

Supporting Information

Simultaneous quantification of exosomal MMP14 expression and proteolysis activity on a spherical dual-probe based fluorescent nanosensor

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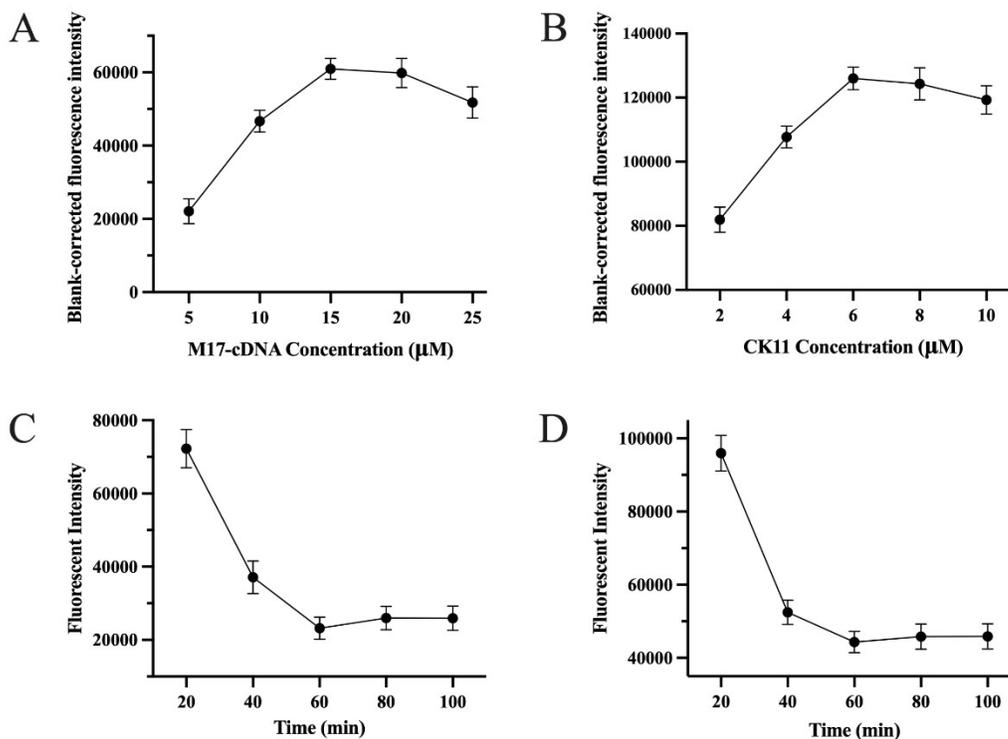


Fig. S1. Effects of M17-cDNA concentration (A), CK11 concentration (B), and incubation times of M17-cDNA (C) and CK11 (D) on fluorescent signals. Error bars were calculated from standard deviations of three independent experiments.

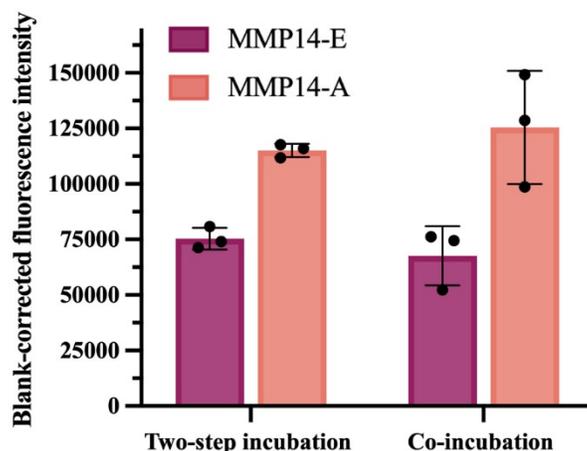


Fig. S2. Comparison of the co-incubation and two-step incubation of two probes for the detection of MMP14-E and MMP14-A using the proposed sensor.

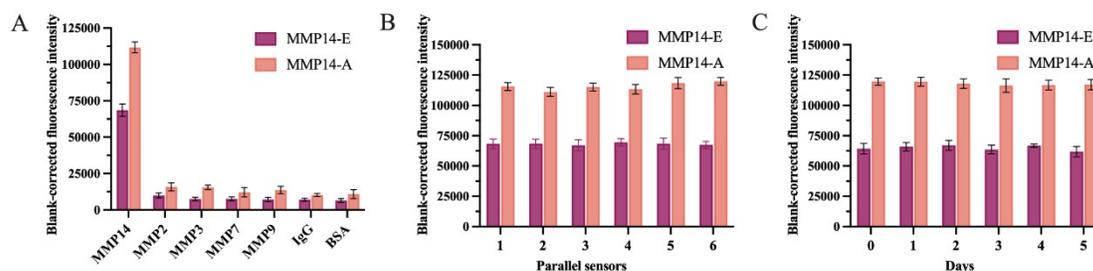


Fig. S3. (A) Selectivity. Concentrations of all proteins was set as 100 ng/L. (B) Reproductivity. Each biosensor was incubated with 100 ng/L of MMP14. (C) Stability.

Table S1 Comparison of sensor techniques for the detection of MMP14.

Sensing platform	Sample	Technique	Linear range (ng/L)	LOD (ng/L)	Ref.
Peptide modified Au/Ag@SiO ₂	Cells and tissues	Fluorescent detection	1000-250000	680	1
Peptide/Gaussia luciferase-based probe	Cells and mouse models	Fluorescent detection	0-80 nM	-	2
Peptide modified electrode	Au Human serum	Electrochemical detection	0.1-50	7	3

Peptide modified electrode	Au	MCF-7 cell	Electrochemical detection	0.2-0.9	0.1	4
Peptide-based antibody-based microfluidic chips	and	Exosomes	Fluorescent detection	10 ² -10 ⁶ EVs/ μ L	~16 EVs/ μ L	5
Aptamer/peptide probe AuNPs	dual-modified	Human serum	Fluorescent detection	1-1000	1.00 (MMP14-E), 1.01 (MMP14-A)	This work

Table S2 Recoveries and precisions of the method (n = 6)

Added (particle s/mL)	MMP14-E			MMP14-A		
	Found-Background (particles/mL)	Recover y (%)	RSD (%)	Found-Background (particles/mL)	Recover y (%)	RSD (%)
10 ²	109.8	109.8	13.29	103.4	103.4	10.09
10 ⁴	8997	89.97	9.628	9830	98.30	5.653

Reference

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