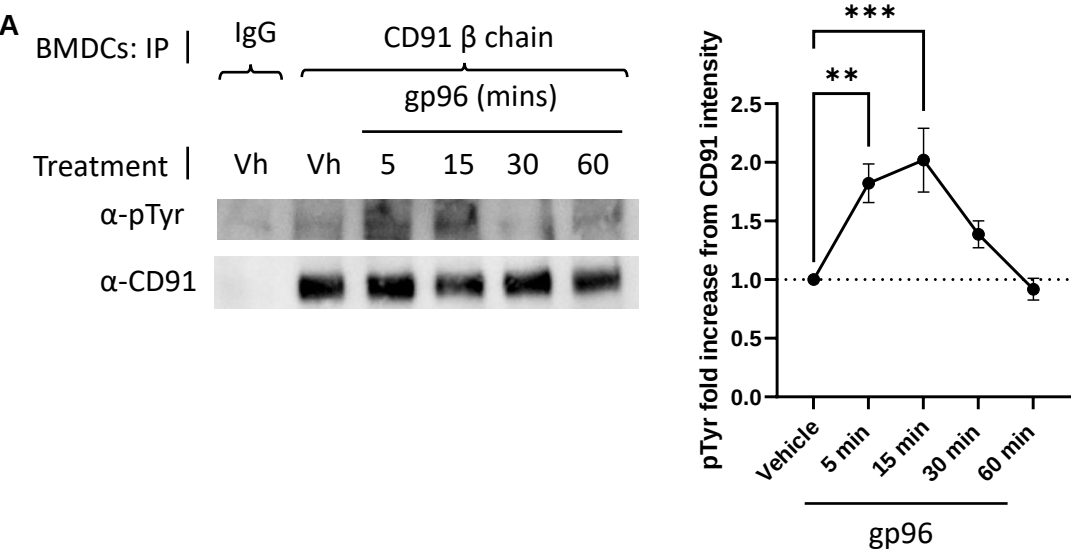
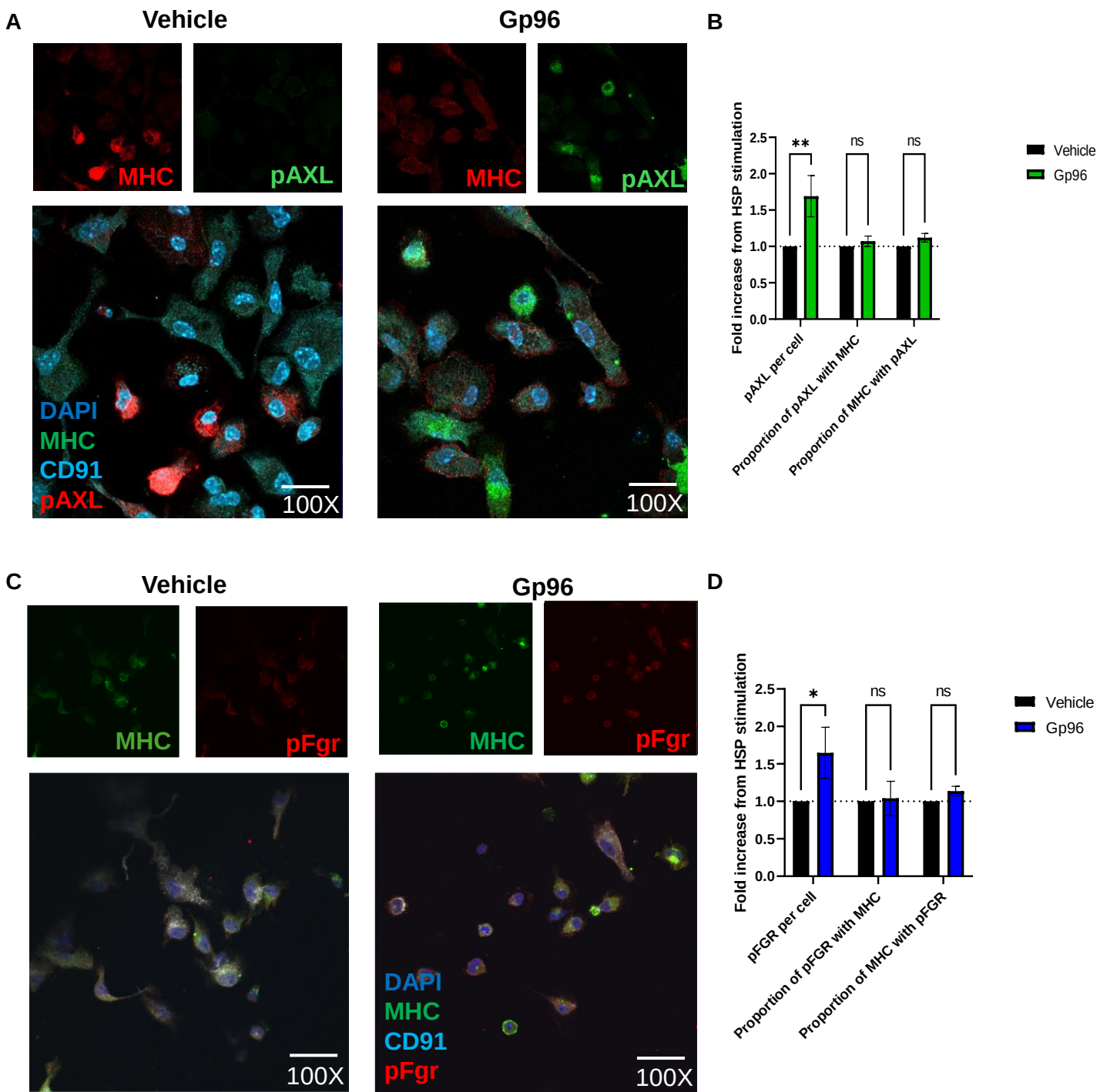
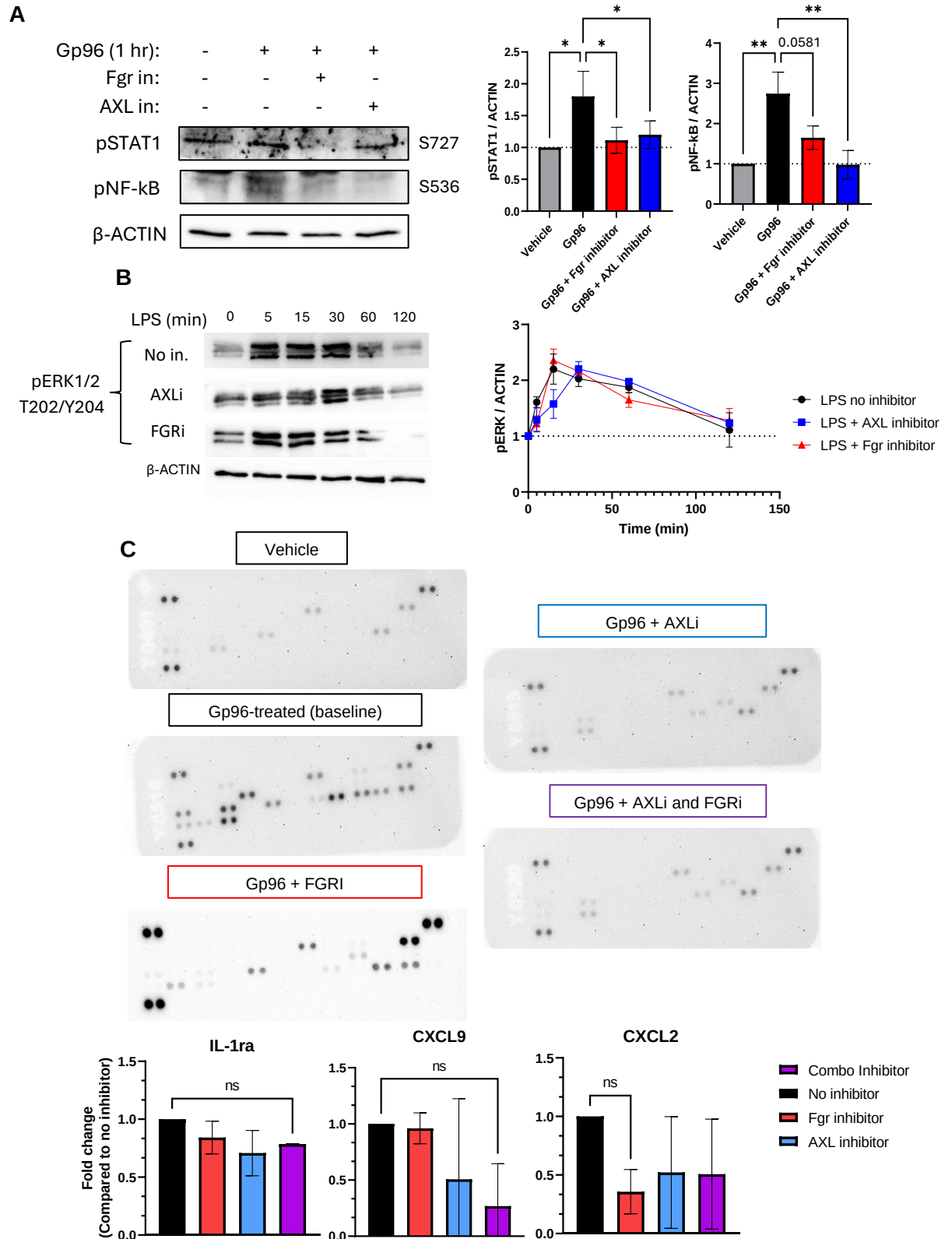


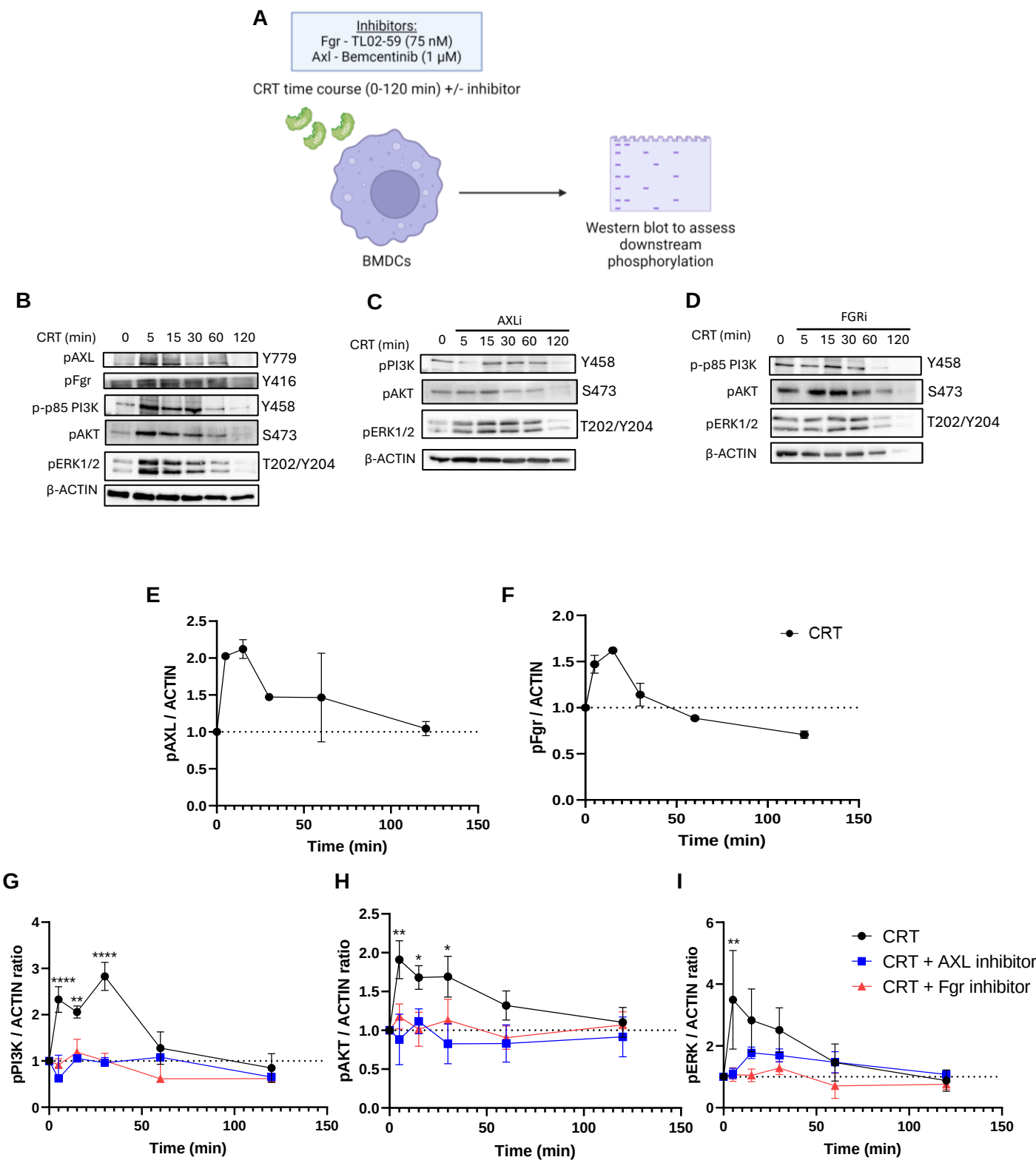
Supplemental Figure 1. (A) Western blot of immunoprecipitation of CD91 β chain following time course treatment with gp96. Immunoprecipitates were probed for pTyr and CD91 to verify pull down. Quantification of pTyr relative to total CD91 pulldown is shown on the left. (B) Western blot of reciprocal pulldown of AXL and CD91. CD91 and AXL were immunoprecipitated and probed for the other protein. Statistical analysis was performed in GraphPad Prism via two-way ANOVA. The significance of each sample is in comparison to gp96-vehicle. Three biological replicates were performed, error bars: SD. *p < .05; **p < .01; ***p < .001.



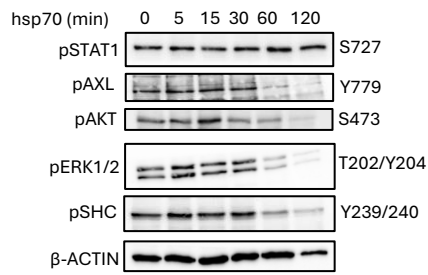
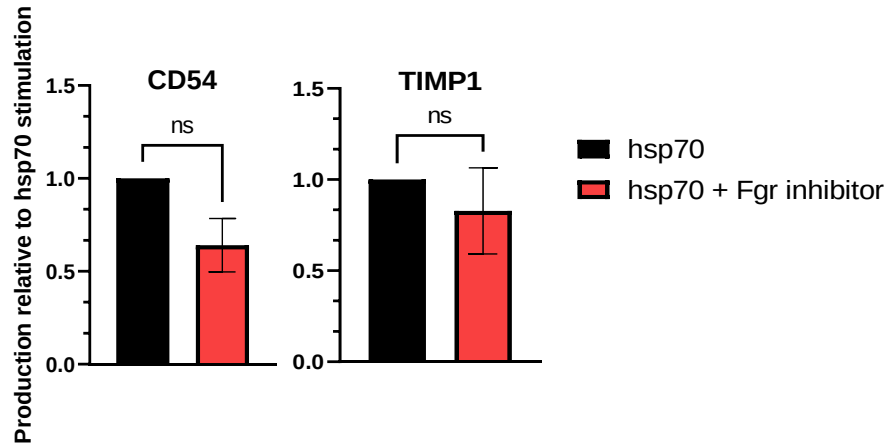
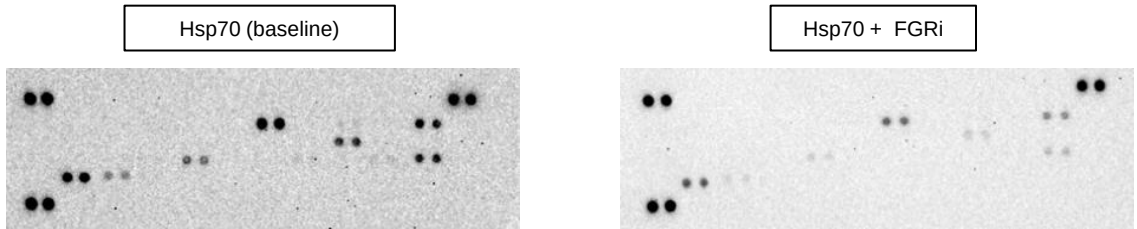
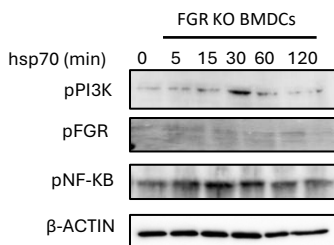
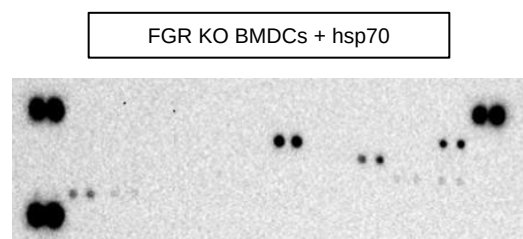
Supplemental Figure 2. (A,C) Representative images of vehicle-treated BMDCs and gp96-treated BMDCs were stained with antibodies for MHC and phosphorylated (A) AXL or (C) Fgr. Phalloidin and DAPI were used to visualize cytoskeleton and nuclei, respectively. (B,D) Quantification of pAXL and pFgr foci upon gp96 treatment. Colocalization proportion of pAXL and pFgr with MHC following foci gp96 treatment. Quantification was performed on NIS-Elements. Statistical analysis was performed in GraphPad Prism via one-way ANOVA. Three biological replicates were performed for all experiments, error bars: SD. * $p < .05$; ** $p < .01$.



Supplemental Figure 3. (A) Western blot of splenic DCs treated with gp96 for 1 hour in presence or absence of Fgr or AXL inhibitor. Phosphorylation of NF-kB and STAT1 was quantified relative to β -actin. (B) Western blot images of pERK1/2 in BMDCs treated with LPS over a time course of 2 hours in the presence or absence of Fgr or AXL inhibitor. Quantification of pERK1/2 relative to β -actin as a loading control. (C) Representative images of cytokine panels from supernatant of BMDCs treated with gp96 with/without inhibitors. Quantification of uninhibited cytokines, IL-1ra, CXCL9, and CXCL2, are shown. Statistical analysis was performed in GraphPad Prism via two-way ANOVA. Three biological replicates were performed, error bars: SD. * $p < .05$, ** $p < .01$.



Supplemental Figure 4. (A) BMDCs were treated with CRT over a time course of two hours in the presence or absence of AXL or Fgr inhibitor. Western blot showing phosphorylation of downstream signaling proteins for (B) CRT time course, (C) CRT with AXLi, (D) CRT with Fgr inhibitor. Graph showing quantification of phosphorylation for (E) AXL, (F) Fgr, (G) PI3K, (H) AKT, and (I) ERK1/2. Relative intensity of phosphorylation was quantified and normalized to β -actin as a loading control. Statistical analysis was performed in GraphPad Prism via two-way ANOVA. The significance of each sample is in comparison to vehicle. Three biological replicates were performed, error bars: SD. * $p < .05$; ** $p < .01$; *** $p < .001$; **** $p < .0001$.

A**B****C****D**

Supplemental Figure 5. (A) Western blot images of phosphorylation of STAT1, AXL, AKT, ERK1/2, and SHC in BMDCs treated with hsp70 over a time course of 2 hours. (B) Representative image of cytokine panel from supernatant of BMDCs treated with hsp70. Quantification of uninhibited cytokines, CD54 and TIMP1, are shown. (C) Western blot images of Fgr KO BMDCs treated with hsp70 over a time course of 2 hours. (D) Representative image of cytokine panel from supernatant of Fgr KO BMDCs treated with hsp70. Three biological replicates were performed, error bars: SD.