

## Supplementary Information

### Optimizing locked nucleic acid modification in double-stranded biosensors for live single cell analysis

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#### Keywords

Homogeneous biosensor, molecular beacon, 3D culture, spheroid, HeLa.

**Table 1.** Nucleic sequences for the dsLNA biosensor.

$\beta$ -actin Probe	/5Alex647N/AG+GT+TT+TG+TC+AA+GA+AA+GG+GT
$\beta$ -actin Quencher 1 (4-LNA)	GA+CA+AA+AC+CT/3IAbRQSp/
$\beta$ -actin Quencher 2 (3-LNA)	GACA+AA+AC+CT/3IAbRQSp/
$\beta$ -actin Quencher 3 (2S-LNA)	GACA+AAAC+CT/3IAbRQSp/
$\beta$ -actin Quencher 4 (2A-LNA)	GACAAA+AC+CT/3IAbRQSp/
$\beta$ -actin Quencher 5 (1-LNA)	GACAAAAC+CT/3IAbRQSp/
$\beta$ -actin Quencher 6 (DNA)	GACAAAACCT/3IAbRQSp/
$\beta$ -actin Target	ACCCTTTCTTGACAAAACCT
$\beta$ -actin Mismatch target	ACCCTTTCTCGACAAAACCT
Random Probe	/5Alex647N/AC+GC+GA+CA+AG+CG+CA+CC+GA+TA
Random Quencher 1 (4-LNA)	CT+TG+TC+GC+GT/3IAbRQSp/
Random Quencher 2 (3-LNA)	CTTG+TC+GC+GT/3IAbRQSp/
Random Quencher 4 (2S-LNA)	CTTG+TCGC+GT/3IAbRQSp/
Random Quencher 3 (2A-LNA)	CTTGTC+GC+GT/3IAbRQSp/
Random Quencher 5 (1-LNA)	CTTGTCGC+GT/3IAbRQSp/
Random Quencher 6 (DNA)	CTTGTCGCGT/3IAbRQSp/
Random Target	TATCGGTGCGCTTGTCGCGT

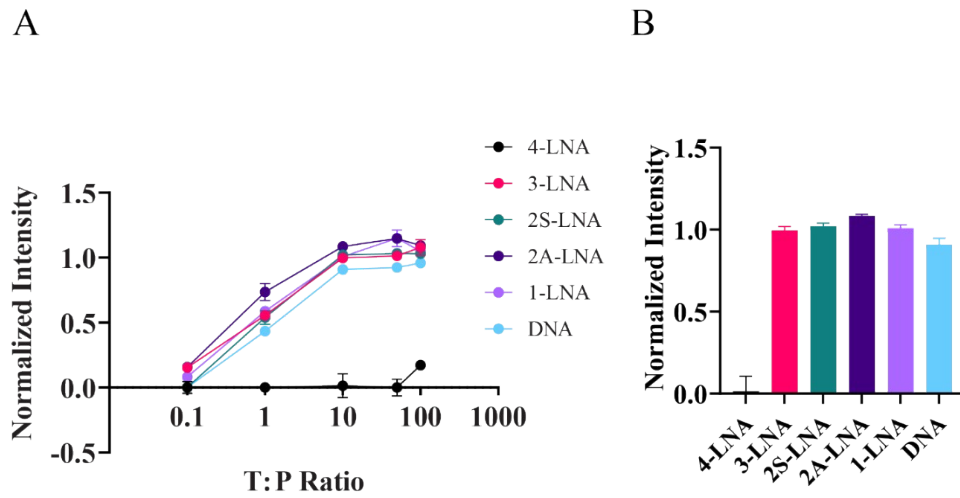
Sequences are in the 5' to 3' direction; + indicates LNA monomers.

**Table 2.** Statistics for data in Figure 4B and D.

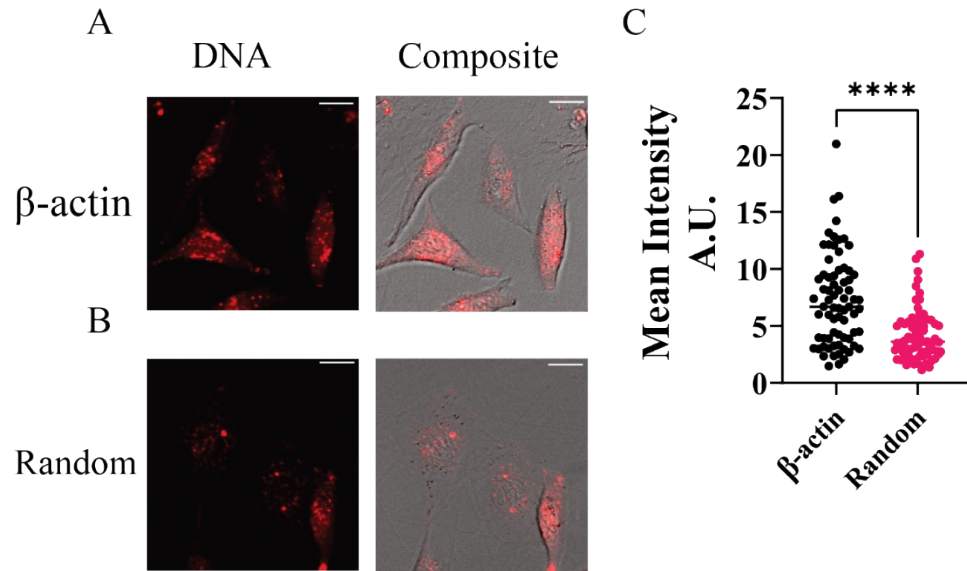
$\beta$ -actin	4 LNA	3 LNA	2 LNA - A	2 LNA - S	1 LNA	DNA
4 LNA		****	****	****	**	ns
3 LNA			ns	ns	ns	****
2 LNA - A				ns	ns	****
2 LNA - S					ns	***
1 LNA						*
DNA						

Random	4 LNA	3 LNA	2 LNA - A	2 LNA - S	1 LNA	DNA
4 LNA		**	**	ns	**	ns
3 LNA			ns	ns	ns	ns
2 LNA - A				ns	ns	ns
2 LNA - S					ns	ns
1 LNA						ns
DNA						

A Brown-Forsythe and Welch ANOVA test and the Dunnett's T3 multiple comparisons test were used to evaluate differences among quenchers for a specific ratio. ns p-value > 0.05, \* p-value < 0.05, \*\* p-value < 0.01, \*\*\* p-value < 0.001, and \*\*\*\* p-value < 0.0001.

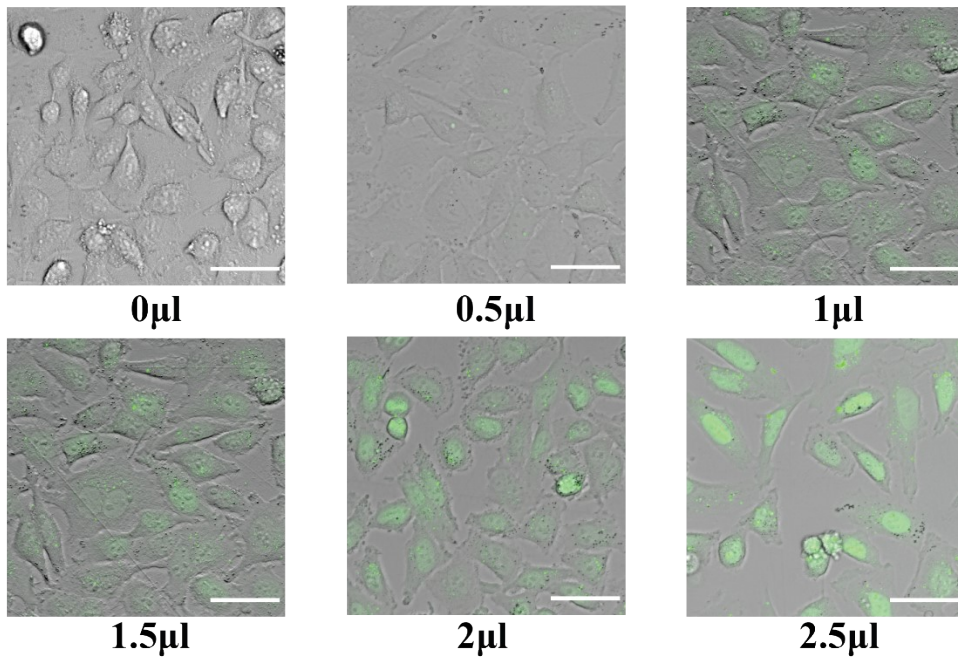


**Figure S1.  $\beta$ -actin probe specificity against a single base mismatch target evaluated for various quencher configurations.** Experimental characterization of the  $\beta$ -actin probe specificity against a mismatch target for the different quenchers. (A) Normalized intensity of the biosensor at multiple T:P ratios. (B) Bar chart of the normalized intensity of  $\beta$ -actin biosensor at a target-to-probe ratio of 10:1. The probe concentration is 250 nM. Error bars represent the standard deviation. A two-way ANOVA test was used to evaluate differences among quenchers and Q:P ratios. A Brown-Forsythe and Welch ANOVA test and the Dunnett's T3 multiple comparisons test were used to evaluate differences among quenchers for the T:P ratio of 10:1 (n=3).

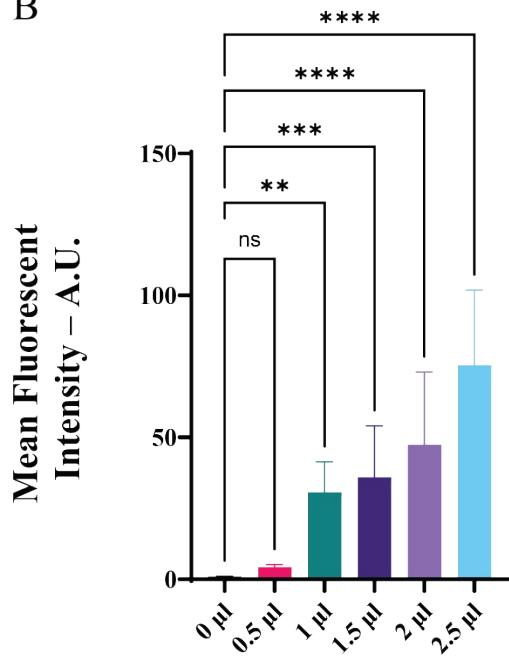


**Figure S2. DNA quencher demonstrates high specificity in live cells. (A-B)** Fluorescence and brightfield overlay images of HeLa cells transfected with (A)  $\beta$ -actin probe or (B) Random probe, respectively. Scale bars, 20  $\mu$ m. **(C)** Quantification of mean fluorescence intensity per cell for both cases. The nonparametric Mann-Whitney test was used to compare across groups. For each experiment  $n > 100$  cells per condition (\*\*\*\* $p < 0.0001$ ).

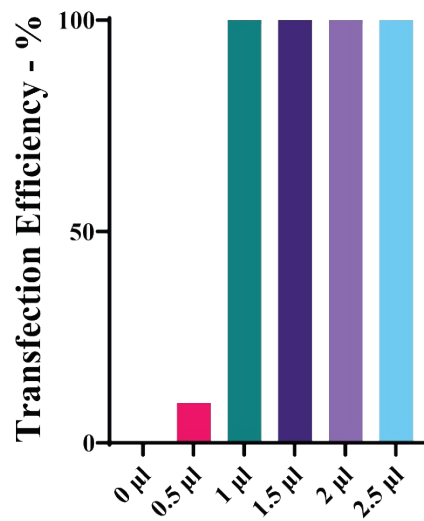
A



B



C



**Figure S3. RNAiMAX allows for high transfection efficiency in HeLa cells.** Block iT™, a non-targeting, fluorescent, double stranded RNA oligo was transfected with varying volumes of RNAiMAX in a 24 well plate according to manufacturer's protocol. Briefly, 6.5  $\mu$ l of Block-iT

(corresponding to approximately 1  $\mu\text{g}$  siRNA) was incubated over night with various volumes of RNAiMAX. Based on this optimization, subsequent experiments with dsLNA biosensors used 1.5 $\mu\text{l}$  RNAiMAX for transfection. **(A)** Representative images of HeLa cells transfected with Block iT<sup>™</sup>. Scale bars, 50  $\mu\text{m}$ . **(B)** Quantification of normalized mean fluorescence intensity per cell for each condition. All values were normalized to the mean fluorescent intensity of the 0  $\mu\text{l}$  RNAiMAX case. A one-way ANOVA test was used to compare between across groups. For each experiment  $n = 10$  cells per condition (\*\*  $p < 0.01$ , \*\*\*  $p < 0.001$  and \*\*\*\* $p < 0.0001$ ). **(C)** Percent of cells transfected with Block iT<sup>™</sup>.  $n > 200$  cells per condition.