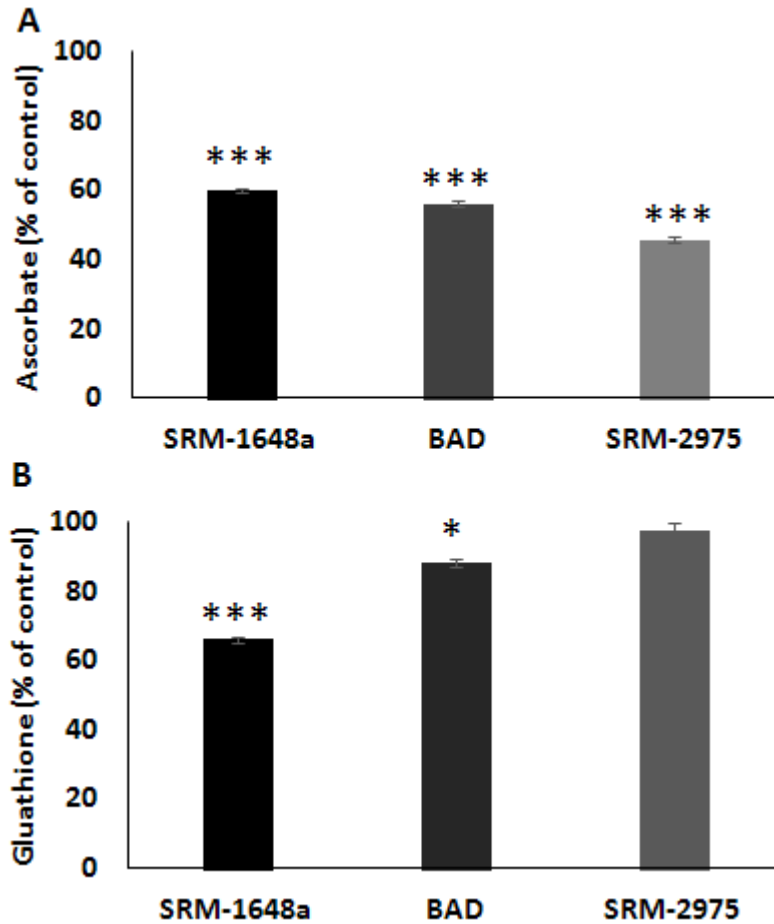


Supplementary material

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Supplementary file 1: Extraction of BAD from filters

The ventilation duct filter contained a yearly collection of abrasion dusts from commercial vehicle (CV) drum brakes that were manufactured by large companies (such as Volvo and Scania) and used in European buses and trucks. The filter contained particles produced during the year 2008 but the specific formula and raw materials that were used in the components cannot be disclosed as this is intellectual property of the manufacturers. Braking was performed in an environmental chamber, fed with filtered air, across a range of speeds and temperatures using a standard CV dynamometer with flywheels, an electric engine and a CV brake installation. Consequently, the sample represents the brake abrasion products of heavy traffic under urban driving and high-speed braking conditions. Air within the chamber was maintained at approximately 20°C and 50% humidity. BAD was extracted from 1 cm³ sections of filter through submersion in 10 mL of high performance liquid chromatography grade methanol with 10 minutes of vortexing. The methanol-solutions were sonicated for 10 minutes at an amplitude of 15 microns, decanted into a pre-weighed 50 ml Falcon tube and dried under a stream of nitrogen gas at 37°C. The dried extract was allowed to equilibrate to room temperature for 24hour prior to re-weighing to establish the extracted mass. Stock solutions were prepared in sterile PBS (1 mg/ml) and stored at -80°C.



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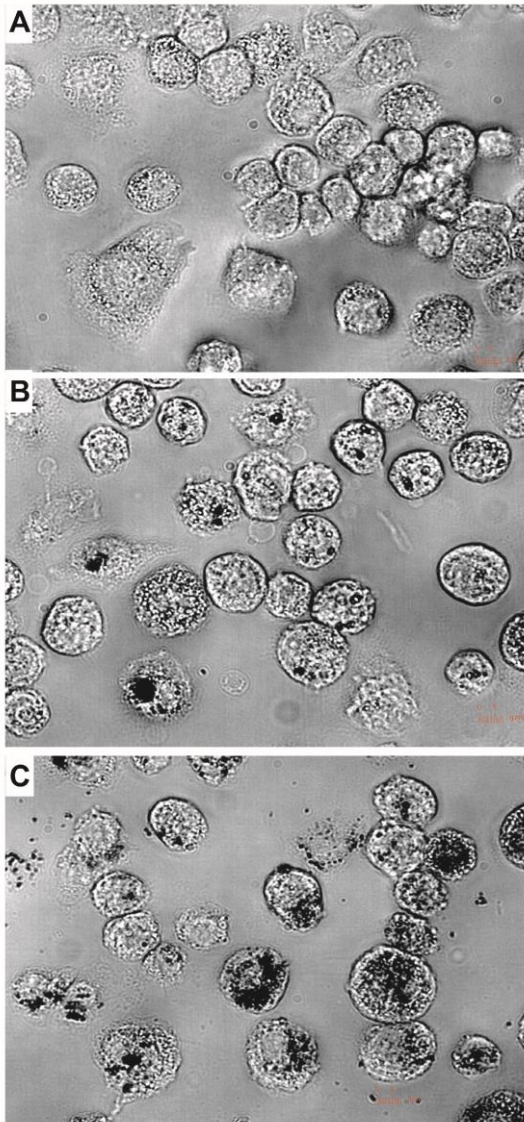
28 **Supplementary Figure 1:** Depletion of (A) ascorbate and (B) glutathione from a synthetic RTL model following 4h incubations with BAD, SRM-2975 (diesel) or SRM-1648a (an urban PM_{2.5} positive control) all at a final concentration of 50 µg/ml. Values are displayed as percentages of a particle-free control and represent the mean ± SE of 3 replicate incubations. Significance differences between values and particle-free control were detected by 1-way ANOVA tests with Bonferroni correction for multiple testing, * p ≤ 0.05, *** p ≤ 0.001

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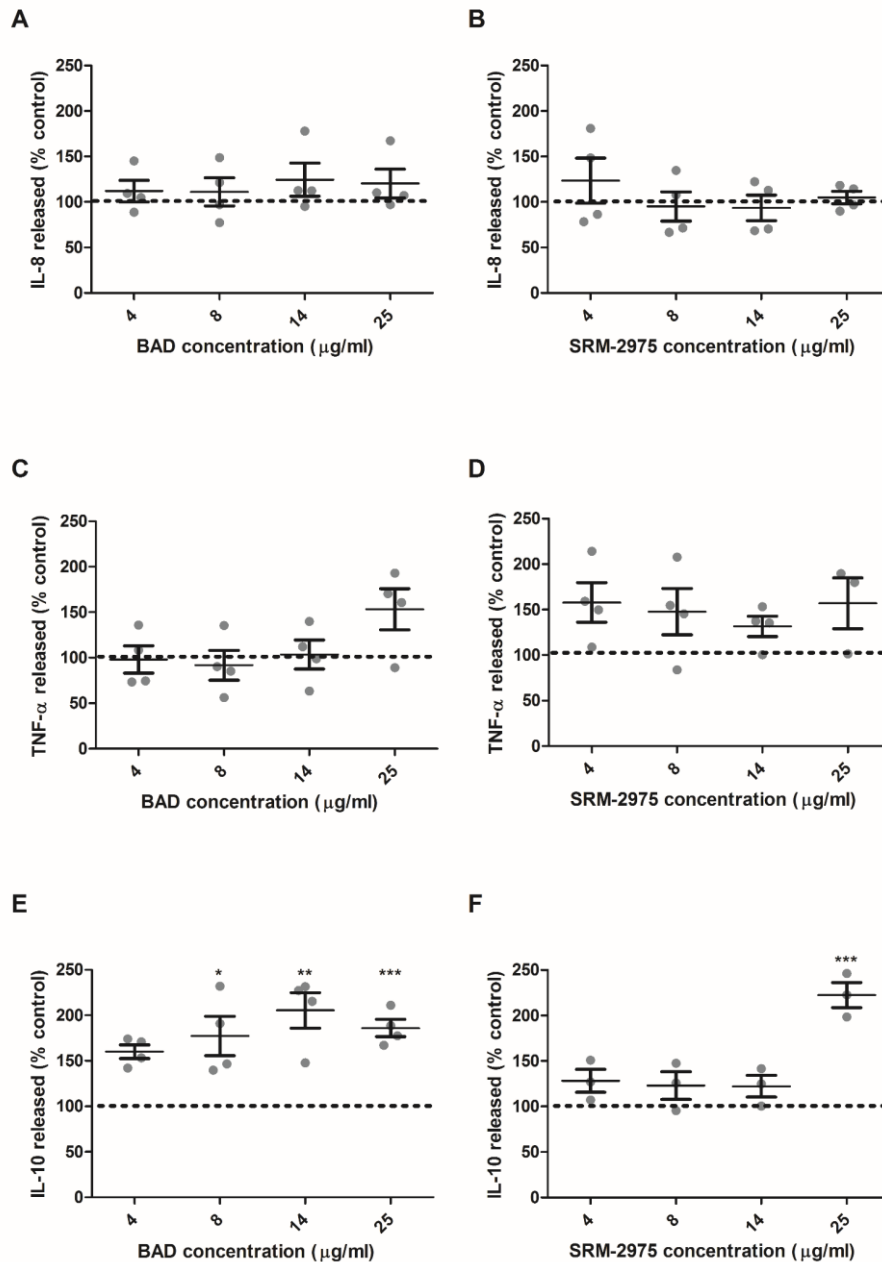


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39 **Supplementary Figure 2:** Representative bright field images of U937 cells after treatment with
40 particle-free media (A) BAD (B) and SRM-2975 (C) (4 µg/ml) for 24 h. These images demonstrate
41 that particles were ingested by the macrophages (scale bar 5 µm). The images were acquired using an
42 IN Cell Analyser 6000 (GE Healthcare) with a 40x objective. Image analysis was performed using IN
43 Cell Developer V1.9.3 (GE Healthcare).

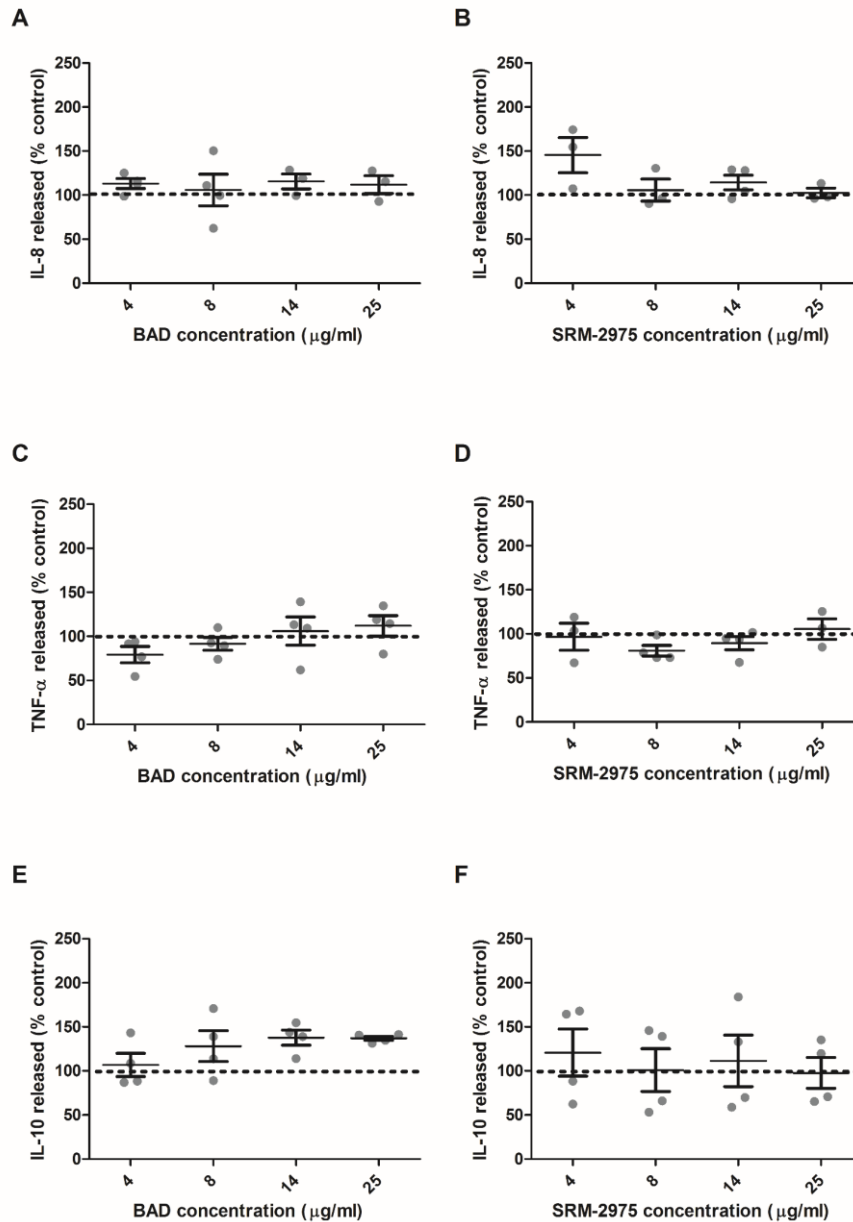
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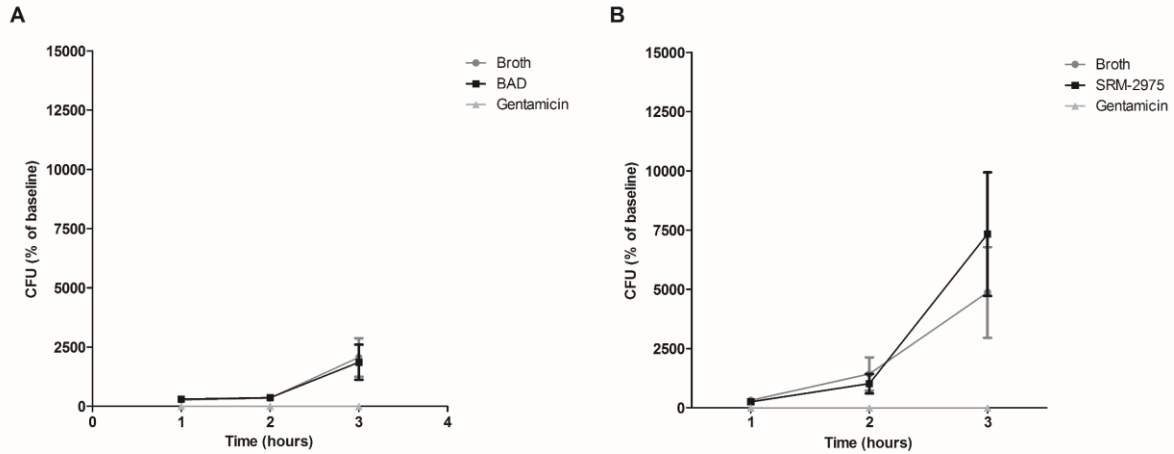
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47 **Supplementary Figure 3:** Concentrations of IL-8 (**A, B**), TNF- α (**C, D**) and IL-10 (**E, F**) measured
 48 within the supernatants of U937s after 24 h exposure to BAD (**A, C, E**) and SRM-2975 (**B, D, F**) in
 49 the presence of metal chelator desferrioxamine (5 $\mu\text{g/ml}$). Values are expressed as percentages of
 50 particle-free controls and normalised to total cellular protein concentrations with error bars depicting
 51 the SEM generated during 5-7 replicates. Significant differences in cytokine concentration were
 52 identified between control and particle-treated cells using 1-way ANOVA tests with Bonferroni
 53 correction. * $p \leq 0.05$, ** $p \leq 0.01$, *** $p \leq 0.001$.



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55 **Supplementary Figure 4:** Concentrations of IL-8 (**A, B**), TNF-α (**C, D**) and IL-10 (**E, F**) measured
 56 within the supernatants of U937s after 24 h exposure to BAD (**A, C, E**) and SRM-2975 (**B, D, F**) and
 57 subsequent incubation in particle-free media for 24 h. Values are expressed as percentages of particle-
 58 free controls and normalised to total cellular protein concentrations with error bars depicting the SEM
 59 generated during 5-7 replicates. Significant differences in cytokine concentration were identified
 60 between control and particle-treated cells using 1-way ANOVA tests with Bonferroni correction. * p
 61 ≤ 0.05 , ** $p \leq 0.01$, *** $p \leq 0.001$.



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63 **Supplementary Figure 5:** The impact of BAD and SRM-2975 exposure on *S. aureus* growth. Data

64 points represent the number of *S. aureus* colonies that grew in MH broth (grey) or MH broth

65 supplemented with 25 µg/ml BAD (A), 25 µg/ml SRM-2975 (B) or 50 µg/ml gentamicin (A and B)

66 after 1,2 or 3 hours of incubation at 37°C. Data are shown as a percentage of the time 0 colony counts

67 for their respective treatment group and error bars represent the SE (n=4). 2-way ANOVA tests with

68 Bonferroni corrections indicated that there were no significant differences (p values > 0.05) in colony

69 counts between treatment groups at any time point.

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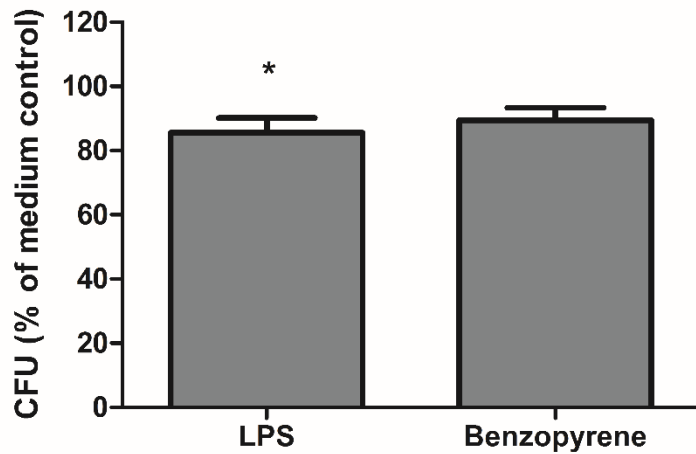
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77 **Supplementary Figure 6:** Quantities of *S. aureus* ingested by U937s over a 2h period subsequent to
 78 24 h incubation with 1 µg/ml LPS or 1 µg/ml benzopyrene. Values were normalised to concentration
 79 of total cellular proteins and presented as percentages of a particle-free control and represent mean ±
 80 SEM of n=6. Significant differences in CFU were identified between control and LPS treated cells
 81 using 1-way ANOVA tests with Bonferroni correction. * p ≤ 0.05.

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