Supplementary Material

TABLE S1. Primer sequences for the quantitative PCR for the mouse genes analyzed. The gene identification number (ID) is the unique identifier number from the Entrez Global Query Cross-Database Search System at the National Center for Biotechnology Information.

Gene symbol	Gene name	Entrez Gene ID		Sequence (5'→3')	Product Size (bp)
Adipoq	adiponectin, C1Q and collagen domain containing	11450	F: R:	gtcagtggatctgacgacaccaa atgcctgccatccaacctg	171bp
Glut1	solute carrier family 2 member 1	20525	F: R:	cttcattgtgggcatgtgcttc aggttcggcctttggtctcag	134bp
Il1b	interleukin 1 beta	16176	F: R:	gcaactgttcctgaactcaact atcttttggggtccgtcaact	89bp
Il6	interleukin 6	16193	F: R:	ccacttcacaagtcggaggctta gcaagtgcatcatcgttgttcatac	112bp
Il10	interleukin 10	16153	F: R:	catggcccagaaatcaagga ggagaaatcgatgacagcgc	91bp
Irs1	insulin receptor substrate 1	16367	F: R:	gcgggctgactccaagaac gctatccgcggcaatgg	76bp
Mcp1	chemokine (C-C motif) ligand 2	20296	F: R:	ttaacgccccactcacctgctg gcttctttgggacacctgctgc	106bp
Ppia	peptidylprolyl isomerase A	268373	F: R:	ctgagcactggggagaaagga gaagtcaccaccctggcaca	87bp
Tnf	tumor necrosis factor	21926	F: R:	catcttctcaaaattcgagtgacaa tgggagtagacaaggtacaaccc	175bp

F: Forward; R: Reverse; Bp: base pair.

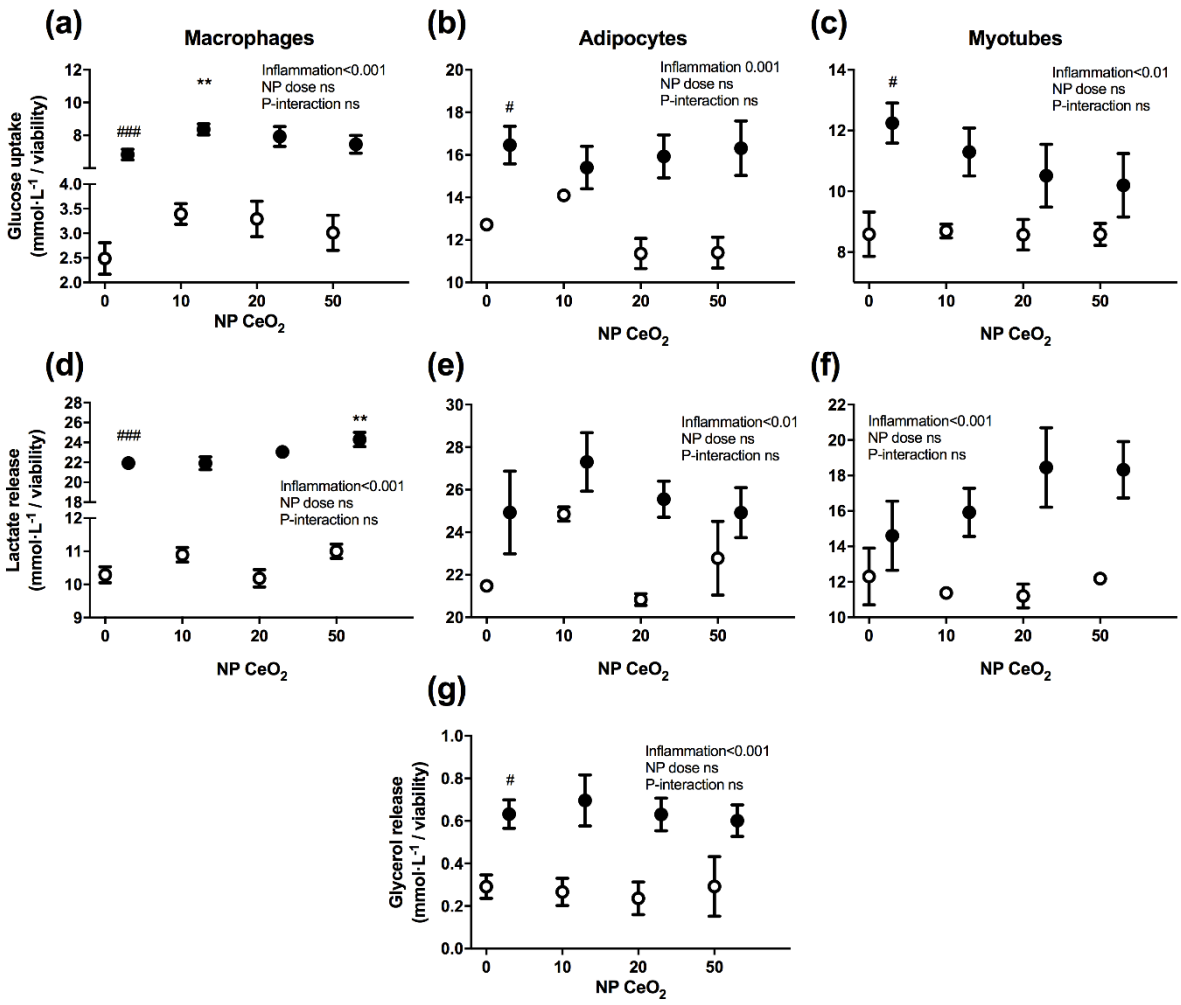

FIGURE S1. Glucose uptake, lactate and glycerol release in RAW 264.7 macrophages (a,d), 3T3-L1 adipocytes (b,e,g) and C2C12 myotubes (c,f) at 24 h after CeO_2 NPs treatment at 10, 20 and 50 µg/ml doses in fold change compared to non-treated control (NTC). White shapes: Control medium; Black shapes: Inflammation in macrophages activated with Lipopolysaccharide (LPS), adipocytes and myotubes treated with conditioned medium (CM); # $p<0.05$, ### $p<0.001$ Control vs. Inflammation; ** $p<0.01$ CeO_2 NPs vs. Inflammation; Data (n=6 /group) are expressed as mean (SEM).

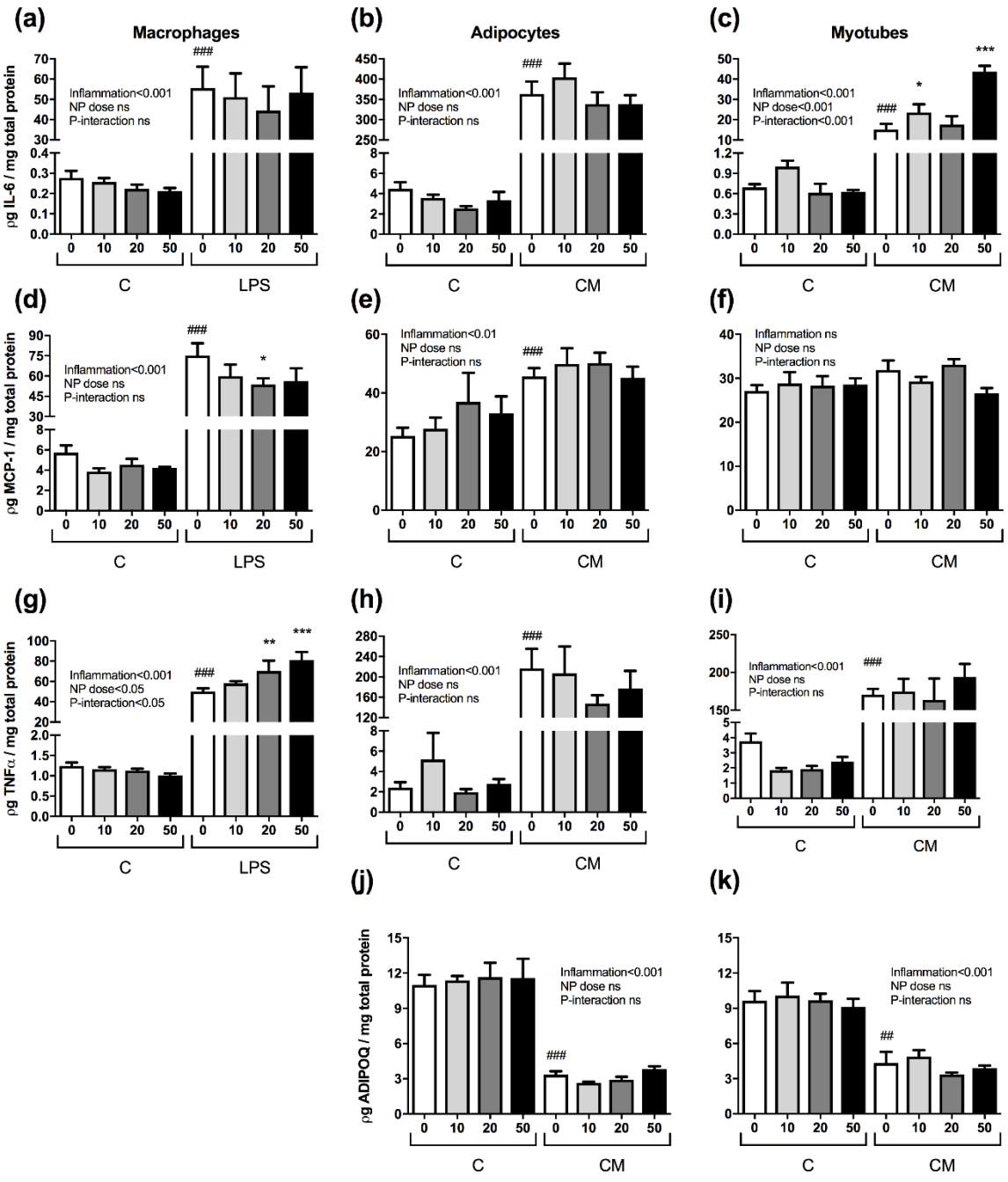

FIGURE S2. Secretion of IL-6, MCP-1, TNF-α and ADIPOQ in RAW 264.7 macrophages (a,d,g), 3T3-L1 adipocytes (b,e,h,j) and C2C12 myotubes (c,f,i,k) at 24 h after CeO_2 NPs treatment at 10, 20 and 50 μg/ml doses in ρg/mg total protein compared to non-treated control (NP0). C: Control medium; LPS or CM: Inflammation in macrophages activated with Lipopolysaccharide (LPS), adipocytes and myotubes treated with conditioned medium (CM); ## $p<0.01$, ### $p<0.001$ Control vs. Inflammation; * $p<0.05$, ** $p<0.01$, ** $p<0.001$ CeO_2 NPs vs. Inflammation; Data (n=6 /group) are expressed as mean (SEM).

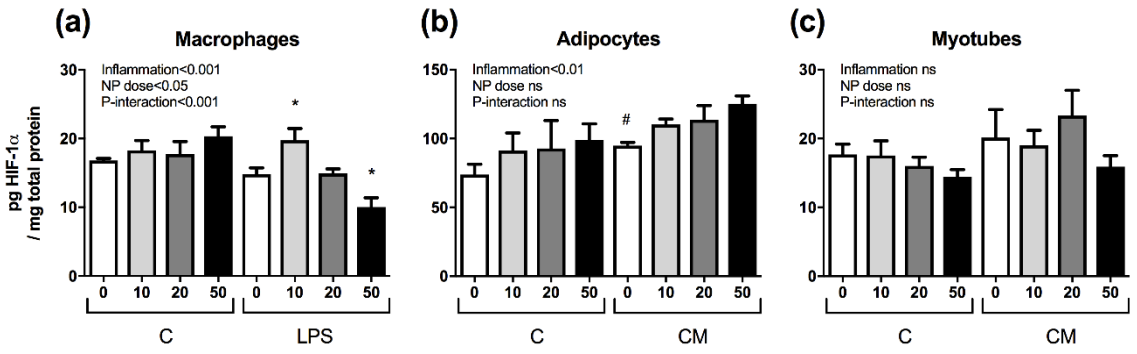

FIGURE S3. HIF-1α total protein in RAW 264.7 macrophages (a), 3T3-L1 adipocytes (b) and C2C12 myotubes (c) at 24 h after CeO_2 NPs treatment at 10, 20 and 50 μg/ml doses in ρg/total protein compared to non-treated control (NTC). C: Control medium; LPS or CM: Inflammation in macrophages activated with Lipopolysaccharide (LPS), adipocytes and myotubes treated with conditioned medium (CM); # $p<0.05$ Control vs. Inflammation; * $p<0.05$ NPs vs. Inflammation; Data (n=6 /group) are expressed as mean (SEM).

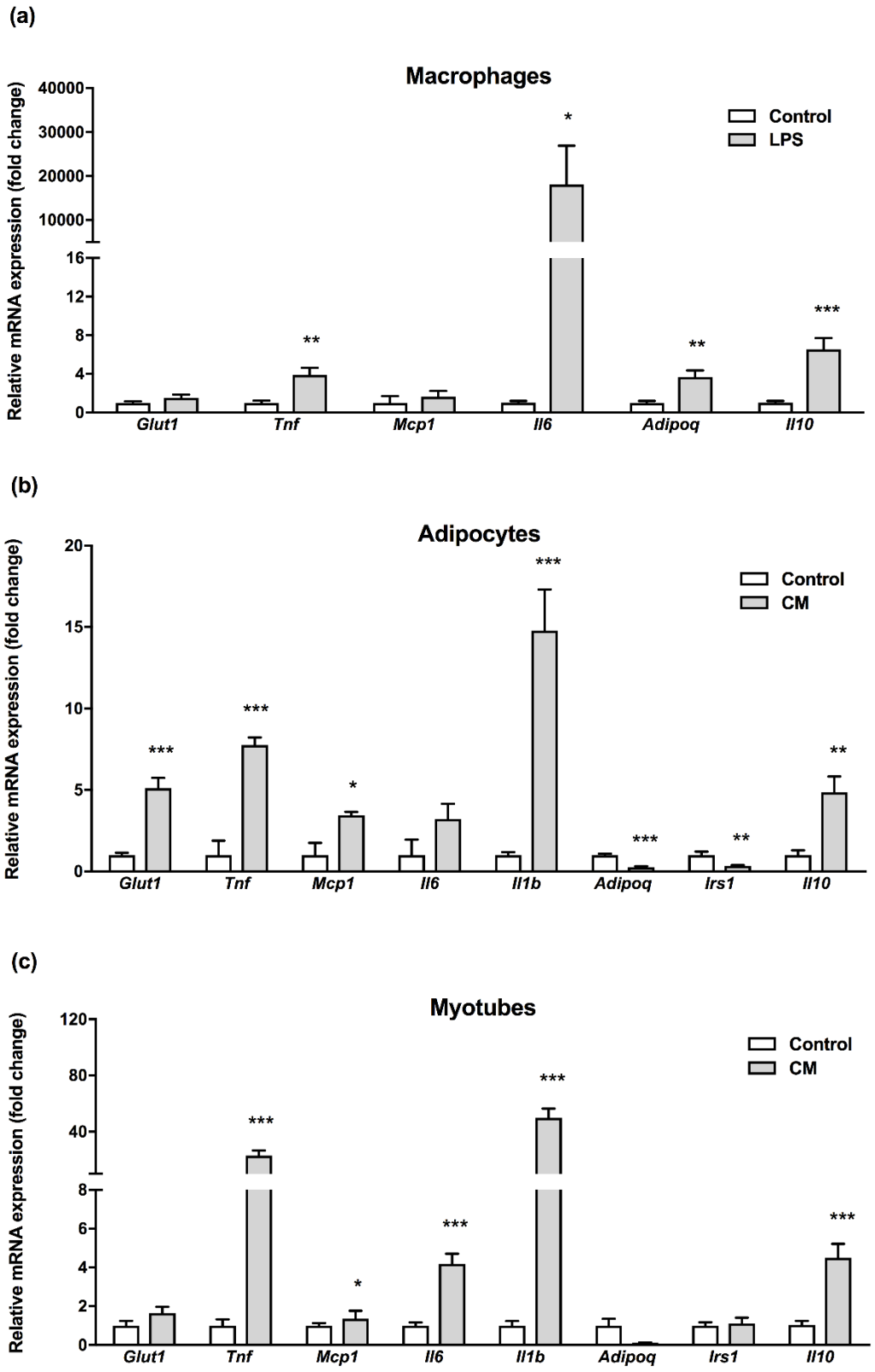

FIGURE S4. Relative mRNA analysis of metabolism-related markers in RAW 264.7 macrophages activated with LPS (a), 3T3-L1 adipocytes (b) and C2C12 myocytes (c) treated with conditioned medium (CM). Results normalized to *Ppia* housekeeping gene. * $p<0.05$, ** $p<0.01$, *** $p<0.001$ Control vs. Inflammation (LPS or CM); Data (n=6 /group) are expressed as mean (SEM).