCCGCGTGGGCCAACAACGTGC
miR-99-5p	F	TTGTAACGCTGAATTCGCATGGGTGGTTCAGTGGTAGAATTCTCGCCTGGCCAGCTGTGAGTG
	R	CTTTCGCTAAGGATCTGCAGTGGTGCATGGGCCGGGAATCGAACCCGGGCCTCCCGCGTGGGCCAACAACGTGC
miR-100-5p	F	TTGTAACGCTGAATTCGCATGGGTGGTTCAGTGGTAGAATTCTCGCCTGGCCAGCTGTGAGTG
	R	CTTTCGCTAAGGATCTGCAGTGGTGCATGGGCCGGGAATCGAACCCGGGCCTCCCGCGTGGGCCAACAACGTGC
miR-146a-5p	F	TTGTAACGCTGAATTCGCATGGGTGGTTCAGTGGTAGAATTCTCGCCTGGCCAGCTGTGAGTG
	R	CTTTCGCTAAGGATCTGCAGTGGTGCATGGGCCGGGAATCGAACCCGGGCCTCCCGCGTGGGCCAACAACGTGC
miR-146b-5p	F	TTGTAACGCTGAATTCGCATGGGTGGTTCAGTGGTAGAATTCTCGCCTGGCCAGCTGTGAGTG
	R	CTTTCGCTAAGGATCTGCAGTGGTGCATGGGCCGGGAATCGAACCCGGGCCTCCCGCGTGGGCCAACAACGTGC

Supplemental Table S3. Sequences of commercial mimics and primers used for real-time qPCR analyses. F, forward primer; R, reverse primer.

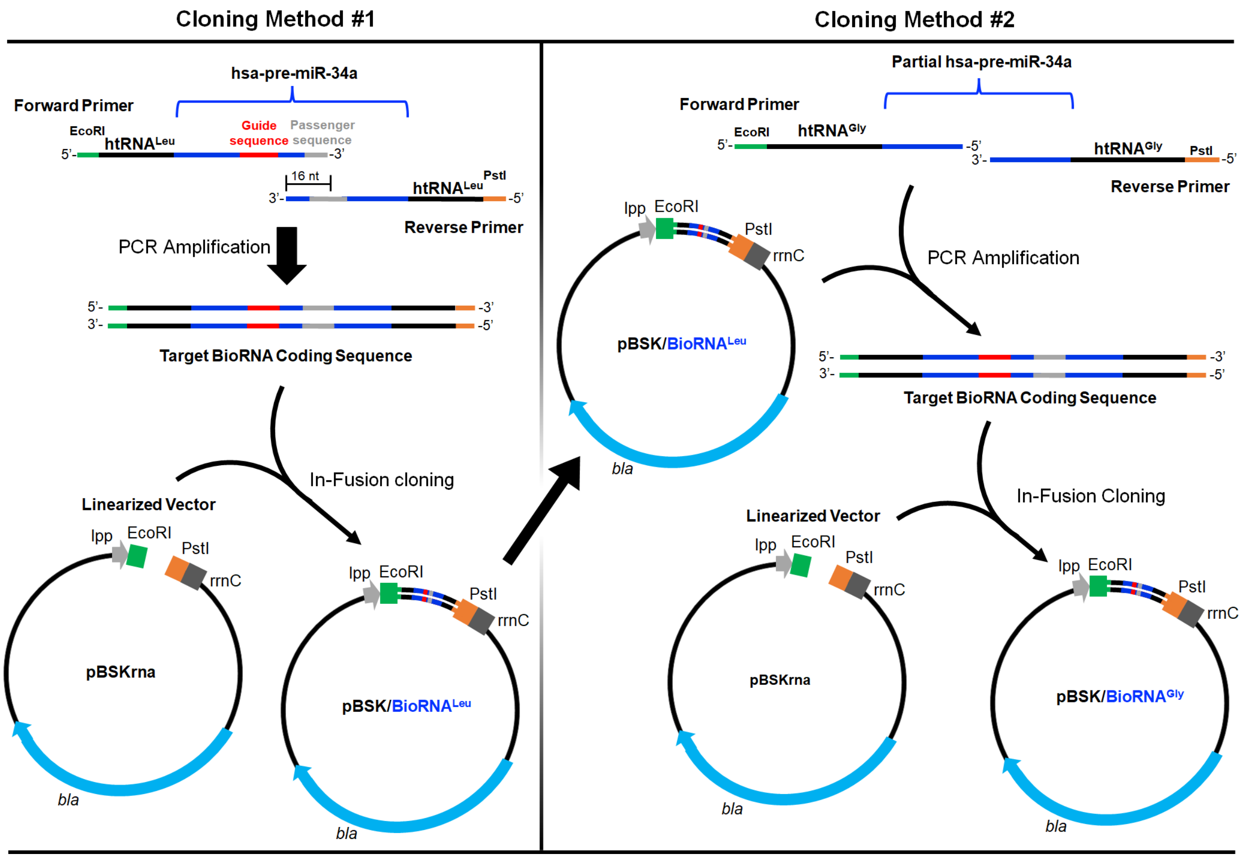
Mimic miRNA		**Sequence (5' to 3')**
miRCURY LNA miR-7-5p (Mimic miR-7-5p)		UGGAAGACUAGUGAUUUUGUUGU (guide sequence)
miRCURY LNA negative control (Mimic Control)		UCACCGGGUGUAAAUCAGCUUG (guide sequence)
Primer		**Primer Sequence (5' to 3')**
hsa-miR-7-5p		
stem-loop RT		GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACCAACAA
qPCR	F	CGCGCTGGAAGACTAGTGATT
	R	GTGCAGGGTCCGAGGT
U6 qPCR	F	CTCGCTTCGGCAGCACA
	R	AACGCTTCACGAATTTGCGT

Supplemental Table S4. RNA sequences used for computational modeling. Underlined, htRNA; Black, respective hsa-pre-miRNA sequence; Red and Green, miRNA guide and passenger strand, respectively; Orange, anticodon; Bold, "CCA" tail. Sequences attained from the Genomic tRNA Database (GtRNAdb), *miRBase.org*, or our recent publications.

Target ncRNA	Length (nt)	Sequence (5' to 3')	MW (Da)
htRNA^{Gly} (anticodon GCC)	74	GCAUGGGUGGUUCAGUGGUAGAAUUCUCGCCUGCCACGCGGGAGGC CCGGGUUCGAUUCCCGGCCCAUGCA**CCA**	24,022
htRNA^{Leu} (anticodon UAA)	86	ACCAGGAUGGCCGAGUGGUUAAGGCGUUGGACUUAAGAUCCAAUGG ACAUAUGUCCGCGUGGGUUCGAACCCCACUCCUGGUA**CCA**	27,905
hsa-pre-miR-34a-5p	114	GGCCGGGCCAGCUGUGAGUGUUUCUUUGGCAGUGUCUUAGCUGGUU GUUGUGAGCAAUAGUAAGGAAGCAAUCAGCAAGUAUACUGCCCUAG AAGUGCUGCACGUUGUUGGCCC	36,975
hsa-pre-miR-124-3p	85	AGGCCUCUCUCUCCGUGUUCACAGCGGACCUUGAUUUAAAUGUCCA UACAAUUAAGGCACGCGGUGAAUGCCAAGAAUGGGGCUG	27,505
hsa-pre-miR-7-5p	110	UUGGAUGUUGGCCUAGUUCUGUGUGGAAGACUAGUGAUUUUGUUG UUUUUAGAUAACUAAAUCGACAACAAAUCACAGUCUGCCAUAUGGC ACAGGCCAUGCCUCUACAG	35,461
hsa-pre-miR-34a/miR-124-3p	109	GGCCAGCUGUGAGUGUUUCUUUAAGGCACGCGGUGAAUGCCGUUGU GAGCAAUAGUAAGGAAGCGGUGUUCCCGUCGUGCCUUCUAGAAGUG CUGCACGUUGUUGGCCC	35,351
hsa-pre-miR-34a/miR-7-5p	109	GGCCAGCUGUGAGUGUUUCUUUGGAAGACUAGUGAUUUUGUUGUGU GAGCAAUAGUAAGGAACAACAAAAUACUCAGUCUUCCCUAGAAGUG CUGCACGUUGUUGGCCC	35,266
BioRNA^{Gly}/miR-34a-5p	180	GCAUGGGUGGUUCAGUGGUAGAAUUCUCGCCUGGCCAGCUGUGAGU GUUUCUUUGGCAGUGUCUUAGCUGGUUGUUGUGAGCAAUAGUAAGG AAGCAAUCAGCAAGUAUACUGCCCUAGAAGUGCUGCACGUUGUUGG CCCACGCGGGAGGCCCGGGUUCGAUUCCCGGCCCAUGCACCA	58,237
BioRNA^{Leu}/miR-34a-5p	192	ACCAGGAUGGCCGAGUGGUUAAGGCGUUGGACUGGCCAGCUGUGAG UGUUUCUUUGGCAGUGUCUUAGCUGGUUGUUGUGAGCAAUAGUAAG GAAGCAAUCAGCAAGUAUACUGCCCUAGAAGUGCUGCACGUUGUUG GCCCGAUCCAAUGGACAUAUGUCCGCGUGGGUUCGAACCCCACUCC UGGUACCA	62,110
BioRNA^{Gly}/miR-124-3p	180	GCAUGGGUGGUUCAGUGGUAGAAUUCUCGCCUGGCCAGCUGUGAGU GUUUCUUUAAGGCACGCGGUGAAUGCCGUUGUGAGCAAUAGUAAGG	58,259

		AAGCGGUGUUCCCGUCGUGCCUUCUAGAAGUGCUGCACGUUGUUGG CCCACGCGGGAGGCCCGGGUUCGAUUCCCGGCCCAUGCACCA	
BioRNA^{Leu}/miR-124-3p	192	ACCAGGAUGGCCGAGUGGUUAAGGCGUUGGACUGGCCAGCUGUGAG UGUUUCUUUAAGGCACGCGGUGAAUGCCGUUGUGAGCAAUAGUAAG GAAGCGGUGUUCCCGUCGUGCCUUCUAGAAGUGCUGCACGUUGUUG GCCCGAUCCAAUGGACAUAUGUCCGCGUGGGUUCGAACCCCACUCC UGGUACCA	62,132
BioRNA^{Gly}/miR-7-5p	180	GCAUGGGUGGUUCAGUGGUAGAAUUCUCGCCUGGCCAGCUGUGAGU GUUUCUUUGGAAGACUAGUGAUUUUGUUGUGUGAGCAAUAGUAAG GAACAACAAAAUACUCAGUCUUCCCUAGAAGUGCUGCACGUUGUUG GCCCACGCGGGAGGCCCGGGUUCGAUUCCCGGCCCAUGCACCA	58,174
BioRNA^{Leu}/miR-7-5p	192	ACCAGGAUGGCCGAGUGGUUAAGGCGUUGGACUGGCCAGCUGUGAG UGUUUCUUUGGAAGACUAGUGAUUUUGUUGUGUGAGCAAUAGUAA GGAACAACAAAAUACUCAGUCUUCCCUAGAAGUGCUGCACGUUGUU GGCCCGAUCCAAUGGACAUAUGUCCGCGUGGGUUCGAACCCCACUC CUGGUACCA	62,093

Supplemental Figure S1. Methods for constructing the pBSK/BioRNA plasmids. The $BioRNA^{Leu}$ and $BioRNA^{Gly}$ plasmids were cloned using an In-Fusion cloning kit where the target inserts were amplified by two methods. In Method #1 ($BioRNA^{Leu}$ in this study), the inserts were obtained directly through PCR amplification using primers with 16-nt complementary base pair overlaps (**Table S2**) and then cloned into the pBSKrna vector. In Method #2 ($BioRNAs^{Gly}$), the inserts were obtained through PCR amplification using respective pBSK/$BioRNA^{Leu}$ plasmids as templates and htRNA specific primers (**Table S2**). The resultant pBSK/BioRNA plasmids were transformed into Stellar™ Competent Cells (*E. coli* HST08 stain) for plasmid propagation and target BioRNA overexpression.



Supplemental Figure S2. Screen for antiproliferative effects of 48 novel BioRNAs against human pancreatic cancer AsPC-1 cells. Cell viability values were determined by CellTiter-Glo assay at 72 h post-transfection with 15 nM recombinant miRNAs, control RNAs or vehicle. Control RNA groups were set as 100%. Values are mean ± SD (N = 4 biological replicates per group). #Several BioRNAs published recently were included for comparison. The data demonstrate an overall similar impact of the BioRNA^{Gly}- and BioRNA^{Leu}-based miRNA on AsPC-1 cell viability. BioRNA/miR-7-5p used for further studies are underlined. *P < 0.05, as compared to respective control RNA (one-way ANOVA with Bonferroni post hoc tests).