

A ISOTYPE CTRL LPS TLR4 surface expression (ΔMFI) TLR4 endocytosis

B *Ifnb1* *Il1b* Relative gene expression (rel. to *Hprt*)

C DMSO DYNASORE *Il1b* *Ifnb1* *Il6* Relative gene expression

D *Ifnb1* *Il1b* Relative gene expression

E *Ifnb1* *Il1b* Relative gene expression

F DMSO FILIPIN DYNASORE PBS MβCD LPS (min): 0 30 60 120 p-TBK1 TBK1 α-tubulin p-TBK1 relative to α-tubulin [A.U.]

(A) Flow cytometric analysis of TLR4 surface expression in WT BMM treated for 60 min with DMSO or dynasore (80 μ M), followed by stimulation with LPS (100 EU/mL) or left unstimulated (CTRL) for 120 min. (B) qRT-PCR analysis of *Irfn1* and *Irfb* expression in WT BMM treated for 60 min with DMSO or dynasore (80 μ M), followed by stimulation with LPS (100 EU/mL) for 90 min. (C) qRT-PCR analysis of *Irfb*, *Irfn1* and *Irf6* mRNA expression in WT BMM treated for 60 min with DMSO or dynasore (80 μ M), followed by stimulation with Pam₂CSK₄ (10 ng/mL), poly I:C (10 μ g/mL), flagellin (0.5 μ g/mL) or CpG DNA (1 μ M), or left unstimulated (CTRL), for 90 min. (D, E) Impact of TAK-242 (1 μ M) or MRT67307 (5 μ M) on LPS-induced (D) *Irfn1* and (E) *Irfb* expression (90 min) in WT BMM treated with filipin (5 μ M), M β CD (10 mM), or DMSO as control. (F) Time-course of LPS-induced TBK1 phosphorylation in WT BMM treated with filipin, M β CD, dynasore or DMSO as solvent control. Data information: Flow cytometry histograms and immunoblot images depict 1 representative of $n = 3$ biological replicates generated in independent experiments. Bar plots are mean \pm SEM of $n = 3-4$ biological replicates generated in independent experiments indicated as data points. Unpaired two-tailed t test performed in (A-C); ordinary two-way ANOVA with Dunnett's multiple comparison test utilized in (D-F); * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$, **** $P < 0.0001$, ns = not significant. Source data are available online for this figure.

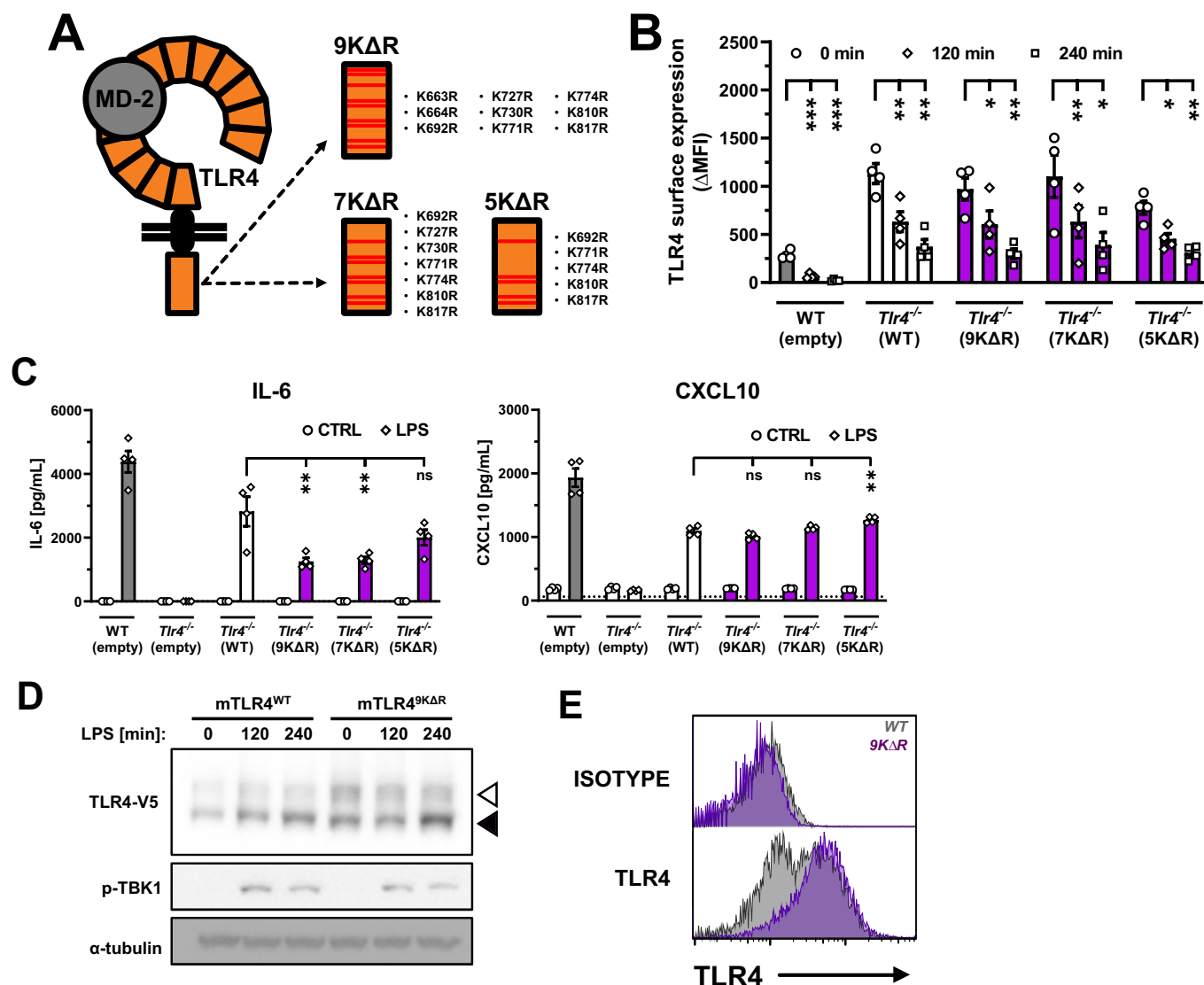


Figure EV2. Lysine residues in the TLR4 TIR domain were not required for LPS-induced TLR4 endocytosis.

(A–C) *Tlr4*^{-/-} BMMs retrovirally reconstituted with (A) mTLR4^{WT}, mTLR4^{9KΔR}, mTLR4^{7KΔR}, mTLR4^{5KΔR} or empty vector were stimulated with LPS (100 EU/mL); (B) TLR4 surface expression assessed at 120 and 240 min post-stimulation and (C) IL-6 and CXCL10 production assessed at 24 h post-stimulation. (D, E) RAW^{TLR4ko} cells were stably transfected with V5-tagged constructs of mTLR4^{WT} or mTLR4^{9KΔR}. (D) Total cellular expression of TLR4-V5 during LPS stimulation (100 EU/mL, 0, 120, 240 min) was assessed via immunoblot. Phospho-TBK1 served as control for cellular activation; α-tubulin served as loading control. Black arrow head indicates low glycosylated intracellular TLR4, white arrow head indicates highly-glycosylated cell surface-expressed TLR4. (E) TLR4 surface expression was assessed in resting cells via flow cytometry. Data information: Immunoblot images depict 1 representative of *n* = 3 biological replicates generated in independent experiments. Flow cytometry histogram represents cells post sorting. Bar plots are mean ± SEM of *n* = 3–4 biological replicates generated in independent experiments indicated as data points. RM two-way ANOVA with Dunnett's multiple comparisons test utilized in (B). Ordinary one-way ANOVA with Dunnett's multiple comparisons test utilized in (C). **P* < 0.05; ***P* < 0.01; ****P* < 0.001, *****P* < 0.0001, ns = not significant. Source data are available online for this figure.

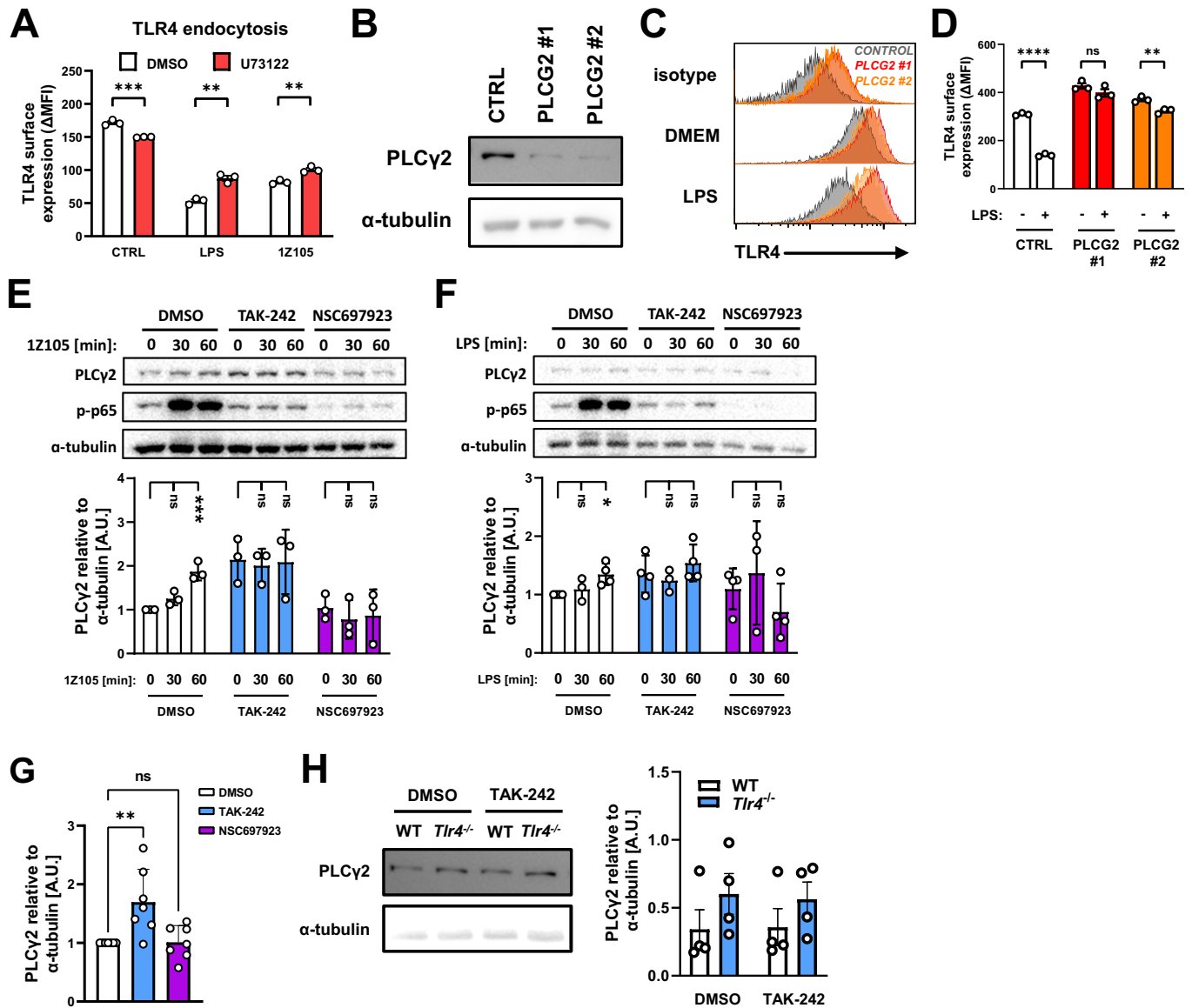


Figure EV3. PLCγ2 regulates TLR4 endocytosis.

(A) Impact of PLC inhibitor (U73122, 10 μM) on LPS- (100 EU/mL) and 1Z105-induced (10 μM) TLR4 endocytosis (120 min) in WT BMM. (B–D) CRISPR/Cas9-mediated knockdown of PLCγ2 expression in WT BMM (B) was verified by immunoblot analysis, and (C, D) shown to impair LPS-induced (100 EU/mL, 120 min) TLR4 endocytosis as assessed by flow cytometry. (E, F) Immunoblot analysis of the impact of TAK-242 (1 μM) or NSC694923 (10 μM) on total PLCγ2, phosphorylated NF-κB p65 and α-tubulin in WT BMM upon stimulation with (C) 1Z105 (10 μM) or (D) LPS (100 EU/mL) for the indicated times. (G) Comparison of PLCγ2 expression in unstimulated cells presented in (E, F). (H) Immunoblot analysis of PLCγ2 cellular expression in WT and *Tlr4*^{-/-} BMM treated with DMSO or TAK-242 (1 μM) for 120 min. Data information: Flow cytometry histograms and immunoblot images depict 1 representative of $n = 3$ –4 biological replicates generated in independent experiments. Bar plots are mean \pm SEM of $n = 3$ –7 biological replicates generated in independent experiments indicated as data points. Unpaired two-tailed t test utilized in (A, D). Ordinary one-way ANOVA with Dunnett's multiple comparisons test utilized in (E–G). * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$; **** $P < 0.0001$; ns = not significant. Source data are available online for this figure.