

## Supporting Information

### **UTRs and Ago-2 / miR-335 complex restricts amylin translation in insulinoma and human pancreatic $\beta$ -cells**

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Supplemental materials contain the following information: *Figure S1*: Bioinformatics analysis of miRNAs seed-sequences in hIAPP 3'UTR, *Figure S2*: Control and hIAPP UTRs cloning sequences, *Tables S1, S2*: mRNA and miRNA primer sequences used for gene expression analysis.

**1. has-miR-124**

5' ...UCCCUUUAUGAAGUGUGCCUUAG... (UTR) **Position 1(1528-1535)**

|||||  
3' CGUAAGUGGCGCACGGAUU (miR)

**2. has-miR-143**

5' ...UUAACAGUGCCCUUUUCAUCUCC... (UTR) **Position 1(193-199)**

||||| |||||  
3' CUCGAUGUCACGA---AGUAGAGU (miR)

5' ...AGCCGAGAUUGCACCACUGCACU... (UTR) **Position 2(731-737)**

|||| |||||  
3' UGGUCUCUACGUCG-UGACGUGG (miR)

**3. has-miR-155**

5' ...GGUAGCUUUGGAAGUAGCAUUAA... (UTR) **Position 1(1369-1376)**

|||||  
3' UGGGGAUAGUGCUAAUCGUAAUU

**4. has-miR-182**

5' ...CCAGCAACAACUUUGUGCCAUU... (UTR) **Position 1(22-28)**

|||||  
3' UCACUUAAGAUGGUCACGGU (miR)

**5. has-miR-330 – overlapped sequences in 3' UTR (highlighted in grey)**

5' ...UUAAAAGUAUAAAACUGCUUUGU... (UTR) **Position 1 (997-1003)**

|||||  
3' AGAGACGUCCGGCACACGAAACG (miR)

5' ...UUAAAAGUAUAAAACUGCUUUGU... (UTR) **Position 2 (1298-1304)**

|||||  
3' AGAGACGUCCGGCACACGAAACG (miR)

5' ...GAAGAUGAAAUGCUUUGCUUUGA... (UTR) **Position 3 (1303-1310)**

|||||  
3' AGAGACGUCCGGCACACGAAACG (miR)

**6. has-miR-335**

5' ...GGACCAGGCGCGGUGGCUCUUGC... (UTR) **Position 1 (505-511)**

|||||  
3' UGUAAAAAGCAAUAACGAGAACU (miR)

**7. has-miR-376**

5' ...AAAAUAAGCAUUUCAAUCUAAG... (UTR) **Position 1 (1467-1471)**

|||||  
3' AUGAGUAUCUCCUCUUAGAUG (miR)

5' ...AUUUUAUAAUAAAUUCUAUGUC... (UTR) **Position 2 (1625-1631)**

||| |||||  
3' UGCACCUUAAAGGAGAUACAA (miR)

8. **has-miR-378**  
 5' ...CAGGCAGAUACAAGGUCAGGAG... (UTR) **Position 1 (558-564)**  
                               |||||  
 3'  UGUGUCCUGGACCUCAGUCCUC  (miR)
9. **has-miR-495**  
 5' ...GUCUGUGUGUCUGAUGUUUGUUG... (UTR) **Position 1(230-236)**  
                               |||||  
 3'  UUCUUCACGUGGUACAAAACAAA  (miR)
- 5' ...UUUUUAAAGUCUAUUGUUUGUUG...(UTR) **Position 2 (950-956)**  
                               |||||  
 3'  UUCUUCACGUGGUACAAAACAAA  (miR)
10. **has-miR-506**  
 5' ...UCCCUUUAUGAAGUGUGCCUAG... (UTR) **Position 1(1529-1535)**  
                               ||| |||||  
 3'  AGAUGAGUCUUCCCACGGAUG
11. **has-miR-634**  
 5' ...AUUGUUUGUUGUGCUUGCUGGUA... (UTR) **Position 1 (962-969)**  
                               ||| |||||  
 3'  CAGGUUUAACCCC-ACGACCAA  (miR)
12. **has-miR-1185 – overlapped sequences in 3' UTR (highlighted in grey)**  
 5' ...UCUGGAAACUCUUUG-CUGUAUAA... (UTR) **Position 1(1189-1196)**  
                               ||| |||||  
 3'  UACUCUCAGAGGGGGACAUUA
13. **has-miR-4789 – overlapped sequences in 3' UTR (highlighted in grey)**  
 5' ...CUGGAAACUCUUUGCUGUAUAAG... (UTR) **Position 1 (1190-1196)**  
                               |||||  
 3'  GUAUGUGUAUAGUCCACAUAUG  (miRNA)
- 5' ...UGGUAGCGGUAGUGAGUGUAUAAG... (UTR) **Position 2 (1590-1596)**  
                               |||||  
 3'  GUAUGUGUAUAGUCCACAUAUG  (miRNA)

**Figure S1.** Bioinformatics analysis of IAPP mRNA 3'-UTR. Databases comprising predicted and validated miRNA-target interactions were used. miRanda (<http://www.microrna.org/microrna/home.do>), DIANA-microT-CDS, mirDB (<http://ophid.utoronto.ca/mirDIP>) and TargetScan ([http://www.targetscan.org/vert\\_71](http://www.targetscan.org/vert_71)) collect predicted miRNA targets. Two databases, miRtarbase (<http://mirtarbase.mbc.nctu.edu.tw>) and DIANATarbase (<http://diana.imis.athena-innovation.gr/DianaTools/index.php?r1/4site/index>), contained validated miRNA targets. Putative miR's seeding positions (underlined) were predicted using TargetScan ([http://www.targetscan.org/vert\\_71](http://www.targetscan.org/vert_71)).

**Control 5'-UTR<sup>1</sup>:** 5'- (HindIII) AAGCTT GGCATTCCGGTACTGTTGGTAAAGCCA CCATGG (NcoI)

**Control 5'-UTR<sup>2</sup>:** 5'- (SpeI)

ACTAGTTAGCAAATGAGGGGGTAAATATTCCAGTGGATACAAGCTTGGACTCTTTTCTTGAAGCTTT  
CTTTCTATCAGAAGCATTTGCTGATATTGCTGACATTGAAACATTAAAAG CCATGG (NcoI)

**Control 3'-UTR:** 5'- (XbaI) TCTAGA GTCGGGG CGGCCGGCC (FseI)

**hiAPP 5'-UTR (152 bp):**

5'GGGTATATAAGAGCTGGATTACTAGTTAGCAAATGAGGGGGTAAATATTCCAGTGGATACAAGCTT  
GGACTCTTTTCTTGAAGCTTTCTTTCTATCAGAAGCATTTGCTGATATTGCTGACATTGAAACATTAAA  
AGAAAATTTGAGAAGCA

**IAPP 3'UTR (1554 bp):**

5'AGGACAATGTAACCTCTATAGTTATTGTTTTATGTTCTAGTGATTTCCCTGTATAATTTAACAGTGCCCT  
TTTCATCTCCAGTGTGAATATATGGTCTGTGTGTCTGATGTTTGTTGCTAGGACATATACCTTCTCAA  
AAGATTGTTTTATATGTAGTACTAAGGTCCCATATAAAAAAGATAGTATCTTTTAAAATGAAATG  
TTTTTGCTATAGATTTGTATTTTAAACATAAGAACGTCATTTTGGGACCTATATCTCAGTGGCACAG  
GTTTAAGAACGAAGGAGAAAAAGGTAGTTTGAACCTTGGTAAATTGTAAACAGCTAATAATGAAGTTA  
TTCTTGACATGAGAAAATCAGTAATTGGACCAGGCGCGGTGGCTCTTGCCTGTAATCCCAGCACTTT  
GGGAGGCCGAGGCAGGCAGATCACAAGGTCAGGAGTTCGAGACCAGCCTGACCAACATGGTGAAA  
CCCTGTCTCTACTAAAAATACAAAAATTAGCCGGGGGTGGTGACATGTGCCTGTAATCCCAGCTACT  
CAGGAGGCTAAGGCAGGAGAATCGCTTAAACCCAGGAGGCGGAGGTTGCAGTGAGCCGAGATTGC  
ACCACTGCACTCCAGCCTGGGTGGCAGAGTGAGACTCGTCTCAAAAAAAGAAAGAAAATTAGTAAT  
TGTAAGTACCCCTGATAAGCAAATTAGTAATTGTCAATACCCCTGTTAAGCAATTCCTTTTTGCAGTA  
TATTTCTGAAATGACAGAATGCTGTTTTAAAAACAAAGAAATAAAATCCTGCTCCTGACTCGGTCAA  
ATATTTTTTAAAGTCTATTGTTTGTGCTTGCTGGTACTAAGAGGCTATTTAAAAGTATAAACTGC  
TTTGTATCCATGAGGGTTTCATTGTGTGTTAGCAGCAGTGAGCTTCTATTAAATGTATATGTCATTTAT  
TTTGTTTAAAGTGGCTTTCAGCAAACCTCAGTCATATTCTTATGCAGGGTATTGCGAAACAACTTGTGT  
TCTATTAATCGTGTCTTCAATTAAGACACAGACTTCTGGAACTCTTTGCTGTATAAGAATTATTT  
CTTTTGTTTAACAAATTAGACATTTCTGGCAGAGGTTATGTATATGATACACTTTTTTTGATAGCAGCT  
GCAATGTTGGACAGAAGATGAAATGCTTTGCTTTGAGTCAGATTCTTATGAATATCTGCTTTTCCCTG  
ACTTTGAGTTAGGTAGCTTTGGAAGTAGCATTAAATCAGATAAACTGCCATCATGCTGCGTTATGCCA  
TTTCTAAAGACACTCAACTTGTACTTTTTAAAAAATAGAAAAAATAAGCATTTCAATCTAAGTGGAAT  
TTGACTCATTGACTTACATTTCTAAGTTAAATTTCCCTTTATGAAGTGTGCCTTAGGTTACCAAATTG  
TAGAGGCTTTCGTTGGTGGTGGTAAGTGGTAGCGGTAGTGAGTGTATAGAGGCAGGGAAATATATT  
TATAATAAATTCTATGTCATGAATTACATATTGAAATAAATAGGTGAATATACAAATTTATA

**Figure S2.** Control and hiAPP UTRs cloning sequences.

Primers	Sequences
hIAPP	F: 5'-AGCTACACCCATTGAAAGTCATC-3' R: 5'-GATGAGAGAATGGCACCAAAGT-3'
Insulin	F: 5'- TGTCTTCTGCCATGGCCCT-3' R: 5'-TTCACAAAGGCTGCGGCTGG-3'
$\beta$ -actin	F:5'-AGGCACCAGGGCGTGAT-3' R:5'-GCCCACATAGGAATCCTTCTGAC-3'
TXNIP	F: 5'-ACAGAAAAGGATTCTGTGAAGGTGAT-3' R: 5'-GCCATTGGCAAGGTAAGTGTG-3'
BIP	F: 5'-GAACGTCTGATTGGCGATGC-3' R: 5'-ACCACCTTGAACGGCAAGAA-3'

**Table S1. mRNA primer sequences used for gene expression.**

Primers	Sequences (3' to 5')	Accession No.	Position
hsa-miR- 124-3p	UAAGGCACGCGUGAAUG CCAA	MIMAT0000422	53–74
hsa-miR-155-3p	CUCCUACAUUUAGCAUUAACA	MIMAT0004658	43-64
hsa-miR- 182-3p	UGGUUCUAGACUUGCCAA CUA	MIMAT0000260	67-87
hsa-miR-376A-3p	AUCAUAGAGGAAAAUCCACGU	MIMAT0000729	44-64
hsa-miR-330-3p	GCAAAGCACACGGCCUGCAGA GA	MIMAT0000751	57-79
hsa-miR-335-3p	UUUUUCAUUAUUGCUCUGAC C	MIMAT0004703	52-73
hsa-miR-378A-3p	ACUGGACUUGGAGUCAGAAGG C	MI0000732	43-64
hsa-miR- 432-3p	CUGGAUGGCUCUCCAUGU CU	MIMAT0002815	62-82
hsa-miR-495-3p	AAACAAACAUGGUGCACUUCUU	MIMAT0002817	50-71
hsa-miR-506-3p	UAAGGCACCCUUCUGAGUAGA	MIMAT0002878	71-91

**Table S2. miRNA primer sequences used for gene expression.**