

Supplementary Figures

Figure S1. Cell viability (%) of the overall WBCs population after exposure to the higher doses of PSNPs (50 and 100 $\mu\text{g}/\text{mL}$) for 24 h. Data represent mean \pm SD from six blood donors.

Figure S2. Gating strategy to quantify the cellular γ -PSNPs uptake in the different populations of WBCs. Lymphocytes (red), Monocytes (blue), and PMNs (green) were separated by SSC-H and FL1-H. The fenced area represents internalized particles of each population (lymphocytes -red-, monocytes -blue-, and PMNs -green-) in the negative control (top) and in the 100 $\mu\text{g}/\text{mL}$ concentration (bottom).

Figure S3. Gating strategy to classify the different populations of WBCs. Lymphocytes (red), monocytes (blue), and PMNs (violet) were separated by SSC and FITC.

Figure S4. Basal levels of genotoxic damage (level of DNA damage detected in non-exposed samples) of lymphocytes, monocytes, and PMNs measured using the comet assay. Representative pictures correspond to basal genotoxic damage (A). As observed, no tails are detected in the population of lymphocytes; tails with low intensity (DNA content) are present in monocytes, and tails with high intensity can be seen in the PMNs population. Graphical representation of the basal levels of genotoxic DNA damage for the three WBC types (B). Data are presented as mean \pm SEM from blood samples of two donors. Results were analyzed with the Student's t-test. *** $P < 0.001$. Dotted lines between bars represent the statistically significant differences between cell populations.

Figure S5. Levels of genotoxic damage observed in unsorted WBCs exposed to 1, 10 and 25 $\mu\text{g}/\text{mL}$ of PSNPs, assessed by the comet assay. As it can be observed no significant levels of genotoxic DNA damage were detected at these concentrations. Data are presented as mean \pm SEM from blood samples of two donors.

Figure S6. Cytokine expression analysis after LPS exposure (positive control). The volcano plot is divided into two areas, the area above the dashed line represents the cytokines significantly expressed (in red), and the lower area depicts the non-significantly expressed cytokines (in black). The X- and Y-axis represent the \log_2 (Fold Change) and the $-\log_{10}$, respectively (P -value $+0.001$). Significance was calculated comparing cytokines expression from exposed sample to non-exposed one by the t-test (in red P -value < 0.05).

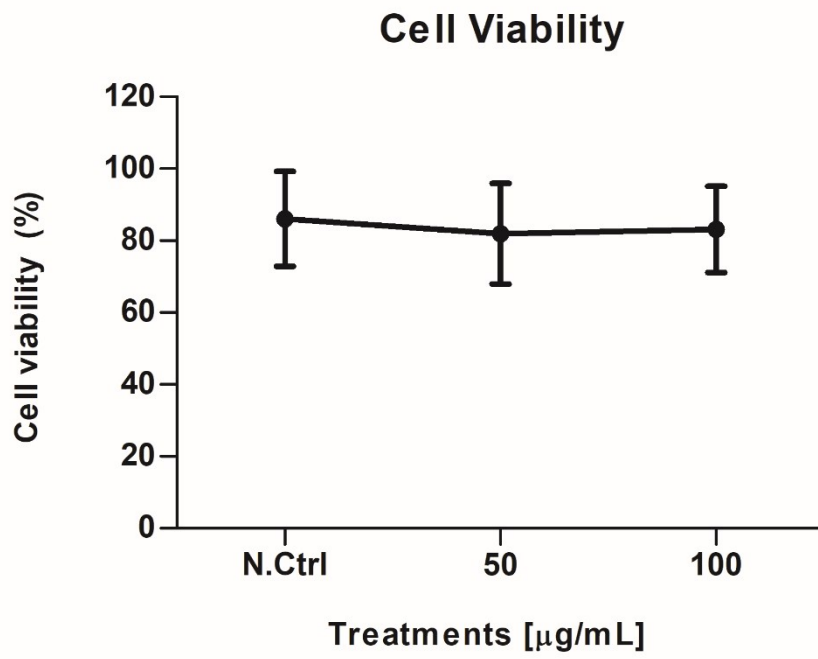


Figure S1

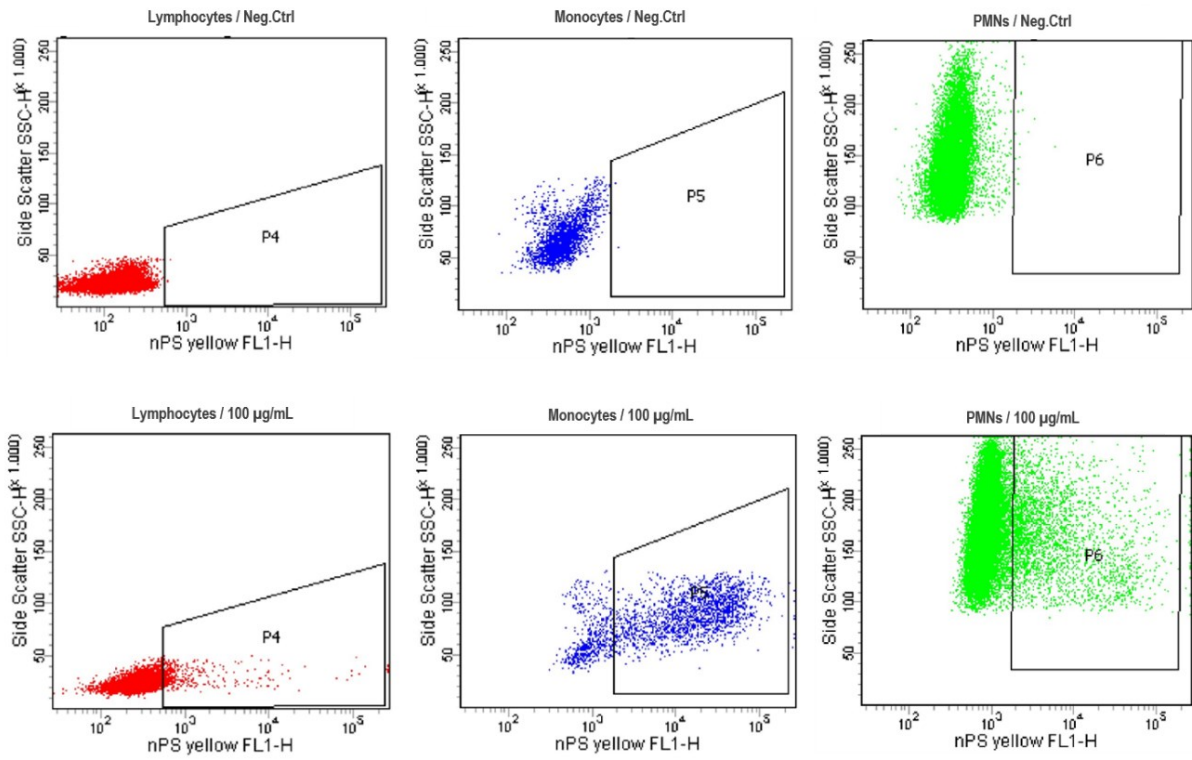


Figure S2

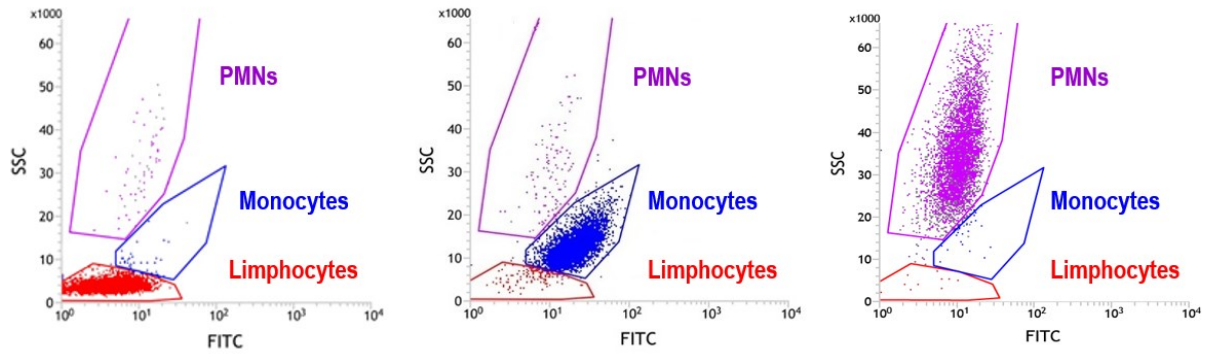


Figure S3

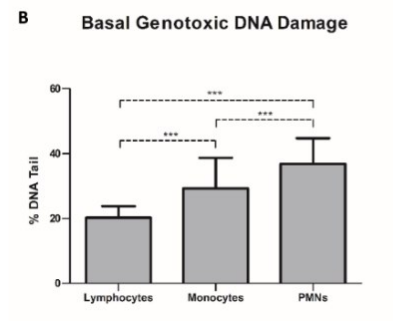
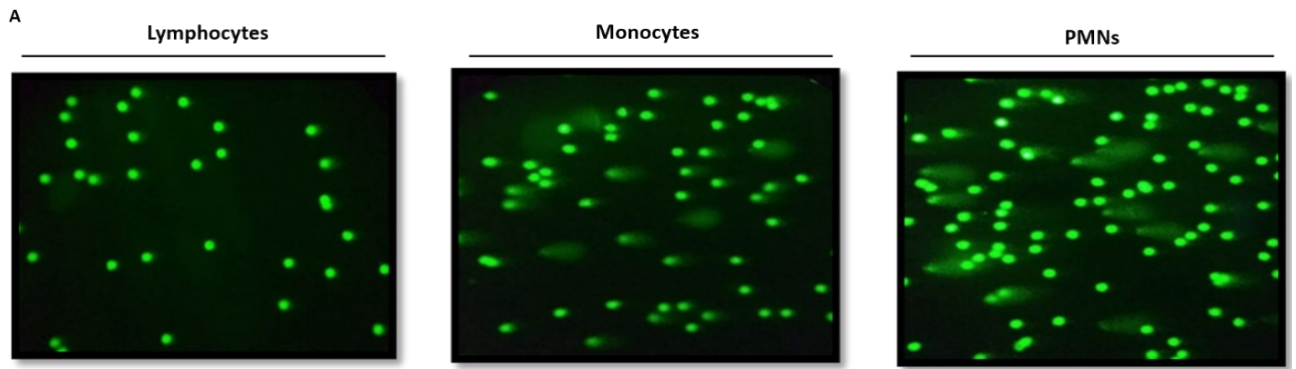


Figure S4

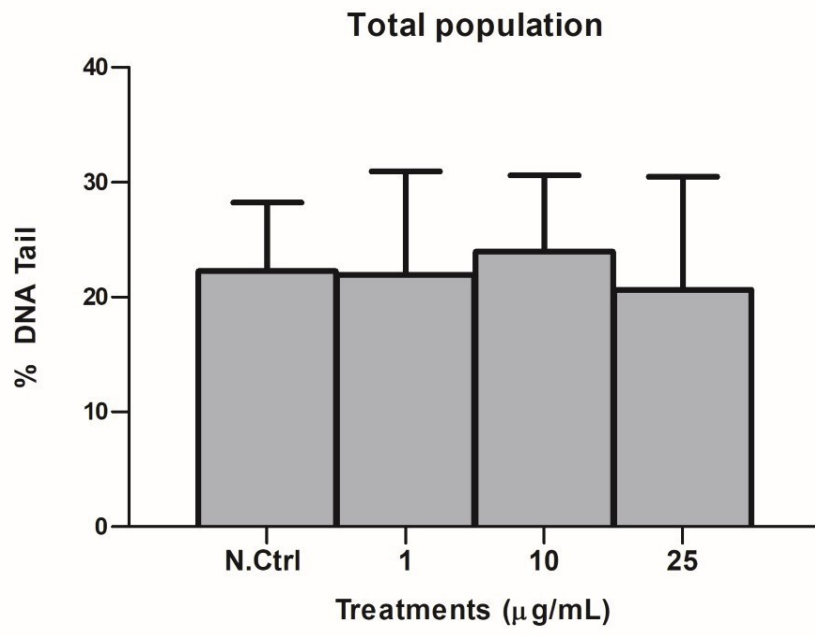


Figure S5

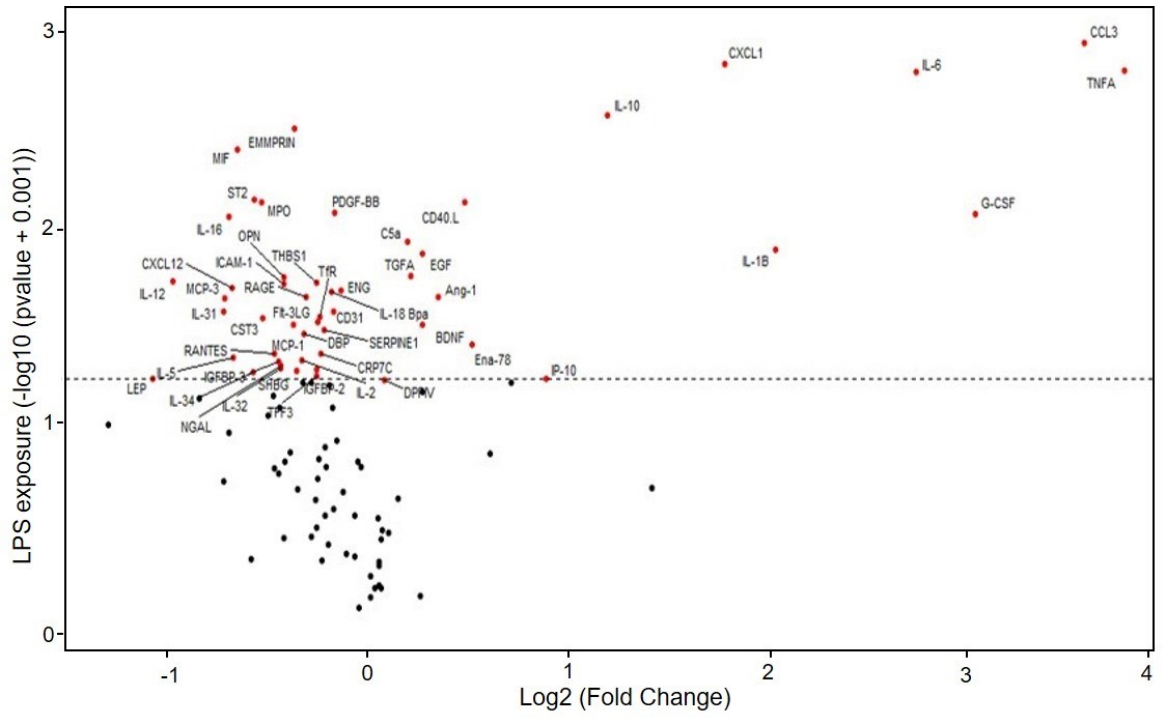


Figure S6