Supporting Information

A dual signal amplification method for exosome detection based on DNA dendrimer self-assembly

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Supporting figures and table

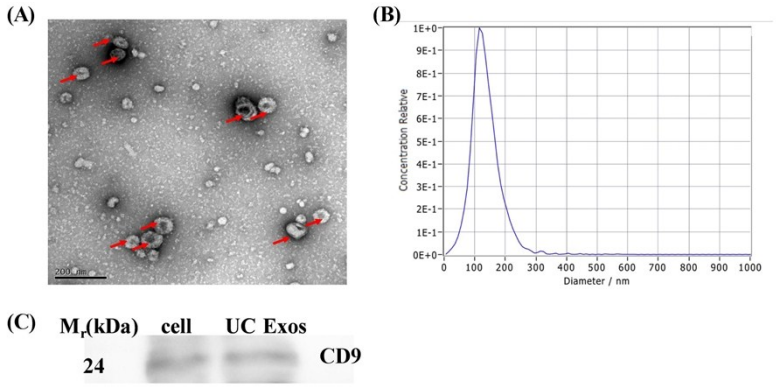

Fig. S1. Characterization of exosomes purified from HepG2 cell culture supernatant. (A) Isolated exosomes were identified by transmission electron microscopy. The red arrows indicate exosomes with a mean diameter of ~100 nm. (B) Size distribution of exosomes by dynamic light scattering measurements. (C) Western blotting images of CD9 proteins from HepG2 cell lysates and exosomes.

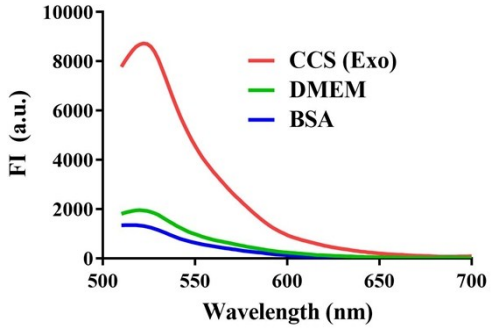

Fig. S2. Fluorescence spectrum of exosome capture process in the presence of CCS, DMEM and 0.1% BSA.

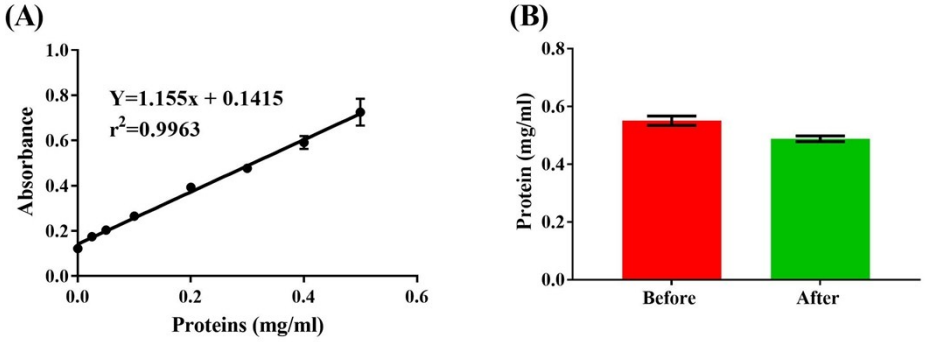

Fig. S3. (A) Standard work curve of the concentration of exosomal proteins and absorbance value obtained by BCA protein quantitation kit. (B) Quantification of the exosomal protein

concentration before the capture (before) and the protein concentration of the captured exosomes (after), using BCA protein quantitation kit.

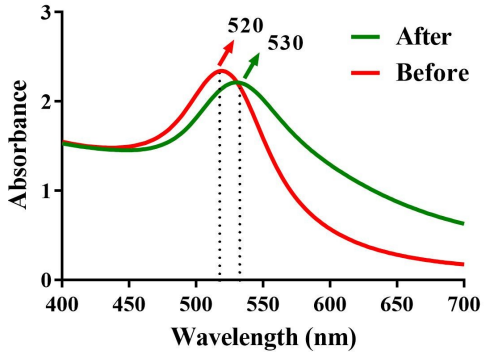

Fig. S4. Absorption spectra of the AuNPs before and after modification of HP_1.

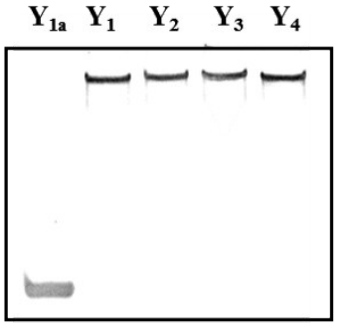

Fig. S5. Native PAGE analysis of Y_1, Y_2, Y_3, and Y_4, while Y_{1a} is as control.

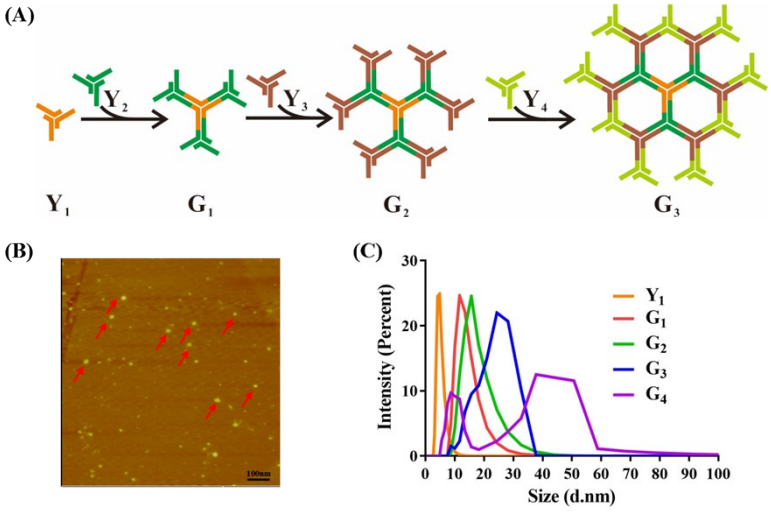

Fig. S6. (A) Schematic illustration of DNA dendrimers generation. (B) AFM imaging for the last generation G_3. (C) DLS experiments for particle size analysis for different dendrimers.

Table S1. Sequences of oligonucleotides used in this work

Name	[a] Sequence (5'-3')
A_1	*ATATACACCCCA*CCTCGCTCCCGTGACACTAATGCTATTTTTT-Biotin
S_1	*TGGGGTGTATAT*-FAM
A_2	CACCCCAC*CTCGCTCCCGTG*ACACTAATGCTATTTTTT-Biotin
S_2	*CACGGGAGCGAG*ATATA-FAM
S_3	TGGGGTGTATATTTCATATATATA
R	ATATACACCCCATTTTTTTTTTTTTTTTTTTTTTTTTTTT
HP_1	CACACACAATATTTCATATATATATTGATGTGTACCTATATATATGAA ATATACACCCCATTTTTT-SH
HP_2	TTGATGTGTACCATATTTCATATATATAGGTACACATCAATATATATA-FAM
Y_{1a}	TGAAATAT TGTGTGTG CCTGTCTGCCTAA TGTGCGTCGTAAG-FAM
Y_{1b}	CTGTCATCGGTCA CTTACGACGCACA AGGAGATCATGAG
Y_{1c}	CTGTCATCGGTCA CTCATGATCTCCTT TAGGCAGACAGG
Y_{2a}	TGACCGATGACAG CCTGTCTGCCTAA TGTGCGTCGTAAG-FAM
Y_{2b}	GACACACTGAGGT CTTACGACGCACA AGGAGATCATGAG
Y_{2c}	GACACACTGAGGT CTCATGATCTCCT TTAGGCAGACAGG
Y_{3a}	ACCTCAGTGTGTC CCTGTCTGCCTAA TGTGCGTCGTAAG-FAM
Y_{3b}	TGCTGTCTGTCCA CTTACGACGCACA AGGAGATCATGAG
Y_{3c}	TGCTGTCTGTCCA CTCATGATCTCCT TTAGGCAGACAGG
Y_{4a}	TGGACAGACAGCA CCTGTCTGCCTAA TGTGCGTCGTAAG-FAM
Y_{4b}	AGGTCAGAACTGT CTTACGACGCACA AGGAGATCATGAG
Y_{4c}	AGGTCAGAACTGT CTCATGATCTCCT TTAGGCAGACAGG

[a] The color of the characters corresponds to the color of probes illustrated in Scheme 1. Italicized characters in A_1, S_1, A_2, and S_2 represent the bases complementary with each other. Underlined characters in S_3 represent the sequence that can open the hairpin structure of HP_1. Underlined characters in HP_2 represent the toehold that is complementary with the hairpin structure of HP_1.