

Supplementary Materials for Wang Q. et al.

Supplementary Figure Legends

supplemental Figure 1. mEB8-ER cells were induced to differentiate in the presence of G-CSF (2 ng/mL), and the mRNA levels of NLRP12 (A), XDH (B), Slfn4 (C), Slc40a1 (D), G0S2 (E), Smarcd1 (F), VPS33b (G) at various time intervals were detected using q-PCR. Three separate experiments were conducted, and quantification of 3 replicates of a typical experiment. Each bar represents the mean \pm SEM (error bars).

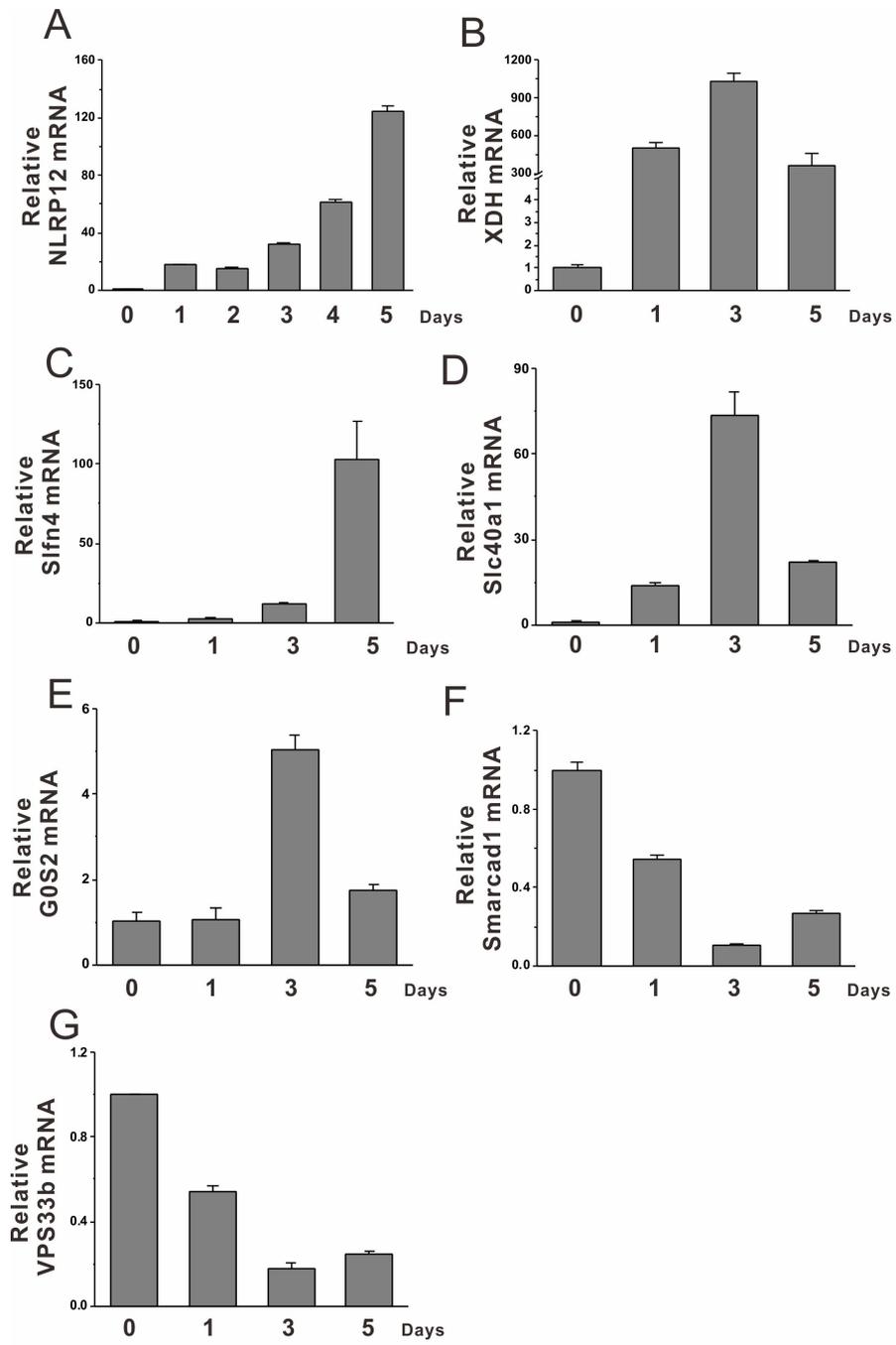
supplemental Figure 2. Two shRNAs targeting NLRP12 were introduced into the mEB8 cells by Gag-pol/VSVG retrovirus, and the cells were induced to differentiate in the presence of G-CSF (2 ng/mL). The mRNA level of NLRP12 (A), CD11b (B) and GR-1 (C) were analyzed using q-PCR. **Percent of CD11b⁺ and GR-1⁺ cells was tested by flow cytometry (D).** For NLRP12 overexpressing, LZRS-GFP was introduced into the mEB8 cells by Gag-pol/VSVG retrovirus. The cells were then induced to differentiate in the presence of G-CSF (2 ng/mL). The mRNA level of NLRP12 was analyzed using q-PCR (E). Three separate experiments were conducted, and quantification of 3 replicates of a typical experiment. Each bar represents the mean \pm SEM (error bars). All values were normalized to the level (=1) in cells of control group. **p < 0.01 and ***p < 0.001.

supplemental Figure 3. mEB8-ER cells with or without NLRP12 depletion were stimulated with G-CSF (2 ng/mL) for the times indicated. The mRNA levels of NIK (A) and ERK (B) were measured by q-PCR. The protein degradation ratio of ERK1/2 in mEB8-ER cells with or without NLRP12 depletion combination with CHX (1 μ g/mL) treatment (C). Three separate experiments were conducted, and quantification of 3 replicates of a typical experiment. Each bar represents the mean \pm SEM (error bars).

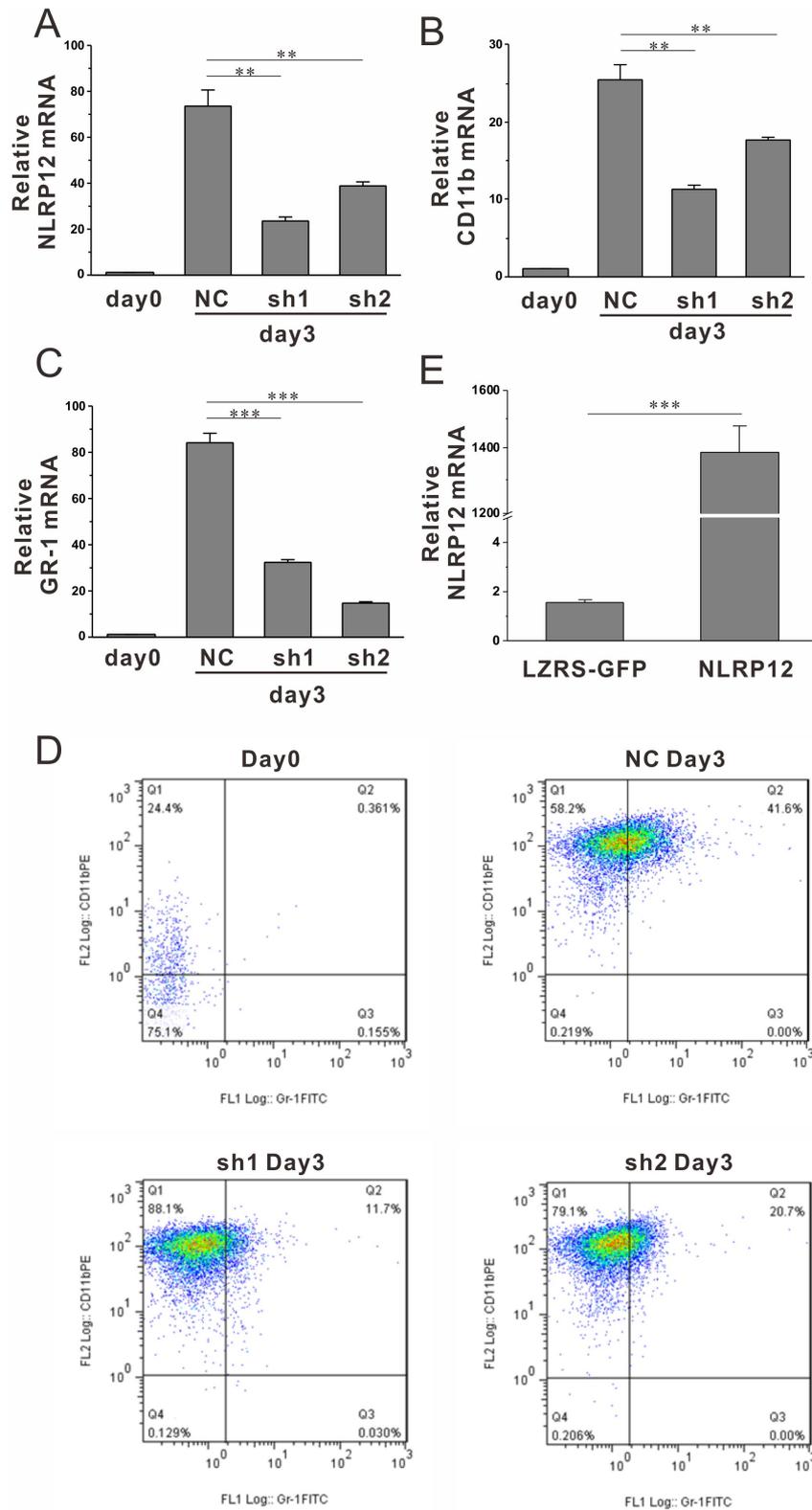
supplemental Figure 4. mEB8-ER cells with or without NLRP12 depletion were induced to differentiate in the presence of G-CSF (2 ng/mL, 3 days). The expression of C/EBP α (A), PU.1 (A) and G-CSFR (B) in each groups were measured by q-PCR. mEB8-ER cells with or without NLRP12 depletion were treated with TNF α (10 ng/mL) (C) or U0126 (10 μ M) (D) and then induced to differentiate in the presence of G-CSF (2 ng/mL). The mRNA levels of G-CSFR were measured by q-PCR. Three separate experiments were conducted, and quantification of 3 replicates of a typical experiment. Each bar represents the mean \pm SEM (error bars). All values were normalized to the level (=1) in cells of control group. * p < 0.05, ** p < 0.01 and *** p < 0.001.

Supplementary Figures

supplemental Figure 1.

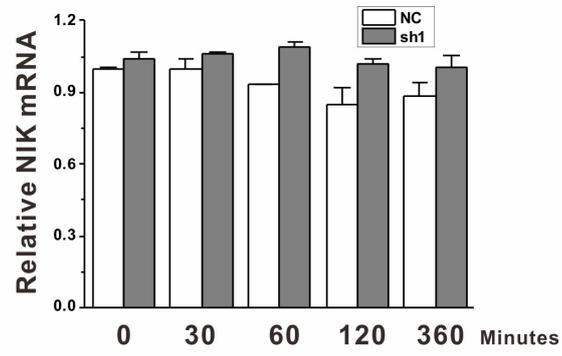


Supplemental Figure 2.

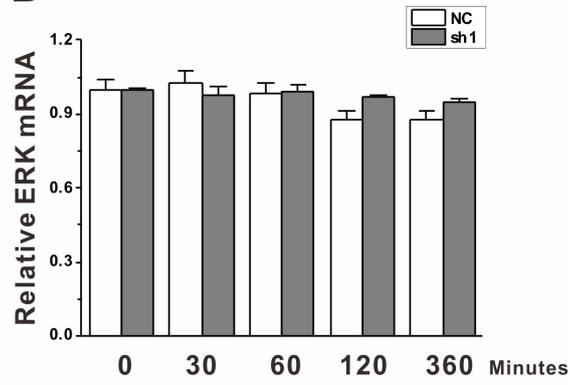


Supplemental Figure 3.

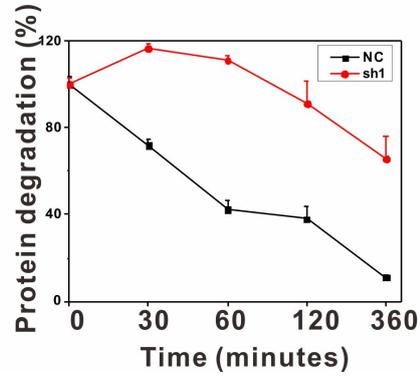
A



B



C



Supplemental Figure 4.

