Supporting Information

Construction of a DNA-AuNP-based satellite network for exosome analysis

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Supporting figures and table

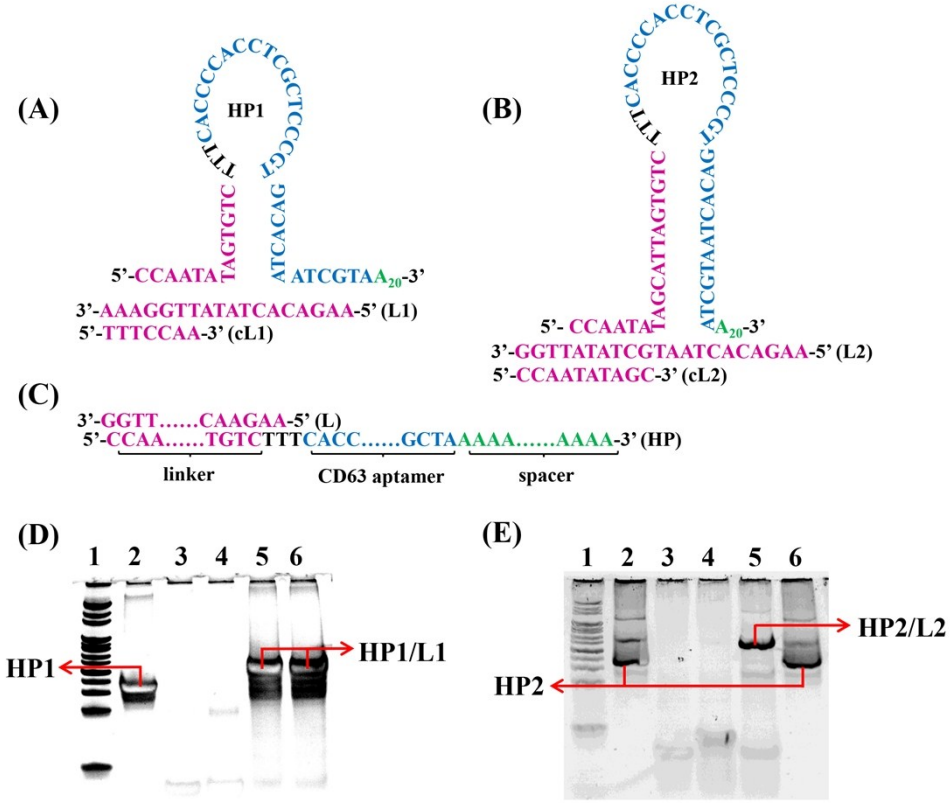

Fig. S1. (A) Sequence schematic of hairpin structure HP1, L1 and cL1. (B) Sequence schematic of hairpin structure HP2, L2 and cL2. (C) Sequence matching schematic between HP and L when the HP was opened in the presence of exosomes. (D) Native polyacrylamide gel electrophoresis to verify non-specific reaction of HP1 and L1/cL1. Lane 1: marker; lane 2: HP1; lane 3: L1; lane 4: L1/cL1; lane 5: mixture of HP1 and L1; lane 6: mixture of HP1 and L1/cL1. (E) Native polyacrylamide gel electrophoresis to verify non-specific reactions of HP2 and L2/cL2. Lane 1: marker; lane 2: HP2; lane 3: L2; lane 4: L2/cL2; lane 5: mixture of HP2 and L2; lane 6: mixture of HP2 and L2/cL2.

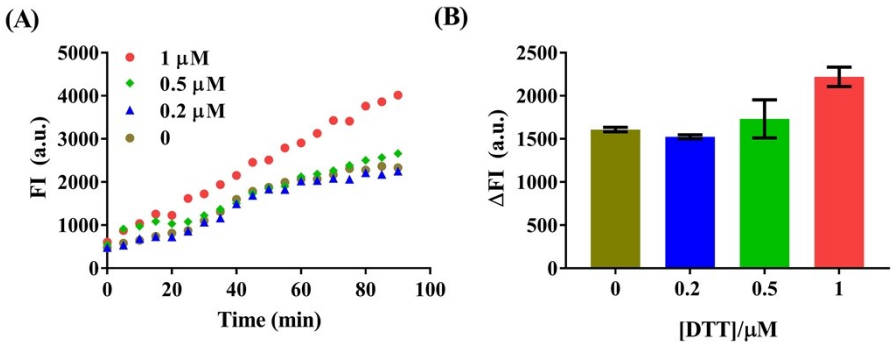

Fig. S2. (A) Spectra of fluorescence signal leakage at different DTT concentrations. (B) Histogram of fluorescence intensity changes at different DTT concentrations. The excitation and emission wavelengths were set to 494 nm and 520 nm.

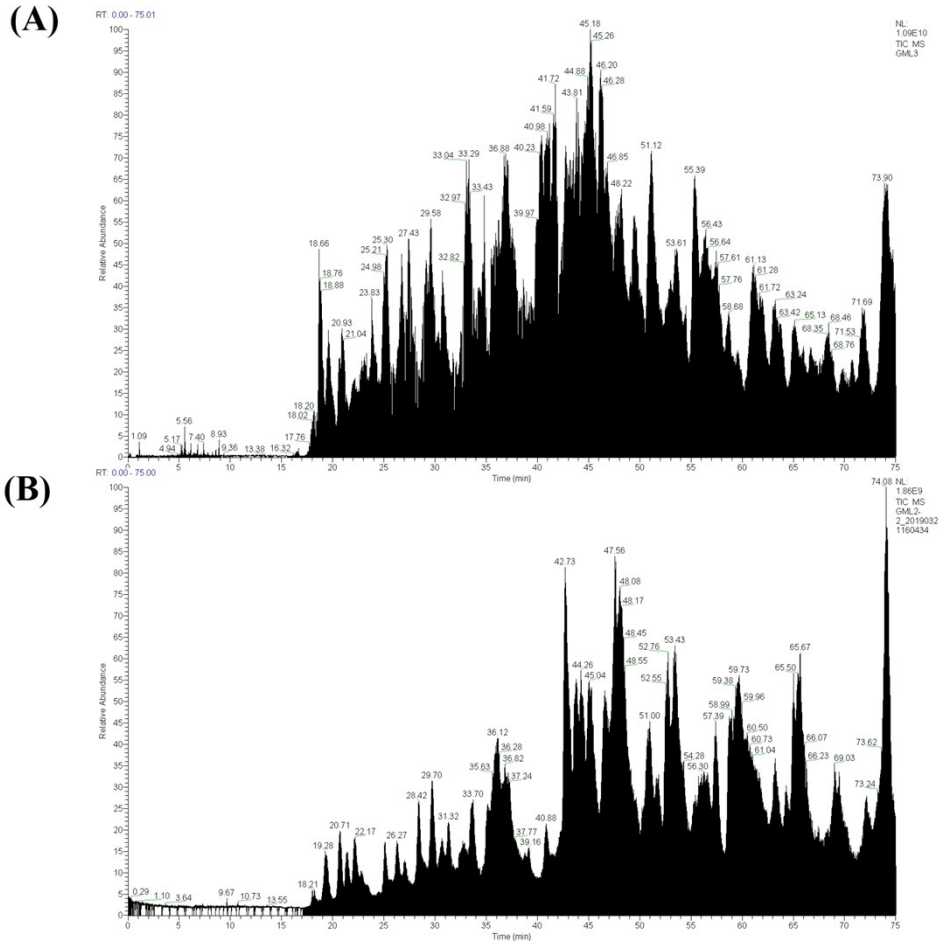

Fig. S3. (A) The relative abundance of exosome protein isolated by our method. (B) The relative abundance of exosome protein isolated by ultracentrifugation.

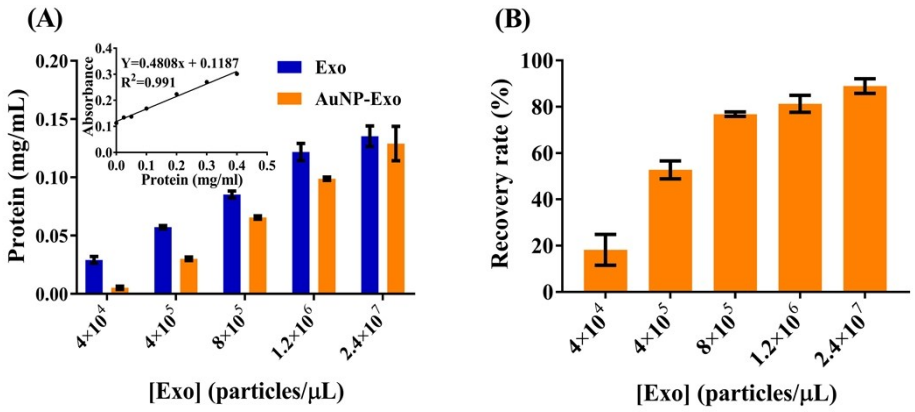

Fig. S4. (A) Histogram of total protein content of standard exosome (Exo) and exosome obtained by our method (AuNP-Exo) at different exosome concentrations. The inset curve shows the standard curve of BCA protein quantification. (B) Histogram of recovery at different exosome concentrations.

Table S1. Sequence information of oligonucleotides used in this work

Name	[a] Sequence (5'-3')
T1	TTTTTTTTTTTTTTTTTTTTAAGACACTAATGCTATATTGGTTGGTTGG
P1	CCAACCAACCAATATAGCAT
T2	GTGGGGTGAAAAAAGACACTAATGCTATATTGGTTGGTTGGTTTTTTT TTTTTTTTTTTTTTAGCATTAGTGTCACGGGAGCGAG
P2	CTTTTTTCACCCCACCTCGCTCCCGTGACA
HP1	CCAATATAGTGTCTTTCACCCCACCTCGCTCCCGTGACACTAATGCTA AAAAAAAAAAAAAAAAAAAA
L1	AAGACACTATATTGGAAAAAAAAA-SH
cL1	FAM-TTTCCAA
HP2	CCAATATAGCATTAGTGTCTTTCACCCCACCTCGCTCCCGTGACACTA ATGCTAAAAAAAAAAAAAAAAAAAA
L2	AAGACACTAATGCTATATTGGAAAA-SH
cL2	FAM-TTCCAATATAGC
HP3	CCAACCAACCAATATAGCATTAGTGTCTTTTTTCACCCCACCTCGCTCC CGTGACACTAATGCTAAAAAAAAAAAAAAAAAAAA
L3	AAGACACTAATGCTATATTGG-SH
cL3	FAM-TTCCAATATAGCATTAGTGT
Poly T	TTTTTTTTTTTTTTTTTTTTT-FAM

[a] The red characters in HP1, HP2 and HP3 represent CD63 aptamers. Underlined characters in HP1, HP2 and HP3 represent the sequence that forms the stem of hairpin structure. The yellow shaded part in L1, L2, L3, HP1, HP2 and HP3 represented the sequence that is complementary between L1 and HP1, L2 and HP2, L3 and HP3.