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ERRATUM

Erratum to: Toxicogenomics of nanoparticulate delivery of etoposide: potential impact on nanotechnology in retinoblastoma therapy

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Unfortunately section 2.13 was not included in the paper. The missing section is given below.

2.13 cDNA Microarray analysis

For microarray analysis, cells were seeded in 6-well plates (Corning, NY, USA) at 1×10^6 cells per well, and after 24 h, they were then treated with (0.0005 μg/ml) the drug either as a solution or encapsulated in nanoparticles for 5 days. Total RNA used for the microarray analysis was isolated from cultured cells using TRIZOL reagent (Invitrogen, USA) and purified using an RNeasy Mini Kit (Qiagen, USA) combined with DNase treatment following the manufacturer's instructions. Total RNA (20 μg) was labeled using a Fluorescent Direct Label Kit (Agilent Technologies) and simultaneously reverse transcribed into cDNA. The labeled samples were cleaned with a QIAquick PCR purification kit (Qiagen, USA) and then hybridized to the Human Whole Genome 44K Oligo Microarray for 17 h at 65°C as recommended by the manufacturer (Agilent Technologies, USA). Data analysis was done using Genespring GX version 10. Agilent Feature Extraction software (G25677AA, Agilent Technologies, 2004) was used to analyze the microarray data. For the differentially regulated genes analysis, i.e., genes showing fold change of >1 (upregulated in etoposide-loaded nanoparticle-treated Y-79 cell lines compared to native etoposide-treated Y-79 cell lines) or less than −1 (downregulated in etoposide-loaded nanoparticle-treated Y-79 cell lines compared to native etoposide-treated Y-79 cell lines) were selected. The experiment was performed in triplicates.

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