Supplementary data for:

Different in vitro exposure regimens of murine primary macrophages to silver nanoparticles induce different fate of nanoparticles and different toxicological and functional consequences

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RT-qPCR analysis of metallothioneingene expression

Total RNA was isolated from Ag-NP-exposed cells using Nucleospin RNA II kit (Macherey-Nagel, France). Reverse transcription was performed using the Enhanced Avian HS RT-PCR cDNA synthesis kit (Sigma, France) according to the manufacturer's instructions. LuminoCTTaq polymerase (Sigma, France) was used for qPCR, using the following primers: Metallothionein I (MT-I) forward 5'-agctcctgcgcctgcaagaac-3'; MT-I reverse 5'-tcaggcacagcacgtcactt-3'; Metallothionein II (MT-II) forward 5'accccaactgctcctgtg-3'; MT-II reverse 5'-acttgtcggaagcctctttg-3'. Amplification was performed in a Cfx96 thermocycler (Bio-Rad, France) with the following cycling program: 95 °C for 20 s, followed by 40 cycles at 95 °C for 5 s and 60 °C for 20 sec. At the end, PCR products were dissociated by incubating at 95 °C. These assays were run in triplicate and data were comparatively analyzed using Cfx software (Bio-Rad Cfx manager). Figure S1.Physico-chemical characterization of the Ag-NPs. Ag-NPs were imaged by scanning electron microscopy (SEM) (A, B); their diameter was deduced from measurement of particle diameter on SEM images (C).



Table S1. Stability of Ag-NPs<sup>a</sup>

-	Diameter ± SEM	% polydispersity ± SEM
Day 0	87.40 ± 0	$22.3 \pm 0$
Day 1	84.40 ± 0.1	$22.5 \pm 0$
Day 2	$69.53 \pm 3.72$	26.5 ± 1.9
Day 3	84.20 ± 1.70	21.1 ± 1.6
Day 4	81.13 ± 1.0	$22.6 \pm 0.3$

<sup>a</sup>NPs were diluted in sterile culture medium at the concentration of 5  $\mu$ g/mL and their hydrodynamic diameter, as well as the percentage of polydispersity of the suspension, were measured once a day during 4 days by DLS.

Figure S2.Cytotoxicity of Ag-NPs. Primary macrophages were exposed for 24h to increasing concentrations of nanoparticles and cell viability was checked by the trypan blue exclusion assay. Results are expressed as mean  $\pm$  SEM.



Figure S3. Metallothionein gene expression.mRNA expression of metallothionein I (MT-I) and metallothionein II (MT-II)in exposed cells was analyzed by RT-qPCR and normalized to mRNA expression of MT-I and MT-II in unexposed cells. Results are expressed as means ± SEM.

