

Supplemental Table 1

Name of the Oligo	Sequence (5'→3')
Fragment 1 FWD	ATGCTGGAAATGCTAGAATAT
Fragment 1 REV	CAGGATCCATCAAGCCCAAG
Fragment 2 FWD	CTTGCAAATGGCAAATACG
Fragment 2 REV	AATGCCGGTTGGCGTGCTCC
Fragment 3 FWD	TGTTGCTCAGAATAACAGGAAC
Fragment 3 REV	CTAACAAAGTGTGCTCCGTCTC
3'-UTR FWD	CGAATCCTCCCTGCACTGC
3'-UTR REV	ACAGAATAACATATTCTTTAAATAG
pBI-GL SENSE	TTACAATTGGACTTCCGCC
pBI-GL ANTI-SENSE	AATGTAACTGTATTCAAGCGATGAC
miR-340 Site I Del SENSE	ATAGCCCAGGATATATTATTAG
miR-340 Site I Del ANTI-SENSE	TTCATATTAAAGGAAAATTATCAAGAAAAC
miR-340 Site II Del SENSE	TGCAAACATTAAAGAAATATGTATTCTG
miR-340 Site II Del ANTI-SENSE	GGGTACTGTATCTTAAGGCAG
sponge-340 DNA oligonucleotide	<i>TCGAGAATCAGTCTCACCTTATAA</i> <u>CCGG</u> AATCAGT CTCTACCTTATAA <u>CCGG</u> AATCAGTCTCACCTTATA <u>CCGG</u> AATCAGTCTCACCTTATAA <u>CCGG</u> AATCAGTC TCTACCTTATAA <u>CCGG</u> AATCAGTCTCACCTTATAA <u>CCGG</u> AATCAGTCTCACCTTATAA <u>AGGGCC</u>
sponge-548c-3p DNA oligonucleotide	<i>TCGAGGCAAAAGTAAAACGATT</i> <u>CCGG</u> GCAAAAG TAAAACGATT <u>CCGG</u> GCAAAAGTAAAACGATT TG <u>CCGG</u> GCAAAAGTAAAACGATT <u>CCGG</u> GCAAAA GTAAAACGATT <u>CCGG</u> GCAAAAGTAAAACGATT TTG <u>CCGG</u> GCAAAAGTAAAACGATT <u>GGGGCC</u>

Supplemental Table 2

Name of the Oligo	Sequence (5'→ 3')
GAPDH FWD	ATGGTTGCCACTGGGGATCT
GAPDH REV	TGCCAAAGCCTAGGGGAAGA
MITF FWD	CCAGGCATGAACACACATTG
MITF REV	GCAGACCTGGTTCCATAAAG
Zebrafish MITF homolog FWD	GGCCGTCAAAAGGGAAATTATC
Zebrafish MITF homolog REV	ATTCCACCTCATGTCTGGATC
Zebrafish <i>α-tubulin</i> FWD	CTGTTGACTACGGAAAGAAGT
Zebrafish <i>α-tubulin</i> REV	TATGTGGACGCTCTATGTCTA
Long 3'-UTR Detection FWD	CCAAGAGGCAGTGGTTGGG
Long 3'-UTR Detection REV	AACCAAATGCTTAATGAGGCTATC
Medium 3'-UTR Detection FWD	GAAAACCGAACTGGGCATATTTC
Medium 3'-UTR Detection REV	GGTTATCAATCTCCAAGAATATTGC
Short 3'-UTR Detection FWD	CGAACCTCCCTGCAGTGC
Short 3'-UTR Detection REV	ACAGAATACATATTCTTAAATAG
Stem-loop RT primer for miR-340	GTCGTATCCAGTGCAGGGTCCGAGGTATTGCACTG GATACGACAATCAGTCT
Forward primer for miR-340:	GC GGCGGT TATAAGCAATG
Universal reverse primer	GC GGGTGCAGGGTCCGAGGT

Supplemental Table 3

Figure	Group	Average half-life (hrs)
2A	Wt	2.5
2A	Ex5	7.1
2B	Wt	2.7
2B	Ex5	5.6
2C	Wt	2.6
2C	Ex5	5.6
3A	Sponge CXCR4	3.2
3A	Sponge-340	6.6
3B	Sponge CXCR4	2.4
3B	Sponge 340	6.8
3D	WT	2.8
3D	340 mutant	5.1
4E	pcDNA	2.8
4E	CRD-BP	14
6A	Control	2.5
6A	Sponge-340	5.4
6A	CRD-BP	5.4
6A	CRD-BP + Sponge-340	5.3
6E	Control	6.4
6E	Sponge-340	7.8
6E	CRD-BP	6.8
6E	CRD-BP + Sponge-340	7.6

The half life of mRNA ($T_{1/2}$) was calculated as follows:

$$T_{1/2} = \frac{T \times \log 2}{\log AmtB/AmtE}$$

Where:

$T_{1/2}$ =Half Life of mRNA

T = Elapsed Time after addition of Doxycycline

AmtB = Average Beginning Amount of mRNA

AmtE = Average Ending Amount of mRNA