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## Cytotoxicity and global transcriptional responses induced by zinc oxide nanoparticles NM 110 in PMA-differentiated THP-1 cells

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1 **Cytotoxicity and global transcriptional responses induced by zinc oxide**  
2 **nanoparticles NM 110 in PMA-differentiated THP-1 cells**

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5 Ramia Safar<sup>a#</sup>, Zahra Doumandji<sup>a#</sup>, Timeh Saidou<sup>a</sup>, Alain LeFaou<sup>b</sup>, Luc Ferrari<sup>a</sup>, Sara Nahlé<sup>a</sup>,  
6 Bertrand H Rihn<sup>a</sup>, Olivier Joubert<sup>a\*</sup>

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9 <sup>a</sup> UMR CNRS 7198, Institut Jean Lamour, Faculté de Pharmacie, Université de Lorraine, Nancy,  
10 France.

11 <sup>b</sup> EA 3452 CITHEFOR, Faculté de Médecine, Université de Lorraine, Nancy, France.

12 <sup>#</sup> both co-authors contributed equally to the work

13  
14  
15 \* To whom correspondence should be addressed:

16 Olivier Joubert,

17 UMR CNRS 7198 Institut Jean Lamour, 2 Allée André Guinier, 54001 Nancy, France

18 Phone: (+33) 372 742 694

19 E-mail: [olivier.joubert@univ-lorraine.fr](mailto:olivier.joubert@univ-lorraine.fr)

20

1 **Abstract**

2         Despite a wide production and use of zinc oxide nanoparticles (ZnONP), their  
3 toxicological study is only of limited number and their impact at a molecular level is seldom  
4 addressed. Thus, we have used, as a model, zinc oxide nanoparticle NM110 (ZnO110NP)  
5 exposure to PMA-differentiated THP-1 macrophages. The cell viability was studied at the  
6 cellular level using WST-1, LDH and Alamar Blue® assays, as well as at the molecular level by  
7 transcriptomic analysis. Exposure of cells to ZnO110NP for 24 h decreased their viability in a  
8 dose-dependent manner with mean inhibitory concentrations (IC<sub>50</sub>) of 8.1 µg/mL.  
9 Transcriptomic study of cells exposed to two concentrations of ZnO110NP: IC<sub>50</sub> and a quarter of  
10 it (IC<sub>50</sub>/4) for 4 h showed that the expressions of genes involved in metal metabolism are  
11 perturbed. In addition, expression of genes acting in transcription regulation and DNA binding,  
12 as well as clusters of genes related to protein synthesis and structure were altered. It has to be  
13 noted that the expressions of metallothioneins genes (*MT1*, *MT2*) and genes of heat-shock  
14 proteins genes (*HSP*) were strongly upregulated for both conditions. These genes might be used  
15 as an early marker of exposition to ZnONP. On the contrary, at IC<sub>50</sub> exposure, modifications of  
16 gene expression involved in inflammation, apoptosis and mitochondrial suffering were noted  
17 indicating a less specific cellular response. Overall, this study brings a resource of transcriptional  
18 data for ZnONP toxicity for further mechanistic studies.

19

20 **Keywords:** zinc oxide nanoparticle, NM110, PMA-differentiated THP-1 cells, transcriptome,  
21 cytotoxicity, metallothionein.

22

## 1 **1. Introduction**

2 Nanoparticles (NP) of metal oxides are attracting more and more interest and are  
3 produced in large quantities. They are widely used in both industrial process and biomedical  
4 research (Girigoswami, 2018). Nevertheless, data on their potential toxicity on living organisms  
5 remain insufficient, particularly at the molecular level. Zinc oxide nanoparticles (ZnONP) have  
6 multiple industrial uses and commercial applications, and it is one of the main NP present in the  
7 market due to its many properties. According to the Project on Emerging Nanotechnologies  
8 Inventory of nanotechnology-based Consumer Products, ZnONP are present in at least 24  
9 commercialized products, primarily sunscreen formulations, due to its UV- absorbing properties  
10 (Vance et al., 2015), with more than 33,000 tons of sunscreens produced containing up to 25 %  
11 of ZnONP (Joo and Zhao, 2017). There are many other pharmaceutical and parapharmaceutical  
12 applications of ZnONP such as ointments, skin creams, toothpaste, deodorants and formulation  
13 of cosmetics. ZnONP have also found industrial applications in rubber, ceramics, optical glasses,  
14 paints and plastics (Mishra et al., 2017).

15 As a result of this numerous applications, toxicity studies on ZnONP have already been  
16 investigated by different research groups. Majority of these studies are limited to qualitative data,  
17 demonstrating that ZnONP induce an increase in the cell death rate (Farcas et al., 2015),  
18 generally associated with inflammation (Sahu et al., 2014), DNA damage, and induction of  
19 oxidative stress (Senapati et al, 2015). However, the molecular mechanisms involved in these  
20 effects remains undefined. In addition, it has been shown that the importance of the toxic effects  
21 of ZnONP is inversely related to size, positive charge and solubility of nanoparticles (Prach et  
22 al., 2013; Buerki-Thurnherr et al., 2013). On the other hand, they vary with the cell line used and

1 macrophages are said to be more sensible when contact with ZnONP than epithelial cells (Farcal  
2 et al., 2015), as well as cancer cells when compared to normal cells (Premanathan et al., 2010).

3       **The present study was performed with the objective to study the toxicity of NP on**  
4 **the respiratory system using *in vitro* models. Given that a human pulmonary macrophage**  
5 **cell line does not exist, the model used for this work was the monocytes THP-1 cell line**  
6 **which are differentiated into macrophages by treatment with PMA showing enhanced**  
7 **adherence and phagocytosis. In addition, the major role of macrophage in the innate**  
8 **defense of the body, especially their strong phagocytic capacity, and their presence in many**  
9 **tissues and organs make it a model of choice for many *in vitro* studies for toxicological**  
10 **impacts of NP (Jones CF, Grainger DW, 2009).**

11       **Then, this manuscript focuses on the toxicity of uncoated zinc oxide nanoparticles**  
12 **NM110 (ZnO110NP) in PMA-differentiated THP-1 macrophages. ZnO110NP is one of**  
13 **representative manufactured nanomaterials in the priority list (NM-Series) which has been**  
14 **established to be well characterized and tested by the European Commission's Joint**  
15 **Research Centre (JRC) in order to enable innovation and development of safe materials**  
16 **and products. Cell viability was assessed using classical tests of toxicology while the**  
17 **molecular response of these cells was established by transcriptomic analysis.**

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## 1 **2. Materials and Methods**

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### 3 **2.1. Chemicals**

4 DMEM medium (Dulbecco's Modified Eagle's Medium- high glucose, D1145), fetal  
5 bovine serum (F7524), L-glutamine [CAS No. 56-85-9], Penicillin [113-98-4], streptomycin  
6 [128-46-1], amphotericin B [1397- 89-3], phorbol 12-myristate 13-acetate (PMA) [1656-9-8],  
7 Dulbecco's Phosphate Buffered Saline (PBS) [16561-29-8], trypan blue solution [72-57-1],  
8 Ethylenediaminetetraacetic acid disodium salt (EDTA) [6381-92-6], Bovine Serum Albumin  
9 (BSA) [9048-46-8], Diethyl pyrocarbonate (DEPC) [150-38-9] were purchased from Sigma-  
10 Aldrich® (Saint Quentin Fallavier, France). APC anti-human CD11c and IgG1-APC isotype  
11 control were purchased from (BD biosciences, Le Pont de Claix, France). 4-[3-(4-Iodophenyl)-2-  
12 (4-nitrophenyl)-2H-5-tetrazolio]-1,3-benzene disulfonate (WST-1) cell proliferation reagent  
13 [150849-52-8] and cytotoxicity detection Kit PLUS LDH, were from Roche® (Meylan, France).  
14 AlamarBlue® Cell Viability Reagent (DAL1025) was from Invitrogen (Villebon sur Yvette,  
15 France). RNA-Solv Reagent® (R6830) from Omega Bio-tek® (Norcross, Georgia). Éthanol 100%  
16 [75-17-5], chloroforme [67-66-3], isopropanol [67-68-0] from Carlo Erba Reagents® (Val de  
17 Rueil, France).

18

### 19 **2.2. Preparation and characterization of nanoparticle suspension**

20 ZnO110NP were obtained from the Joint Research Center (NM 110, JRS). They are  
21 suspended in ultrapure water (18 MΩ) at a concentration of 2.56 mg/mL (**Phuyal et al, 2017**),  
22 sonicated using a 3-mm probe (Vibracell 75022, Bioblock, Illkirch, France) at 30 % magnitude  
23 for 6 min under continuous cooling with ice. Immediately after sonication, ZnO110NP

1 suspension was physico-chemically characterized and working dilutions in the culture medium  
2 were prepared.

3 The hydrodynamic diameter and size distribution of ZnO110NP suspension, expressed as  
4 polydispersity index (PdI), were measured using dynamic light scattering (DLS, Zetasizer™  
5 3000E, Malvern Instruments Worcestershire, UK). Zeta potential was calculated using the  
6 *Smoluchowski's* equation (Sze et al., 2003). All measurements were performed in triplicate at  
7 25 °C.

8

### 9 **2.3. Cell culture**

10 THP-1 human monocytic cell line was obtained from American Type Culture Collection  
11 (ATCC, TIB-202™, Manassas, VA, USA). Cells were cultured in DMEM medium  
12 supplemented with 15 % of heat-inactivated fetal bovine serum, 100 U/mL of penicillin, 100  
13 µg/mL of streptomycin, 0.25 µg/mL of amphotericin and 2 mM of L-Glutamine in incubator at  
14 37°C under 5 % CO<sub>2</sub> atmosphere. They were split every 2-3 days to prevent the cell density from  
15 exceeding one million per mL. For each experiment, cells were differentiated into macrophages  
16 by exposure to 10 ng/mL (16 nM) of PMA in a plate appropriate to the test for 24 h. The density  
17 of 5 x 10<sup>4</sup> cells per mL was respected for all tests.

18

### 19 **2.4. Cell phenotype study**

20 After differentiation, cell phenotype was verified by flow cytometry. THP-1 cells were  
21 treated with and without PMA in 6 wells UpCell plate (Thermo-Fisher, Illkirch, France). After  
22 24 h, cells were harvested using Versene solution (PBS and EDTA 0.1%). After 5 min of  
23 centrifugation at 400 x g, cell pellet was resuspended in PBS-BSA. 4 x 10<sup>5</sup> cells were incubated

1 with fluorescein isothiocyanate (FITC)-labeled monoclonal antibodies against CD11c for 30  
2 min, then washed with PBS-BSA, and were analyzed by flow cytometry (BD Biosciences, Le  
3 Pont de Claix, France). Non-differentiated unstained cells were used as control.

## 4 5 **2.5. Cytotoxicity study**

6 After treatment with PMA for 24 h, the medium was removed by aspiration and cells  
7 were incubated with 0 (control), two times dilution from 20 to 0.6  $\mu\text{g}/\text{mL}$  of ZnO110NP in  
8 serum free medium for 24 h. The cell viability was checked using WST-1, LDH and,  
9 AlamarBlue<sup>®</sup> assays. Unexposed cells were used as control and considered as having 100 % of  
10 cell viability. Six wells and four test replicates were used per culture condition. The inhibitory  
11 concentration ( $\text{IC}_{50}$ ) was calculated with the Reed and Muench method (Reed and Muench,  
12 1938).

### 13 **2.5.1. WST-1 assay**

14 WST-1 (water soluble tetrazolium) assay was performed as previously described  
15 (Ronzani et al., 2014). Briefly, after 24 h of exposure to ZnO110NP, cells were incubated with 5  
16 % WST-1 reagent for 2 h at 37 °C. Then, the absorbance was read at 450 nm with 690 nm as  
17 reference (iMark<sup>TM</sup> Microplate Absorbance Reader, Bio-Rad).

### 18 **2.5.2. LDH assay**

19 Lactate dehydrogenase (LDH) assay was performed according to manufacturer's  
20 instructions. Briefly, after 24 h of exposure to ZnO110NP, cells were incubated with 100  $\mu\text{L}$  of  
21 (LDH reaction buffer + substrate) for 30 min at room temperature, Then, 50  $\mu\text{L}$  of stop solution  
22 was added and the absorbance was read at 490 nm (iMark<sup>TM</sup> Microplate Absorbance Reader,  
23 Bio-Rad). For the positive control, cells were exposed to lysis buffer for 15 min before the test.



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### **2.5.3. AlamarBlue<sup>®</sup> assay**

AlamarBlue<sup>®</sup> assay was performed according to manufacturer's instructions. Briefly, cells were incubated with 10 % of reagent for 3 h at 37 °C. Fluorescence was read at 590 nm after excitation at 560 nm using spectrofluorimetry (JASCO, FMP-825, Bouguenais, France)

## **2.6. Transcriptomic study**

### **2.6.1. RNA extraction**

1x10<sup>6</sup> THP-1 cells were exposed, after differentiation, to ZnO110NP at concentrations of the IC<sub>50</sub> or one fourth of IC<sub>50</sub> (IC<sub>50</sub>/4) for 4 h using unexposed cells as control. As previously described (Eidi et al., 2012; Safar et al., 2015), total RNA was, then, extracted using RNA-Solv Reagent<sup>®</sup> according to manufacturer's protocols. The quality of the extracted RNA was assessed by spectrophotometry (BioSpec-nano, Shimadzu) and capillary electrophoresis using RNA 6000 Nano<sup>®</sup> (2100 Bioanalyzer<sup>™</sup>, Agilent Technologies, Santa Clara, CA). All RNA samples showed a ratio A<sub>260nm</sub>/A<sub>280nm</sub> > 1.8 with RNA integrity number (RIN) > 8.

### **2.6.2. Microarray hybridation**

cDNA and Cy3-dye-labeled cRNA synthesis were carried out with 100 ng of total RNA according to the manufacturer protocol (One-Color Microarray-Based Gene Expression Analysis, version 6.6). Then, 600 ng of labelled cRNA were hybridized using Microarray slides (SurePrint G3 Human GE v3 8x60K, Agilent Technologies) at 65 °C during 17 h. After washing, the arrays were scanned by Agilent DNA microarray scanner (Agilent). Acquisition of images and quantification of fluorescence signal as well as primary data analysis were performed using the Agilent Feature Extraction Software version 11.0.1.1.

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### **2.6.3. Bioinformatics analyses**

Data were first normalized with Lowess' method using GeneSpring (version 13.0, Agilent Technologies Pty Ltd). Then, a principal component analysis (PCA), was performed using GeneSpring as a quality control step where the outlier's samples were removed. Student's *t*-test followed by Benjamini-Hochberg correction and filtering criteria were then applied to identify genes whose expression level was significantly modified. Genes showing expression changes of at least 1.5-fold change (FC) in either direction as compared to control with  $p \leq 0.05$  were considered significantly differentially expressed and were used in the following analysis.

The selected genes were analyzed using the Database for Annotation, Visualization, and Integrated Discovery version 6.8 (DAVID; <http://david.abcc.ncifcrf.gov>). Indeed, genes were grouped among clusters according to different criteria such as Gene Ontology (GO) terms (GO BP: biological process, GO CC: cellular component, GO MF: molecular function) and pathways (KEGG and BIOCARTA). For the biological interpretation, we have considered GO biological process (GO BP) and pathways with  $p$ -value  $\leq 0.05$  within the cluster with Enrichment Score above to 1.3 (Huang da et al., 2009). All raw data of the microarrays are available on NCBI Gene Expression Omnibus database (GEO, <http://www.ncbi.nlm.nih.gov/geo/>), using the GSE599435 accession number.

### **2.7. Statistical analysis**

Cell viability data are presented as means  $\pm$  standard error of the mean (SE) of four biological replicates. Statistical differences were determined by one-way analysis of variance (ANOVA) followed by Dunnett's test using Prism software<sup>TM</sup>.

1 **3. Results**

2

3 **3.1. Nanoparticle characterization**

4 The mean hydrodynamic diameter of ZnO110NP was  $261.5 \pm 4$  nm with a polydispersity  
5 index of  $0.170 \pm 0.017$  and the zeta potential was  $+21.6 \pm 1.8$  mV (Figure 1). **TEM images**  
6 **showed that each unit on NP have at least one dimension less than 100 nm (see Figure S2 in**  
7 **supplementary data). Size of particles was checked by DLS immediately and after 24 hours**  
8 **in the medium of exposure, showing no aggregation nor changes in the size of particles (see**  
9 **Table S7 in supplementary data).**

10

11 **Figure 1**

12

13 **3.2. Cell phenotype study**

14 The exposure to PMA increase the CD11c<sup>+</sup> cells number from 62.9 % to 93.9 % (Figure  
15 2) suggesting that, in our macrophage culture conditions, notable part of the cells was already at  
16 least partially differentiated. PMA pretreatment allows uniformity of the cell phenotype before  
17 the NP exposure.

18

19 **Figure 2**

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21 **3.3. Cytotoxicity study**

22 Whatever the assays (Figure 3), exposure of cells to ZnO110NP for 24 h decreased their  
23 viability in a dose-dependent manner. WST-1 (Figure 3A) and AlamarBlue<sup>®</sup> (Figure 3B) assays

1 gave similar results and a viability of 9.6 % and 7.5 %, respectively at the higher concentration  
2 of ZnO110NP (20  $\mu\text{g/mL}$ ). In contrast, for LDH assay (Figure 3C), the decrease of viability with  
3 NP concentration was slow and a viability of 42 % was solely reached at 20  $\mu\text{g/mL}$ . However,  
4 there was no significant difference in  $\text{IC}_{50}$  (Figure 3) for the three tests and the mean of 8.1  
5  $\mu\text{g/mL}$  (which correspond to 2.1  $\mu\text{g/cm}^2$ ), was considered and retain for the transcriptomic assay.

### 7 **Figure 3**

#### 9 **3.4. Transcriptomic study**

10 Cells were exposed for 4 h to ZnO110NP at concentrations of 2.0 and 8.1  $\mu\text{g/mL}$ :  
11 namely,  $\text{IC}_{50}/4$  and  $\text{IC}_{50}$  corresponding to 0.5 and 2.1  $\mu\text{g/cm}^2$ , respectively. PCA analysis showed  
12 a clear segregation of results for the three groups corresponding to the three conditions (control,  
13 cells exposed to  $\text{IC}_{50}/4$ , or to  $\text{IC}_{50}$ ) (Figure S1 in supplementary informations). As compared to  
14 control, 360 significantly differentially expressed genes were identified following exposure to  
15 2.0  $\mu\text{g/mL}$  of ZnO110NP, a non-cytotoxic concentration. Among them, 33 were up-regulated  
16 and 327 were down-regulated. Not surprisingly, the exposure to 8.1  $\mu\text{g/mL}$  of ZnO110NP  
17 induced the modification of a far greater number of genes, 3202 genes were differentially  
18 expressed with 872 and 2330 up and down-regulated respectively (Table 1). All these genes are  
19 listed in the supplementary information Table S1, S2 for 2.0  $\mu\text{g/mL}$  concentration and S3, S4 for  
20 8.1  $\mu\text{g/mL}$  concentration.

21 Functional Gene Ontology (GO) analysis revealed similar clusters of genes in both  
22 exposed cell populations. In fact, cluster containing genes involved in or related to ZnO  
23 metabolism was found for both conditions with three identical GO BP, namely “cellular response

1 to zinc ion”, “cellular response to cadmium ion” and “negative regulation of growth” and one  
2 KEGG pathway “Mineral absorption”. Other clusters of genes with modified responses were also  
3 common to both conditions: clusters related to virus, perturbation of gene transcription  
4 regulation and to protein synthesis and structure (Figure 4). The lower dose (2.0 µg/mL) of  
5 ZnO110NP induced modification gene expression belonging to the clusters related to  
6 transduction mechanism, i.e “lipid phosphorylation” cluster. On the contrary, at 8.1 µg/mL,  
7 modifications of expression of genes involved in inflammation, apoptosis and mitochondrial  
8 suffering were noted indicating a less specific cellular response. The analyzed transcriptomic  
9 results are summarized and illustrated in Fig. 4. Biological process (GOTERM\_BP) and  
10 pathways (KEGG, BIOCARTA) of each cluster were presented in supplementary information  
11 table S5 for 2.0 µg/mL concentration and table S6 for 8.1 µg/mL concentration.

12 Moreover, there were 27 genes whose expression was increased after exposition of cells  
13 to both concentrations (Figure 5A). The FC values for majority of these genes vary in dose-  
14 dependent manner (Table 2). The STRING 10.5 (Search Tool for the Retrieval of Interacting  
15 Genes; <http://string-db.org/>) database (Szklarczyk et al., 2014) analysis shows that they belong to  
16 two families of genes: metallothioneins and heat shock proteins (HSP) (Figure 5B).

17

18

**Figure 4**

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**Figure 5**

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**Table 2**

21

#### 1 4. Discussion

2           **The present study was performed with the objective of studying the toxicity of**  
3 **ZnO110NP on the respiratory system using an *in vitro* macrophage model, the PMA-**  
4 **differentiated THP-1 monocytic cell line monocytes. The use of PMA allowed us to**  
5 **uniformize the cell phenotype before NP exposure.**

6           When exposed to ZnO110NP, the viability of THP-1 cells decreased in a dose-dependent  
7 manner. Calculated IC<sub>50</sub> was assessed to 8.1 µg/mL using the three tests. In the same way, Farcal  
8 and collaborators (2015) studied ZnO110NP toxicity on nine different cellular types which  
9 includes primary human macrophages (HMDM), murine peritoneal macrophage-like cells  
10 (RAW264.7) and murine alveolar macrophage-like cells (MH-S). ZnO110NP was highly toxic to  
11 all the cellular lines tested. However, the IC<sub>50</sub> value was > 100 µg/mL for HMDM, 18.40 µg/mL  
12 for RAW264.7 and 19.68 µg/mL for MH-S cells using different tests. In our study, PMA-  
13 differentiated THP-1 macrophages were more sensitive to ZnO110NP as IC<sub>50</sub> was found to be  
14 8.1 µg/mL. This difference between IC<sub>50</sub> values is probably due to the fact that Farcal et al  
15 resuspended the NP in water with ethanol and BSA *versus* water alone in our study. Although  
16 ZnO110NP have the same size and charge in both studies, a plasma protein corona formation  
17 around nanoparticles could probably impair their bioreactivity and make them less toxic  
18 (Hussien et al, 2013; Rihn and Joubert, 2015; Hongying et al., 2018) by limiting their uptake by  
19 cells. In addition, in ours study, cell exposition to ZnO110NP was performed in serum free  
20 medium which would allow the nanoparticles to freely exert their cytotoxicity. Finally, THP-1 is  
21 a cancerous cell line, and according to a previous study, ZnONP exhibited much higher cytotoxic  
22 effects on malignant cells than on normal cells (Premanathan et al, 2011). Furthermore, Liang et  
23 al (2018) studied the cytotoxicity of ZnO110NP on THP-1 macrophages, their observations are

1 generally in agreement with our results. Other forms of ZnONP exists and are also considered as  
2 toxic, this toxicity may differ depending on their physicochemical properties as well as the  
3 cellular model being used (Yin et al., 2015; Hanley et al, 2009a; 2008b).

4         Several studies have proposed different mechanisms to explain the toxicity of ZnONP  
5 based on oxidative stress and inflammatory response induction (Roy et al., 2013; De Berardis et  
6 al., 2010; Moos et al., 2011). Thus, we decided to study the global transcriptional responses  
7 following 4 h exposure to low ( $IC_{50/4} = 2.0 \mu\text{g/mL}$  or  $0.5 \mu\text{g/cm}^2$ ) or high ( $IC_{50} = 8.1 \mu\text{g/mL}$  or  
8  $2.1 \mu\text{g/cm}^2$ ) concentrations in order to identify early adverse effects of ZnO110NP. **The zinc**  
9 **concentration was measured in the cells after  $IC_{50/4}$  exposure by ICP-AES (see Table S8).**  
10 Indeed, a non-cytotoxic low concentration of ZnO110NP allows us to study the adaptive  
11 response, while the cytotoxic high concentration gives a hint of the causes of toxicity and cellular  
12 death as shown in Fig. 4. After exposure to the high concentration, the number of genes whose  
13 expression significantly changed were much higher than the one observed for the lower one  
14 (nearly 10 times). However, in both conditions, we observed clusters of genes associated with  
15 “cellular response to zinc and cadmium ions” and “mineral absorption pathway” as also  
16 described by Moos et al (2011) using four human cell lines: CaCo-2, RKO, HaCaT, SK Mel-28  
17 following a 4 h-exposure period with 1 and  $5 \mu\text{g/cm}^2$  of ZnONP. This response was observed  
18 regardless of cellular model indicating that these gene clusters could be considered as a specific  
19 response to ZnO. Among these genes, we noticed that a Zn efflux transporter gene (*SLC30A1*)  
20 and metallothioneins genes (*MT1*, *MT2*) were strongly activated. So, this response of cells is  
21 early and is a sensitive exposure biomarker of ZnONP that has been also observed by Tuomela et  
22 al (2013) with three immune cell lines: human monocyte-derived macrophages (HMDM),  
23 monocyte-derived dendritic cells (MDDC), and Jurkat T cell leukemia-derived cell line. In

1 addition, Moos et al demonstrated that this family of genes was also up-regulated following their  
2 exposure to soluble  $Zn^{+2}$  ( $ZnCl_2$ ). This suggested that this response is related to a liberation of  
3  $Zn^{+2}$  by degradation of ZnONP. This might occur in the intravacuolar compartment, an acidic  
4 environment created by the lysosomes (Gwak et al., 2015). These results, corresponding to  
5 intracellular mechanism of defense against to  $Zn^{2+}$  are in favor of the hypothesis that states that  
6 ZnONP dissolution occurs inside the endosomes (Senapati et al., 2015) and less likely in the  
7 extracellular compartment (Buerki-Thurnherr et al., 2013). This intracellular hypothesis, is  
8 reinforced by the non-specific response, namely, over expression of heat shock proteins (*HSPA6*,  
9 *HSPA1A*, and *HSPA1B*) genes at 6912, 1586, 461 times respectively, which was observed after  
10 exposure to both Zn110NP concentrations representing a well-known stress response to metal  
11 toxicity (Bauman et al., 1993).

12 Beside the induction of metal responsive genes, the most characteristic clusters  
13 influenced by high and low concentrations of ZnO110NP were related to regulation of gene  
14 transcription and DNA binding. This may be not surprising as  $Zn^{2+}$  ion is a cofactor in the  
15 structure of many zinc finger motif proteins that are transcription factors and of DNA binding  
16 proteins. This effect was limited for the lower concentration, but more visible for higher one  
17 such as clusters of “DNA damage recognition” and “RNA splicing”. However, for this latter, it is  
18 possible that these proteins are subject to disruption by a high concentration of  $Zn^{2+}$  (Hartwig,  
19 2001).

20 In addition, it is only at high concentration that, inflammation and mitochondrial  
21 dysfunctions, as well as apoptosis pathway, could be identified indicating a non-specific  
22 mechanism of toxicity as shown in several studies using different cellular models (Gao et al.,  
23 2016; Wang et al., 2018; Wilhelmi et al., 2013; Chevallet et al., 2016).





1 **5. Conclusion**

2 In summary, this study brings additional sources of transcriptional data for ZnONP  
3 toxicity for further mechanistic studies. Indeed, exposure of PMA-differentiated THP-1 cells to a  
4 low non-cytotoxic ZnONP concentration ( $IC_{50}/4$ ) has shown that they have a cellular metabolic  
5 alteration giving specific sensitive markers of exposition related to Zn metabolism. At the high  
6 cytotoxic concentration ( $IC_{50}$ ), markers of cytotoxicity and cell death are not specific but the  
7 markers of exposition to Zn are still present. The metallothioneins genes family (*MT1*, *MT2*) was  
8 strongly upregulated in both conditions. **The proteins encoded by these genes are known to**  
9 **participate in the metabolism of Zn and Cu and in the detoxification of heavy metals (e.g. Cd).**  
10 Thus, the genes coding these proteins might be used as an early marker of exposition to metallic  
11 NP.

12

13

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18

19 **Conflict of interest**

20 The authors declare that they have no conflicting interests.

21

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1 **Tables**

2

3 **Table 1:** Numbers of PMA-differentiated THP-1 genes having at least 1.5 fold change up or  
4 down regulated ( $p \leq 0.05$ ) after exposure to both high and low concentrations of ZnO110NP,  
5 namely,  $8.1 \mu\text{g/mL} = 2.1 \mu\text{g/cm}^2$  ( $\text{IC}_{50}$ ) and  $2.0 \mu\text{g/mL} = 0.5 \mu\text{g/cm}^2$  ( $\text{IC}_{50}/4$ ). Data from three  
6 independent experiments was normalized using GeneSpring and submitted to a *t*.test student  
7 following Benjamini-Hochberg correction.

|                      | <b>IC<sub>50</sub>/4</b> | <b>IC<sub>50</sub></b> |
|----------------------|--------------------------|------------------------|
| All genes            | 360                      | 3202                   |
| Up-regulated genes   | 33                       | 872                    |
| Down-regulated genes | 327                      | 2330                   |

8

1 **Table 2:** Common significant ( $p \leq 0.05$ ) up-regulated genes with their Fold Change following  
 2 exposure of PMA-differentiated THP-1 cells to both high and low concentrations of ZnO110NP.

| Gene Symbol     | Gene Name   | Fold Change         |                  |
|-----------------|---|---------------------|------------------|
|                 |   | IC <sub>50</sub> /4 | IC <sub>50</sub> |
| <b>HSPA6</b>    | Heat shock 70kDa protein 6                            | 81.53               | 6912.33          |
| <b>MT1M</b>     | Metallothionein 1M                                    | 56.88               | 57.64            |
| <b>MT1E</b>     | Metallothionein 1E                                    | 34.34               | 44.76            |
| <b>MT1H</b>     | Metallothionein 1H                                    | 28.91               | 83.36            |
| <b>MT1X</b>     | Metallothionein 1X                                    | 28.40               | 44.55            |
| <b>MT1G</b>     | Metallothionein 1G                                    | 26.15               | 57.57            |
| <b>MT1L</b>     | Metallothionein 1L                                    | 23.55               | 29.40            |
| <b>MT1B</b>     | Metallothionein 1B                                    | 22.87               | 73.67            |
| <b>MT1HL1</b>   | Metallothionein 1H-like 1                             | 17.37               | 69.38            |
| <b>HSPA1A</b>   | Heat shock 70kDa protein 1A                           | 16.73               | 1586.45          |
| <b>MT1A</b>     | Metallothionein 1A                                    | 12.21               | 33.17            |
| <b>MT2A</b>     | Metallothionein 2A                                    | 12.16               | 7.24             |
| <b>FAM189A2</b> | Family with sequence similarity 189, member A2        | 9.68                | 4.45             |
| <b>HSPA1B</b>   | Heat shock 70kDa protein 1B                           | 9.42                | 461.72           |
| <b>WNT6</b>     | Wingless-type MMTV integration site family, member 6  | 7.27                | 20.87            |
| <b>ASCL2</b>    | Achaete-scute family bHLH transcription factor 2      | 6.08                | 4.93             |
| <b>ZBTB2</b>    | Zinc finger and BTB domain containing 2               | 5.60                | 2.97             |
| <b>ASB13</b>    | Ankyrin repeat and SOCS box containing 13             | 5.58                | 4.37             |
| <b>MT1F</b>     | Metallothionein 1F                                    | 4.63                | 3.45             |
| <b>SLC30A1</b>  | Solute carrier family 30 (zinc transporter), member 1 | 4.44                | 5.71             |
| <b>HMOX1</b>    | Heme oxygenase (decycling) 1                          | 2.86                | 2.76             |
| <b>CDCA7L</b>   | Cell division cycle associated 7-like                 | 2.61                | 3.04             |
| <b>CNKSR3</b>   | CNKSR family member 3                                 | 2.17                | 1.92             |
| <b>WFS1</b>     | Wolfram syndrome 1 (wolframin)                        | 2.06                | 2.71             |
| <b>DMRTA2</b>   | DMRT-like family A2                                   | 1.91                | 1.58             |
| <b>GPANK1</b>   | G patch domain and ankyrin repeats 1                  | 1.74                | 2.17             |
| <b>CCNE1</b>    | Cyclin E1   | 1.56                | 2.26             |

3

1 **Figures**

2

3 **Figure 1:** Zinc oxide nanoparticles NM110 (ZnO110NP) characterization. (A): size and (B): zeta  
4 potential as measured by DLS.

5

6 **Figure 2:** Cell phenotype study of THP-1 cells differentiated into macrophages by incubation for  
7 24 h with (10 ng/mL = 16 nM) of phorbol 12-myistate 13-acetate (PMA). Cell differentiation  
8 was confirmed by flow cytometry using CD11c antibody. (A): Control, non-differentiated  
9 unstained cells (B): Cells not treated with PMA. (C): PMA treated cells.

10

11 **Figure 3:** Cytotoxic study of PMA treated THP-1 cells exposed to ZnO110NP as assessed by  
12 (A) WST-1 assay, (B) LDH assay, (C) AlamarBlue® assay. Un-exposed cells are considered as  
13 negative control, 100 % of cell viability. Data are expressed as mean  $\pm$  S.E of four biological  
14 replicates. \*\*\*  $p < 0.001$  et \*  $p < 0.05$

15

16 **Figure 4:** Functional annotations of significantly up- and down-regulated genes of PMA-  
17 differentiated THP-1 cells exposed to both high and low concentrations of ZnO110NP, namely,  
18 8.1  $\mu\text{g/mL} = 2.1 \mu\text{g/cm}^2$  ( $\text{IC}_{50}$ ) and 2.0  $\mu\text{g/mL} = 0.5 \mu\text{g/cm}^2$  ( $\text{IC}_{50/4}$ ). On the left, the functional  
19 annotations (Biological process (GOTERM\_BP) and pathways (KEGG, BIOCARTA)) obtained  
20 for  $\text{IC}_{50/4}$  concentration, on the right the annotations obtained for  $\text{IC}_{50}$  concentration.

21

22 **Figure 5:** Significant upregulated genes of PMA-differentiated THP-1 cells exposed to both high  
23 and low concentrations of ZnO110NP, namely, 8.1  $\mu\text{g/mL} = 2.1 \mu\text{g/cm}^2$  ( $\text{IC}_{50}$ ) and 2.0  $\mu\text{g/mL} =$

1 0.5  $\mu\text{g}/\text{cm}^2$  ( $\text{IC}_{50}/4$ ) for 4h. (A) Venn diagram of the number of common and unique up-regulated  
2 genes (at least 1.5-fold change and  $p \leq 0.05$ ). (B) Interactions between the 27 common  
3 upregulated genes as retrieved from the STRING database. Among them, we identified genes  
4 belong to families: metallothioneins (*MT1*, *MT2*) and heat shock protein (*HSP*).

1 **Supplementary informations**

2

3 **Figure S 1:** Graphical representation of the principal component analysis (PCA) giving the  
4 distribution of analyzed samples by GeneSpring. Each condition (control, IC<sub>50</sub>/4, IC<sub>50</sub>) is  
5 represented by three independent experiments.

6 **Figure S 2:** Characterization of ZnO nanoparticles studied by transmission electron microscopy.

7 **Table S 1:** Full list of significant ( $p \leq 0.05$ ) up-regulated genes following exposure of PMA-  
8 differentiated THP-1 cells to 2.0  $\mu\text{g/mL}$  (IC<sub>50</sub>/4) of ZnO110NP.

9 **Table S 2:** Full list of significant ( $p \leq 0.05$ ) down-regulated genes following exposure of PMA-  
10 differentiated THP-1 cells to 2.0  $\mu\text{g/mL}$  (IC<sub>50</sub>/4) of ZnO110NP.

11 **Table S 3:** Full list of significant ( $p \leq 0.05$ ) up-regulated genes following exposure of PMA-  
12 differentiated THP-1 cells to 8.1  $\mu\text{g/mL}$  (IC<sub>50</sub>) of ZnO110NP.

13 **Table S 4:** Full list of significant ( $p \leq 0.05$ ) down-regulated genes following exposure of PMA-  
14 differentiated THP-1 cells to 8.1  $\mu\text{g/mL}$  (IC<sub>50</sub>) of ZnO110NP.

15 **Table S 5:** Significant clusters (Enrichment Score  $> 1.3$ ) with Gene Ontology Biological  
16 Processes (GOTERM\_BP) and pathways following exposure of PMA-differentiated THP-1 cells  
17 to 2.0  $\mu\text{g/mL}$  (IC<sub>50</sub>/4) of ZnO110NP.

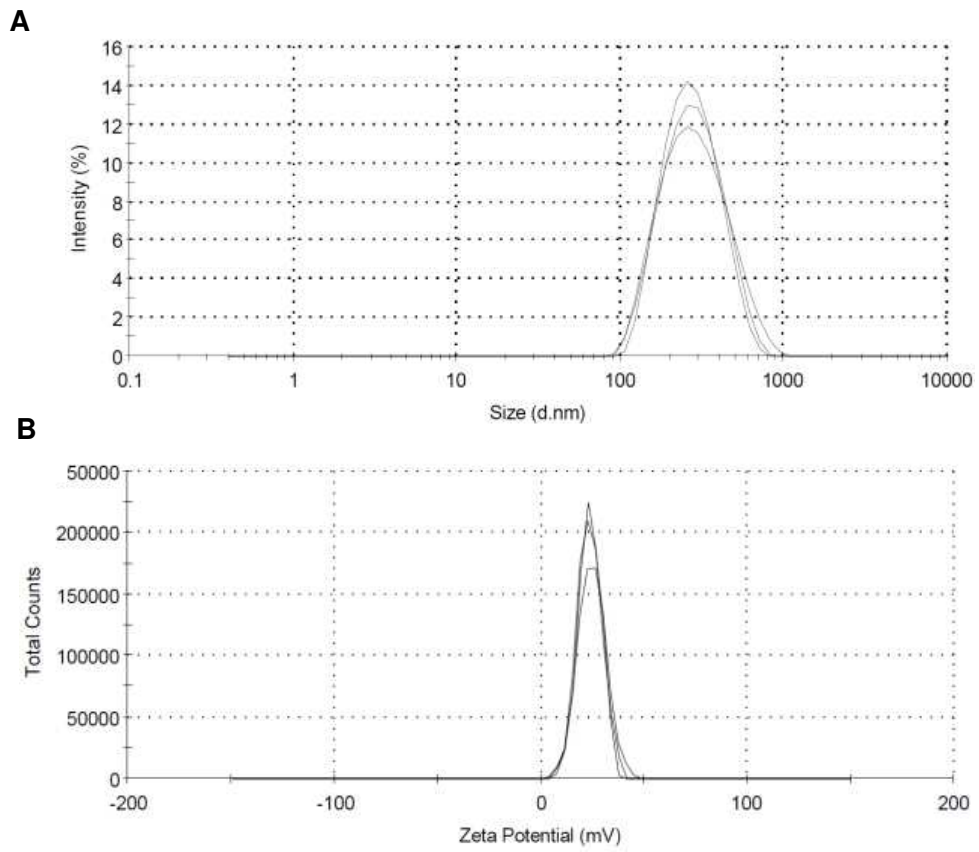
18 **Table S 6:** Significant clusters (Enrichment Score  $> 1.3$ ) with Gene Ontology Biological  
19 Processes (GOTERM\_BP) and pathways following exposure of PMA-differentiated THP-1 cells  
20 to 8.1  $\mu\text{g/mL}$  (IC<sub>50</sub>) of ZnO110NP.

21 **Table S 7:** Characterization of ZnO nanoparticles by dynamic light scattering, after 0h or 24h in  
22 the medium of exposure (serum-free medium).

- 1 **Table S 8:** Measure of zinc (Zn) in the cell layers in contact with or inside the cells by
- 2 Inductively Coupled Plasma-Optical Emission Spectrometer.
- 3

1 **Figure 1**

2





1 **Figure 2**

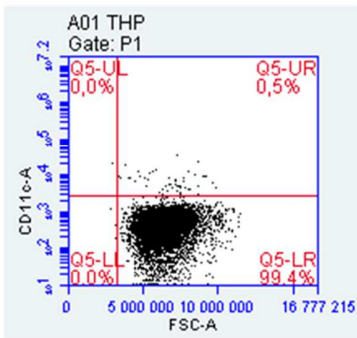
2

Unstained cells

Stained cells

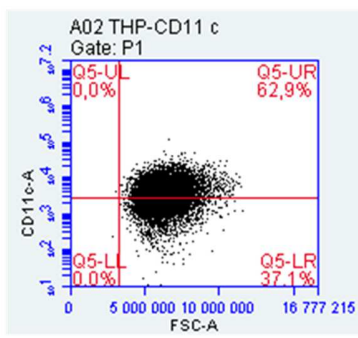
**A**

THP-1



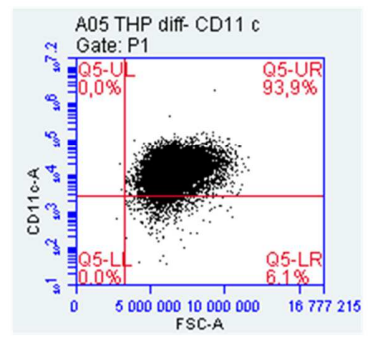
**B**

THP-1



**C**

THP-1 + PMA

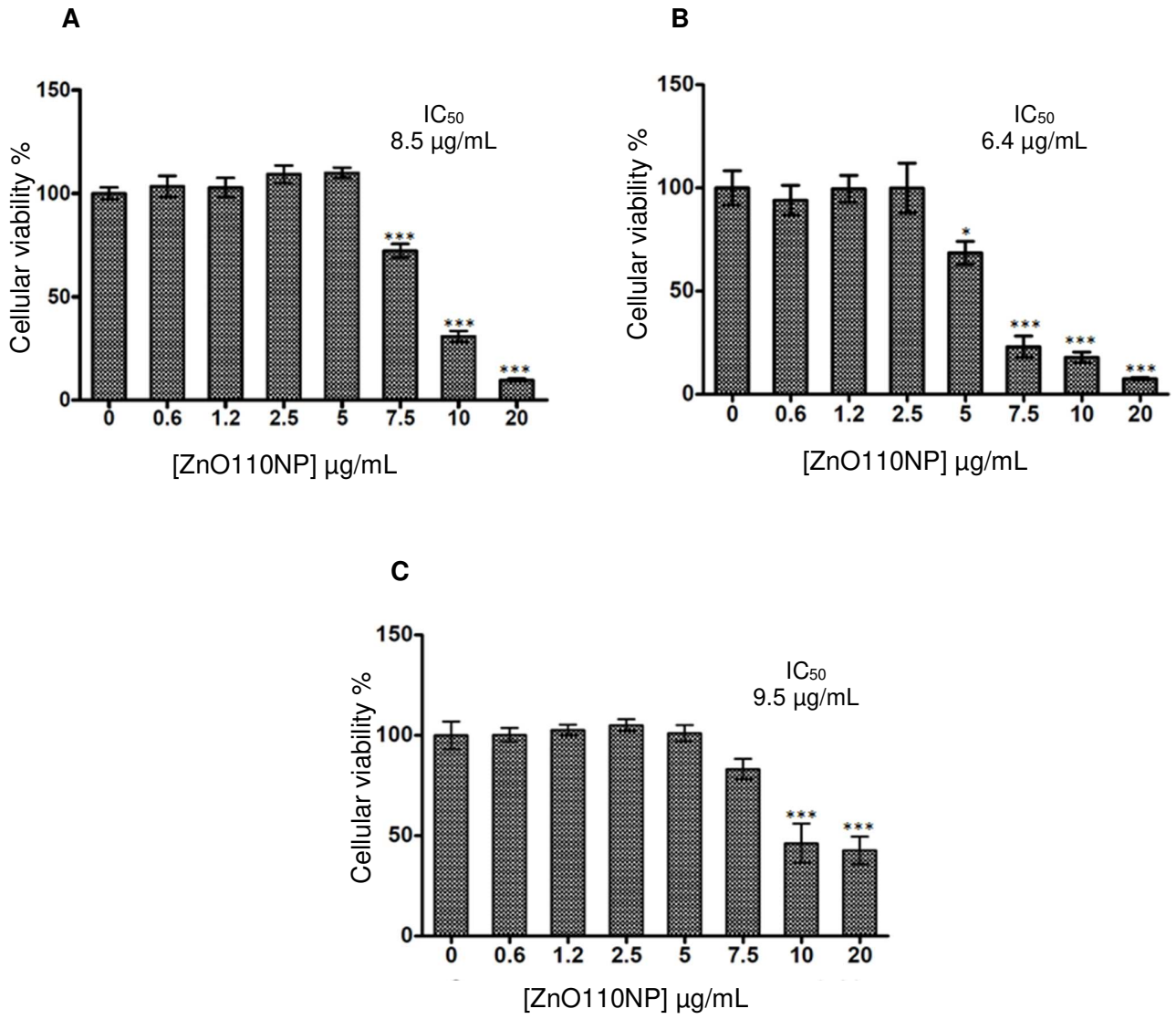


**62,9% CD11c<sup>+</sup> cells**

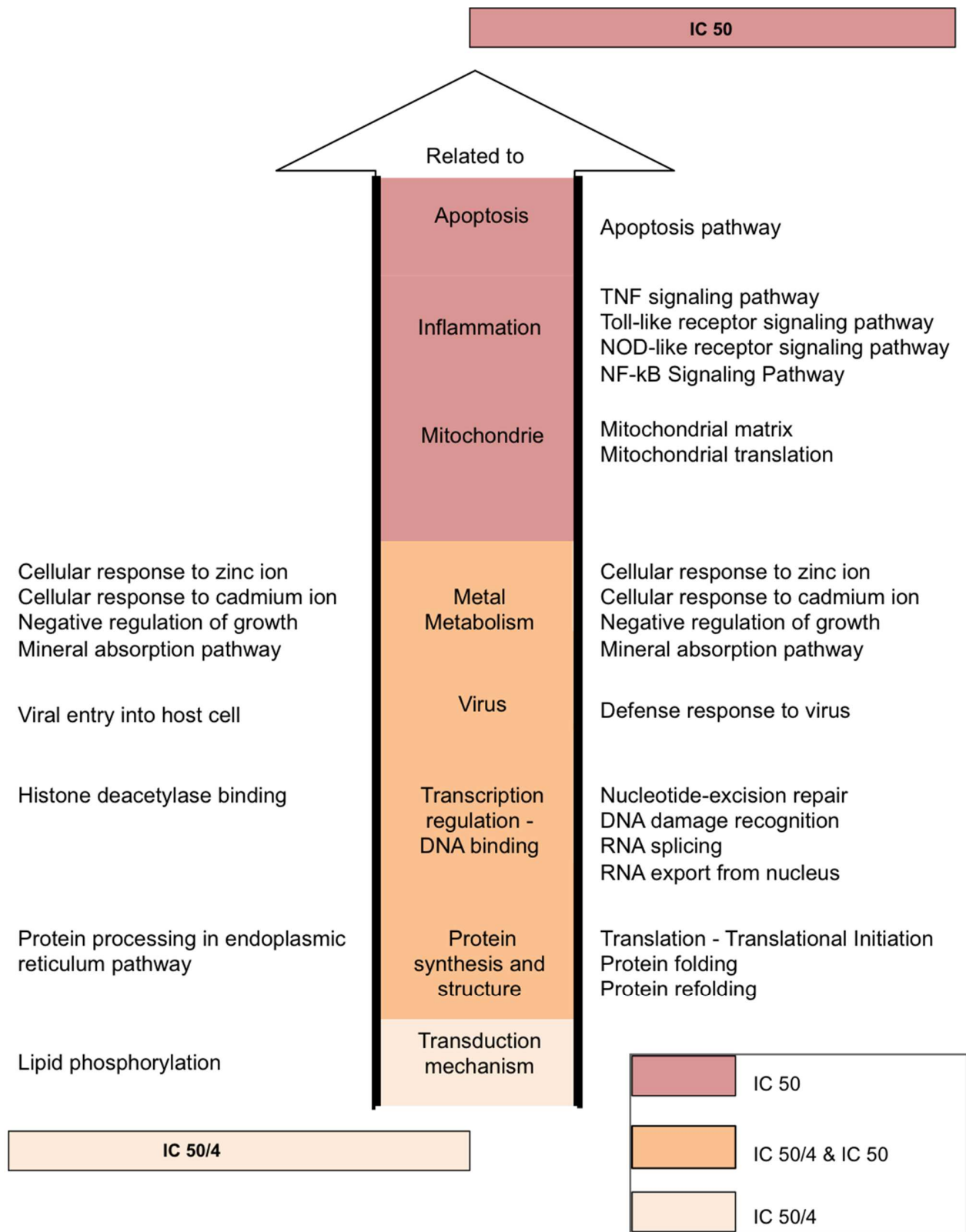
**93,9% CD11c<sup>+</sup> cilles**

1 **Figure 3**

2



1 **Figure 4**



1 **Figure 5**

2

3

