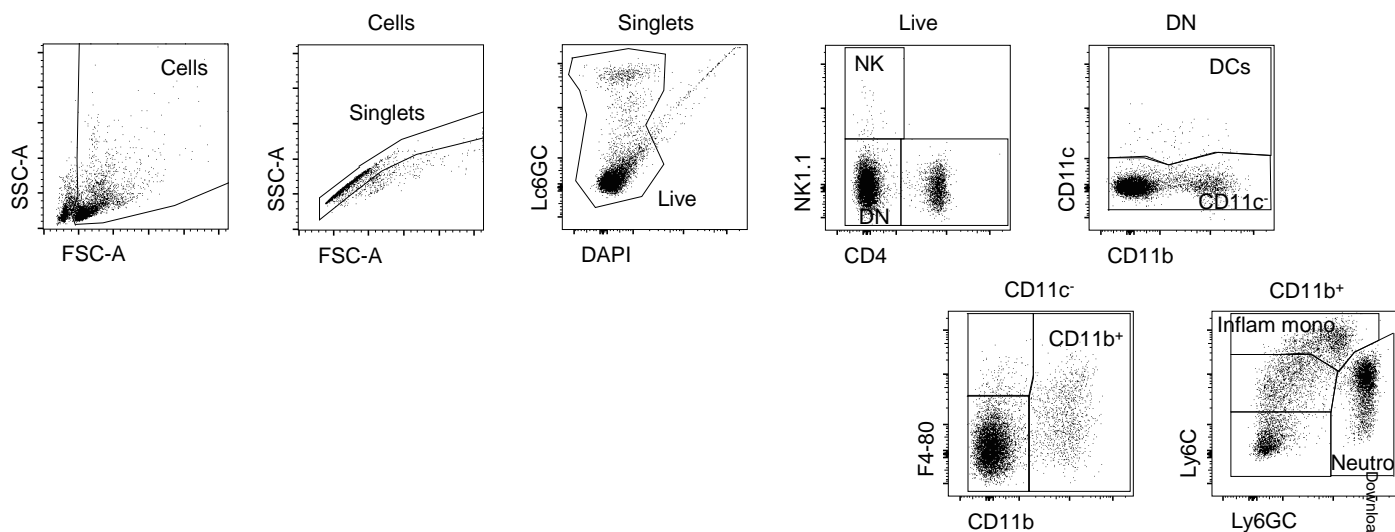
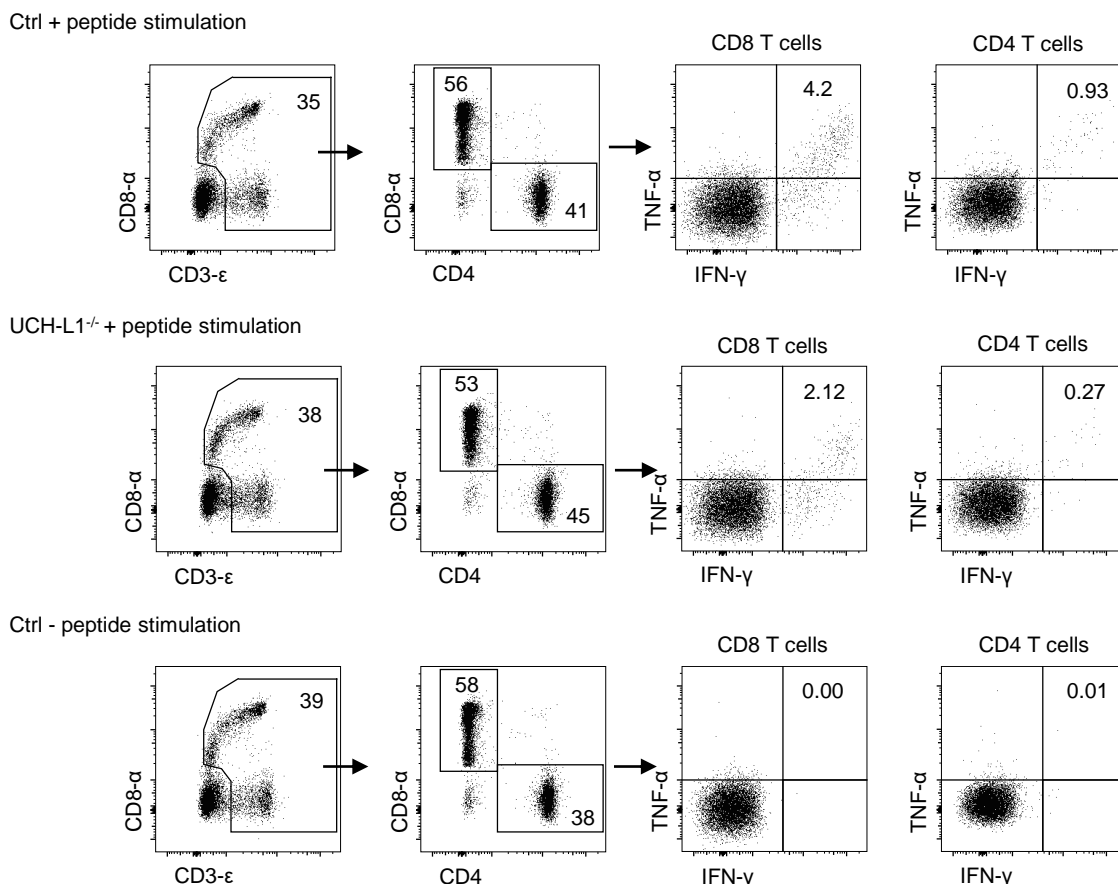


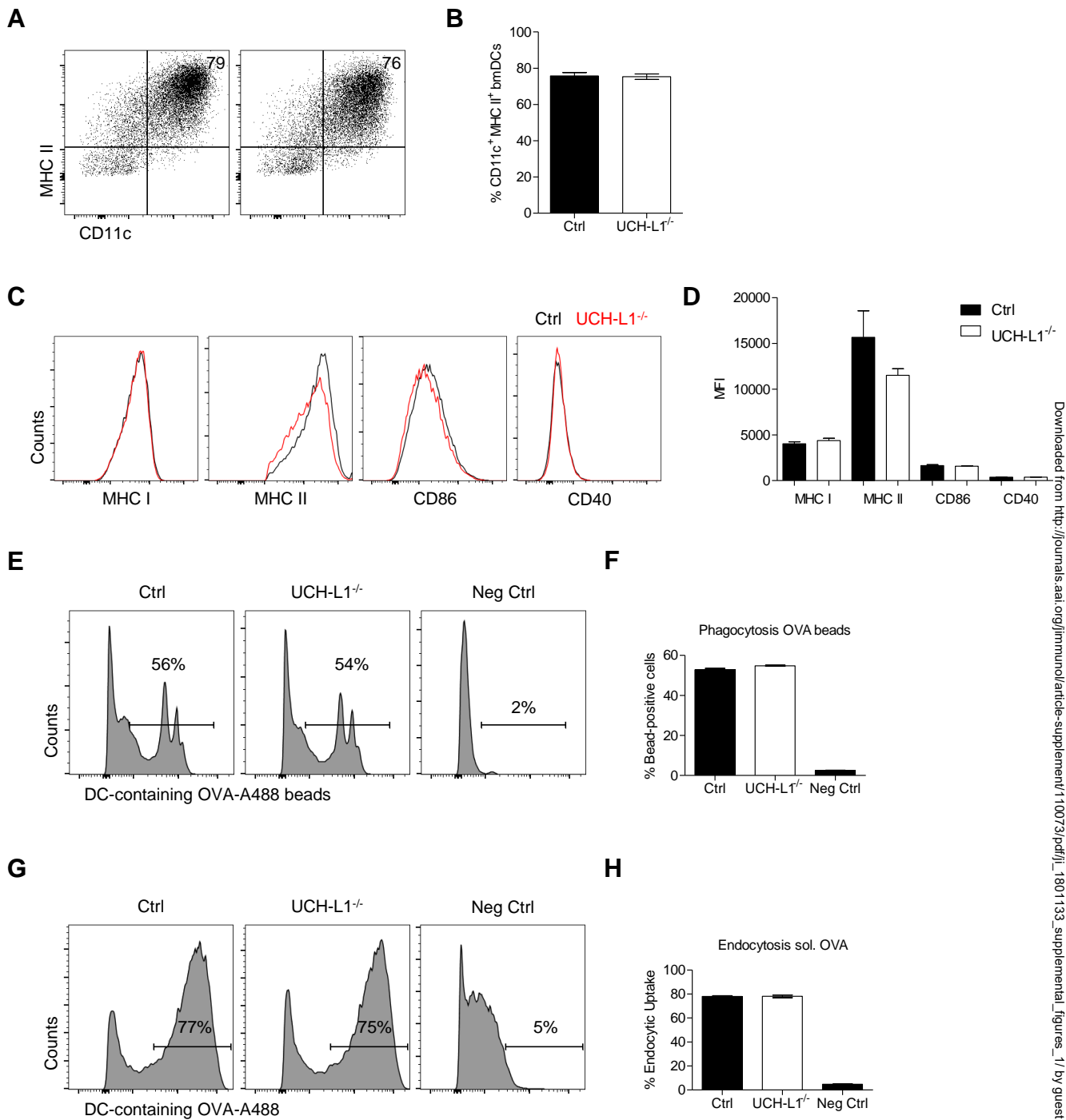
Supplemental figure 1: Immune cell population sorting from mouse spleen and human PBMCs for UCH-L1 mRNA expression analysis.

A: Mouse spleen cells are gated on forward scatter area (FSC-A)/ side scatter area (SSC-A) to gate cells, FSC-W (width) /FSC-H (height) to gate singlets, NIR⁻ to gate live cells, and FSC-A/CD45⁺ to gate haematopoietic cells. **B:** CD8⁺ and CD4⁺ T cells are gated from CD45⁺/CD3⁺ gates, while CD3⁻ cells are further gated with CD11c and MHC II to define DCs with gated CD8⁺ and CD8⁻ subsets. **C:** B cells are gated from CD45⁺/CD19⁺ gates. CD19⁻ cells are further gated to define CD3⁻/NK1.1⁺ NK cells, and CD3⁺/NK1.1⁺ NKT cells. CD3⁺ cells are further gated $\gamma\delta$ ⁺ to define $\gamma\delta$ T cells. **D:** Human PBMCs are gated on FSC-A/SSC-A to gate cells, FSC-W/FSC-H to gate singlets, CD45⁺/SSC-A to gate haematopoietic cells. T and B cells are gated from CD3⁺/CD20⁻ and CD3⁻/CD20⁺ respectively. Double negative (DN) cells are gated as HLA-DR⁺ cells and DCs and monocytes are further gated as CD14⁺/CD16⁻ and CD14⁺/CD16^{hi}, respectively. DC subsets are defined as CD123^{hi}/CD11c⁻ pDCs, CD123⁺/CD11c⁺ mDCs. mDCs are further defined as CD1c⁺/CD141^{inter} cDC2 subset, CD1c⁻/CD141^{hi} cDC1 subset, and CD1c⁻/CD141⁻ DN subset.

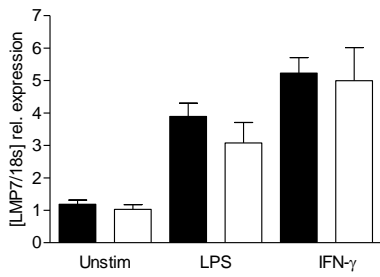
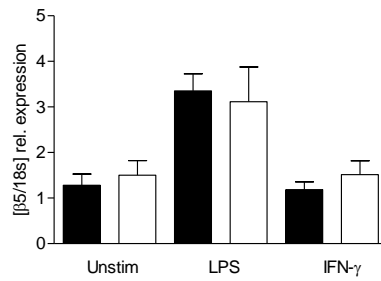
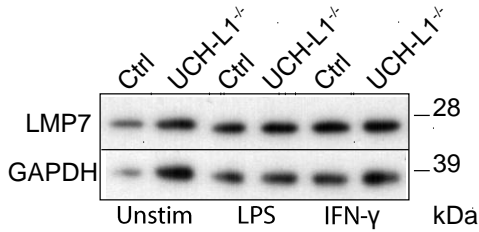
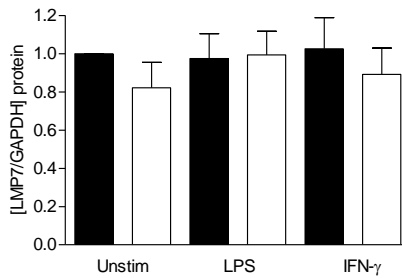
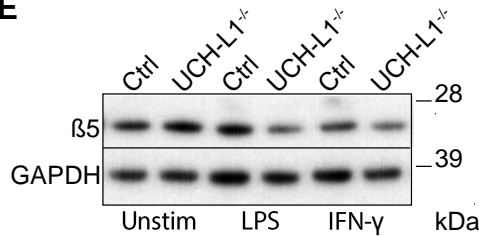
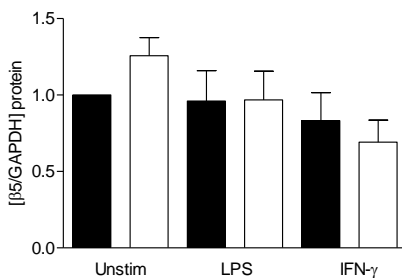
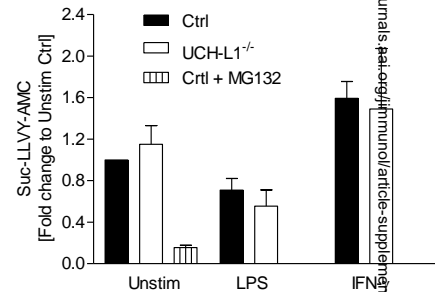
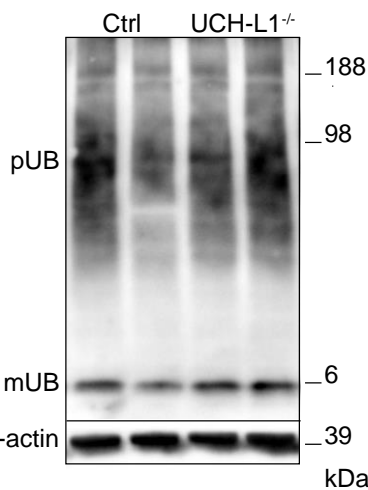
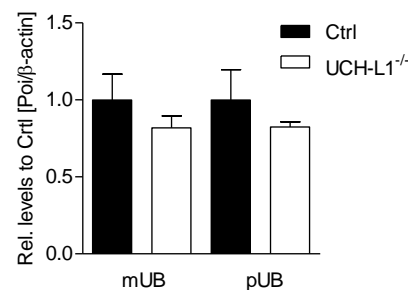
A**B**

Supplemental figure 2: Gating strategies to identify cell populations and intracellular cytokine staining in spleen post listeria infection. **A:** Sample data from control spleen following 3 day infection with LmEGD. Cells are gated on forward scatter area (FSC-A)/ side scatter area (SSC-A), FSC-A (area) /FSC-H (height) to gate singlets, and DAPI negative to identify live cells. CD4⁻, NK1.1⁺ cells are gated as NK cells. CD4⁻, NK1.1⁻ double negative (DN) cells are further gated as CD11c⁺, CD11b^{+/-} DCs. CD11b⁺ cells are further gated as Ly6GC^{hi}, Ly6C⁺ neutrophils and Ly6GC⁺, Ly6C^{hi} inflammatory monocytes. **B:** Intracellular staining of IFN- γ and TNF- α cytokine secreting CD8 and CD4 T cells on day 9 post listeria infection. Example dotplots of intracellular staining of splenic T cells from control (Ctrl) and UCH-L1-deficient (UCH-L1^{-/-}) littermate mice following stimulation with MHC I- and MHC II-restricted peptides (+ peptide stimulation) or unstimulated (Ctrl – peptide stimulation) are shown. T cells are gated on CD3- ϵ and CD8- α and further gated based on CD4 and CD8- α markers. The percentage IFN- γ and TNF- α double positive CD8- α and CD4 T cell subsets are indicated.

Downloaded from http://journals.aai.org/immunol/article-supplement/110073/pdf/11801133_supplemental_figures_1/ by guest on 05 August 2015



Supplemental figure 3: Phenotype of control and UCH-L1-deficient bmDCs. **A:** Surface expression of CD11c and MHC II on bmDCs from control (Ctrl) and UCH-L1-deficient (UCH-L1^{-/-}) littermates **B:** Quantification of frequency of CD11c⁺MHCII⁺ DCs, mean +/- SEM, n= 10. **C:** Surface staining of MHC I, MHC II and co stimulatory markers on naïve bmDCs. **D:** Mean fluorescence intensity (MFI) of surface staining is quantified, mean +/- SEM, n=3 animal bmDC cultures per group. **E:** Phagocytic uptake of fluorescent OVA coated 3 µM beads is measured in control (Ctrl) and UCH-L1-deficient (UCH-L1^{-/-}) littermate bmDCs by flow cytometry following a 5 hour incubation with OVA-A488 adsorbed beads at 37°C. Cells incubated with OVA-A488 adsorbed beads at 4°C serve as negative controls. Plots are representative of similar results obtained in 2 separate experiments **F:** Quantification of frequencies of uptake, mean +/- SEM, n= 2. **G:** Receptor-mediated endocytosis is measured in control and UCH-L1-deficient littermate bmDCs by flow cytometry following 20 min incubation with fluorescent soluble OVA-A488 at 37°C. Cells incubated with OVA-A488 at 4°C serve as negative controls. Plots are representative of similar results obtained in 2 separate experiments. **H:** Quantification of frequencies of uptake, mean +/- SEM, n= 3 animal bmDC cultures per group.

A**B****C****D****E****F****G****H****I**

Supplemental figure 4: Ubiquitin Proteasome System is equivalent in control and UCH-L1-deficient littermate bmDCs. **A, B:** qPCR for LMP7 and $\beta 5$ subunit transcripts in unstimulated (Unstim), LPS or IFN- γ 24h stimulated control (Ctrl) and UCH-L1-deficient (UCH-L1^{-/-}) bmDCs, n=6-9 bmDC cultures per group. **C:** Western blot of LMP7 in unstimulated, LPS or IFN- γ 24h stimulated control and UCH-L1-deficient bmDCs. Blot is representative of similar data obtained in 3 separate experiments **D:** Quantification of LMP7 protein with GAPDH as housekeeper control. Values are calculated relative to unstimulated controls +/- SEM, n= 4 bmDC cultures per group. **E, F:** As in C, D for $\beta 5$. **G:** Chymotrypsin-like activity as measured by cleavage of the fluorogenic substrate Suc-LLVY-AMC in unstimulated, LPS or IFN- γ 24h stimulated control and UCH-L1^{-/-} bmDCs. Control plus the proteasome inhibitor MG132 (Ctrl + MG132) serves as negative control for the assay. Values are calculated relative to unstimulated controls +/- SEM, n= 4 animal bmDC cultures per group. **H:** Western blot of polyubiquitin (pUb) and monoubiquitin (mUb) levels in control and UCH-L1-deficient littermate bmDCs. Blot is representative of similar data obtained in 2 separate experiments **I:** Quantification of pUb or mUb protein of interest (Poi) with β -actin as housekeeper control. Values are calculated relative to unstimulated controls +/- SEM, n= 4 animal bmDC cultures per group.