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Supplementary Information

Experimental part.

Synthesis of the cationic lipid Au nanoparticles (NP)

The gold nanoparticles were prepared by reducing the $HAuCl_4$ with $NaBH_4$ in the presence of *N,N,N*-Trimethyl(11-mercaptoundecyl) ammonium bromide in an aqueous solution. The Au/$NaBH_4$/ Trimethyl(11-mercaptoundecyl) ammonium bromide ratio was 56:0.1:85 (mol/mol/mol). The color of the solution changed from faint yellow to wine red within 2 min indicating the formation of AuNPs. The cationic lipid AuNPs solution was then dialyzed and stored at room temperature for further use. The cationic lipid AuNPs solution was highly stable in water and no precipitate and an aggregate formation were detected up to 6 months.

Preparation AuNPs carrying premiR-145 expressing plasmid DNA complex

The AuNPs-premiR-145/GFP complexes were prepared with varying w/w ratio (10:1, 20:1, respectively). For AuNPs-premiR-145/GFP (10:1) the amounts are 44 µg:4.4 µg, and for (20:1) are 44 µg:2.2 µg. respectively.

Methods.

Transmission Microscopy

The morphology and size of the cationic lipid AuNPs were characterized by Transmission Electron Microscope (TEM), JEM- 1200EX model. A drop of the sample solution was allowed to dry on a copper grid (400 mesh, electron microscopy sciences).

Zeta Potential

The electrical charge of the AuNPs was measured by using a Zeta potential analyzer (Zetasizer Nano-ZS). AuNPs and AuNPs-premiR145/GFP were diluted with distilled water and the determination of zeta potential was performed.

Fluorescence microscopy

Fluorescence microscopy was performed using an Apo-Tome microscope, Zeiss. GFP (green fluorescence protein) emission was detected at at λ =509 nm, using an excitation wavelength of λ = 489 nm.

Cell culture

The glioma cell line A172, was obtained from the American Type Culture Collection (Manassas, VA). Cells were grown on tissue culture dishes at a concentration of 2×10^5 cells/mL in Dulbecco's modified Eagle medium DMEM containing 10% heat-inactivated fetal calf serum (FCS), 2 mmol/L glutamine, penicillin (50 units/mL), and streptomycin (0.05 mg/mL). The medium was changed every 3 to 4 days and cultures were split using 0.25% trypsin. Equal numbers of cells (2×10^5 cells/mL) were plated for all the experiments.

Transfection

Plasmid DNA, encoding for premiR145 and green fluorescent protein (GFP) was used in the transfection studies. The A172 glioma cells were grown in tissue culture dishes at a concentration of 2×10^5 cells/mL in Dulbecco's modified Eagle medium DMEM containing 10% heat-inactivated fetal calf serum (FCS), 2 mmol/L glutamine, penicillin (50 units/mL), and streptomycin (0.05 mg/mL). At a confluence level of 70–80%, the media was replaced, and the cells were incubated with 2 ml fresh media. The transfection complexes of AuNPs-premiR145/GFP expressing plasmid DNA were added to the cells at 37°C. Transfection with the Mirus reagent was performed according to the manufacture's instructions. Briefly, 2.5 µg plasmid (in 2.5 µl) was mixed with 200 µl of OptiMEM and 7.5 µl of Mirus reagent. Cells were incubated with this mixture for 1-2 hr and then 2 ml of complete medium was added.

The cells were incubated with the vectors for 3 h. The transfection media was then replaced with fresh culture media, and the cells were incubated for a 72 h. After the incubation the cells were collected using 0.25% trypsin.

Real-time PCR analysis

Total RNA was isolated from cultured cells using QIAzol reagent (Qiagen, CA) according to the manufacturer's protocol. 0.5 µg of RNA was used to synthesize cDNA by Thermoscript (Invitrogen) with oligo dT primers. To detect the CTGF mRNA we employed the SYBR green qPCR method using the following primers: CTGF - forward; reverse.

For internal control we employed S12 mRNA levels: forward TGCTGGAGGTGTAATGGACG reverse CAAGCACACAAAGATGGGCT). The expression of miR-145 was determined using TaqMan miRNA assays and real-time PCR. All the miRNA assays (hsa-miR-145; 002278 and sn-RNU6B; 001973) were obtained from Applied Biosystems (Foster City, CA) and the reactions were run in triplicates. The relative expression of the specific miRNAs was calculated using the comparative Ct method after normalization to snRNU6B. The level of extracellular miRNAs was determined in a fixed volume (500 µl) of culture supernatants and calculated based on their Ct values that were normalized by cel-miR-39: 000200 (Applied Biosystems), which was spiked in each aliquot of the real-time RT–PCR. Quantitative miRNA or mRNA expression data were acquired and analyzed using the ABI Prism 7000 Sequence Detection System (Applied Biosystems). Data were further analyzed by Comparative CT (ΔΔCT) method, and results are expressed in arbitrary units.

Results.

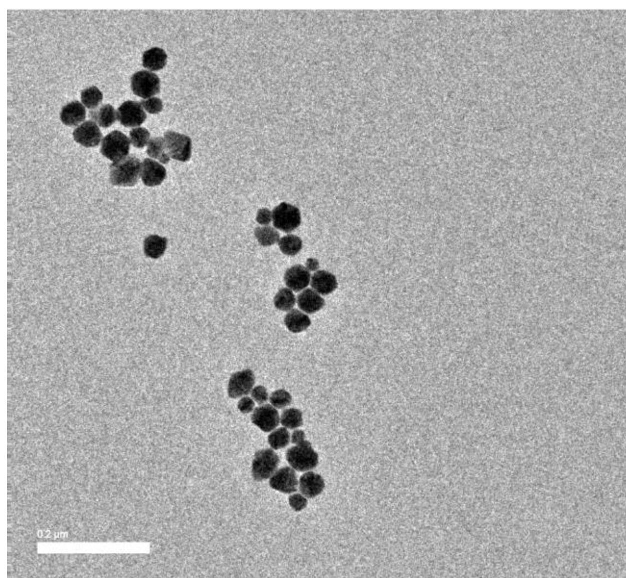
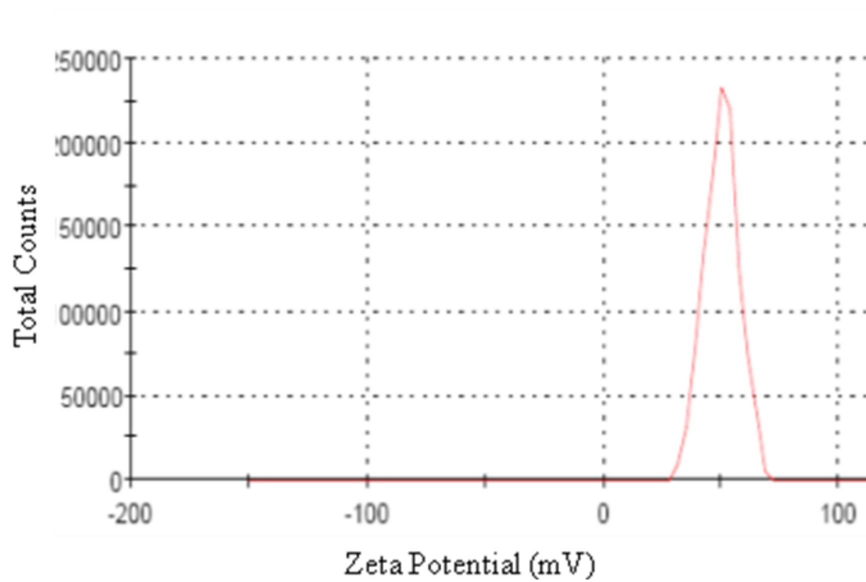


Figure SI1. HR-TEM image of AuNPs**.** The scale = 200 nm**.**



FigureSI2. Zeta potential measurements of the AuNPs.

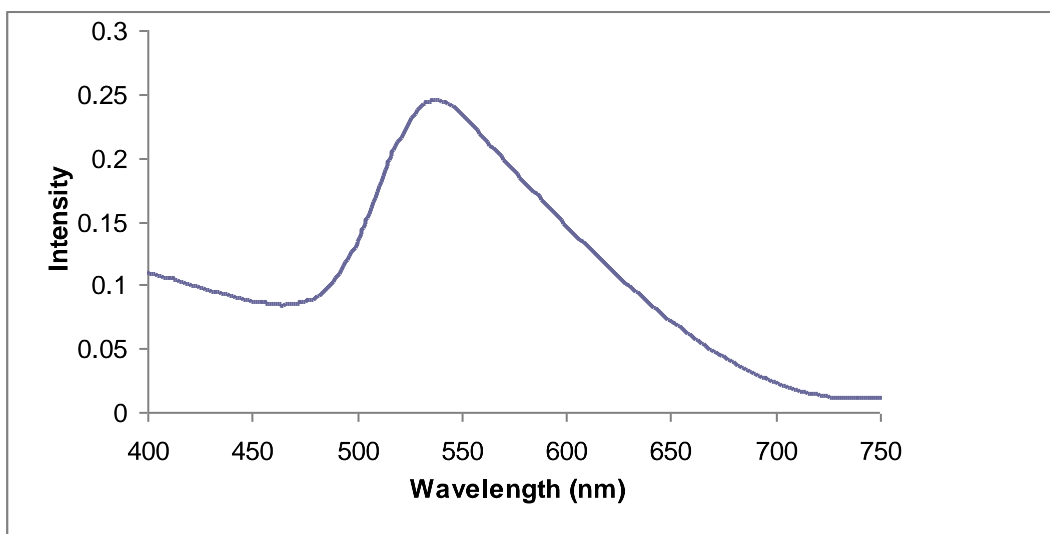


Figure SI3. UV/vis spectra of the as prepared AuNPs.

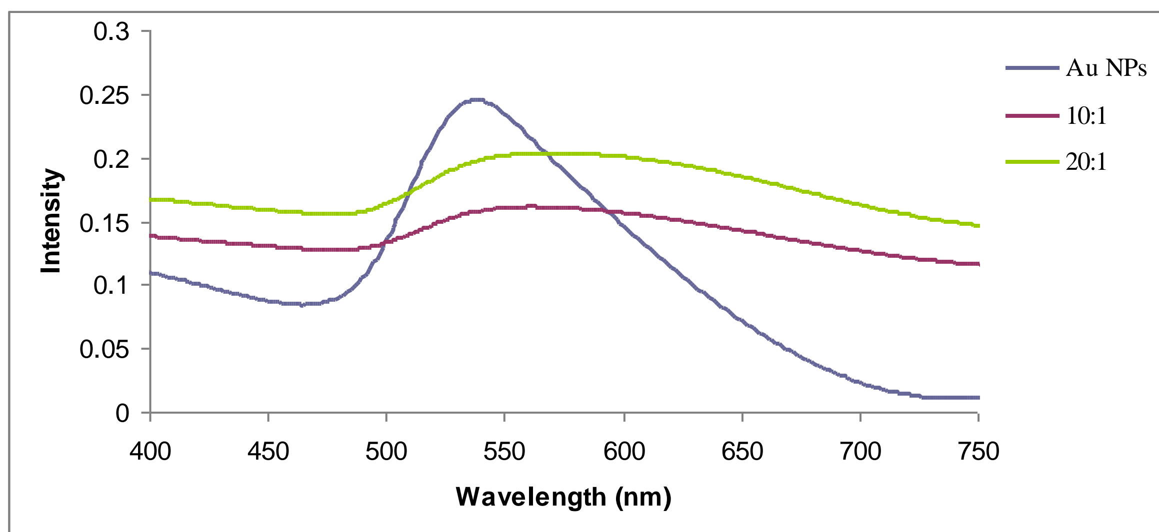


Figure SI4. UV/vis spectra of AuNPs (blue line), AuNPs/premiR-145 (10:1) (purple line), AuNPs/premiR-145 (20:1) (green line).

	AuNPs	**10:1**	**20:1**
λmax (nm)	538	562	568
intensity max	0.245	0.161	0.203