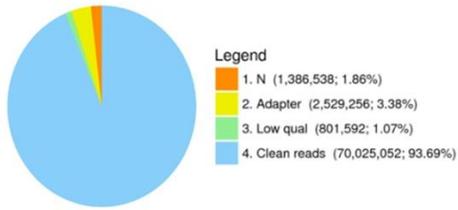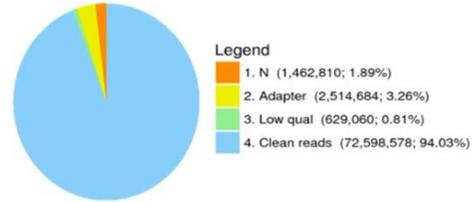**Supplementary Figure 1 Representative electropherograms by bioanalyser.** A: RNA samples for untreated HepG2 cells; B: RNA samples for *Catharanthus roseus*-silver nanoparticles treated HepG2 cells.

A

Legend
1. N (1,386,538; 1.86%)
2. Adapter (2,529,256; 3.38%)
3. Low qual (801,592; 1.07%)
4. Clean reads (70,025,052; 93.69%)

B

Legend
1. N (1,462,810; 1.89%)
2. Adapter (2,514,684; 3.26%)
3. Low qual (629,060; 0.81%)
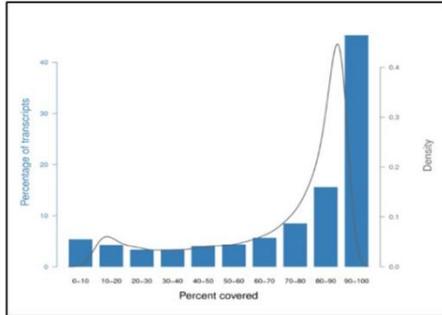4. Clean reads (72,598,578; 94.03%)

Supplementary Figure 2 Filter composition of raw data. A: RNA samples for untreated HepG2 cells; B: RNA samples for *Catharanthus roseus*-silver nanoparticles treated HepG2 cells.
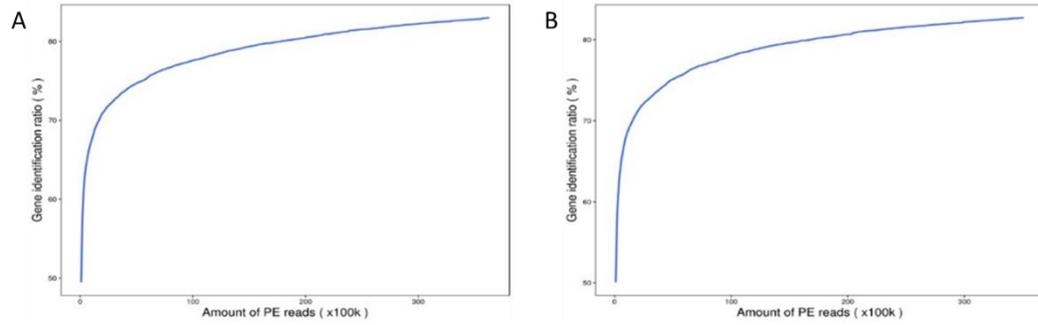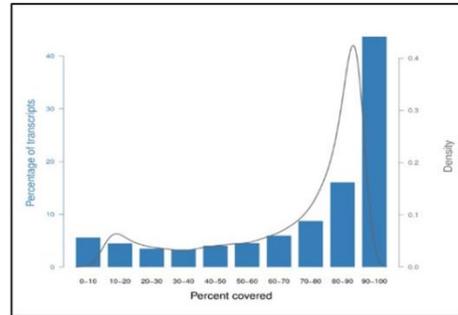
Supplementary Figure 3 Saturation analysis. A: Untreated HepG2 cells; B: *Catharanthus roseus*-silver nanoparticles treated HepG2 cells.
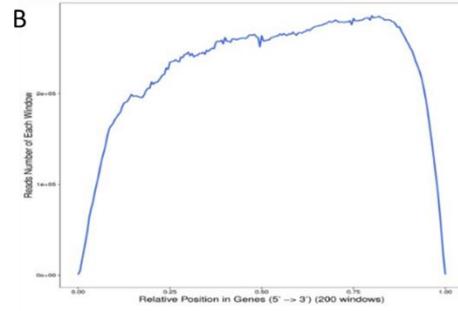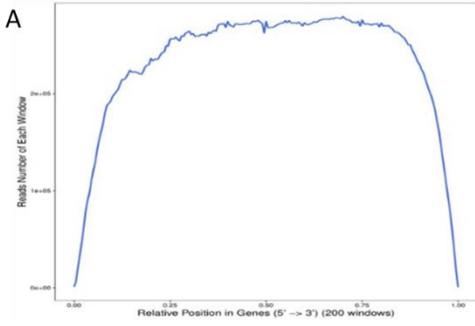
Supplementary Figure 4 Read coverage on transcripts. The X-axis represents the read coverage. Left Y-axis represents the percentage of transcripts. The right Y-axis represents the density of transcripts. A: Untreated HepG2 cells; B: *Catharanthus roseus*-silver nanoparticles treated HepG2 cells.

Supplementary Figure 5 Read coverage on transcripts. The X-axis represents the position along with transcripts. Left Y-axis represents the number of reads. A: Untreated HepG2 cells; B: *Catharanthus roseus*-silver nanoparticles treated HepG2 cells.