

Expanded View Figures

Figure EV1. Prdx4 does not impact priming of inflammasome components or associated factors (relates to Fig 3).

A qRT-PCR analysis of *Nlrp3*, *Il1b*, *Il18*, *Asc*, *caspase-1*, *Nlrp1*, *Trxnip*, and *Nos2* relative to *Gapdh* mRNA in Prdx4 WT and KO BMDMs, primed for 6 h with LPS or left untreated.

B Western blot analysis of NLRP3, pro-caspase-1, ASC, pro-IL-1 β , Prdx4, and β -actin (loading control) in Prdx4 WT and KO BMDMs at 6 h after LPS stimulation.

C Western blot analysis of NLRP3, Prdx4, and β -actin (loading control) in Prdx4 WT and KO BMDMs at 6 h after LPS stimulation and CHX treatment for the time points indicated.

Data information: (A) Each dot represents a biological replicate; horizontal lines indicate mean. Vertical lines indicate SD (C). n.s. not significant (two-tailed *t*-test). Data are representative of one experiment with $n = 4$ mice per genotype with $n = 2$ technical replicates (A) or two (B, C) independent experiments with $n = 3$ mice per genotype.

Source data are available online for this figure.

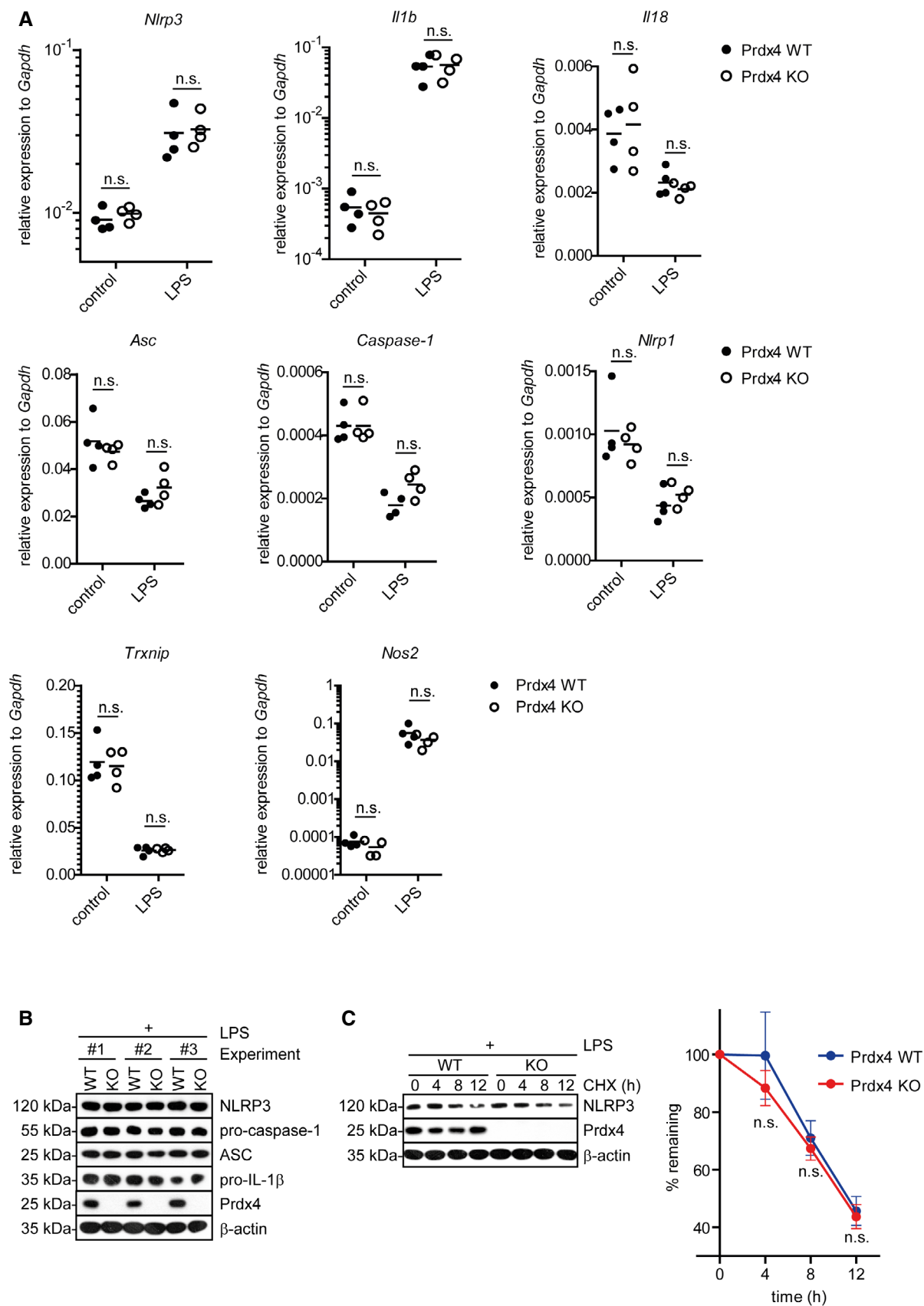


Figure EV1.

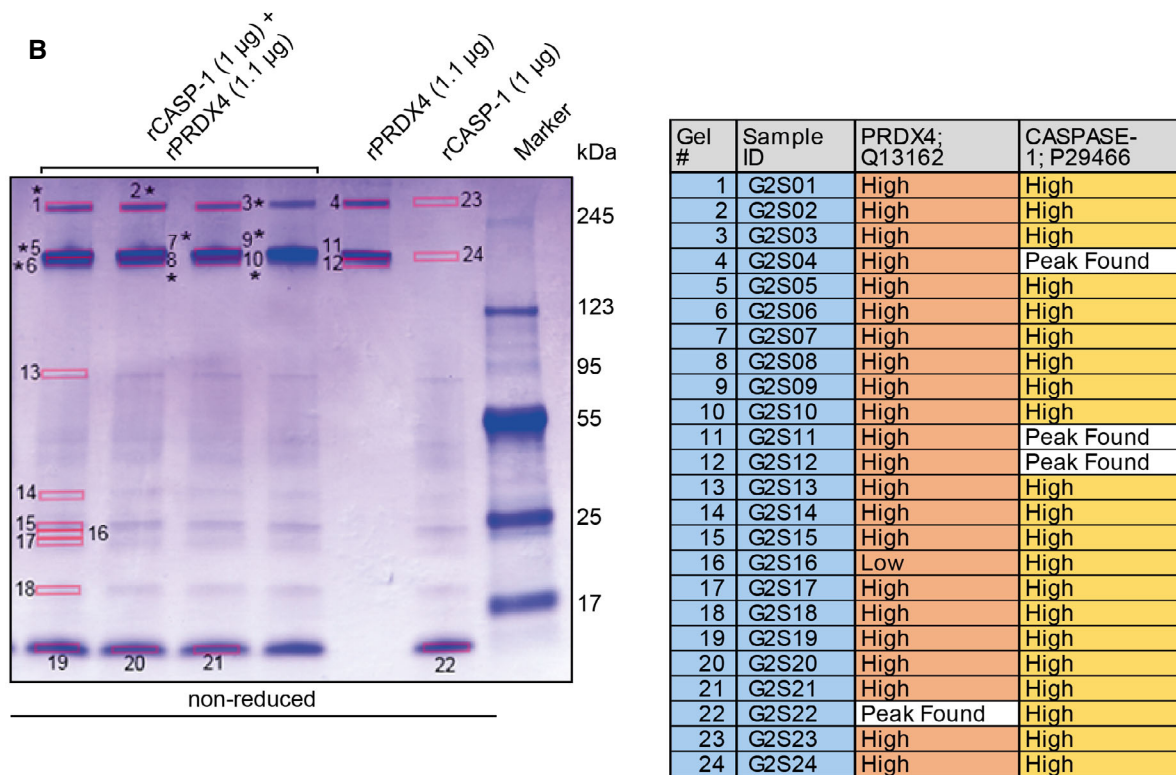
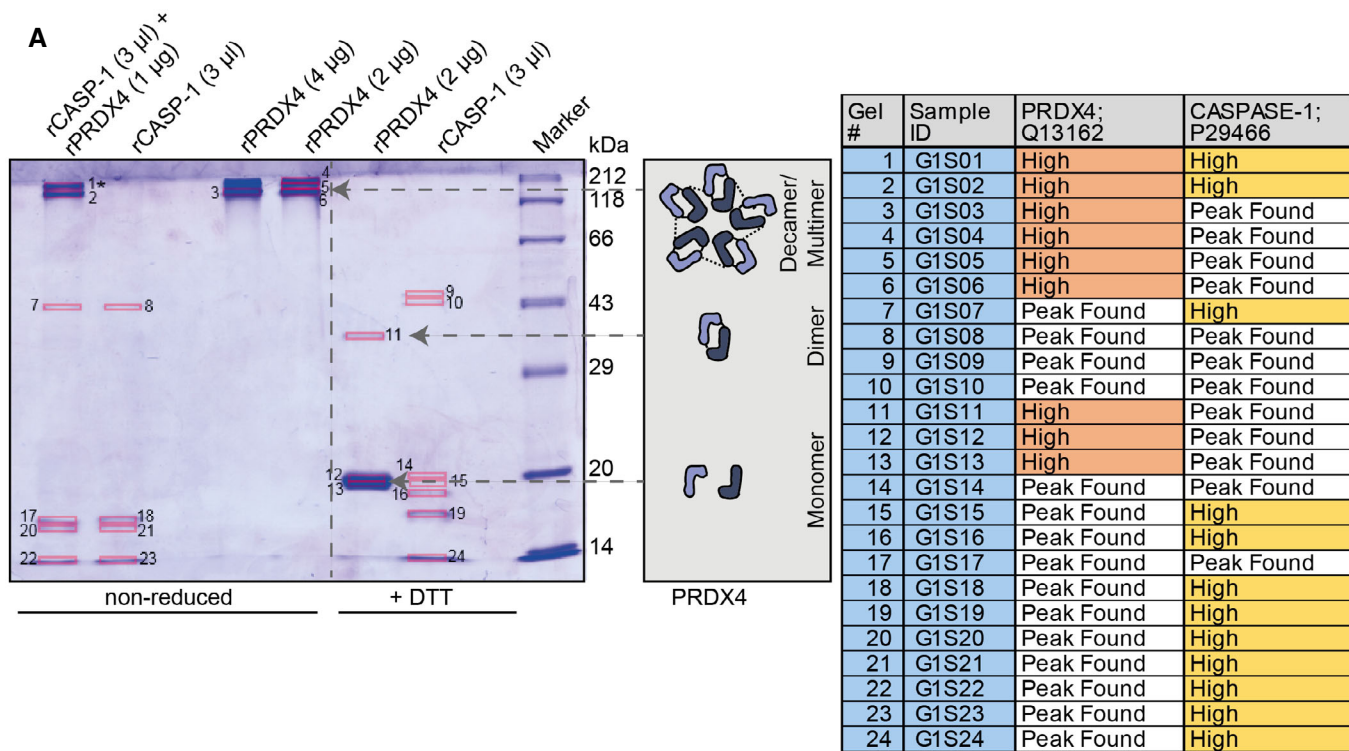


Figure EV2.

Figure EV2. Analysis of caspase-1 HMW complex by mass spectrometry (relates to Fig 4).

A, B SDS-PAGE and mass spectrometry analyses of rPRDX4, rCASP-1, or co-incubated rPRDX4+rCASP-1. (A) rPRDX4, rCASP-1, or co-incubated rPRDX4+rCASP-1 as well as rPRDX4 and rCASP-1 treated with DTT were loaded onto the gel, and SDS-PAGE was performed on a 4% polyacrylamide stacking gel followed by a 10% gel for separation. The gray box depicts a schematic illustration of Prdx4 decamers/multimers, dimers and monomers. Excised spots (1–24), analyzed by in-gel digestion and LC-ESI MS, are indicated (red rectangles). Gel spots were digested with pepsin, and peptide extracts were analyzed by LC-ESI MS with an Orbitrap Velos mass spectrometer. Both HCD and ETD spectra were acquired. Caspase-1 was identified by three peptides together with Prdx4 in-gel spot 1 (asterisk). (B) SDS-PAGE was performed on a 4–20% gradient gel. Excised spots (1–24), analyzed by in-gel digestion and LC-ESI MS, are indicated (red rectangles). Gels spots were digested with pepsin, and peptide extracts were analyzed on two LC-ESI MS platforms. HCD spectra were acquired with a QExactive MS, and both HCD and ETD spectra were acquired using an Orbitrap Velos MS instrument. Spots where at least two caspase-1 peptides could be detected on Prdx4 gel spots are indicated by asterisk.

Source data are available online for this figure.

Figure EV3. Characterization of EV isolates, obtained from inflammasome-activated BMDMs (relates to Fig 6).

A Dynamic light scattering (DLS) measurements from EVs, isolated from the supernatant of unstimulated or LPS+ATP-treated BMDMs.
B Transmission electron microscopy (TEM) and high magnification of EVs, isolated from the supernatant of unstimulated or LPS+ATP-treated BMDMs. Scale bar indicates 100 nm.
C Reducing SDS-PAGE (left panel) or non-reducing SDS-PAGE (right panel) followed of EV and whole-cell lysates followed by Western blot analysis using antibodies to Prdx4, inflammasome components (NLRP3, pro-caspase-1, pro-IL-1 β , and ASC), CD63 as a positive EV marker, Grp94, mitofilin, and cytochrome c as negative markers and β -actin as control.

Source data are available online for this figure.

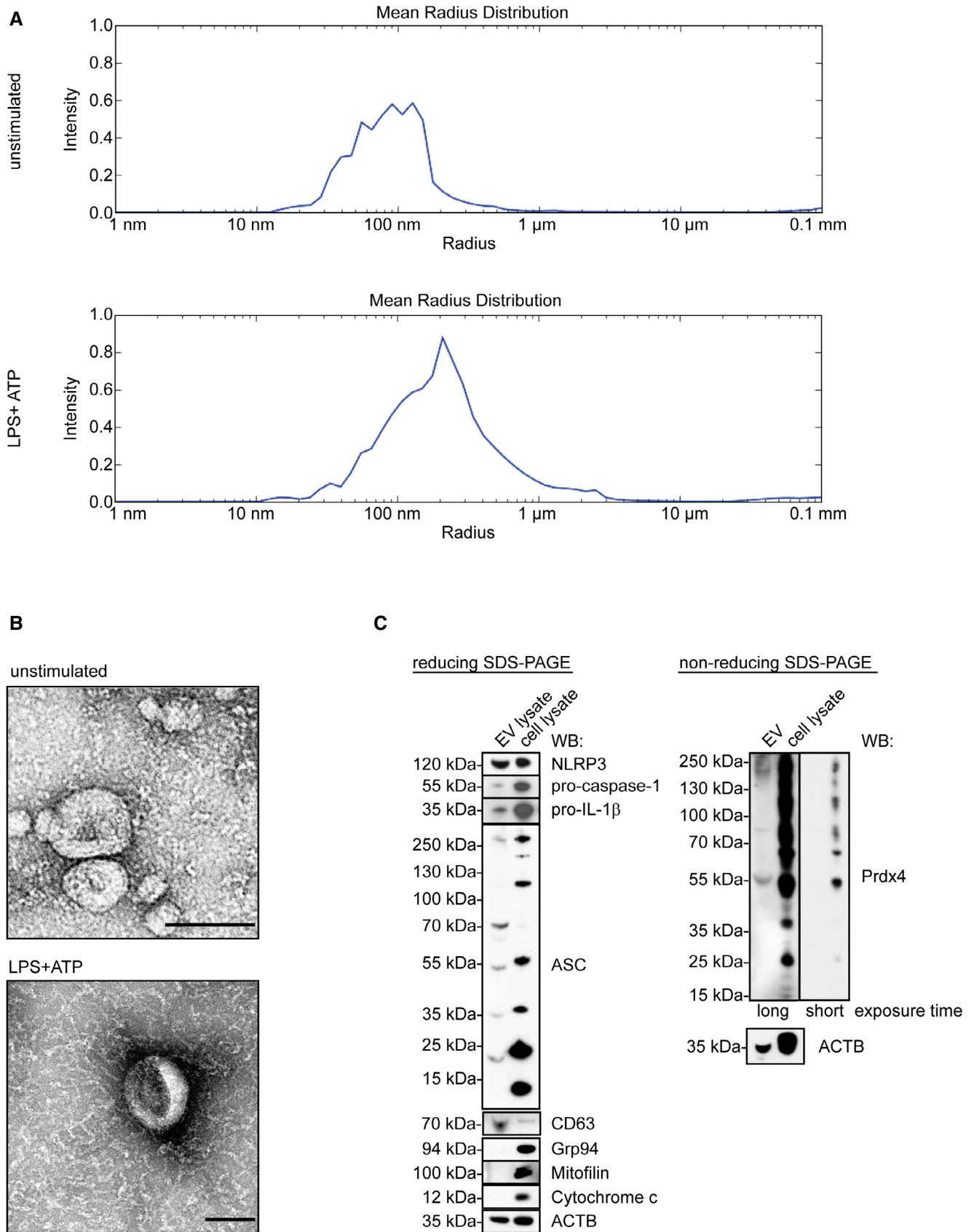


Figure EV3.

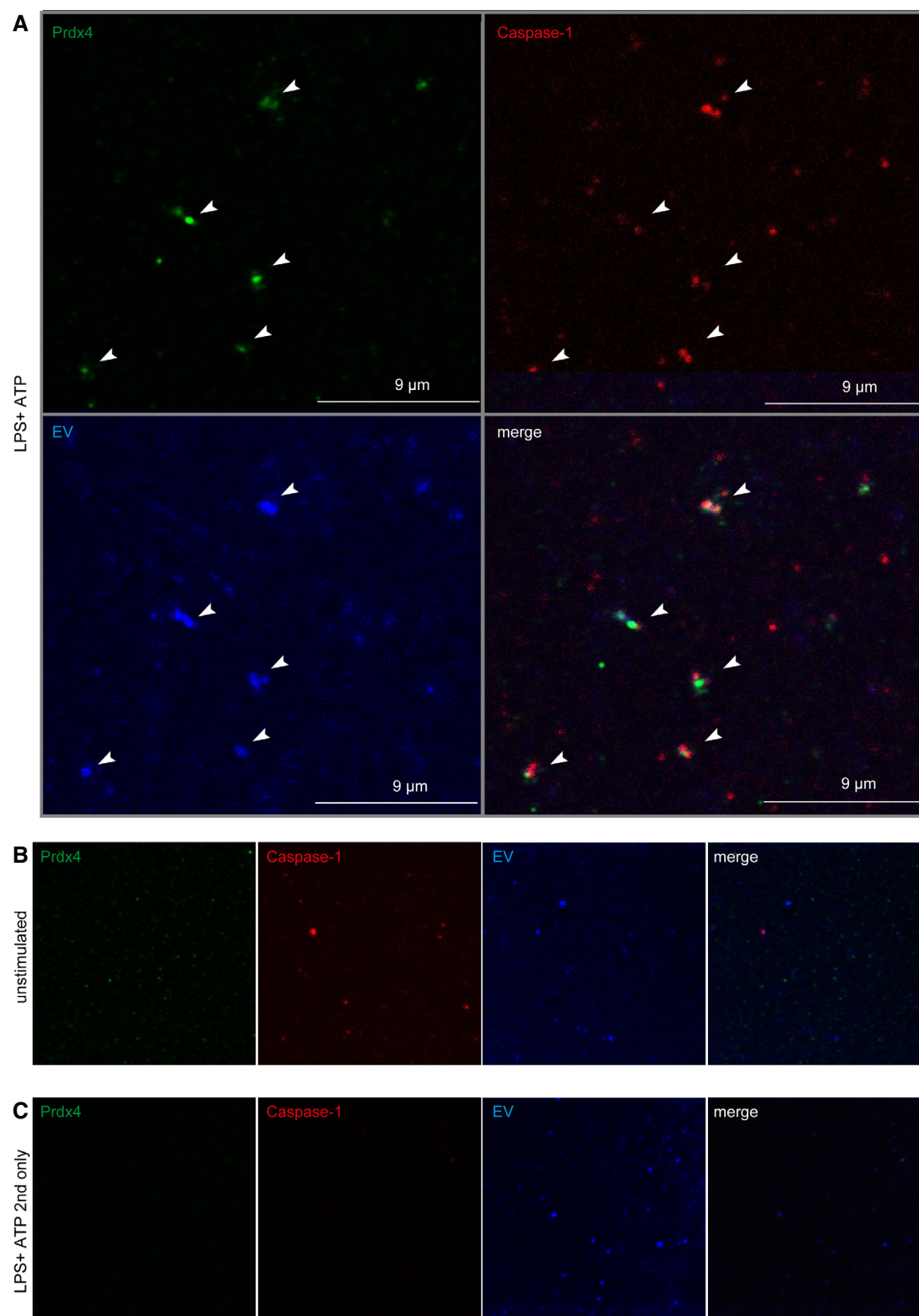


Figure EV4. Prdx4 and caspase-1 co-localize in EVs (relates to Fig 6).

A–C Fluorescence microscopy of EVs isolated from the supernatant of LPS+ATP-treated (A) or unstimulated (B) BMDMs. EV membrane was stained with CellVue Burgundy, EVs were then fixed and stained with antibodies to Prdx4 (green) or caspase-1 (red) (A, B) or second antibodies only as control (C).