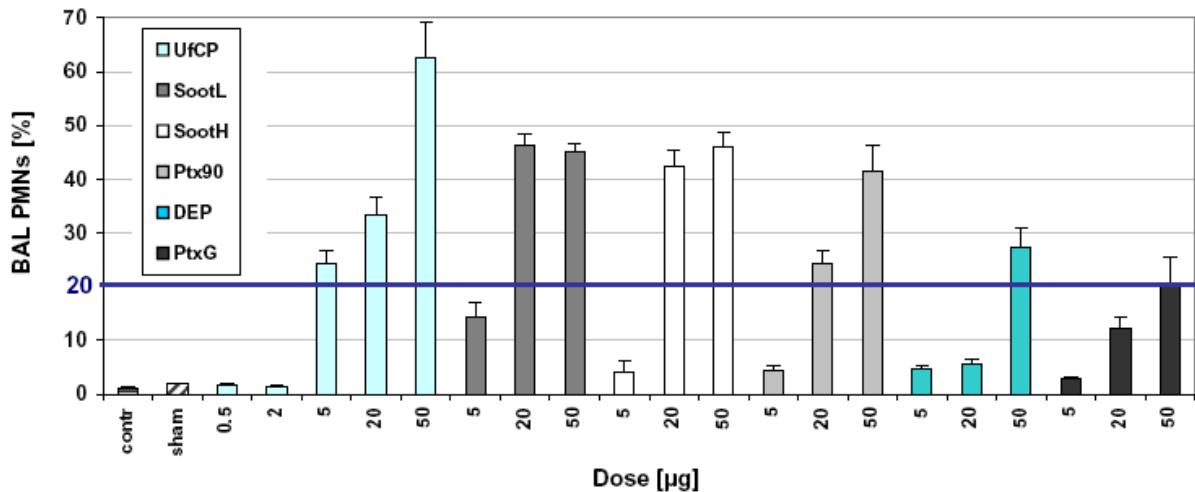


Supplemental Material, Table 1

| RefSeq | Gene Name | Gene Abbr. | Forward Primer Sequence | Reverse Primer Sequence |
|--------------|---|----------------|-----------------------------------|-----------------------------|
| NM_007436 | aldehyde dehydrogenase family 3, subfamily A1 | <i>Aldh3a1</i> | AGC TCC CAC CAT CCT AGT | GTC ATT GGC TGT CAC TCC |
| NM_009969 | colony stimulating factor 2 (granulocyte-macrophage) | <i>Csf2</i> | GCC ATC AAA GAA GCC CTG AA | GCG GGT CTG CAC ACA TGT TA |
| NM_008176 | chemokine (C-X-C motif) ligand 1 | <i>Cxcl1</i> | CCG AAG TCA TAG CCA CAC | GTG CCA TCA GAG CAG TCT |
| NM_009141 | chemokine (C-X-C motif) ligand 5 | <i>Cxcl5</i> | GAC TCT GAC CCC AGT GAA G | GTG AGA TGA GCA GGA AGC |
| NM_009992 | cytochrome P450, family 1, subfamily a, polypeptide 1 | <i>Cyp1a1</i> | GCT GGG TTT GAC ACA GTC | ATA GGG CAG CTG AGG TCT |
| NM_009994 | cytochrome P450, family 1, subfamily b, polypeptide 1 | <i>Cyp1b1</i> | GCC TCA GGT GTC TAG GTC T | GTG GAC TGT CTG CAC TAA GG |
| NM_010295 | glutamate-cysteine ligase, catalytic subunit | <i>Gclc</i> | GGA GAC CAG AGT ATG GGA GT | AGC CTA GTC TGG GGA ATG |
| NM_008160 | glutathione peroxidase 1 | <i>Gpx1</i> | GGG ACT ACA CCA AGA TGA | CAG GTC GGA CGT ACT TGA |
| NM_001037741 | glutathione peroxidase 4 | <i>Gpx4</i> | AGC CCC AGG TGA TAG AGA | CCT GCC GTG CTA TCT CTA |
| NM_010344 | glutathione reductase 1 | <i>Gsr</i> | AGG GCC ACA TCC TAG TAG AC | GTG GCT GAA GAC CAC AGT AG |
| NM_008181 | glutathione S-transferase, alpha-1 | <i>Gsta1</i> | AGG AGA GAG CCC TGA TTG | CTG TTG CCC ACA AGG TAG |
| NM_010442 | heme oxygenase (decycling) 1 | <i>Hmox1</i> | AGG TGA TGC TGA CAG AGG | GTG TCT GGG ATG AGC TAG TG |
| NM_010479 | heat shock protein 1A | <i>Hspa1a</i> | GAC AAG TCG GAG AAC GTG | GAG TAG GTG GTG AAG GTC TG |
| NM_008361 | interleukin 1 beta | <i>Il1b</i> | CAA CCA ACA AGT GAT ATT CTC CAT G | GAT CCA CAC TCT CCA GCT GCA |
| NM_031168 | interleukin 6 | <i>Il6</i> | GTT CTC TGG GAA ATC GTG GA | TGT ACT CCA GGT AGC TAT GG |
| NM_013599 | matrix metallopeptidase 9 | <i>Mmp9</i> | GAA GTG GGG TTT CTG TCC | AGC CCT CGA GGT AGC TAT AC |
| NM_013602 | metallothionein 1 | <i>Mt1</i> | GGT CTT CTC TGT TGG GGA CA | GCT GGG TTG GTC CGA TAC TA |
| NM_008630 | metallothionein 2 | <i>Mt2</i> | TAG ATG GAT CCT GCT CCT GC | CAC TTG TCG GAA GCC CTC TT |
| NM_008706 | NAD(P)H dehydrogenase, quinone 1 | <i>Nqo1</i> | CAG GTG AGC TGA AGG ACT C | CCT GCT ACG AGC ACT CTC T |
| NM_010957 | 8-oxoguanine DNA-glycosylase 1 | <i>Ogg1</i> | GAG ACT GCT GAG ACA AGA CC | GTG AGT CTC TGC TTC TGG AC |
| NM_011198 | cyclooxygenase 2; COX2 (mitogen-inducible) | <i>Ptgs2</i> | CAA CAC CTG AGC GGT TAC | GTT CCA GGA GGA TGG AGT |
| NM_013693 | tumor necrosis factor | <i>Tnfa</i> | CAC CAC GCT CTT CTG TCT | GGC TAC AGG CTT GTC ACT |
| NT_039649.7 | 18S ribosomal RNA | <i>Rn18s</i> | GAC TGT CTC GCC GGT GTC | GGA GAG CCG GAA CGT CGA |

List of genes with the respective primer pairs used for the quantitative PCR analysis. Transcript sequences are identified by the NCBI Reference Sequences ID. All genes are abbreviated by their official MGI symbol (Mouse Genome Informatics, <http://www.informatics.jax.org>). Primer were derived by Primer3 open source software, (<http://primer3.sourceforge.net/>) using the primer picking conditions: GC: 55-60%; annealing: 55°C.

Supplemental Material, Figure 1



The data point '50 μ g UfCP' deviates by 13% (55.1% now 62.5%) from Stoeger et al. (2006) due to an averaging error

Inflammatory dose response in lungs of mice ($n = 8$) 24h after particle instillation. Polymorphonuclear leucocytes (PMNs) recovered by BAL are given as percentage of total BAL cells. The inflammatory efficacy of the particles was defined as the 20% PMN effect level (blue line) divided by the particle mass causing this effect level. The respective mass values were derived by linear interpolation between the data points of the dose response relations (Table 1).

Supplemental Material, Figure 2

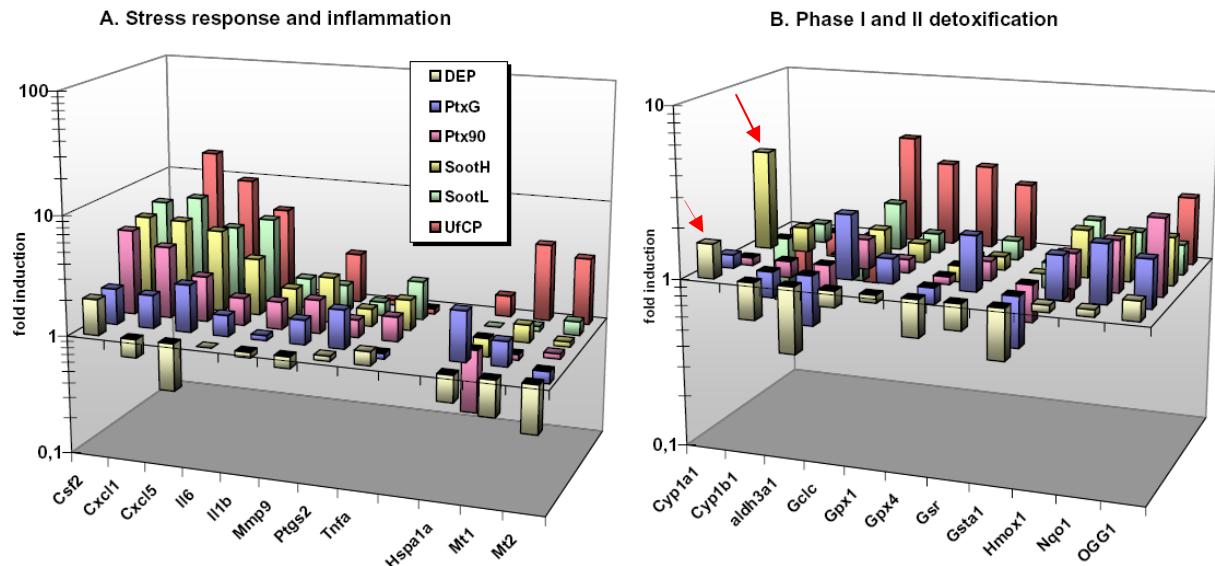


Illustration of gene expression (mRNA levels) of selected marker enzymes (Table 2) characterizing stress response and inflammation (A) as well as phase I and II detoxification (B). cDNA samples from four animals were pooled for quantitative PCR analysis. Expression levels were normalized to 18S rRNA and displayed as fold induction relative to sham control mice. The red arrows indicate the 1.6 and 3.9 fold induction of Cyp1a1 by DEP and SootH particle instillation.