Supporting Information

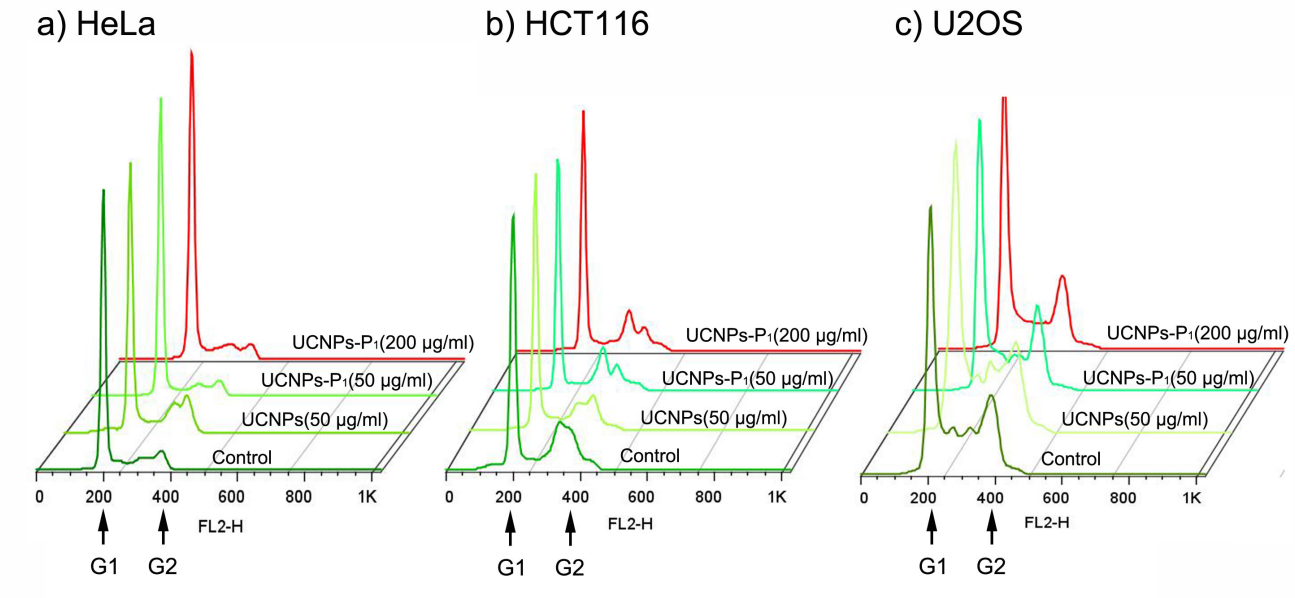

Fig S1. Representative cell cycle distribution graphs of cells, (a) Hela, (b) HCT116 and (c) U2OS for statistics in **Figure 7**. The merged raw data of cell cycle distribution was graphed using Flowjo software (7.6.5).

Table S1. The DLS data for UCNPs-P1 and UCNPs

UCNPs-P1				
Run	Pos.	KCps	Mob.	Zeta
1	50	2304.4	-0.351	-4.5
2	50	2256.4	-0.448	-5.7
3	50	2027.2	-0.452	-5.7
Average		2196	-0.417	-5.3
UCNPs				
Run	Pos.	KCps	Mob.	Zeta
1	50	2163.4	1.824	23.2
2	50	2167.8	1.861	23.7
3	50	2165.9	1.88	23.9
Average		2165.7	1.855	23.6

Experimental procedures

1. Pull down assay

Exponential growing 1x10^8 HeLa cells were trypsin harvested and centrifuged (4000 rpm, 5min) to collect cells. Cell pallets were resuspended with PBS (137 mmol/L NaCl, 2.7 mmol/L KCl, 1.76 mmol/L KH_2PO_4, 10 mmol/L Na_2PO_4) twice. Then Cells were resuspended in 1.5 mL lysis buffer (25 mM Tris pH 7.4, 150 mM NaCl, 0.5% NP-40, 1 mM PMSF and protease Inhibitors) on ice for 15 min. Unresolved debris were cleared by 13,000 rpm centrifugation fro 10 min. Supernatant were equally distributed, and incubated with Nanoparticles **UCNPs** or **UCNPs-P_1** at 4 ^oC, for 2 hours. Then Nanoparticles and its bound proteins were spin down and washed with lysis buffer for three times, to remove the unbound proteins. Nanoparticles and is bound proteins were denatured in 1x SDS sample buffer (62.5 mmol/L Tris, pH 6.8, 2% SDS, 5% beta-mercaptoethanol, 10% glycerol and 0.01% bromophenol blue) and treated in boiling water bath for 10 min. Finally, the proteins were separated by 10% SDS-PAGE gel, transferred to nitro-cellular membrane, and probed with antibodies, respectively (anti-Cyclin D1 or Geminin).

2. Flow cytometry analysis

Cells subjected to cell cycle analysis were typsin digestion detached, centrifugation (2000 rpm, 3 min) collected and resuspended in PBS, then cells were spin down and fixed in 70% cold ethanol for 120 minutes (4 ^oC). Before analysis, cells were spin down again to remove the ethanol and resuspended in PBS, then stained of nucleic acids by adding propidium iodide (20 μg/mL)/RNase A (50 μg/mL) working solution, at 37 ^oC for 30 min. Finally, cells were analyzed in BD Biosciences FACSCalibur Flow Cytometer and the results were processed with Modifit LT 3.0 software, for counting the cell phase percent of G1, G2 and S phases. Finally, the cell phase distributions of each sample were presented as column chart, graphing by GraphPad Prism 5 software.