## SUPPORTING INFORMATION

# An artificial enzyme cascade amplification strategy for highly sensitive and specific detection of breast cancer-derived exosomes

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#### Table of content:

- 1. Supporting figures (Fig. S1-5)
- 2. Supporting table (Table S1-2)



Fig. S1 Optimization of the G-quadruplex mimicking DNAzyme sequence by comparing the relative signal generated from five common G-quadruplex mimicking DNAzyme sequence. A is the absorbance at 420 nm in the presence of exosomes and  $A_0$  is the absorbance at 420 nm in the absence of exosomes. Error bars show the standard deviation of three experiments.



**Fig. S2** Optimization of the switch strands. (A) Absorption spectra of the SDT sensing scaffold coupled with different switch strands (B1, B2, B3, B4, B5, and B6) in the presence and absence of exosomes. (B) The relative signal of the SDT sensing scaffold coupled with different switch strands.



**Fig. S3** (A) The relative signal of different concentration of SDT for detection of MCF-7 exosomes. (B) The relative signal of different concentration of hemin for detection of MCF-7 exosomes.



**Fig. S4** (A) The relative signal of the SDT sensing scaffold at 420 nm after incubated with different concentration of glucose. (B) Time-course absorbance monitoring of the SDT sensing scaffold after adding all the reagents in the presence and absence exosomes.



**Fig. S5** Influence of temperature (4, 27, and 35°C) on the formation of G-quadruplex. (C) Histogram of absorbance change ratio  $(A/A_0-1)$  for the different reaction temperature.

## **2** Supporting Tables

DNA	Sequence (from 5' to 3')					
P1	GGG TTG GGC GGG ATG GG <mark>G GTA TCCA</mark>					
P2	TTT GGG TAG GGC GGG TTG GG <mark>G GTA TCC A</mark>					
P3	GGG TAG GGC GGG TTG GG <mark>G GTA TCC A</mark>					
P4	CTG GGA GGG AGG GAG GGA GGT ATC CA					
P5	ACC TGG GGG AGT ATT GCG G <mark>TA TCC A</mark>					
A76	TCAACTTTGGGTAGGGCGGGTTGGGGGGTATCCATGATAAAACGACACTACGT GGGAATCTACTATGGCGGCTCTTC					
B76	TTCAGTTTGGGTAGGGCGGGTTGGGGGGTATCCAAATGTGCTTCCCACGTAGT GTCGTTTGTATTGGACCCTCGCAT					
C59	CTGAATTTTTATTACAGCTTGCTACACTTTTTGAAGAGCCGCCATAGTATTTTA CATT					
D59	GTTGATTTTTGTGTAGCAAGCTGTAATTTTTTATGCGAGGGTCCAATACTTTTT ATCA					
B1	TTGATCCTTTGGATACC CCC AAC					
B2	TTGATCCTTTGGATACC CCC AAC CCG					
В3	TTGATCCTTTGGATACC CCC AAC CCG CCC					
B4	TTGATCCTTTGGATACC CCC AAC CCG CCC TAC					
B5	TTGATCCTTTGGATACC CCC AAC CCG CCC TAC CCA					
B6	TTGATCCTTTGGATACC CCC AAC CCG CCC TAC CCA AA					

Table S1. Sequence of oligonucleotides designed in this study<sup>a</sup>

<sup>a</sup> Bold bases are the G-quadruplex sequence, and underlined bases are MUC1 aptamer.

Platform	Linear range (particles/mL)	LOD (particles/mL)	Method	Assay time	Reference
B-Chol anchor assay with enzyme-linked HCR	$2.3  imes 10^{6}$ - $2.3  imes 10^{8}$	$2.2 \times 10^{6}$	Colorimetric	~16.5 h	1
large-AR AuNBP@MnO <sub>2</sub> NSs	$8.5 \times 10^5$ - $8.5 \times 10^7$	1.35 × 10 <sup>5</sup>	Colorimetric	~2.5 h	2
Aptamer-based DNA nanodevices	10 <sup>6</sup> - 10 <sup>11</sup>	106	Fluorescence	-	3
"on-off"-type aptasensor	1.0×10 <sup>8</sup> - 1.6×10 <sup>9</sup>	4.2 ×10 <sup>7</sup>	Fluorescence	32 min	4
Aptasensor based on g- C3N4 nanosheets	$1.9  imes 10^9$ - $3.38  imes 10^{10}$	1.35 × 10 <sup>9</sup>	Colorimetric	~30 min	5
HRP-pSC <sub>4</sub> - AuNPs@COFs	$5 \times 10^{5}$ - $1.5 \times 10^{10}$	1.6 × 10 <sup>5</sup>	electrochemical	~3 h	6
Switchable DNA tetrahedral scaffolds	$3.8 \times 10^{6}$ - $1.2 \times 10^{8}$	1.51 × 10 <sup>5</sup>	Colorimetric	~2 h	This work

#### Table S2. Comparison of our method and reported methods for exosomes detection.

#### REFERENCES

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