Supplementary Information (SI) for Analyst.
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Supporting information

Table. S1. Oligonucleotide sequences used in this study.

Title	Sequence (5' to 3')
BRCA-1	GAA CAA AAG GAA GAA AAT CA
H1	AAC ATC ATG TGA TAC AAT TAT TAA CAA GGA ACG ACC CAA GUA GCU UAU CAG ACU GAU GUU GA
H2	SH-AAA ATT TTT CG TCA ACA TCA GTC TGA TTT TAA GCT ATG TTG -FAM
crRNA	UAA UUU CUA CUC UUG UAG AUG AUU UUC UUC CUU UUG UUC A
"2"	UGA GGU AGU AGG UUG UAU AGU U
DH probe	A*A*G* A*A*T* T*C*T* T*A*A* G*A*A* T*T*C* T*T* TCA ACA TCA CCG ACC TTC CAC CGA GCT AGA TCC CTG GAC GAC TTG AAA AAC TAT ACA ACC TAC TAC CTC A TTT CAA GTC GTC CAG TTG AAA

Supplemented experimental section:

Cell culture and cfDNA extracton

MCF-7 cells were grown in Dulbecco's modified Eagle medium (DMEM) containing 10% fetal bovine serum (FBS), 100 U/mL penicillin, and 100 g/mL streptomycin at 37 °C in a 5% CO_2 humidified atmosphere. HEK293 cells were grown in RPMI 1640 medium supplemented with 10% FBS, 100 U/mL penicillin, and 100 g/mL streptomycin at 37 °C in a humidified 5% CO_2 atmosphere. Applied Biosystems MagMAX free DNA extraction kit was used to extract the cfDNA from the cell culture fluid. The extraction procedure refers to the instruction of the kit.

Immobilization of H0 probe on the surfaces of SMBs

The surfaces of MBs were labeled with H0 probe as follows, First, 5 μl H0 probe was mixed with 37.5 μl 1× PBS and prehybridized with a PCR machine (90 °C for 5 min, cooled to 4 °C at a speed of 4 °C/min). Then MBs (10 μl, 10 mg/ml) were washed three times with washing buffer and diluted to 1 mg/ml. H0 probe (10 μl) was added to the diluted MB solution and mixed for 30 min at room temperature, followed by magnetic separation of the H0@MBs. The H0@MBs complexes obtained were washed twice with washing solution.

pp Probe Preparation

pp Probe was prepared according to a previously reported procedure; its spectra were in accordance with those described [1]. HR-FAB MS: calculated m/z 727.2350, found 727.2353; FTIR (KBr/cm): 3450, 2970, 1600, 1588, 1465, 1354, 1147.

Statistical analysis

All data collected in the research were shown as mean ± standard deviations. The two-tailed Student's t test was used to obtain the differences between two groups and P <

0.01 was used to evaluate the significance.

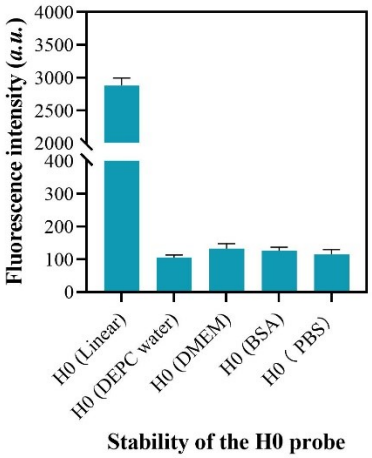

Figure S1. Fluorescence intensity of the H0 probe when mixed with different buffer solutions.

References:

1. Pandith, A.; Seo, Y. J., Label-free sensing platform for miRNA-146a based on chromo-fluorogenic pyrophosphate recognition. *J. Inorg. Biochem.* **2020,** *203*, 110867.