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# Dicer によるマイクロ RNA 前駆体 (pre-miRNAs) 切断反応に 及ぼす小分子

# A Study of The Effects of Small Molecules on Dicermediated Cleavage of Precursor miRNAs (pre-miRNAs)

Ph.D. Thesis

Ву

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## ABSTRACT

MicroRNA (miRNA) is a small (18-22 nucleotides) and evolutionary conserved noncoding RNA that is expressed as a post-transcriptional regulator of living cells and is known to be implicated in various cellular processes and diseases. On the normal condition, miRNA was tightly regulated in the cells, however, the aberrant expression of this type of non-coding RNA would result in cancer, and this type of miRNA is commonly referred to as oncomirs. Inhibition is preferred to overcome this unfavorable overexpression.

A combination screening strategy was used to find a small molecule with the potential to be an inhibitor of miRNA production. This type of screening strategy was a hybrid of targetbased screening and cell-based screening. The goal of this combination was to overcome the limitations of target-based screening, which did not take into account the physiological aspects of the living organism, and also cell-based screening, that considered as mechanismagnostic screening. The combination of both types of screening would increase the relevance of screening results to physiological conditions and make it easier to track the mechanism of action behind the inhibition.

Uterine corpus endometrial carcinoma (UCEC) was chosen to apply those screening concepts due to the lack of alternative drugs available to cure this kind of cancer. Several UCEC-associated miRNAs reported by Favier A., et al. then were used to demonstrate the inhibition of small molecules to the production of UCEC-associated miRNAs (miR-182, miR-31, miR-30d). Nakatani group, on the other hand, developed small molecules with nucleobase recognition sites, such as guanine recognition by N-Acyl-2-amino-7-methyl-1,8-naphthyridine, adenine recognition by 7-methyl-2-oxo-1,8-naphthyridine (azaquinolone), and cytosine recognition by protonated 2-amino-7-methyl-1,8-naphthyridine. These small molecules are designed to specifically bind the complementary nucleobase on the nucleic acids. If those small molecules can bind to miRNA precursors, they may inhibit oncogenic miRNA production.

The first chapter of this dissertation described the framework and background of the research. In chapter 2, the use of Real-time PCR (qPCR) to determine the kinetical properties of an *in-vitro* Dicer reaction was investigated. However, due to a number of challenges, the results of this experiment did not meet the expected results.

In chapter 3, We demonstrated a multistep qPCR-based screening of an in-house chemical library that targets UCEC-associated miRNA production using the screening strategy that

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combined the target-based screening and cell-based screening assay. *In-vitro* Dicer-mediated processing of pre-miR-182, pre-miR-31, and pre-miR-30d was used for the initial screening. The first screening yielded 48 different compounds with significant inhibition effects on miRNA production. The inhibitory effect of the identified compounds on the biogenesis of the miRNA targets on the cells was then investigated. We discovered eight hit compounds with potential inhibitory effects on pre-miR-182 and pre-miR-31 processing in vitro and in cells. Furthermore, the interaction of eight compounds with pre-miRNAs was studied using the Surface Plasmon Resonance (SPR) assay and gel analysis. Among eight hit compounds, only 2 compounds showed favorable binding to pre-miRNAs. This suggested two possible ways of inhibition may occur, first, the compounds bind to the pre-miRNA and interfere with the Dicer-mediated cleavage processing, or the compounds directly interact with Dicer and affected the cleavage processing.

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# Abbreviation

AGO I	Argonaute RISC Component 1
ATP	Adenosine Triphosphate
BSA	Bovine Serum Albumin
CCK-8	Cell-counting kit 8
cDNA	complementary DNA
CT value	Cycle Threshold Value
DANP	N,N'-bis(3-aminopropyl)-2,7-diamino-1,8-naphthyridine
dNTP	deoxynucleoside triphosphate
EDTA	Ethylenediaminetetraacetic acid
FDA	Food and Drug Administration (agency within the United States Department of Health and Human Services)
IC <sub>50</sub>	Inhibition Concentration- 50
Km	Michaelis Constant
MBLs	Mismatch Binding Ligands
miR-X	microRNA-X
miRNA	microRNA
MOA	Mechanism of Action
NA	Naphtiridine Azaquinolone
ND	Naphtiridine Dimer
PCR	Polymerase Chain Reaction
pre-miRNA	precursor microRNA
qPCR	quantitative / Real-time Polymerase Chain Reaction
RISC	RNA-Induced Silencing Complex
RNA	Ribonucleic Acids
RNA Pol II	RNA Polymerase II
RT	Reverse Transcription
RT-qPCR	Reverse Transcription - quantitative / Real-time Polymerase Chain Reaction
SA	Streptavidin
SPR	Surface Plasmon Resonance
TCGA	The Cancer Genome Atlas
TRBP	Transactivation Response element RNA-binding Protein
UCEC	Uterine Corpus Endometrial Carcinoma
Vmax	Maximum rate of reaction
WST	Water-soluble Tetrazolium

# CHAPTER I General Introduction

# **1.1** MicroRNA (miRNA) as a Post-transcriptional Gene Regulator and Cancer Therapeutics

miRNAs are a class of evolutionary conserved small non-coding RNA with 18-22 nucleotides in length, which regulate gene expression through translational repression and mRNA degradation. (1,2) The biogenesis of miRNAs as illustrated in Figure 1.1, begins with the transcription of the miRNA gene in the nucleus by RNA Pol II, and the primary miRNAs (pri-miRNAs) are capped, spliced, and polyadenylated. RNase III-type enzyme Drosha cleaves long pri-miRNAs into precursor miRNAs (pre-miRNAs), and the resulting pre-miRNAs are exported from the nucleus to the cytoplasm by Exportin. Another RNase III-type enzyme Dicer then processes the pre-miRNA to produce mature miRNA. The RNA-induced silencing complex (RISC), which includes TRBP and AGO I, complements target mRNAs for post-transcriptional gene silencing. (3)



Figure 1.1 microRNA Biogenesis

The expression of miRNA is tightly regulated in normal cells, but dysregulation of miRNA expression has been observed in many types of cancer (oncogenic miRNA / oncomirs). The dysregulation of miRNA expression can cause some types of cancer including breast cancer, pancreatic cancer, prostate cancer, and lung cancer. (3-8) Several strategies have been developed to treat these cancers, by targeting the oncogenic miRNAs.

Krutzfeldt et al. developed antisense oligonucleotides (antagomirs), which are miRNA inhibitors that work by annealing to the mature miRNA's guide strand and inducing degradation or stoichiometric duplex formation, to block the overexpressed oncomirs. Their research focuses on improving the stability and specificity of antagomirs by adopting 2'-OMe-modified nucleotides with a phosphorothioate linkage that complements miR-122. (9,10) The antagomirs against miR-122 (antagomir-122) were administered to mice, and could decreased endogenous miR-122 level to undetectable level as long as 23 days post-injection. (11,12) Another strategy for inhibiting oncomir overexpression is genome editing using CRISPR/Cas9. Zhao et al used this strategy to downregulate miR-17-92 cluster and miR-21 by in vitro experiment. (13) Other researchers applied Cas9 mRNA and guide RNA into zebrafish embryos, as the result they reported chromosomal deletions and inversions. (14)

These strategies reported previously are shown to have adverse effects. Galbraith W.M., et al. reported that after administering antagomirs to monkeys, peripheral white blood cell counts decreased. Another issue raised by the use of antisense oligonucleotides is that these miRNA inhibitors may be unable to distinguish between members of the same family of miRNA. In contrast to the antisense oligonucleotide strategy, CRISPR/Cas9 gene-editing results in permanent gene modifications. However, the off-target effects have not been precisely profiled, this genome editing method must be improved further before being used as a substitute for cancer/disease therapy. (15,16,17)

Due to the challenges that come with those miRNA inhibitors, it may be useful to develop another strategy for inhibiting miRNA functions. Numerous strategies could be used to discover a novel method of inhibiting oncomirs overexpression. It is not necessary to develop inhibitors from scratch, rather, it is possible to repurpose currently available small molecules/drugs for miRNA inhibition by screening for the most suitable inhibitor candidates while also obtaining a drug candidate.

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Target-based screening or biochemical assay is one of the strategies that are usually used if the target was identified. Coussens N.P. et al. describe this type of assay as having a variety of schemes, for example, to detect the binding between a small molecule and the target can be observed directly using fluorogenic products, or it can be coupled to a reporter that facilitates detection, such as luciferases. This biochemical assay is frequently used in combination with another analytical instrument, such as mass spectrometry, to quantify reaction products. (18-20)

Another screening approach is phenotypic assay. The advantage of target-based screening or biochemical assays is that they are more direct methods for quantifying or analyzing the effect of a small molecules on a target of interest, however, these strategies do not always reflect the biochemical processes in complex cellular environments. It is common for drug candidates to appear potent when tested in biochemical assays but fail to work in the cellular environment. Phenotypic assays cover a wide range of assessment techniques, from the simplest such as cell death or growth arrest to the use of animal models. The limitation of this type of assay is that it is mechanism-agnostic, which means that it cannot be used to determine the mechanism of action. (21-24)



Figure 1.2 Dicer-mediated pre-miRNA maturation inhibition pathway

With the desire to find a new inhibitor of disease-associated miRNAs, the middle point of those two screening strategies would be preferred. We have attempted to target the biogenesis process of miRNAs by a small molecule (Figure 1.2), to inhibit the diseaseassociated miRNA. From the miRNA biogenesis process, we chose Dicer-mediated cleavage of pre-miRNA for a target-based screening. We also adopted a cell-based assay to see the effect of small-molecule on endogenous miRNA production. The adoption of a mechanism-specific assay, such as an in-vitro Dicer cleavage reaction, would resolve the phenotypic assay's mechanism-agnostic problem. On the other hand, adopting a cell-based assay would more reflect the biochemical processes in complex cellular environments. (25)

Applying those concepts to tackling the disease, we choose Uterine Corpus Endometrial Carcinoma (UCEC) as a cancer case model. UCEC is a malignant tumor of the female reproductive system that develops from the uterus's inner lining cells and is a major threat to women's health worldwide. (26,27) Additionally, UCEC accounts for approximately 20%-30% of female reproductive system cancers, ranking second only to cervical cancer. (28) Only a few drugs have been approved by the FDA for the treatment of this type of cancer. These drugs includes Pembrolizumab (Keytruda), Dostarlimab-gxly (Jemperly), Lenvatinib (Lenvima), and Megastrol (Megace). Due to the limited alternatives of available drugs, the discovery of novel drug candidates holds great promise for risk management and personalized therapeutic approaches for UCEC. (29)

A study by Favier A. et al. demonstrated a significant increase in the level of several miRNA expressions associated with this type of carcinoma, including miR-182, miR-31, and miR-30d. Similarly, the Cancer Genome Atlas (TCGA) revealed similar findings. In this study, we selected those three miRNAs as a model for implementing the combination of target-based and cell-based assay as described previously. (30)

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Figure 1.3 Stem-loop Reverse Transcription Real-Time PCR (RT-qPCR) Scheme

To evaluate miRNA production during the Dicer-mediated cleavage reaction, as well as miRNA expression during the cell-based assay, we used real-time PCR as the main instrument due to its fast and high-throughput detection and quantification of target nucleic acids sequences. (31) Due to specificity and sensitivity to detect and amplify the mature miRNA during reverse transcription (RT) reaction, stem-loop RT primer was used as illustrates in Figure 1.3. (32)

## **1.2 Sequence-Specific Small Molecules**

Nakatani group has developed a number of sequence-specific DNA mismatch binding ligands (MBLs) that are capable of recognizing and binding to bulged sites and mismatched base pairs in duplex DNA (Figure 1.4). The developed molecules work by occupying the spaces and forming hydrogen bonds to the mismatched nucleotide bases. These ligands are then stabilized through stacking interactions with adjacent base pairs. (33)



**Figure 1.4** Nucleobase recognition parts. (a) Guanine recognition by *N*-Acyl-2amino-7-methyl-1,8-naphthyridine, (b) Adenine recognition by 7-methyl-2oxo-1,8-naphthyridine (azaquinolone), (c) Cytosine recognition by protonated 2-amino-7-methyl-1,8-naphthyridine

Naphtiridine Dimer (ND) is a dimeric form of *N*-acyl-2-amino-1,8-naphtiridine, which was the first compound designed to recognize G-G mismatches. From a structural perspective, this molecule was consists of two naphtyridine heterocycles connected by a linker. Two naphtyridine form hydrogen bonding with the guanine, and the linker that contained a secondary amino group offers the appropriate conformational restriction to the dynamic motion of two heterocycles besides providing attractive electrostatic interaction to negatively charged DNA and gained water solubility. (34-36)

8-azaquinolone, which is a complement to adenine in terms of its hydrogen bonding surface was utilized to develop another molecule that could recognize G-A mismatches, naphtiridine-azaquinolone (NA). In another case, a hydrogen bonding rearrangement of the donor-donor-acceptor groups of cytosine was required to develop C-C mismatch recognition, which was achieved through the development of a protonated form of 2-amino-1,8-naphtiridine. This molecule meets the requirement that needed, and it is also reported that 2-amino-1,8-naphtiridine is strongly and selectively bound to C-C mismatch. (37-40)

Due to the specific nucleobase recognition properties of the small molecules synthesized and developed by Nakatani group, it is highly likely that those small molecules will bind to pre-miRNAs that has the unpaired nucleotides in their structure, which may affect the miRNA maturation process. If small molecules could inhibit UCEC-associated oncogenic miRNA production *in vitro* and also in cells, then those small molecules have the potential to be drug candidates.

#### **I.3 Objectives**

The objective of this research is to analyze the effect of the small molecule on the Dicer-mediated cleavage of pre-miRNA *in vitro* and in cells, seeking for potential small-molecule candidates for treating UCEC that are associated with miRNA dysregulation. To achieve that objective, we demonstrated a combination of assays between target-based assay and cell-based assay to screen the small molecules that shows the potential inhibitory activity to mature miRNA production.

Aside from that, the results and the screening methods from this research could be used for consideration in the development of a high throughput screening system of the small molecules that targeting UCEC-associated miRNA.

# CHAPTER II Utilization of Real-Time PCR to determine Kinetical Properties of Invitro Dicer reaction

# 2.1 Introduction

A small molecule that binds to a specific pre-miRNA and inhibits or accelerates its processing can be a tool for modulating miRNA-mediated gene regulation. It was previously reported that by protonating the nitrogen in the 2,7-diamino-1,8-naphthyridine chromophore, N,N'-bis(3-aminopropyl)-2,7-diamino-1,8-naphthyridine (DANP) could form hydrogen bonds with cytosine as shown in Figure 2.1 A. (39) This compound, however, has a limitation in that it does not bind to RNA. To address this issue, this compound was modified by the addition of an expanded ring system (BzDANP) (Figure 2.1 B), which may improve stacking interaction with neighboring base pairs in RNA. (40)



Figure 2.1 DANP could form hydrogen bonding with cytosine (A) and BzDANP (B)

Further studies of BzDANP by Otabe, et.al shows that BzDANP reduced the initial velocities of the pre-miR-136 Dicer cleavage reaction, resulting in a significant decrease in Vmax.(41) BzDANP has the potential to be used in other pre-miRNAs, but one of the major

challenges is determining the kinetical properties of this compound in Dicer-mediated cleavage reactions in a more direct and convenient way than isotope labeling. One option is to directly detect the product, which is miRNA, which can be done with real-time PCR. Here we conducted an experiment to determine the kinetical properties by using real-time PCR.

## 2.2 Results and Discussions

To determine the kinetical properties of *in vitro* dicer reaction, several different concentrations of substrates (pre-miR-136) were used, ranging from 25 nM to 400 nM, as well as different incubation times at the in vitro dicer reaction. The aliquots of the reaction solution separated after 2.5, 5, 10, 20, 40, 80, and 180 minutes incubation. Figure 2.2 and 2.3 shows the correlation between concentration miR-136 product and time for every variation concentration of substrate.

Table 2.1 shows every initial velocity from various substrate concentrations. The initial velocity then was plotted against substrate concentrations and the obtained plots were analyzed by least-squares fitting to the Michaelis-Menten equation. The Michaelis-Menten analysis for the *in vitro* dicer reaction of pre-miR-136 yielded a *Km* of 9.71 x 10<sup>15</sup> nM, and V<sub>max</sub> 4.31 x 10<sup>19</sup>nM min<sup>-1</sup>. The results obtained here are far different compared to the previous study by Otabe, et.al, in which they obtained Km of 52.6 ± 8.6 nM and Vmax of 1.52 ± 0.08 nM min<sup>-1</sup>.

The differences between these two result raised from the different methods that used. It is important to note that using qPCR as an instrument to measure the kinetical aspect especially in this *in-vitro* dicer reaction is still needs to be improved. Several critical points often occur during the experiments, the technical handling problem quite often becomes a problem due to multi-step procedures, from the sampling, preparation for reverse transcription, and the preparation for real-time PCR, especially for the standard curve technique. This makes the results are often difficult to reproduce in the same quality. Unfortunately, because of the limitation of time to overcome this problem, it is difficult to continue this experiment.

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Figure 2.2 Velocity plot of in vitro Dicer reaction by several different substrate concentration



Figure 2.3 Velocity plot of in vitro Dicer reaction by several different substrate concentrations

pre-miR	-136 (nM)	25	50	100	200	300	400
Vo	(nM/min)	0.0002	0.0019	0.0211	0.0064	0.0561	0.1224

# **2.3 Conclusion**

We have demonstrated the utilization of real-time PCR to investigate the kinetical properties of the *in vitro* dicer reaction. Compared to the previous study conducted by Otabe, et.al, we obtain significantly different results. As mentioned in the results and discussion section, the methods for utilizing real-time PCR to investigate the kinetic properties of enzymatic reactions particularly those used in the *in vitro* dicer reaction still require improvement. It would be preferable to reduce the systematical error aas possible, for example by using one-step RT-qPCR reagents, or digital droplet PCR which eliminates the need to create a standard curve.

# 2.4 Methods

#### 2.4.1 Time-dependent Dicer Cleavage Reaction

In the presence of a buffer reaction, phosphorylated precursor microRNA (25 nM), 50 mM MgCl<sub>2</sub>, 10 mM ATP, 0.05 percent BSA, and Dicer (50 nM) were mixed. 6 different variation concentration (25, 50, 100, 200, 300, 400 nM) of BzDANP was then added, with RNAse-free water serving as a negative control. After that, the mixture was incubated at 37°C for several variation time (0, 2.5, 5, 10, 20, 40, 80, 180 minutes). The reaction was then halted by adding 10 mM EDTA.

#### 2.4.2 Reverse Transcription Real-time PCR (RT-qPCR)

The 100 mM dNTP Mix, the Multiscribe Reverse Transcriptase, and the 5X Reverse Transcription primer were combined and incubated according to the manufacturer's protocol. After that, the mixture was mixed with the Taqman Master Mix. This mixture was then loaded to the real-time PCR instrument, and the resulting data were analyzed using the real-time PCR instrument's software.

# CHAPTER III Study of Mechanism of Action (MOA)-based Screening Assay of Small Molecules Targeting Uterine Corpus Endometrial Carcinoma (UCEC)-associated microRNA

## **3.1 Introduction**

UCEC is a malignant tumor of the female reproductive system that develops from the cells of the uterus's inner lining. It is a major threat to women's health globally. (26,27) Additionally, UCEC accounts for approximately 20%-30% of female reproductive system cancers, trailing only cervical cancer in this category. (28)

Because the available drugs to treat this type of cancer are still limited, it would be preferable to discover a new drug to treat this type of cancer. From a mechanism of action standpoint, the majority of drugs used to treat UCEC were either PD-1 binders or kinase inhibitors. For this reason, an alternative to searching for a new drug is to identify a potential pathway associated with this cancer that could be used as a starting point for drug discovery.

In this chapter, the screening of small molecules to find the UCEC drug candidates was demonstrated. All of the small molecules that used in this screening shows in Figure 3.1. MicroRNA biogenesis was adopted into the screening system to mimic the Dicer-mediated pre-miRNAs maturation process. This process is conducted in-vitro as previously mentioned as target-based screening. (18,19) The compounds obtained from this screening then continued to the in-cell screening, to know the effect of the small molecules in the living cells environment.

Further analysis was then performed on the small molecules that may possess the potential oncogenic miRNA inhibitors, such as SPR analysis to analyze the small molecule's binding affinity to the pre-miRNA and its viability, which measures the effect such as IC<sub>50</sub>.

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10G (10B_(N14266)ljx344)	9G (8A_(N14249)jjx238)	- 8G	7G (6C_(N160035) NCD-C3- NH2)	6G (2G_(N160007) PQA- C3-amide)	5G (5G_(N14031)NN246)	4G (11F_N132078)	3G (4E_N132021)	2G (6G_N131039)
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10E (9H_(N14264)ljx372)	9E (7E_(N14245)ijx107)	8E	7E (5A_(N160025) CMBL5a)	6E (2B_(N160002) 5H-iQ)	5E (5C_(N14027)YM011)	4E (9F_N132062)	3E (2A_N132001)	2E (6A_N131033)
WINNER	finition with			anteritan Anteritan		H CONCOLOR	$\stackrel{H_2N}{} \underbrace{\stackrel{NH_2}{}}_{N} \stackrel{H_2SO_4}{}_{NH_2} \stackrel{H_2SO_4}{}_{H_2O}$	
10D (9F_(N14262)ljx289)	9D (7D_(N14244)Jjx253)	8D	7D (4G_(N160023) CMBL4)	6D (10E_(N14069)NCT6)	5D (4H_(N14024)SM-221)	4D (8H_N132056)	3D (11H_N131080)	2D (4G_N131023)
Charles and a second	Murinian Station	HANNAR	munund	1.5 M 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	NH2 NH2	на 11 - 11 - 11 - 11 - 11 - 11 - 11 - 11		
10C (9B_(N14258)ljx188)	9C (7C_(N14243)BzNA)	8C (9A_(N160057) bAla- Nap)	7C (4C_(N160019) Am- BzND)	6C (8F_(N14054)BzDANP)	5C (4B_(N14018)SA029)	4C (6F_N132038)	3C (10B_N131066)	2C (4B_N131018)
	Winnigh	HAN N N N N N N N N N N N N N N N N N N	N N N NH2	H <sub>2</sub> N-{ -N -N -N -N -N -N -N -N -N -N	HOTLOH	AND		
10B (9A_(N14257)ljx280)	<sup>1</sup> 9B (7B_(N14242)ljx249)	8B (8D_(N160052) ih 039)	7B (4B_(N160018) Am-BzN)	6B (8A_(N14049)otb003)	5B (3H_(N14016)AIK112)	4B (5C_N132027)	3B (9H_N131064)	2B (2H_N131008)
Church Bornie	the for the second second	HO N N N N N N N N N N N N N N N N N N N				w. Wight we will		
10A (8H_(N14256)ljx305)	<sup>1</sup> 9A (7A_(N14241)jjx106)	8A (7H_(N160048)	7A (3C_(N160011) DDAP)	6A (7F_(N14046)5-	5A (2B_(N14002)AIK041)	4A (5B_N132026)	3A (8D_N131052)	2A (2B_N131002)

Figure 3.1 67 Library compounds from Nakatani Laboratory group

## **3.2** Results and Discussions

#### 3.2.1 In Vitro Dicer Reaction Screening

To determine the effects of small molecules in the dicer processing reaction, we performed *in vitro* dicer reaction by using pre-miR-182, pre-miR-31, and pre-miR-30d as the miRNA targets and 67 selected small molecules from the Nakatani laboratory library as tested compounds. The products of this reaction were either promoted or inhibited mature miRNA. However, to measure the product we need to perform a reverse transcription reaction to transcribe miRNA products to cDNA. This cDNA was then quantified using qPCR.

Figure 3.2 , 3.3, and 3.4 shows the qPCR results of three different miRNAs, each of which was replicated twice. The  $2^{-\Delta CT}$  expressions were used to evaluate the amount of cDNA that is directly proportional to the amount of miRNA products affected by each tested compound. For every compound that shows the  $2^{-\Delta CT}$  value greater than 1, this indicates that the compound promoted miRNA production, on the other hand, any compound with  $2^{-\Delta CT}$  value less than 1 inhibits miRNA production during the dicer processing reaction. To screen the compounds that would be used in the next step of screening, we introduced a  $2^{-\Delta CT}$  value of 0.5 as a threshold which is analogous to  $IC_{50}$  which indicates that certain compounds inhibited 50% of miRNA production. In this case, a lower  $2^{-\Delta CT}$  value indicates greater inhibition which is preferable. Aside from  $2^{-\Delta CT}$  expressions, the replication was also considered when selecting compounds for the next step of the screening, only compounds that passed the threshold twice were chosen for the next screening.

According to the criteria described above, Figure 3.2 demonstrates that 26 compounds pass the 0.5 threshold and also meet the replication criteria, indicating that those 26 compounds may exhibit inhibitory activity against the dicer-mediated pre-miR-182 processing reaction. The inhibition of pre-miR-31 and pre-miR-30d processing reaction shows in Figure 3.3 and 3.4, there are 31 and 22 different compounds that have shown potential inhibitory activity to the pre-miR-31 and pre-miR-30d.

The in vitro dicer reaction result was summarized in Figure 3.5, which shows 48 different small molecules inhibiting three different dicer-mediated pre-miRNA processing. All of it could be divided into three categories: compounds that appear to preferentially inhibit

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one type of miRNA, compounds that appear to preferentially inhibit two types of miRNAs, and compounds that appear to preferentially inhibit all three types of miRNAs.

Following that, we performed in-cell screening to investigate the biological significance of those 48 compounds in living cells.





Figure 3.2 In vitro Dicer screening of hsa-miR-182









Figure 3.4 In vitro Dicer screening of hsa-miR-30d

Figure 3.5 In vitro Dicer screening results and its summary

				_	_			
Total	miR-182-31-30d	miR-31 and miR 30d	miR-182 and miR-31	miR-182 and miR-30d	miR-30d	miR-31	miR-182	microRNA
48	8	л	6	4	л	12	∞	compound that inhibit
	niR-31 +		4	6 6		00		miR-182

3E      2E (6A, N131003) 	2B 2B (2H_N131008)	miR 182
	2F 2F (6B_N131034)	miF
10E 10E (PIL, N14364)[6372) 10F 10F (IOL, N143659][6372) 10H 10H (IOL, N143659][6380] 10H 10H (IOL, N143659][6389] 10H 10H (IOL, N143659][6389] 10H 10H (IOL, N143659][6389]	9G 9G (8A_(N14249)ljx238)	R-31
3D 3D 64C, N131023) 4 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,	2C 2C (4B_N131018)	miR-30d
3H      3H (HL, NI)324)        5D      5D (HL, NI)4045(NL210)        7H      7H (F, NI)4046(NL210)        7H      7H (F, NI)4046(NL210)        7H      7H (F, NI)4046(NL210)	2A 2A (2B_N131002)	miR 182-30d
411 411 (111 313300) 410 010 (011 000) (011 000 (011 000 (011 000 (011 000 (011 000 (011 000 (011 000	4D 4D (8H_N132056)	miR 182 - 31
3C 3C (108 N131060) 3D 3D (1018 N131060) 3	2G 2G (6G_N131039)	miR 30d - 31
3A 5A (6D, NI 31052) 3B 3A (6D, NI 31052) 3B 3B (6H, NI 31064) 3C 7C (4C, (NI 6001 3) AmBRO 7D 7D (4C, (NI 6001 3) AmBRO	2H 2H (7C_N131043)	AII

#### 3.2.2 Feasibility Assay of HeLa cell-line

In order to confirm the feasibility of HeLa cells as a model organism in this study, we examined the expression of three types of miRNA (hsa-miR-182, hsa-miR-31, and hsa-miR30d) in these cells. The HeLa cells were cultured and lysed using standard technique, and the miRNAs of interest were quantified by applying RT-qPCR. We found that the average CT value of all three types of miRNAs was less than 30 (out of 40) as shown in Table 3.1, implying that the difference in value before and after the addition of the compounds could be easily counted, and we concluded that HeLa cells are viable to use in this study.

	Replication	microRNA					
e	Replication	182	31	30d			
CT Valu	I	27.276	20.357	24.583			
	II	25.926	20.295	24.928			
	III	26.625	20.178	25.307			
	Average	26.609	20.277	24.939			

Table 3.1 CT value summary of miR-182, miR-31, and miR-30d in HeLa cells

#### 3.2.3 In-Cell Screening

To investigate the effects of previously-screened small molecules on the expression of hsa-miR-182, hsa-miR-31, and hsa-miR-30d in living cells, we added those compounds to the cells and incubated them overnight to reveal their biological effects. After incubation, the cells were lysed, and the expression of miRNAs was quantified using RT-qPCR techniques similar to the *in vitro* dicer reaction.

Figure 3.6, 3.7, and 3.8 shows the expression of hsa-miR-182, hsa-miR-31, and hsamiR-30d on the triplication of each miRNA, respectively. In contrast to the *in-vitro* dicer reaction, to evaluate the amount of cDNA products, we used  $2^{-\Delta\Delta CT}$  expressions rather than  $2^{-\Delta CT}$  because of the differences in normalization calculation between the two. The CT value of compound-affected miRNA was normalized to the CT value of the untreated product in terms of *in-vitro* dicer reaction. In the cell-based assay, we used two-step normalization, first normalizing the CT value of treated cells to the CT value of untreated cells, then normalizing it again to the internal control gene, in this case, U6 snRNA. Even though the expression used is different, the practical definition of the two is the same. If the  $2^{-\Delta\Delta CT}$  expressions value is less than 1, there is an inhibition effect on miRNA expression and vice versa.

To determine which compounds exhibit potential inhibitory activity, we set the  $2^{-\Delta\Delta CT}$  expressions value of 0.5 as a threshold, and compounds with  $2^{-\Delta\Delta CT}$  values less than the threshold have significant inhibition effects. Similar to the screening criteria in the previous *in vitro* dicer reaction screening, we considered replication in addition to the  $2^{-\Delta\Delta CT}$  expressions value. If a compound showed the  $2^{-\Delta\Delta CT}$  expressions value less than the threshold more than or equal to two times replication, we considered this compound as a potential inhibitor.

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Figure 3.6 In-Cell screening results of hsa-miR-182



Figure 3.7 In-Cell screening results of hsa-miR-31



Figure 3.8 In-Cell screening results of hsa-miR-30d



According to the criteria provided above, Figure 3.6 demonstrates that 5 compounds reach the 0.5 threshold and also meet the replication criteria, indicating that these 5 compounds may possess inhibitory activity against the pre-miR-182 processing reaction. The inhibition of pre-miR-31 and pre-miR-30d processing reaction shows in Figure 3.7 and 3.8. While 5 different compounds have demonstrated potential inhibitory activity against hsamiR-31 production, there are no compounds that meet all of the criteria listed above for hasmiR-30d production.

The summary of compounds that inhibit hsa-miR-182 and hsa-miR-182 production is shown in Figure 3.9. Compounds 2A, 3A, and 5C inhibit the production of has-miR-182, whereas compounds 2B, 4C, and 7B inhibit the production of hsa-miR-31. In contrast to the other six compounds, which appear to preferentially inhibit one type of miRNA, compounds 2D and 3D inhibit both types of miRNA production.



Figure 3.9 In-Cell screening results summary

#### 3.2.4 Confirmation Experiment In Cell Reaction

To verify the validity of the criteria used in the *in vitro* dicer reaction screening, we performed a similar experiment on the 19 compounds that were excluded from the in-cell screening. These compounds were used to treat HeLa cells in a similar manner, and the results of this experiment were evaluated similarly to those from the in-cell screening.

As presented in Figure 3.10, 3.11, and 3.12, none of the compounds significantly inhibited has-miR-182, has-miR-31, or has-miR-30d production by failing to pass the  $2^{-\Delta\Delta CT}$  expressions threshold, and even when several compounds did pass the threshold, those compounds did not meet the replication criteria, defined as passing the threshold more than twice. The validity of the screening criteria is concluded as a result of these findings.



expression of hsa-miR-182. This results indicates that none of the compounds that pass the Figure 3.10 In cell assay of 19 compounds that excluded after first screening to confirm the threshold and meet the replication criteria



expression of hsa-miR-31. This results indicates that none of the compounds that pass the Figure 3.11 In cell assay of 19 compounds that excluded after first screening to confirm the threshold and meet the replication criteria

expression of hsa-miR-30d. This results indicates that none of the compounds that pass the Figure 3.12 In cell assay of 19 compounds that excluded after first screening to confirm the threshold and meet the replication criteria



#### 3.2.5 Surface Plasmon Resonance (SPR) Analysis

It was previously reported that the small molecule could bind to precursor miRNAs and then interfere with the cleavage processing of the dicer. (41) To verify this possibility, SPR analysis was used to determine the mechanism of action (MOA) of the small molecules that inhibited hsa-miR-182, hsa-miR-31, and hsa-miR-30d production. This study will assess the binding ability of 8 small molecules identified through in-cell screening (2A, 2B, 2D, 3A, 3D, 4C, 5C, and 7B) to the precursors of hsa-miR-182, hsa-miR-31, and hsa-miR-31.

Binding experiments were generally carried out on the SA chip with amounts of immobilized pre-miR-182, pre-miR-31, and pre-miR-30d corresponding to 1606.8, 2150.0, and 1950.7 RU, respectively. Figure 3.13 and 3.14 depicts typical binding curves monitored during contact time with an 8-compound solution. It demonstrates that compounds 3D and 4C have better binding profiles than the other six compounds. A comparison of compound 3D and 4C binding to pre-miRNAs reveals that pre-miR-182 has the highest response, followed by pre-miR-31 and pre-miR-30d, respectively.







**Figure 3.14** SPR binding assay of compound 2B, 7B, 2D, and 3D to the pre-miR-182/31/30d immobilized surface. Ligand was added at concentration of 50 uM. The amount of pre-miR-182/31/30d immobilized on SA chip was 1606.8, 2150, 1950.7 RU respectively

#### 3.2.6 WST-8 Viability Assay

To assess the biological significance of eight compounds from the previous screening, we used a WST-8 viability assay to measure cell viability and proliferation. The cells were cultured and pre-incubated before adding varying concentrations of each of the eight compounds ranging from 0 to 100 uM. After another incubation, the cells' absorbance at 450 nm was measured using a microplate reader.

The results of this assay are depicted in Figure 3.15 and 3.16, which shows the effects of compound concentration on cell viability. The common pattern that appears in all eight figures is that the higher the concentration of the compounds, the lower the cell viability. However, among those eight compounds, compounds 3D and 4C show significant inhibition, and based on this data, we can predict that the IC<sub>50</sub> for 3D is around 5 uM and 0.2 uM for 4C.





Figure 3.15 Viability assay of compound 2D, 3D, 2A and 3A



Figure 3.16 Viability assay of compound 2B, 4C, 5C and 7B

#### 3.2.7 The Mechanism of Action

Based on the screening results, it was known that the the miRNA production was inhibited by all of the hit compounds, however, among 8 hit compounds (2A, 2B, 2D, 3A, 3D, 4C, 5C, and 7B), only 2 compounds that shows binding affinity to miRNA precursors (3D and 4C). To understand this phenomenon, we could refer to the first screening assay. From that assay (the *In vitro* dicer reaction), the reaction condition has been limited to the miRNA precursors, Dicer, and buffer. It means there are two possibilities regarding the miRNA production inhibition mechanism as shown in Figure 3.16, either by binding to the miRNA precursors and inhibit the Dicer-mediated cleavage reaction, or these compounds directly affecting the Dicer thereby inhibit the miRNA production.



Figure 3.17 Inhibition mechanism; (Inhibition 1) small molecule bind to pre-miRNA and inhibit Dicer-mediated cleavage reaction, (Inhibition 2) small molecule affecting the Dicer, and it makes the inhibition occurred.

## **3.3 Conclusions**

We performed a screening assay based on our understanding of miRNA biogenesis. We used the *in vitro* dicer cleavage reaction in our primary screening and we were able to found 48 compounds from the initial 67 compounds as potential inhibitors. These 48 compounds then subjected to in-cell screening as the secondary screening, and we were able to obtain 8 compounds (2A, 2B, 2D, 3A, 3D, 4C, 5C, and 7B) with promising results.

Aside from that, we conducted a similar in-cell screening for 19 excluded compounds from the primary screening to evaluate our screening criteria, and the result shows that all 19 compounds did not pass the second screening, indicating that the criteria that were used in the first screening are valid.

Additional assays were also performed to learn more about the biological significance of those eight compounds. According to the SPR analysis and viability assay, compound 3D was the most promising result as an inhibitor to miR-182 production. Compound 4C also shows similar results, however, its low IC<sub>50</sub> value during viability assay makes the second screening of this compound compromised and needs to be analyzed further before using this compound on the further assay.

## 3.4 Methods

#### 3.4.1 The Library Compounds and pre-microRNA targets

All chemical compounds and microRNA precursors (pre-miR-182/31/30d) belong to the Nakatani laboratory library. 67 different compounds that were used in this experiment were selected by considering the structural difference of every compound group. To make it easier to identify, the nomenclature in this experiment was used by giving letters and numbers according to the location of the compounds in the library well-plate. The rearrangement of the 48-compounds also applied after the first screening.

#### 3.4.2 In Vitro Dicer Cleavage Reaction

In the presence of a buffer reaction, phosphorylated precursor microRNA (0.5 uM), 50 mM MgCl<sub>2</sub>, 10 mM ATP, 0.05 percent BSA, and Dicer (50 nM) were mixed. The sample from the library compounds was then added, with RNAse-free water serving as a negative control. After that, the mixture was incubated at 37°C for 6 hours. The reaction was then halted by adding 10 mM EDTA. To remove non-nucleic acids, ethanol precipitation was used, followed by RNAse-free water to solute the nucleic acids.

#### 3.4.3 In-cell Reaction

HeLa cells were cultured and expanded using standard techniques. The cells were then plated in multi-well plates and incubated in the incubator overnight (37°C, 5% CO<sub>2</sub>). At each well, the cell density is 5000 cells per 100 uL. Following incubation, HeLa cells were treated with a final concentration of the target compounds of 1 uM. Another overnight incubation was performed to ensure that the desired biological effect was achieved. Following treatment, the lysis and cDNA procedures were carried out in accordance with the kit's manufacturer's instructions.

#### 3.4.4 WST-8 Cell Viability Assay

After dispensing 100uL of cell suspension (5000 cells/well) into a 96-well plate, a 24hour pre-incubation period in a humidified incubator was performed. Following that, 10 uL of the substances to be tested at various concentrations was added. Another 24-hour incubation period was required to determine the effect of the substances. Then CCK-8 was added and incubated for an additional 1-4 hours. After that, using a microplate reader, determine the absorbance at 450 nM.

# **CHAPTER IV**

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# SUPPLEMENTARY DATA

S1	Well plate rearrangement , this arrangement used for 48 compound In-Cell screening, SPR analysis, and viability assay
S2	In vitro Dicer reaction detail calculation for hsa-miR-182
S3	In vitro Dicer reaction detail calculation for hsa-miR-31
S4	In vitro Dicer reaction detail calculation for hsa-miR-30d
S5	In cell screening detail calculation for hsa-miR-182
S6	In cell screening detail calculation for hsa-miR-31
S7	In cell screening detail calculation for hsa-miR-30d
S8	Additional In cell Assay detail calculation for hsa-miR-182
S9	Additional In cell Assay detail calculation for hsa-miR-31
S10	Additional In cell Assay detail calculation for hsa-miR-30d
S11	Detail calculation of 25 nM and 50 nM substrate for velocity plot
S12	Detail calculation of 100 nM and 200 nM substrate for velocity plot
S13	Detail calculation of 300 nM and 400 nM substrate for velocity plot

# Well Plate Rearrangement

2A (2B_N131002)	3A (8D_N131052)	4H (11H_N132080)	6G (2G_(N160007) PQA-	7G (6C_(N160035) NCD-	9F (7G_(N14247)ljx224)
			C3-amide)		Go in the
					0.0 (0.4 (1)14 40 40)1; 0.00)
2B (2H_N131008)	3B (9H_N131064)	5B (3H (N14016)AIK112)	6H (3B_(N160010) PQAD-	7H (7F_(N160046) AIK216)	9G (8A_(N14249)ijx238)
2C (4B_N131018)	3C (10B_N131066)	5C	7A (3C_(N160011) DDAP)	8A (7H_(N160048)	9H (8B_(N14250)ljx223)
		(4B_(N14018)SA029)		AIK248)	
			gentalagg	но~~µ <sup>(N</sup> , <sup>N</sup> ) µ~~о	
2D (4G_N131023)	3D (11H_N131080)	5D (4H_(N14024)SM-	7B (4B_(N160018) Am-	8B (8D_(N160052) ih	10C (9B_(N14258)ljx188)
0	NHa	<sup>221)</sup>	BzN)	039)	~
L <sub>N</sub> CCoto^					HANNY RUNNY CO
2E (6A_N131033)	3E (2A_N132001)	5E	7C (4C_(N160019) Am-	9B (7B_(N14242)ljx249)	10E (9H_(N14264)ljx372)
	H <sub>2</sub> N LN N OEI		BZND)		${}_{H_{1}M} \sim \sim {}_{H}^{M} \overset{\text{for }}{\underset{M}{\leftarrow}} \underset{M = 0}{\overset{\text{for }}{\underset{M = 0}{\leftarrow}}}$
2F (6B_N131034)	3H (4H_N132024)	5F (5E_(N14029)NN146)	7D (4G_(N160023)	9C (7C_(N14243)BzNA)	10F (10A_(N14265)ljx380)
	Lang in a stand water and the stand in the second s	uptou			${}_{H_2N} \sim \sim \sum_{\underline{H}} \left( \sum_{N} \left( \sum_{\underline{H} \in \underline{V}} \right)^{O} \right)^{NH_2} $
2G (6G_N131039)	4B (5C_N132027)	5H	7E (5A_(N160025)	9D (7D_(N14244)ljx253)	10G (10B_(N14266)ljx344)
		(6G_(N14039)Thioflavin)	CMBL5a)		
2H (7C_N131043)	4D (8H_N132056)	6D	7F (5H_(N160032) NCD-	9E (7E_(N14245)ljx107)	10H (10D_(N14268)ljx358)
	NHA ND HOIN HOI		C4-SH)	Mailon with the	NH NH

**S1** Well plate rearrangement , this arrangement used for 48 compound In-Cell screening, SPR analysis, and viability assay

Comula	has-miR-182 (C	T value)	dCT		2^-dC1	Г	Thresh	nold <0.5	
Sample	I	=	- 1	=		=	Ι	=	ĸ
2A	20.967	20.554	3.558	3.144	0.085	0.113	1	1	OK
2B	20.900	20.571	3.491	3.162	0.089	0.112	1	1	ОК
2C	16.413	16.126	-0.996	-1.283	1.995	2.434	0	0	-
2D	16.614	16.456	-0.795	-0.954	1.735	1.937	0	0	-
2E	20.359	20.246	2.950	2.837	0.129	0.140	1	1	OK
2F 2G	16 140	16.317	-1 269	-0.548	2 4 10	2 131	0	0	
2H	20.438	20.484	3.029	3.075	0.123	0.119	1	1	ок
3A	20.133	20.808	2.724	3.399	0.151	0.095	1	1	OK
3B	21.252	21.725	3.843	4.316	0.070	0.050	1	1	ок
3C	16.153	16.974	-1.257	-0.435	2.389	1.352	0	0	-
3D	15.838	16.146	-1.572	-1.263	2.972	2.400	0	0	-
3E	20.776	20.952	3.367	3.543	0.097	0.086	1	1	ок
3F	15.944	16.240	-1.465	-1.169	2.761	2.248	0	0	-
3G	16.943	16.962	-0.466	-0.447	1.381	1.363	0	0	-
30	22.494	17 149	5.065	0.261	1.590	1 109		0	UK
4A 4B	16.091	16 457	-1.318	-0.201	2 4 9 3	1.190	0	0	
4C	16.922	17.267	-0.487	-0.142	1.402	1.104	ŏ	õ	-
4D	22.016	22.071	4.607	4.662	0.041	0.040	1	1	ок
4E	16.308	16.554	-1.101	-0.855	2.145	1.808	0	0	-
4F	16.102	16.149	-1.307	-1.260	2.475	2.395	0	0	-
4G	16.819	16.714	-0.591	-0.695	1.506	1.619	0	0	-
4H	18.854	18.835	1.444	1.426	0.367	0.372	1	1	ок
5A	16.063	16.719	-1.346	-0.691	2.543	1.614	0	0	-
5B	20.596	21.048	3.187	3.638	0.110	0.080	1	1	OK
50	20.689	21.183	3.279	3.773	0.103	0.073	1	1	OK
55	16 500	16 400	-0.909	-1 009	1 878	2 013		0	UK -
5F	22.066	21.932	4.657	4.523	0.040	0.044	1	1	ок
5G	16.308	16.252	-1.101	-1.157	2.145	2.230	0	0	-
5H	22.123	22.000	4.714	4.591	0.038	0.041	1	1	ок
6A	15.436	16.143	-1.973	-1.266	3.926	2.405	0	0	-
6B	16.774	17.817	-0.635	0.408	1.553	0.754	0	0	-
6C	16.488	17.383	-0.921	-0.026	1.893	1.018	0	0	-
6D	23.421	24.057	6.012	6.648	0.015	0.010	1	1	ок
6E	16.539	16.712	-0.870	-0.697	1.828	1.621	0	0	-
6G	16 958	17 383	-1.251	-0.023	2.360	1.040	0	0	
6H	17.948	18.259	0.538	0.850	0.689	0.555	ő	0	
7A	22.986	22.429	5.576	5.020	0.021	0.031	1	1	ок
7B	19.617	20.033	2.207	2.624	0.217	0.162	1	1	ок
7C	24.398	24.750	6.989	7.341	0.008	0.006	1	1	ОК
7D	26.438	26.395	9.029	8.985	0.002	0.002	1	1	ок
7E	21.963	22.541	4.554	5.132	0.043	0.029	1	1	OK
7F	22.584	22.961	5.175	5.552	0.028	0.021	1	1	OK
7G	19.315	19.964	1.906	2.555	0.267	0.170	1	1	OK
84	17 083	24.370	-0.326	0.907	1 254	0.008	0	0	
88	15 972	16 623	-1 437	-0 786	2 707	1 724	0	0	
8C	17.682	18.644	0.273	1.235	0.827	0.425	ő	1	
9A	17.210	17.690	-0.200	0.280	1.148	0.823	0	0	-
9B	16.660	16.498	-0.749	-0.911	1.681	1.880	0	0	-
9C	17.635	18.068	0.226	0.659	0.855	0.633	0	0	-
9D	16.245	17.194	-1.164	-0.215	2.241	1.161	0	0	-
9E	21.765	22.215	4.355	4.806	0.049	0.036	1	1	ок
9F	16.396	16.811	-1.013	-0.598	2.019	1.514	0	0	•
90	17.024	17 110	-0.275	0.938	1 207	1 222	0	0	
10A	16 782	16 640	-0.627	-0.290	1.297	1.704	0	0	
10B	17.566	17.681	0.157	0.271	0.897	0.829	ő	õ	-
10C	21.061	20.977	3.652	3.568	0.080	0.084	1	1	ок
10D	17.785	17.729	0.376	0.320	0.771	0.801	0	0	-
10E	18.471	18.423	1.061	1.014	0.479	0.495	1	1	ОК
10F	17.587	17.703	0.178	0.293	0.884	0.816	0	0	-
10G	16.964	17.187	-0.445	-0.222	1.361	1.167	0	0	-
10H	17.413	17.448	0.004	0.039	0.997	0.974	0	0	-
Reference	17.409								

**S2** In vitro Dicer reaction detail calculation for hsa-miR-182

Comula	has-miR-31 (	CT value)	dCT		2^-d0	т	Thresh	old <0.5	
Sample	-	II	I	Ш	I	Ш	I	II	ĸ
2A	15.295	14.664	-0.758	-1.390	1.691	2.620	0	0	-
2B	15.775	15.386	-0.278	-0.667	1.212	1.588	0	0	-
20	16.301	15.069	0.248	-0.680	0.842	0.989	0	0	-
2E	16.887	16.431	0.833	0.378	0.561	0.770	0	0	-
2F	17.223	17.270	1.170	1.216	0.444	0.430	1	1	ок
2G	17.367	17.361	1.313	1.308	0.402	0.404	1	1	ок
2H	17.345	17.368	1.292	1.314	0.409	0.402	1	1	OK
3A 20	18.994	18.526	2.941	2.472	0.130	0.180	1	1	OK
30	17.907	17 198	1.655	1.054	0.277	0.316	1	1	OK
3D	18.603	18.340	2.550	2.287	0.171	0.205	1	1	ок
3E	16.841	16.731	0.788	0.678	0.579	0.625	0	0	-
3F	16.216	15.853	0.163	-0.200	0.893	1.149	0	0	-
3G	16.560	16.239	0.507	0.186	0.704	0.879	0	0	-
3H 4A	16.409	16.294	0.356	0.241	0.781	0.846	0	0	-
4A 4B	17 782	17 509	1 729	1 4 5 6	0.302	0.365	1	1	OK -
4C	16.778	16.678	0.724	0.624	0.605	0.649	0	0	-
4D	19.425	19.258	3.371	3.204	0.097	0.108	1	1	ок
4E	16.188	16.009	0.135	-0.045	0.911	1.031	0	0	-
4F	16.550	16.550	0.497	0.497	0.709	0.709	0	0	-
4G	16.357	16.523	0.304	0.470	0.810	0.722	0	0	-
4H	19.145	19.328	3.091	3.275	0.117	0.103	1	1	OK
5A 5B	16.663	16 149	0.704	0.466	0.614	0.724	0	0	-
5C	16.964	16.772	0.911	0.719	0.532	0.607	õ	0	-
5D	16.755	16.444	0.702	0.391	0.615	0.763	0	0	-
5E	16.103	16.049	0.050	-0.005	0.966	1.003	0	0	-
5F	16.065	15.879	0.012	-0.175	0.992	1.129	0	0	-
5G	15.996	15.716	-0.057	-0.337	1.040	1.263	0	0	-
5H	15.096	14.///	-0.957	-1.276	1.942	2.422	0	0	-
6B	16 357	16.302	-0.157	0.364	0.810	0.842	0	0	-
6C	16.745	16.631	0.692	0.577	0.619	0.670	õ	0	-
6D	20.875	20.556	4.822	4.503	0.035	0.044	1	1	ок
6E	15.414	15.410	-0.639	-0.643	1.557	1.562	0	0	-
6F	16.080	16.247	0.026	0.193	0.982	0.875	0	0	-
6G	17.685	17.540	1.632	1.487	0.323	0.357	1	1	OK
6H 7A	22.738	22.976	0.085	6.923	0.010	0.008	1	1	OK
7B	16.809	16.687	0.755	0.634	0.592	0.644	0	0	-
70	20.206	19.769	4.153	3.716	0.056	0.076	1	1	ок
7D	24.883	24.534	8.830	8.481	0.002	0.003	1	1	ок
7E	19.597	19.508	3.544	3.454	0.086	0.091	1	1	ок
7F	22.339	22.534	6.286	6.481	0.013	0.011	1	1	OK
7G	19.407	19.319	3.353	3.265	0.098	0.104	1	1	ок
84	21 585	21 387	-0.145	5 3 3 4	0.022	0.025	1	1	- -
8B	15.136	15.071	-0.917	-0.982	1.888	1.975	ò	0	-
8C	13.753	13.855	-2.300	-2.198	4.924	4.588	0	0	-
9A	14.995	14.727	-1.058	-1.326	2.082	2.508	0	0	-
9B	17.979	17.846	1.926	1.793	0.263	0.289	1	1	OK
9C	20.919	20.884	4.866	4.831	0.034	0.035	1	1	OK
9D	21.625	21.392	5.572	5.339	0.021	0.025	1	1	OK
9E 9F	17 755	17 440	1 702	1.387	0.015	0.016	1	1	OK
9G	35.006	35.217	18.953	19.164	0.000	0.000	1	1	ок
9H	23.997	23.881	7.943	7.828	0.004	0.004	1	1	ок
10A	16.557	16.341	0.504	0.288	0.705	0.819	0	0	-
10B	16.034	15.694	-0.020	-0.359	1.014	1.283	0	0	-
10C	20.795	20.586	4.742	4.532	0.037	0.043	1	1	ок
10D	15.751	15.574	-0.302	-0.479	1.233	1.394	0	0	-
10E	24 209	24 154	3.555	3.394	0.085	0.095	1	1	OK
10G	16.289	16.197	0.236	0.144	0.849	0.905	o	0	-
10H	24.786	24.592	8.733	8.539	0.002	0.003	1	1	ОК
Peference	16.052								

S3 In vitro Dicer reaction detail calculation for hsa-miR-31

0	hsa-miR-30d (C	T value)	dC1	r	2^-d0	т	Thresh	nold <0.5	_
Sample	I	11	I	Ш	Ι	Ш	I	I	к
2A	16.119	16.099	1.683	1.663	0.311	0.316	1	1	OK
2B	15.342	15.393	0.906	0.957	0.533	0.515	0	0	-
2C	15.956	15.953	1.520	1.517	0.349	0.349	1	1	OK
2D	16.281	16.199	1.845	1.763	0.278	0.295	1	1	ок
2E	14.843	14.807	0.407	0.371	0.754	0.773	0	0	-
2F 2G	14.007	14.536	1 278	1 273	0.000	0.932	1	1	- -
20 2H	15 927	15.709	1 4 9 1	1.273	0.356	0.343	1	1	OK
3A	18.211	18,168	3.776	3.732	0.073	0.075	1	1	ок
3B	17.709	17.613	3.273	3.177	0.103	0.111	1	1	OK
3C	16.028	15.960	1.593	1.524	0.332	0.348	1	1	ок
3D	17.012	16.931	2.576	2.496	0.168	0.177	1	1	ОК
3E	14.540	14.374	0.104	-0.062	0.930	1.044	0	0	-
3F	14.597	14.560	0.161	0.124	0.895	0.918	0	0	-
3G 21	15.076	14.933	0.641	0.497	0.641	0.709	0	0	-
30	13 268	13.730	-1 168	-1 210	2 247	2 313	0	0	UK
4B	13 739	13 604	-0.697	-0.831	1 621	1 780	0	0	
4C	14.857	14.675	0.421	0.239	0.747	0.847	ŏ	õ	-
4D	15.444	15.368	1.009	0.932	0.497	0.524	1	0	-
4E	13.995	13.906	-0.440	-0.530	1.357	1.444	0	0	-
4F	13.558	13.410	-0.878	-1.026	1.837	2.036	0	0	-
4G	14.236	14.118	-0.200	-0.318	1.148	1.247	0	0	-
4H	14.778	14.629	0.342	0.193	0.789	0.875	0	0	-
5A	13.822	13.768	-0.614	-0.668	1.530	1.588	0	0	-
58	13.964	13.787	-0.471	-0.649	1.386	1.568	0	0	-
50 5D	16 310	16 231	-0.465	-0.650	0.273	0.288	1	1	- -
5E	15.535	15.498	1,100	1.062	0.467	0.479	1	1	ок
5F	14.681	14.615	0.245	0.179	0.844	0.884	0	0	-
5G	15.053	14.882	0.618	0.446	0.652	0.734	0	0	-
5H	15.582	15.378	1.146	0.942	0.452	0.521	1	0	-
6A	14.212	14.371	-0.224	-0.065	1.168	1.046	0	0	-
6B	14.971	15.073	0.535	0.638	0.690	0.643	0	0	-
6C	14.440	14.501	0.004	0.065	0.997	0.956	0	0	-
6D	13.529	13.621	-0.907	-0.815	1.876	1.759	0	0	-
0E 6E	13.957	13.650	-0.476	-0.500	1.393	1.501	0	0	-
6G	14.676	14.832	0.241	0.397	0.846	0.760	0	0	
6H	17.277	17.367	2.841	2.932	0.140	0.131	1	1	ок
7A	18.869	18.787	4.433	4.351	0.046	0.049	1	1	ок
7B	14.476	14.409	0.040	-0.027	0.973	1.019	0	0	-
7C	19.365	19.372	4.929	4.936	0.033	0.033	1	1	ок
7D	19.639	19.637	5.203	5.201	0.027	0.027	1	1	OK
7E	15.990	15.823	1.554	1.387	0.340	0.382	1	1	OK
75	17.933	17.837	3.498	3.401	0.089	0.095	1	1	OK
7G 7⊔	15.200	15.242	0.024	0.000	0.565	0.572	1	1	-
8A	14.628	14.518	0.193	0.082	0.875	0.945	0	0	-
8B	15.901	15.776	1,465	1.340	0.362	0.395	1	1	ок
8C	13.991	13.990	-0.444	-0.446	1.361	1.362	0	0	-
9A	13.627	13.432	-0.809	-1.004	1.752	2.005	0	0	-
9B	13.970	13.957	-0.466	-0.479	1.381	1.394	0	0	-
9C	12.953	12.914	-1.482	-1.522	2.794	2.871	0	0	-
9D	13.908	13.898	-0.528	-0.538	1.442	1.451	0	0	-
9E	14.314	14.315	-0.121	-0.121	1.088	1.088	0	0	-
9F	13.760	13.675	-0.676	-0.761	1.597	1.695	0	0	-
<u>ан</u>	18.375	18 329	3 9 3 9	3 802	0.065	0.067	1	1	- -
10A	12.831	12.665	-1.605	-1.771	3.042	3.413	0	0	-
10B	14.277	14,173	-0.159	-0.263	1.117	1.200	ō	õ	-
10C	13.769	13.541	-0.667	-0.894	1.587	1.859	0	0	-
10D	13.731	13.506	-0.705	-0.930	1.630	1.905	0	0	-
10E	13.895	13.871	-0.541	-0.565	1.455	1.480	0	0	-
10F	13.913	13.802	-0.523	-0.634	1.436	1.551	0	0	-
10G	15.696	15.445	1.260	1.009	0.417	0.497	1	1	ок
10H	15.260	15.076	0.824	0.641	0.565	0.641	0	0	-

# S4 In vitro Dicer reaction detail calculation for hsa-miR-30d

									10.634	11.200	11,319	24,966	13.915	24.694	24.803	25,400	14.060	II 13,604	14.081	Average Sample 0
										dCT			Average							•
													۳ ا	ndetermined	Indetermint Ur	Undetermint U	29.069	(Undetermine	Undetermin	8H
							0	\d]- [U6]) sample	T 182/31/30	samplex - ([C	/31/30d] - [U6]	f=([CT 182,	ddc	ndetermined	Indetermint Ur	Undetermint U	Undetermin	(Undetermine	Undetermin	96
														ndetermined	Indetermine Un	Undetermine U	Undetermine	(Undetermine	Undetermin	ŝĤ
			L									25.308	13.731	25.144	25.055	25.726	13.992	12.857	14.345	8D
												24.805	14.047	25.103	24.323	25.559	13.989	13.978	14.174	80 88
												24.888	14.185	24.495	24.840	25.328	14.437	14.047	14.072	8A
	000		0.540	0.620	0.623	0.889	0.690	-0.332	11.522	11.890	12.002	24.983	14.241 13.178	24.748	23.102 24.985	25.216	14.95z 13.226	13.095	14.135	7H
	1		0.758	0.359	0.616	0.399	1.479	0.698	11.033	12.679	12.018	25.433	13.523	25.173	25.292	25.834	14.140	12.613	13.816	7F
	0		1.572	1.861	1.369	-0.653	-0.896	-0.454	9.981	10.304	10.866	25.121	14.737	24.875	25.289	25.198	14.894	14.985	14.333	7E
			0.403	0.758	0.802	1.484	0,400	0.319	11.945	11.600	11.609	25.263	13.468 13.292	25.352	25.247	25.189	13.234	13,435	13.552	70 70
	0		0.217	0.555	0.553	2.204	0.851	0.854	12.838	12.050	12.173	25.462	13.108	25.797	25.104	25,485	12.959	13.054	13.312	7B
	0		0.683	0.981	0.653	0.550	0.027	0.615	11.183	11.227	11.935	25.292	13.844	25.445	24.790	25.641	14.262	13.563	13.707	7A
			0.808	1.065	0.843	0.308	-0.091	0.247	11.072	11.109	11.566	25.146	13.940	25.052	24.901	25.484	14.110	13.792	13.917	6G
	1 0 0		0.770	0.716	0.407	0.378	0.483	1.297	11.011	11.682	12.616	25.259	13.489	24.974	25.272	25.530	13.963	13.589	12.91/	65
			0.640	0.408	0.991	0.644	1.294	0.014	11.278	12,493	11.333	25.320	13.618	25,159	25.471	25.329	13.881	12.978	13.996	68 8
			1.976	1.367	1.451	-0.982	-0.451	-0.537	9.651	10.749	10.783	24.787	14.392	24.675	24.734 25 065	24.951	15.023	13.984	14.169	6C
	0 0 1		0.496	0.596	0.752	1.011	0.747	0.411	11.645	11.947	11.730	25.215	13.441	25.148	25.198	25.300	13.503	13.251	13.570	6B
	00		0.516	0.635	1.168	0.955	0.656	-0.224	11.589	11.855	11.096	24.683	13.170	24.436	24.826	24.788	12.847	12.970	13.693	6A
			0.815	0.540	0.731	0.295	0.890	0.452	10.929	12.090	11.771	24.944	13.302	24.705	24.890	25.089	13.776	12.884	13.318	54 6
			1.344	0.665	0.579	-0.426	0.588	0.787	10.208	11.788	12.107	24.968	13.601	24.872	24.795	25.238	14.664	13.007	13.132	55
	0 0 0 0		0.831	1.012	0.624	0.267	-0.017	0.680	10.901	11.183	12.000	25.011	13.650	24.629	25.217	25.188	13.728	14.035	13.188	5E
UK			0.48/	0.442	1.002	1.039	1.1/6	-0.002	11.6/2	12.3/6	11.31/	25.151	13.363	24.859	25.113	25.482	13.186	12./3/	14.165	5 6
ę '	. 11		0.985	0.364	2.193	0.022	1.457	-1.133	10.656	12.657	10.187	25.346	14.180	25.354	25.605	25.080	14.698	12.948	14.894	5B
	0		0.738	0.863	1.000	0.438	0.212	0.001	11.071	11.412	11.320	24.988	13.720	24.654	25.104	25.206	13.583	13.692	13.886	5A
	0		0.568	0.808	0.552	0.816	0.307	0.858	11.450	11.507	12.178	24.782	13.071	24.351	24.860	25.135	12.901	13.353	12.958	4
	0 0 0 0		0.571	0.548	0.622	-0.214	0.358	-0.110	11.441	12.067	12.005	25.220	13.382 14.044	24.897	25.230 25.381	25.533	13.455	13.163	13.528	4G 4F
	0		0.902	0.605	0.930	0.149	0.725	0.104	10.783	11.924	11.423	25.024	13.647	24.470	25.108	25.493	13.687	13.183	14.070	4
	0		0.837	0.548	1.037	0.257	0.867	-0.053	10.891	12.067	11.266	25.382	13.975	24.704	25.925	25.519	13.813	13.858	14.252	4D 40
	- 0		0.867	0.903	1.012	0.207	0.147	-0.017	10.840	11.347	11.303	25.107	13.944	24.765	25.229	25.326	13.925	13.883	14.024	5 <del>8</del>
	0		0.912	0.882	0.667	0.133	0.181	0.584	10.767	11.381	11.903	24.939	13.589	24.390	24.979	25.448	13.624	13.598	13.546	4A
	1 0		0.826	0.422	0.825	-0.389	1.246	0.277	10.245	11.685	11.596	24.934 25.099	13.514 13.448	24.441 24.785	25.603	25.392	13.875	13.157	13.312	3H
	0		1.392	0.514	0.882	-0.478	0.961	0.181	10.156	12.161	11.500	25.025	13.753	24.823	24.871	25.381	14.667	12.711	13.883	ЗF
' Ç	0 +		0.746	0.676	0.465	0.422	0.566	1.105	11.056	11.766	12,424	25.123	13.375	24.793	24.992	25.584	13.737	13.227	13.160	38
5 .	. 0		1.183	0.743	0.620	-0.242	0.428	0.689	10.391	11.627	12.009	24.962	13.619	24.323	25.084	25.477	13.932	13.456	13.469	30
	0 0		1.134	0.954	1.352	-0.181	0.068	-0.435	10.453	11.268	10.885	25.037	14.169	24.677	25.300	25.135	14.224	14.032	14.250	3B
9 R	1 0 1		0.370	0.503	0.488	1.435	0.991	1.036	12.069	12.191	12.355	25.195	12.990	24.968	25.138	25.480	12.899	12.947	13.124	3A
	00		0.700	0.784	0.747	0.515	0.351	0.421	11.149	11.550	11.740	24.934	13.454	25.024	24.862	24.915	13.875	13.311	13.175	2H
	1		0.581	0.479	0.938	0.784	1.063	0.092	11.418	10 200	11.411	24.989	13.292	24.967	24.741	25.260	13.550	12.478	13.849	2F
	0 0		0.837	0.935	0.532	0.256	0.096	0.912	10.890	11.296	12.231	24.903	13.431	24.461	24.976	25.272	13.571	13.680	13.040	2E
Ŗ	1 1 1		0.443	0.297	0.308	1.176	1.749	1.699	11.809	12.949	13.018	25.434	12.842	25.260	25.246	25.796	13.451	12.297	12.777	2D
	00		0.562	0.980	0.514	0.831	0.272	0.959	11.464	11.472	12.278	25.382	13.644 13.699	25.193	24.989 25.048	25.963 25.314	13.729 14.066	13.819	13.685	2B 2C
OK	0 1 1		0.391	0.463	0.774	1.356	1.110	0.369	11.990	12.309	11.689	25.238	13.242	25.262	25.108	25.345	13.272	12.798	13.656	2A
;	=	_	≡	=	-	≡	=	_	≡	=	-	182	9U	≡	=	-	≡	=	_	Combin
0	Score X<0.5			^-ddCT	2	dCT 0)	T sample -	ddCT (dC		T 182-U6	dC	ge	Avera		1-miR-182	hsa		90		وعسماه

S5 In cell screening detail calculation for hsa-miR-182

										4.774	II 5.549	5.024	31 19.030	U6 13.915	III 18.833	II 19.153	I 19.105	III 14.060	II 13.604	ا 14.081	Average Sample 0
											dCT			werage							-
															ndeterminec	Indetermin: U	Undetermine L Undetermine L	Undetermine 29.069	«Undetermin«	Undetermin	8H 8G
									U6]) sample O	2/31/30d]-	iplex - ([ CT 18	0d] - [U6]) sam	CT 182/31/3	ddCT = ([	ndetermined	Indetermine U	Undetermine L	Undetermine	« Undetermin«	Undetermin	°₽ °E
													18.840	13.731	18.285	19.024	19.210	13.992	12.857	14.345	8D
9													19.082 19.023	13.695 14.047	19.097 18.797	19.081 19.185	19.067 19.087	13.822 13.989	13.531	13.733	8C
66													19.177	14.185	19.153	19.320	19.056	14.437	14.047	14.072	8A
lr	10	0 0	0 0	0.039	1.145	0.630	-0.688 4.697	-0.196	-0.499 0.666	4.086 9.471	5.354	4.525 5.690	18.896 20.080	14.241 13.178	19.038 22.696	18.985 18.640	18.664 18.904	14.952 13.226	13.632	14.13	7G 7H
าเ	0	0 0		0.754	0.517	1.014	0.408	0.950	-0.021	5.181	6.499	5.003	19.084	13.523	19.321	19.113	18.819	14.140	12.613	13.816	7F
ce	0	0	0	1.527	3.081	1.558	-0.611	-1.623	-0.640	4.163	3.926	4.384	18.895	14.737	19.057	18.911	18.717	14.894	14.985	14.333	7E
211	1 0	0 0		0.510	1.040	0.754	0.973	-0.056	0.407	5.746	5.636	5.431	19.025 19.004	13.468 13.292	18.981 18.973	19.111 19.072	18.982 18.966	13.234 12.889	13.618	13.55	7C
₽ S(	4	0	1	0.431	0.757	0.385	1.215	0.402	1.377	5.988	5.951	6.401	19.222	13.108	18.947	19.005	19.713	12.959	13.054	13.312	78
cre	0 0	0 0	0 0	1.041	0.584	0.750	-0.058	0.547	0.416	5.546 4.715	5.584	5.440 5.310	18.943 19.047	13.249 13.844	18.863 18.977	19.040 19.147	18.926 19.017	13.317 14.262	12.943	13.48, 13.70	6H 7A
ee	0	0		0.931	1.552	1.005	0.103	-0.634	-0.008	4.876	4.915	5.016	18.876	13.940	18.987	18.707	18.934	14.110	13.792	13.917	66
ni	00	0 0	1 0	0.942	0./31	0.854	0.086	-0.325	0.227	4.860 4.993	6.001 5.224	5.251 6.306	18.989	13.618 13.489	18./41 18.956	18.979 18.814	19.247 19.220	13.881 13.963	12.978	13.99t 12.91/	6 6 Fi Fi
ng	0	0.0		0.903	0.906	0.951	0.147	0.142	0.072	4.920	5.691	5.096	19.094	13.858	19.150	18.973	19.159	14.230	13.282	14.06	60
ξC	0 0			1 526	0.835	0.559	0.773	0.260	0.840	5.546	5.809	5.864	19.181	13.441	19.049	19.060	19,434	15,003	13.251	13.570	6B
de		0	0	0.346	0.640	0.784	1.533	0.644	0.352	6.307	6.193	5.376	19.129	13.170	19.154	19.164	19.068	12.847	12.970	13.69	6A
ta	- 0			0.865	0.892	0.653	0.209	0.165	0.616	4.982	5.714	5.640	18.808	13.362	18.949	18.756	18.718	13.967	13.042	13.079	5G
il	0	0	0	1.065	0.823	0.602	-0.091	0.282	0.731	4.682	5.831	5.755	19.024	13.601	19.347	18.838	18.887	14.664	13.007	13.13	51
с	0	0	0	0.710	1.351	0.567	0.494	-0.434	0.818	5.268	5.115	5.842	19.059	13.650	18.996	19.150	19.030	13.728	14.035	13.188	5
al	0 0	0 0		0.515	0.617	1.244	0.956	0.696	-0.315	5.730	6.245	4.708	18.924 19.120	13.363	18.916	18.983	18.874	13.186 13.742	12.737	14.165	5 5
cι	0	0	0	1.074	0.539	1.730	-0.104	0.892	-0.790	4.670	6.441	4.233	19.295	14.180	19.368	19.389	19.127	14.698	12.948	14.89/	5B
ila	0 +	0 0		0.571	0.925	0.775	0.808	-0.4400	0.368	5.582	5.662	5.392	19.266	13.720	19.165	19.354	19.278	13.583	13.692	13.886	5A
ati	. 0			0.844	1.373	1.029	0.245	-0.457	-0.041	5.019	5.092	4.982	19.075	14.044	19.041	18.915	19.269	14.022	13.824	14.286	40
io	1	0	0	0.490	0.870	0.843	1.030	0.200	0.247	5.804	5.749	5.271	18.990	13.382	19.259	18.912	18.799	13.455	13.163	13.528	4F
n	0 0	0 0		0.583	1.371 1.018	0.980	0.778	-0.455	-0.098 0.029	5.552 5.121	5.094 5.524	4.926 5.053	19.165 18.879	13.975 13.647	19.365 18.808	18.953 18.707	19.178 19.123	13.813 13.687	13.858	14.252	4 d
° fc	1	0	1	0.337	0.728	0.434	1.569	0.458	1.205	6.343	6.007	6.229	19.074	12.882	19.119	18.900	19.204	12.776	12.894	12.975	40
or	0 0	0 0		0.673	1.081 1.585	0.696	0.571	-0.112 -0.664	0.523	5.344 5.260	5.437	5.547	19.032 19.061	13.589 13.944	18.968 19.185	19.035 18.768	19.093 19.229	13.624 13.925	13.598	13.546 14.024	4B
hs	0	0	0	0.965	1.258	0.716	0.052	-0.331	0.483	4.825	5.218	5.506	18.631	13.448	18.700	18.376	18.818	13.875	13.157	13.312	3Н
a-	0 0	0 0	0 0	1.107	0.544	0.569	-0.347	0.878	0.011	4.427	5.595	5.838	19.049	13.753	19.094 18.823	19.137	18.916	14.667 14.196	12.711	13.88	3G
'n	0	0	0	0.792	1.015	0.644	0.337	-0.021	0.636	5.111	5.528	5.660	18.808	13.375	18.848	18.755	18.820	13.737	13.227	13.160	3E
∘ nil	0.0			0.538	0.406	0,496	0.894	1.300	1.011	5.667	6.849	6.035	19.164	12.980	19.245	19.051	19.194	13.578	12.202	13.160	30
R-:	0 0	0 0		0.825	1.419	0.856	0.278	-0.505	0.224	5.051	5.044	5.247	19.283	14.169	19.275	19.076	19.498	14.224	13.456	14.250	30
3:	4	0	0	0.374	0.823	0.538	1.418	0.280	0.894	6.192	5.829	5.918	18.970	12.990	19.091	18.777	19.042	12.899	12.947	13.12/	зA
1	1 0	0 0	0 0	0.693	1.639 0.774	1.091	0.528	-0.713 0.369	-0.125 0.673	5.302	4.836	4.899 5.697	18.816 19.297	13.803 13.454	18.784 19.790	18.757 19.230	18.906 18.872	13.483 13.875	13.920	14.007	2G 2H
	0.0	1		0.611	0.493	0.965	0.711	1.021	0.052	5.484	6.570	5.076	19.002	13.292	19.034	19.048	18.924	13.550	12.478	13.849	2F
QK			, 11	0.556	0.399	0.420	0.847	1.326	1.251	5.620	6.875	6.275	19.098	12.842	19.071	19.171	19.052	13.451	12.297	12.77	20
	0	0	0	0.817	1.334	0.606	0.292	-0.416	0.723	5.065	5.133	5.747	19.014	13.699	19.131	18.952	18.959	14.066	13.819	13.212	2C
× '	1 0	- 0		0.521	0.597	0.833	0.942	2.107	0.328	5.787	6.294 7.656	5.287	19.887	13.242	18.987	19.09Z	19.008	13.272	12./98	13.68	2A 2B
	=	=	-	=	=	-	≡	=	-	≡	=	-	ĥ	6	=	=	-	=	=	-	
₽		ore X<0.5	s	:	^-ddCT	2	dCT 0)	T sample -	ddCT (dC	:	CT 31-U6		; Se	Avera		a-miR-31	. hs	;	U6	·	Sample

								8.384	8.885	I 8.099	182 22.371	U6 13.915	III 22.444	II 22.488	I 22.180	III 14.060	II 13.604	I 14.081	Average Sample 0
									qCI			d Average	Indetermined	Indetermine U	Undetermine L	29.069	Undetermine	Undetermine	8H
						le O	30d] - [U6]) samp	CT 182/31/3	5]) samplex - ([	2/31/30d] - [U6	T=([CT 182	ddo	Indetermined	Indetermine U	Undetermine L	Undetermine	Undetermine	Undetermine	86
												]	Indetermined	Indetermine U	Undetermine L	Undetermine	Undetermine	Undetermine	ŝŝ
											22.280	13.731	22.345	22.315	22.179	13.992	12.857	14.345	8D
											22.348 22.758	13.695 14.047	22.662	22.459 22.976	21.922 22.555	13.822 13.989	13.531 13.978	13.733	8C 8B
											22.098	14.185	22.024	22.203	22.066	14.437	14.047	14.072	8A
-	0 0	2.232	1.154	1.271	-1.158	-0.206	-0.346	7.226	8.858	7.753	22.127	14.241 13.178	22.178	22.310 21.953	21.892	14.952	13.632	14.139	7G 7H
	0 0	1.257	0.780	0.986	-0.330	0.358	0.021	8.054	9.243	8.120	21.995	13.523	22.194	21.856	21.936	14.140	12.613	13.816	76
	0 0	1.811	3.033	1.245	-0.857	-1.601	-0.317	7.527	7.284	7.783	22.269	14,737	22.422	22.269	22.115	14.894	14.985	14.333	7E - C
	0 0	0.472	1.393	0.838	1.082	-0.132	0.256	9.466	8.407	8.355	22.210	13.468 13.292	22.701	22.025	21.906	13.234	13.618	13.551	7D 7C
_	0 0	0.449	0.748	0.566	1.155	0.420	0.822	9.539	9.304	8.921	22.363	13.108	22.498	22.359	22.234	12.959	13.054	13.312	7B
	1 0	0.955	1.224	0.447	0.066	-0.292	1.160	8.450	8.593	9.260	22.611	13.844	22.712	22.156	22.966	14.262	13.563	13.707	7A
		0.728	0.002	0.660	0.458	536.8	0.600	8.847	17.848	8,699	25.045	13,249	22.079	20.791	27, 186	13 317	12.943	13.487	6H G
	, 1	1.055	1.244	0.462	-0.077	-0.315	1.114	8.307	8.570	9.214	22.186	13,489	22.270	22.159	22.128	13.963	13.589	12.914	6 FI
	0 0	0.868	0.632	0.900	0.204	0.662	0.152	8.588	9.546	8.251	22.414	13.618	22.469	22.524	22.247	13.881	12.978	13.996	6E
	0 0	1.051	0.865	1.068	-0.072	0.208	-0.096	8.312	9.093	8.004	22.328	13.858	22.542	22.375	22.067	14.230	13.282	14.063	6D
	0 0	1.927	1.259	1.191	-0.946	-0.333	-0.252	7.438	8.552	7.847	22.338	14.392	22,461	22.537	22.016	15.023	13.984	14.169	60
		0.453	0.906	0.942	1.143	0.444	0.086	9.528	9.329	8.185	22.184	13.170	22.375	22.299	21.877	12.847	13.951	13.693	68 6
-	0	1.124	0.722	0.712	-0.169	0.470	0.491	8.215	9.354	8.590	22.046	13.326	21.992	22.238	21.908	13.776	12.884	13.318	5H
-	0 0	1.102	0.890	0.549	-0.140	0.169	0.866	8.244	9.054	8.965	22.117	13.362	22.211	22.096	22.044	13.967	13.042	13.079	56
	0	1.670	0.949	0.583	-0.739	0.076	0.778	7.645	8.961	8.878	22.095	13.601	22.309	21.968	22.009	14.664	13.007	13.132	뛰
-	0 1	0.799	1.010	0.565	0.513	-0.506	0.824	8.707	8.379	9.360	22.630	13.588	22.639	21.93/	23.313	13./42	14.035	13.954	5E 5D
-	. 0	0.600	0.576	1.256	0.737	0.796	-0.329	9.121	9.681	7.770	22.220	13.363	22.307	22.418	21.936	13.186	12.737	14.165	5C
_	0 0	1.281	0.748	1.821	-0.358	0.419	-0.865	8.026	9.304	7.235	22.368	14.180	22.724	22.252	22.128	14.698	12.948	14.894	5B
	0	0.707	1.442	0.881	0.501	-0.528	0.182	8.885	8.356	8.282	22.228	13.720	22.468	22.048	22.168	13.583	13.692	13.886	5A
	1 0	0.696	1.119	0.486	0.523	-0.163	1.042	8.907	8.722	9.142	21.994	13.071	21.809	22.075	22.099	12.901	13.353	12.958	4 č
-		0.684	1.240	1 193	0.549	-0.310	-0.067	8.933	8.5/4	8.166	21.940	14 044	22.388	21./3/	21.694	13,455	13.163	14 286	40
_	0	0.767	0.988	1.015	0.382	0.017	-0.022	8.766	8.902	8.078	22.229	13.647	22.453	22.085	22.148	13.687	13.183	14.070	â m
	0 0	0.873	1.530	0.553	0.196	-0.614	0.854	8.580	8.271	8.954	22.576	13.975	22.393	22.129	23.206	13.813	13.858	14.252	40
	0	0.396	0.870	0.546	1.338	0.202	0.874	9.722	9.086	8.973	22.142	12.882	22,497	21.980	21.949	12.776	12.894	12.975	40
	0 0	0.744	1.307	0.858	0.427	-0.386	-0.172	8.811	8.499	8.320	22.132	13.589 13.944	22.435	22.097	21.865	13.624 13.925	13.598	13.546	4B 4
_	0	1.139	1.049	0.605	-0.188	-0.069	0.725	8.196	8.815	8.824	22.060	13.448	22.071	21.973	22.136	13.875	13.157	13.312	ЗH
	0	1.151	1.236	0.622	-0.203	-0.305	0.685	8.181	8.579	8.785	22.029	13.514	22.377	21.864	21.846	14.196	13.285	13.061	3G
-		1.803	0.746	0.941	-0.851	0.423	0.088	7.533	9.308	8.188	22.096	13.753	22.200	22.018	22.069	14.667	12.711	13.881	a µ
		0.207	0.531	0.543	2.272	0.915	0.880	10.656	9.799	8.980	22.792	12,980	24.234	22.001	22.139	13.578	12.202	13.160	3D
	0 0	0.800	1.234	0.693	0.322	-0.304	0.529	8.707	8.581	8.628	22.258	13.619	22.639	22.037	22.097	13.932	13.456	13.469	3C
	0 0	0.913	1.227	1.397	0.131	-0.295	-0.482	8.515	8.590	7.617	22,409	14.169	22.739	22.621	21.868	14.224	14.032	14.250	38
		0.518	1.056	0.400	0.071	-0.079	0.748	765.0	8 805	2 247	21 986	12.990	77 733	21 753	21 971	12 800	12 947	13 124	34
_	- 0	0.674	1.821	0.711	0.570	-0.865	0.492	8.954	8.020	8.592	22.325	13.803	22.437	21.940	22.599	13,483	13.920	14.007	2G
-	0 0	0.749	0.654	0.821	0.417	0.612	0.284	8.801	9.497	8.383	22.186	13.292	22.351	21.975	22.232	13.550	12.478	13.849	2F
	0 0	0.951	1.473	0.604	0.073	-0.559	0.727	8.457	8.326	8.826	21.967	13.431	22.029	22.006	21.867	13.571	13.680	13.040	2E
-		0.551	0.506	0.415	0.860	0.982	1.270	9.244	9.866	9.369	22.335	12.842	22.695	22,163	22.147	13,451	12.297	12.777	2D 20
		0.572	1.215	0.674	0.806	-0.281	0.568	9.190	8.603	8.668	22.464	13.644	22.920	22.120	22.352	13.729	13.517	13.685	2B
_	0 0	0.543	0.818	0.804	0.881	0.290	0.316	9.265	9.175	8.415	22.194	13.242	22.537	21.973	22.071	13.272	12.798	13.656	2A
_	-	≡	=	-	≡	=	-	≡	=	-	30d	90	≡	=	-	≡	=	_	Jampie
5	Score X<0.		^-ddCT	2	dCT 0)	T sample -	ddCT (dC	0,	T 30d-U6	đ	ge	Avera		-miR-30	hsa		90		وعسماه
				,				'				,							1

**S7** *In cell* screening detail calculation for hsa-miR-30d

		9N		hsa	-miR-182		Avera	age	dC	T 182-U6		קקכב (קכ	T sample	-dCT 0)	2	^-ddCT		S	core X<0	5	
sample	-	=	≡	-	=	≡	90	182	-	=	≡	-	=	≡	-	=	≡	-	=	≡	7
3F.	12.693	13.033	13.389	24.219	24.560	23.935	13.038	24.238	11.526	11.527	10.546	1.435	0.083	0.597	0.370	0.944	0.661	_	0	0	'
3G.	13.053	13.221	13.758	24.102	25.166	24.499	13.344	24.589	11.049	11.945	10.741	0.958	0.500	0.792	0.515	0.707	0.577	0	0	0	
4A.	12.722	13.177	13.606	24.130	24.567	24.169	13.169	24.289	11.408	11.390	10.563	1.317	-0.055	0.614	0.401	1.039	0.653	-	0	0	
4C.	12.793	13.574	13.579	24.621	23.769	24.227	13.315	24.206	11.828	10.195	10.648	1.738	-1.249	0.699	0.300	2.377	0.616	-	0	0	
ŧĒ.	12.767	14.211	13.885	24.339	23.905	24.425	13.621	24.223	11.572	9.694	10.539	1.482	-1.750	0.590	0.358	3.365	0.664	_	0	0	,
4F.	13.659	14.144	13.480	24.379	23.670	24.009	13.761	24.019	10.720	9.526	10.528	0.629	-1.918	0.579	0.646	3.780	0.669	0	0	0	
4G.	13.752	14.099	14.411	24.546	23.841	24.248	14.087	24.212	10.795	9.742	9.837	0.704	-1.703	-0.111	0.614	3.255	1.080	0	0	0	
5A.	14.625	16.062	13.626	24.797	24.144	24.167	14.771	24.370	10.173	8.082	10.541	0.082	-3.362	0.592	0.945	10.284	0.663	0	0	0	
5G.	13.837	13.240	13.855	23.990	24.652	23.894	13.644	24.179	10.153	11.412	10.039	0.063	-0.032	0.090	0.957	1.023	0.940	0	0	0	
6A.	14.315	13.934	13.800	24.659	24.845	24.601	14.016	24.702	10.344	10.911	10.802	0.253	-0.533	0.853	0.839	1.447	0.554	0	0	0	
6B.	13.911	13.833	13.480	24.304	24.299	23.891	13.741	24.165	10.394	10.466	10.411	0.303	-0.978	0.462	0.811	1.970	0.726	0	0	0	
6C.	13.261	14.380	14.723	24.968	23.897	23.982	14.121	24.282	11.707	9.517	9.259	1.617	-1.927	-0.690	0.326	3.803	1.613	_	0	0	
6E.	13.817	14.653	14.068	24.270	24.771	24.172	14.179	24.404	10.453	10.118	10.104	0.363	-1.327	0.156	0.778	2.508	0.898	0	0	0	
6F.	14.038	15.354	13.932	24.307	24.012	23.815	14.441	24.045	10.269	8.658	9.884	0.178	-2.786	-0.065	0.884	6.897	1.046	0	0	0	
8C.	13.941	15.029	14.231	24.123	24.484	24.412	14.400	24.340	10.182	9.455	10.181	0.091	-1.989	0.232	0.939	3.971	0.851	0	0	0	
9A.	13.472	14.950	14.227	24.601	24.438	24.504	14.216	24.514	11.129	9.488	10.277	1.039	-1.957	0.328	0.487	3.881	0.797	-	0	0	
10A.	13.211	12.768	13.786	24.079	24.716	24.126	13.255	24.307	10.868	11.948	10.341	0.777	0.504	0.392	0.583	0.705	0.762	0	0	0	
10B.	14.454	13.806	13.763	24.427	25.146	23.923	14.008	24.499	9.974	11.340	10.160	-0.117	-0.105	0.211	1.084	1.075	0.864	0	0	0	
10D.	14.432	13.954	13.872	24.214	24.850	23.879	14.086	24.314	9.781	10.896	10.006	-0.309	-0.548	0.058	1.239	1.462	0.961	0	0	0	,
Sample 0	15.058	13.158	14.322	25.148	24.602	24.271	14.179	24.674	10.090	11.444	9.949	0.000	0.000	0.000	1.000	1.000	1.000	0	0	0	

S8 Additional In cell Assay detail calculation for hsa-miR-182

		2		<u>ب</u>	2 mi0_21		Avor	Ş	2	112										<u></u>	
Sample		8			0-1111-01			260	5	1 31-00		0001 (00	ampie	4 (		-duci		4	016 7/0.	ľ	R
Jampic	-	=	=	-	=	=	90	31	-	=	=	-	=	=	-	=	=	-	=	≡	;
3F.	12.693	13.033	13.389	18.193	17.998	17.979	13.038	18.057	5.500	4.965	4.590	2.041	-0.073	0.450	0.2430	1.0520	0.7322	_	0	0	
3G.	13.053	13.221	13.758	18.098	18.192	18.068	13.344	18.119	5.045	4.971	4.310	1.586	-0.067	0.169	0.3331	1.0474	0.8892	_	0	0	
4A.	12.722	13.177	13.606	18.049	18.200	18.280	13.169	18.176	5.327	5.022	4.674	1.869	-0.016	0.533	0.2738	1.0111	0.6910	_	0	0	
4C.	12.793	13.574	13.579	18.140	18.135	18.161	13.315	18.145	5.348	4.562	4.581	1.889	-0.476	0.441	0.2700	1.3910	0.7369	-	0	0	
4E.	12.767	14.211	13.885	18.175	18.258	18.548	13.621	18.327	5.408	4.047	4.663	1.949	-0.991	0.522	0.2589	1.9877	0.6965	_	0	0	
4F.	13.659	14.144	13.480	18.268	18.235	18.492	13.761	18.332	4.610	4.091	5.011	1.151	-0.947	0.871	0.4503	1.9277	0.5469	_	0	0	
4G.	13.752	14.099	14.411	18.440	18.132	18.456	14.087	18.342	4.688	4.033	4.045	1.229	-1.005	-0.096	0.4265	2.0075	1.0690	_	0	0	
5A.	14.625	16.062	13.626	18.809	18.300	18.465	14.771	18.525	4.184	2.238	4.839	0.726	-2.800	0.698	0.6048	6.9646	0.6163	0	0	0	
5G.	13.837	13.240	13.855	18.323	18.285	18.085	13.644	18.231	4.486	5.045	4.229	1.028	0.007	0.089	0.4905	0.9952	0.9404	_	0	0	
6A.	14.315	13.934	13.800	18.602	18.284	18.393	14.016	18.427	4.287	4.350	4.593	0.829	-0.688	0.453	0.5631	1.6110	0.7307	0	0	0	
6B.	13.911	13.833	13.480	18.198	18.173	18.132	13.741	18.168	4.288	4.340	4.652	0.829	-0.697	0.511	0.5629	1.6217	0.7017	0	0	0	
6C.	13.261	14.380	14.723	18.123	18.134	18.215	14.121	18.157	4.862	3.754	3.492	1.404	-1.284	-0.649	0.3779	2.4349	1.5680	-	0	0	
6E.	13.817	14.653	14.068	18.392	18.037	18.636	14.179	18.355	4.575	3.383	4.569	1.117	-1.655	0.428	0.4612	3.1485	0.7434	_	0	0	
6F.	14.038	15.354	13.932	18.663	18.190	18.370	14.441	18.408	4.625	2.837	4.438	1.167	-2.201	0.298	0.4454	4.5984	0.8136	_	0	0	
8C.	13.941	15.029	14.231	18.559	18.232	18.549	14.400	18.446	4.618	3.203	4.318	1.159	-1.835	0.177	0.4478	3.5681	0.8847	-	0	0	
9A.	13.472	14.950	14.227	18.953	18.465	18.717	14.216	18.712	5.482	3.515	4.490	2.023	-1.523	0.349	0.2461	2.8731	0.7849	_	0	0	
10A.	13.211	12.768	13.786	18.190	17.949	18.147	13.255	18.095	4.979	5.181	4.361	1.520	0.143	0.220	0.3487	0.9054	0.8583	_	0	0	
10B.	14.454	13.806	13.763	18.141	18.094	18.424	14.008	18.220	3.688	4.288	4.660	0.229	-0.750	0.519	0.8532	1.6817	0.6976	0	0	0	
10D.	14.432	13.954	13.872	18.616	17.943	18.461	14.086	18.340	4.184	3.989	4.588	0.725	-1.049	0.447	0.6048	2.0690	0.7333	0	0	0	
Sample 0	15.058	13.158	14.322	18.516	18.196	18.463	14.179	18.391	3.459	5.038	4.141	0.000	0.000	0.000	1.0000	1.0000	1.0000	0	0	0	

S9 Additional In cell Assay detail calculation for hsa-miR-31

		9		ns.	a-min-suc		AVera	age	8	1 300-06		aacı (ac	, I sample						Score X <c< th=""><th>ü</th><th>,</th></c<>	ü	,
Sample	-	=	≡	-	=	≡	06	30d	-	=	≡	-	=	≡	-	=	≡	-	=	≡	,
3F.	12.693	13.033	13.389	23.001	23.487	23.481	13.038	23.323	10.308	10.454	10.093	1.397	0.217	0.625	0.3797	0.8603	0.6484			0	'
3G.	13.053	13.221	13.758	22.979	23.408	23.491	13.344	23.293	9.926	10.187	9.733	1.014	-0.050	0.265	0.4951	1.0354	0.8319		1	0	'
4A.	12.722	13.177	13.606	22.853	23.223	23.565	13.169	23.214	10.131	10.046	9.959	1.220	-0.191	0.491	0.4294	1.1419	0.7113		1 6	0	'
4C.	12.793	13.574	13.579	22.988	23.369	23.689	13.315	23.349	10.195	9.796	10.110	1.284	-0.441	0.642	0.4107	1.3578	0.6407		1 0	0	'
4Ē	12.767	14.211	13.885	23.300	23.380	23.664	13.621	23.448	10.532	9.169	9.778	1.621	-1.068	0.311	0.3252	2.0967	0.8062		1 0	0	1
4F.	13.659	14.144	13.480	23.262	23.628	23.854	13.761	23.581	9.603	9.484	10.373	0.692	-0.753	0.906	0.6190	1.6857	0.5338		0	0	'
4G.	13.752	14.099	14.411	23.404	23.588	23.594	14.087	23.529	9.652	9.489	9.183	0.741	-0.748	-0.285	0.5985	1.6796	1.2183		0	0	'
5A.	14.625	16.062	13.626	24.051	32.956	23.641	14.771	26.883	9.426	16.894	10.015	0.515	6.657	0.548	0.7000	0.0099	0.6842		2	0	1
5G.	13.837	13.240	13.855	23.376	23.567	23.682	13.644	23.542	9.540	10.327	9.827	0.628	0.090	0.359	0.6470	0.9396	0.7798			0	1
6A.	14.315	13.934	13.800	23.349	23.026	23.262	14.016	23.212	9.034	9.092	9.462	0.122	-1.145	-0.006	0.9187	2.2119	1.0041		0	0	'
6B.	13.911	13.833	13.480	23.533	23.438	23.664	13.741	23.545	9.622	9.606	10.184	0.711	-0.631	0.716	0.6109	1.5489	0.6086		0	0	'
6C.	13.261	14.380	14.723	23.342	23.468	23.644	14.121	23.485	10.081	9.088	8.921	1.170	-1.149	-0.546	0.4445	2.2171	1.4604		1 C	0	'
6E.	13.817	14.653	14.068	23.444	23.570	24.002	14.179	23.672	9.627	8.916	9.935	0.715	-1.321	0.467	0.6090	2.4979	0.7235		0	0	'
6F.	14.038	15.354	13.932	24.040	23.750	23.710	14.441	23.833	10.002	8.396	9.779	1.091	-1.841	0.311	0.4696	3.5829	0.8060		1 0	0	'
8C.	13.941	15.029	14.231	23.897	23.723	23.824	14.400	23.815	9.956	8.694	9.593	1.045	-1.543	0.125	0.4847	2.9148	0.9168		1 C	0	'
9A.	13.472	14.950	14.227	24.045	24.350	23.991	14.216	24.129	10.573	9.400	9.764	1.662	-0.837	0.296	0.3161	1.7865	0.8143		1 0	0	'
10A.	13.211	12.768	13.786	23.407	23.319	23.545	13.255	23.424	10.196	10.551	9.760	1.284	0.314	0.292	0.4105	0.8044	0.8168		1 0	0	1
10B.	14.454	13.806	13.763	23.912	23.480	23.923	14.008	23.772	9.459	9.673	10.160	0.547	-0.564	0.692	0.6845	1.4782	0.6190		0	0	1
10D.	14.432	13.954	13.872	23.925	23.419	23.733	14.086	23.692	9.493	9.465	9.860	0.581	-0.772	0.393	0.6684	1.7080	0.7617		6	0	'
Null RT	15.058	13.158	14.322	23.969	23.395	23.789	14.179	23.718	8.912	10.237	9.468	0.000	0.000	0.000	1.0000	1.0000	1.0000		0	0	_

S10 Additional In cell Assay detail calculation for hsa-miR-30d

## Substrate 25 nM

Time Sampling	CT mear	n Value	Conc (uN	/l) mean	<b>Δ</b> CT to 0
(min)	Ct Value	SD	Conc (uM)	SD	min
0	33.488	0.7355	0.00710	7.59.E-06	0.0000
2.5	32.258	0.1585	0.00684	3.53.E-06	1.2301
5	32.156	0.4772	0.00959	9.18.E-06	1.3323
10	30.820	0.0661	0.01216	4.20.E-06	2.6681
20	30.128	0.0519	0.02293	2.63.E-05	3.3602
40	30.147	0.0193	0.02960	1.52.E-05	3.3411
80	29.109	0.0460	0.10214	1.28.E-04	4.3797
180	27.467	0.0142	0.15325	1.61.E-04	6.0209

Substrate 50 nM

Time Sampling	CT mean Value		Conc (uM) mean		<b>Δ</b> CT to 0
(min)	Ct Value	SD	Conc (uM)	SD	min
0	32.855	0.0989	0.00546	3.76.E-05	0
2.5	31.698	0.1315	0.00323	3.15.E-06	1.156601
5	32.045	0.1335	0.00294	1.08.E-05	0.809743
10	31.241	0.1030	0.00473	2.30.E-05	1.613736
20	28.993	0.1065	0.02149	3.23.E-05	3.861771
40	28.943	0.0782	0.02607	2.38.E-05	3.912268
80	27.624	0.0773	0.10497	5.74.E-04	5.230887
180	26.126	0.0885	0.38511	2.24.E-03	6.728572

 ${\bf S11}$  Detail calculation of 25 nM and 50 nM substrate for velocity plot

# Substrate 100 nM

Time Sampling	CT mean Value		Conc (uM) mean		<b>Δ</b> CT to 0
(min)	Ct Value	SD	Conc (uM)	SD	min
0	29.508	0.0486	0.06489	1.43.E-04	0
2.5	30.811	0.0916	0.15440	9.02.E-05	0.32676
5	32.382	0.1918	0.02403	3.15.E-05	-1.19671
10	30.717	0.0719	0.07559	8.01.E-05	-0.30246
20	30.246	0.1046	0.52890	1.47.E-04	1.909919
40	30.136	0.0210	0.89781	2.55.E-04	2.727061
80	29.867	0.1016	0.76997	2.91.E-03	3.364975
180	27.966	0.0899	4.18384	4.63.E-03	5.561035

Substrate 200 nM

Time Sampling	CT mean Value		Conc (uM) mean		<b>Δ</b> CT to 0
(min)	Ct Value	SD	Conc (uM)	SD	min
0	28.963	0.1185	0.00630	1.98.E-02	0
2.5	27.124	0.1121	0.02376	2.06.E-01	1.83901
5	24.958	0.0143	0.07054	1.26.E-01	4.004938
10	24.538	0.0639	0.09258	2.83.E-01	4.425247
20	23.639	0.0941	0.16015	4.96.E-01	5.324462
40	22.217	0.0538	0.37632	9.31.E-01	6.74645
80	22.257	0.0316	0.39424	2.23.E+00	6.705735
180	20.325	0.1173	1.17342	1.07.E+00	8.638033

**S12** Detail calculation of 100 nM and 200 nM substrate for velocity plot

# Substrate 300 nM

Time Sampling	CT mean Value		Conc (uM) mean		<b>Δ</b> CT to 0
(min)	Ct Value	SD	Conc (uM)	SD	min
0	26.884	0.0249	0.25513	4.85.E-04	0
2.5	26.780	0.1028	0.26920	4.11.E-04	0.103791
5	24.641	0.0516	1.03634	1.20.E-03	2.24324
10	26.052	0.0258	0.60742	3.12.E-03	0.831655
20	25.140	0.0174	0.78602	1.79.E-03	1.744209
40	24.442	0.0210	1.21573	2.58.E-03	2.442131
80	24.021	0.0653	1.56371	2.72.E-03	2.862636
180	20.999	0.0176	11.62720	3.76.E-02	5.884878

# Substrate 400 nM

Time Sampling	CT mean Value		Conc (uM) mean		<b>Δ</b> CT to 0
(min)	Ct Value	SD	Conc (uM)	SD	min
0	29.001	0.0494	0.07517	2.35.E-04	0
2.5	27.045	0.0270	0.37456	2.12.E-03	1.955842
5	23.948	0.0034	1.64587	4.58.E-03	5.052423
10	23.198	0.0114	2.53681	5.79.E-03	5.802208
20	22.416	0.0187	3.92261	3.66.E-03	6.585011
40	24.739	0.0251	0.93875	8.95.E-04	4.262106
80	21.759	0.0095	8.59525	4.47.E-02	7.241521
180	19.526	0.0501	23.16750	1.72.E-02	9.474163

 ${\bf S13}$  Detail calculation of 300 nM and 400 nM substrate for velocity plot

# List of presentations

- Muhammad Nurrohman Sidiq, Asako Murata, and Kazuhiko Nakatani, "Screening of small molecules that interfere dicer-mediated processing of pre-miR-182/31/30d", Japan Society of Chemical Biology, virtual meeting, June 2021 (Poster)
- Muhammad Nurrohman Sidiq, Asako Murata, and Kazuhiko Nakatani, "qPCR-based screening methods for small molecules that modulate dicer-mediated pre-miR-182/31/30d", The 48<sup>th</sup> International Symposium of Nucleic Acids Chemistry, virtual meeting, November 2021 (Poster)