Supplemental Figure S1

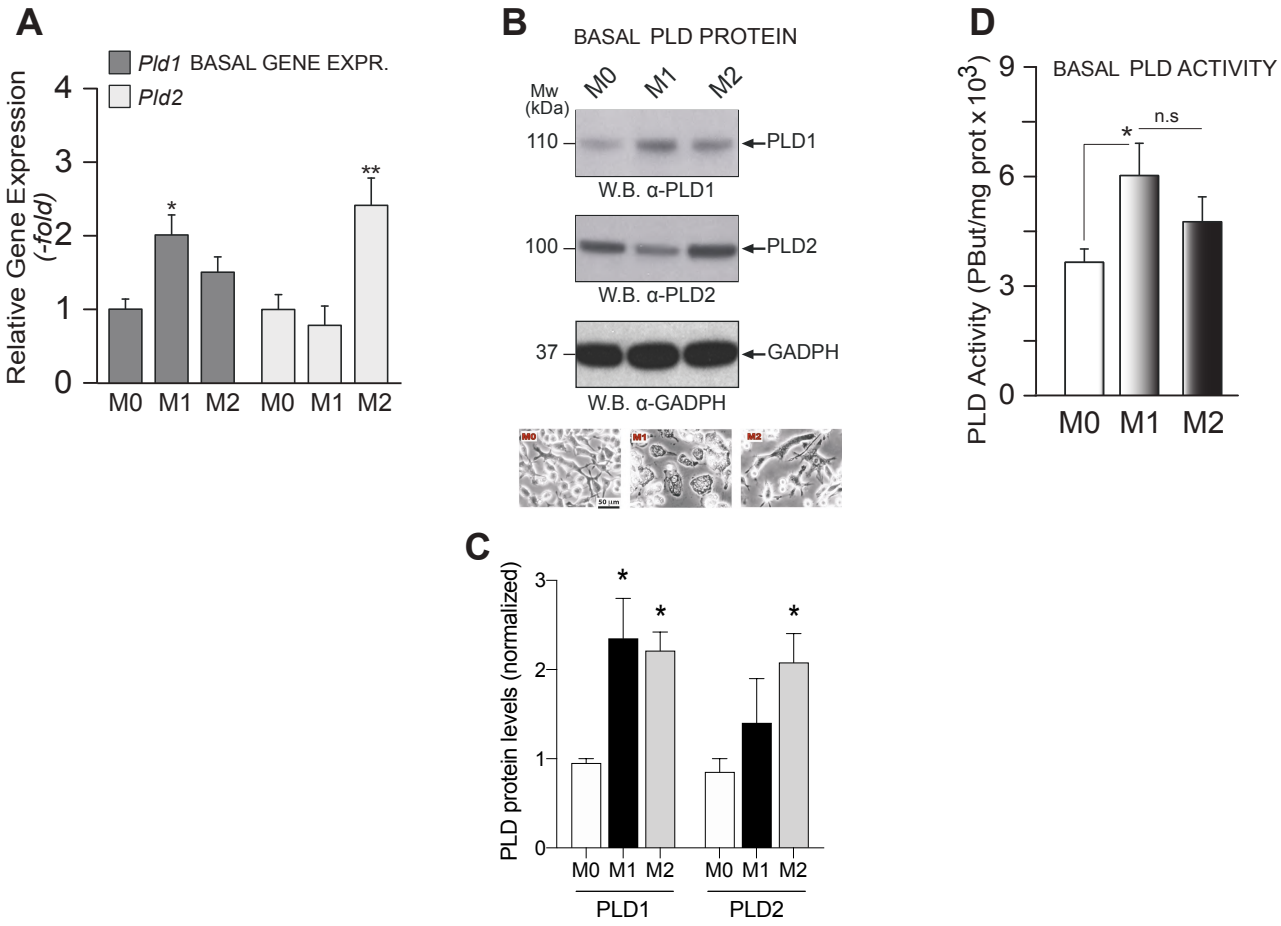

Figure S1. Assessment of gene, protein, activity , and functional levels in M1 and M2 macrophages. (A) Basal gene expression levels of Pld1 and Pld2 in M0, M1 and M2 macrophages (n=3). (B-C) Protein expression of PLD1 and PLD2 by Western blotting (GAPDH are loading . controls) and densitometry with inset showing photomicrographs of representative morphology for M0, M1 and M2 macrophages by bright field microscopy scale= 50 μm (n=3). (D) Phospholipase activity in M0, M1 and M2 macrophages (n=4). Data in bar graphs are mean ± SEM; statistical significance (*$p < 0.05$ and **$p < 0.01$; n.s.=not significant) was evaluated with one-way ANOVA and Tukey's post hoc comparing conditions to the M0 normalized controls for each panel

Supplemental Figure S2

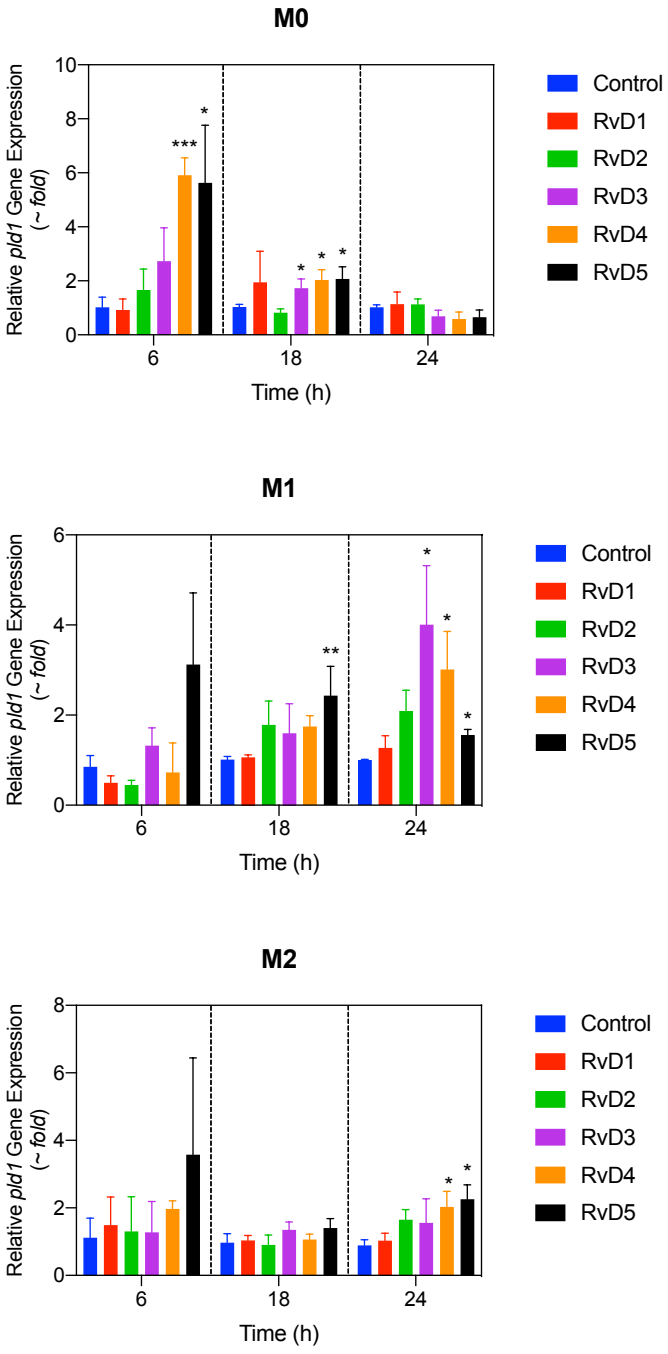

Figure S2. PLD1 gene expression in M0, M1 and M2 macrophages at different time lengths of macrophage incubation with RvDs. See main Fig 1 for specific *Pld1* gene expression changes at 24 hrs of M1 or M2 incubation with RvD's. Data shown are relative *Pld1* gene expression upon D-series resolvins treatment for 6 (n=3), 18 (n=3) and 24 h (n=3) as means ± SEM; statistical significance (*$p < 0.05$, **$p < 0.01$, and ***$p < 0.001$) was evaluated with one-way ANOVA and Tukey's post hoc comparing samples with controls (vehicle only) for each panel.

Supplemental Figure S3

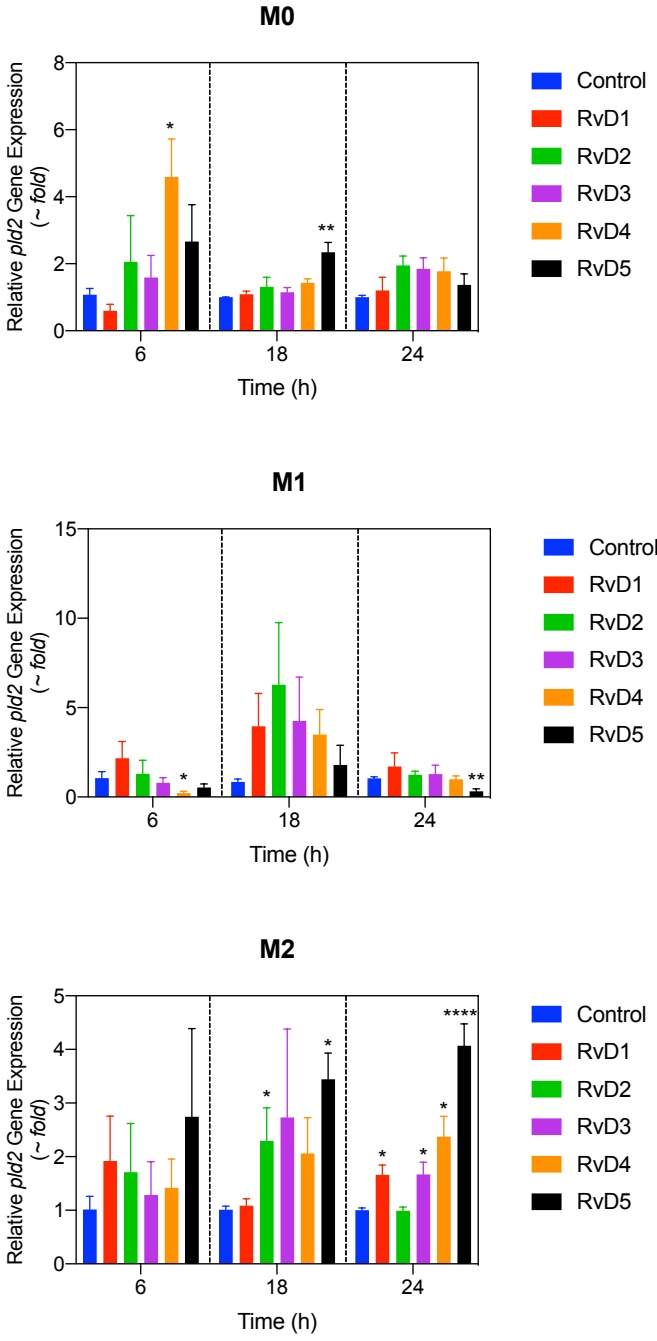

Figure S3. PLD2 gene expression in M0, M1 and M2 macrophages at different time lengths of macrophage incubation with RvDs. See main Fig 1 for specific *Pld2* gene expression changes at 24 hrs of M1 or M2 incubation with RvD's. Data shown are relative *Pld2* gene expression upon D-series resolvins treatment for 6 (n=3), 18 (n=3) and 24 h (n=3) as means ± SEM; statistical significance (*$p < 0.05$, **$p < 0.01$, and ***$p < 0.001$) was evaluated with one-way ANOVA and Tukey's post hoc comparing samples with controls (vehicle only) for each panel.

Supplemental Figure S4

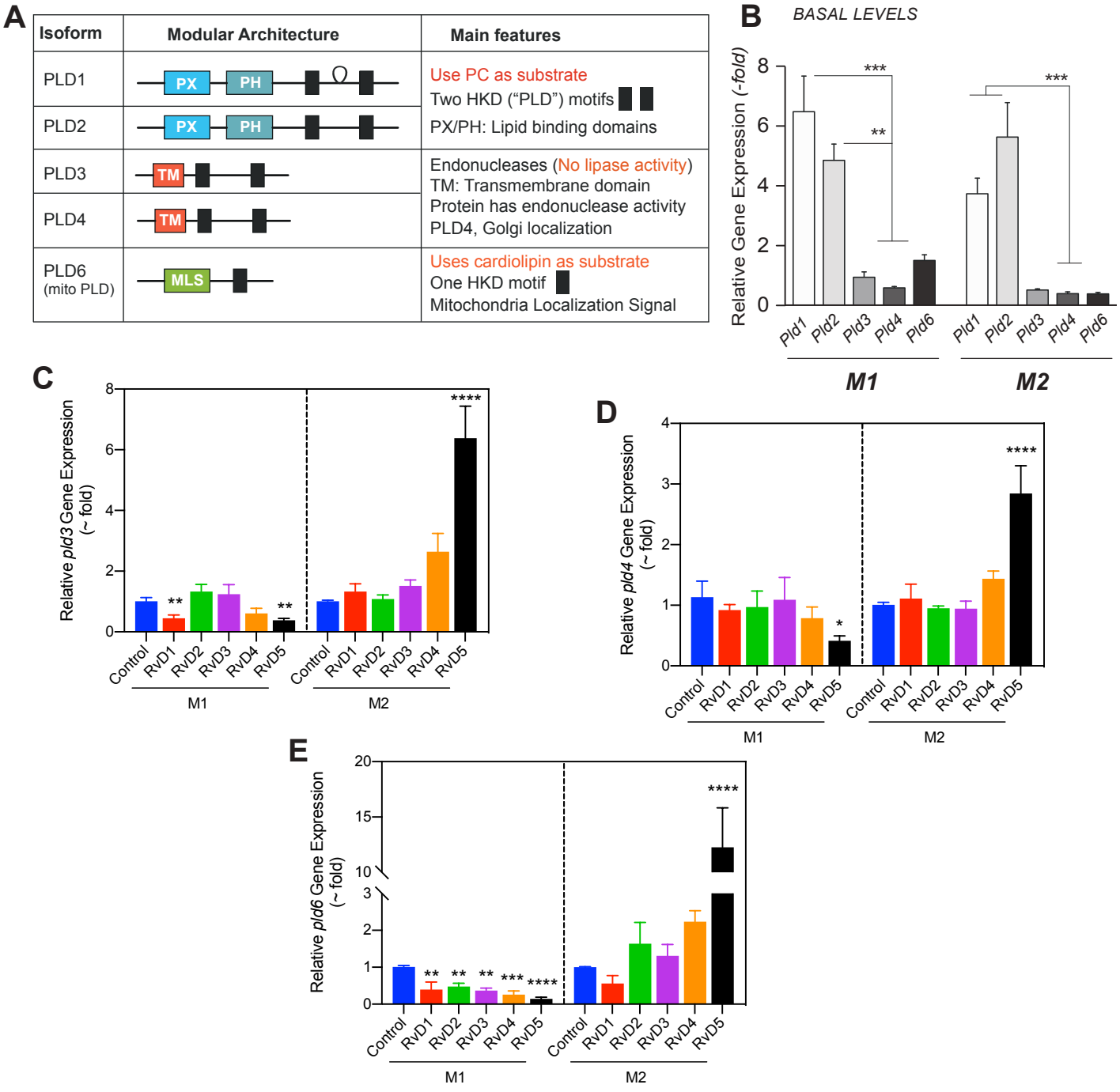

Figure S4. Classical and Non-classical PLD's and their basal levels in M1 and M2 macrophages. (A) Scheme showing the molecular architecture and features of the "classical" (PLD1 and PLD2) and "non-classical" (PLD3, PLD4 and PLD6) mammalian PLD's. HKD=catalytic site/lipase signature motif; PX=phox homology and PH=pleckstrin homology regulatory domains; or TM=transmembrane and MLS=mitochondria localization signal. (Note: PLD5 has not been fully described). (B) Comparison of basal gene expression levels between *Pld1, Pld2, Pld3, Pld4, Pld6* using qRT-PCR in M1 and M2 macrophages (n=3). Gene expression levels of *Pld3* (C), *Pld4* (D), *Pld6* (E) measured by qRT-PCR in M1 or M2 macrophages with 10 nM D-series resolvins treatment for 24 hours (n=3). Data presented are means ± SEM; statistical significance (*$p < 0.05$, **$p < 0.01$, and ***$p < 0.001$) was evaluated with one-way ANOVA and Tukey's post hoc comparing samples to the control (vehicle) for each panel and each phenotype.

Supplemental Figure S5

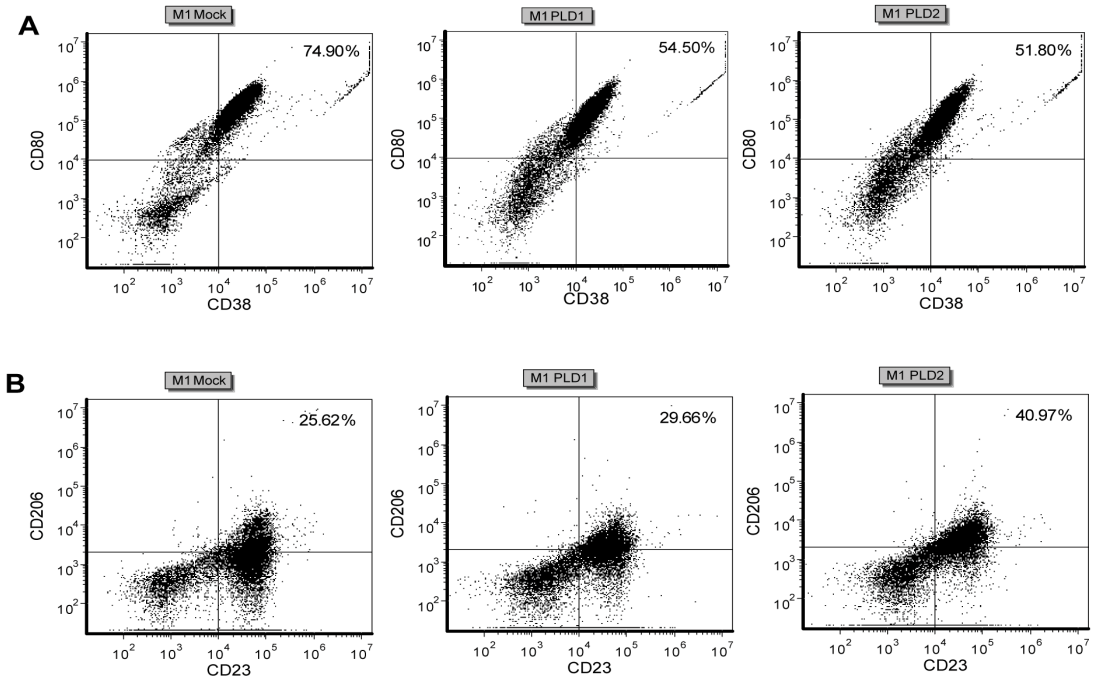

Figure S5. PLD ectopic expression causes macrophage polarization. See Main Figure 4D for plotting of this data.

Supplemental Figure S6

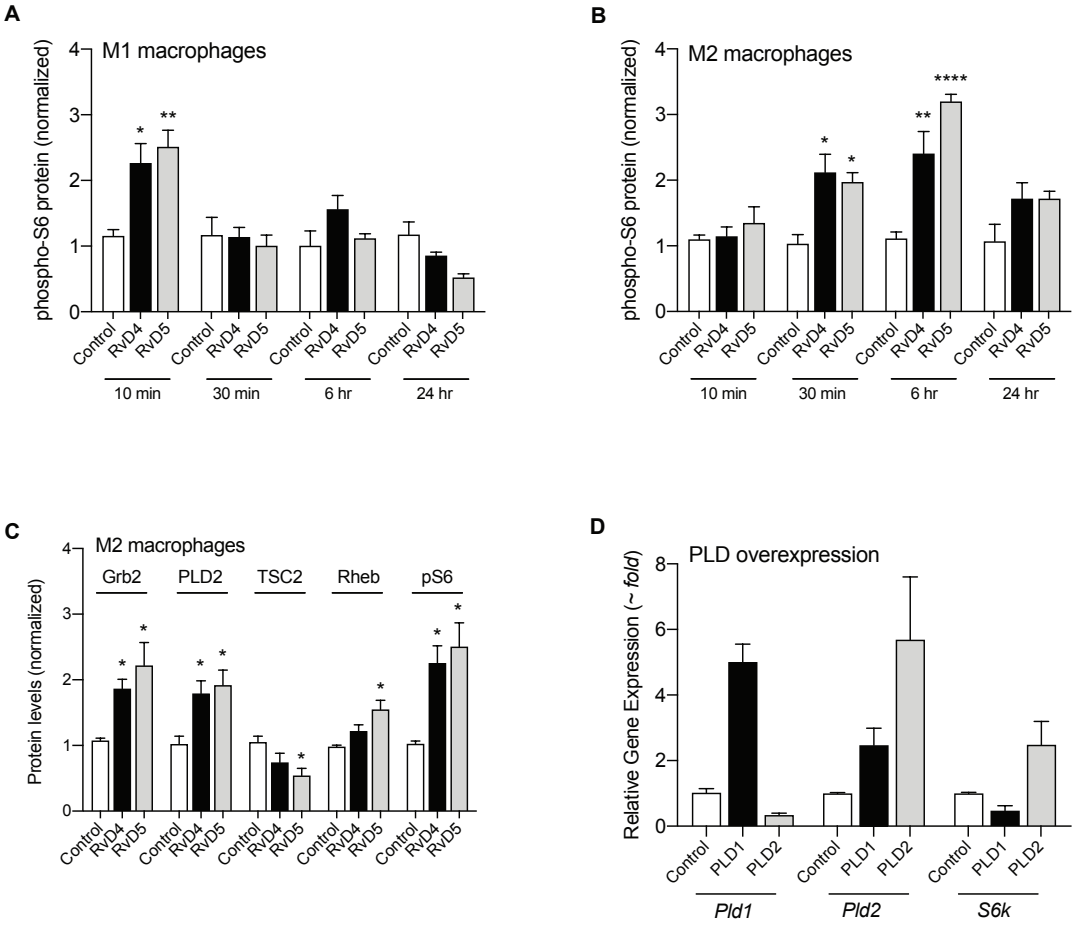

Figure S6. Densitometry of RvD5-PLD2 signaling in M2 macrophages. (A-B) Densitometric quantification of protein bands in Figure 6C showing levels of phospho-S6 protein in M1 and M2 macrophages (normalized to GAPDH) (n=3). (C) Densitometry quantification of protein bands in Figure 6F (n=4). (D) Gene expression levels of *Pld1, Pld2* and S6k in macrophages transfected with control, PLD1 or PLD2 plasmids (n=2). Data presented are means ± SEM; statistical significance (*$p < 0.05$, **$p < 0.01$, and ***$p < 0.001$) was evaluated with one-way ANOVA and Tukey's post hoc multiple comparisons.