

Supplemental Table 2

<u>Name of the Oligo</u>	<u>Sequence (5' → 3')</u>
GAPDH FWD	ATGGTTGCCACTGGGGATCT
GAPDH REV	TGCCAAAGCCTAGGGGAAGA
MITF FWD	CCAGGCATGAACACACATTC
MITF REV	GCAGACCTTGTTTTCCATAAAG
Zebrafish MITF homolog FWD	GGCCGTCAAAAGGGAATTATC
Zebrafish MITF homolog REV	ATTCCACCTCATGTCTGGATC
Zebrafish <i>α-tubulin</i> FWD	CTGTTGACTACGAAAGAAGT
Zebrafish <i>α-tubulin</i> REV	TATGTGGACGCTCTATGTCTA
Long 3'-UTR Detection FWD	CCAAGAGGCAGTGGTTTGGG
Long 3'-UTR Detection REV	AACCAAATGCTTTAATGAGGCTATC
Medium 3'-UTR Detection FWD	GAAAACCGAACTGGGCATATTTT
Medium 3'-UTR Detection REV	GGTATCAATCTCCAAGAATATTGC
Short 3'-UTR Detection FWD	CGAATCCTCCCTGCACTGC
Short 3'-UTR Detection REV	ACAGAATACATATTTCTTTAAATAG
Stem-loop RT primer for miR-340	GTCGTATCCAGTGCAGGGTCCGAGGTATTTCGCACTG GATACGACAATCAGTCT
Forward primer for miR-340:	GCGGCGGTTATAAAGCAATG
Universal reverse primer	GCGGGTGCAGGGTCCGAGGT

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:

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

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