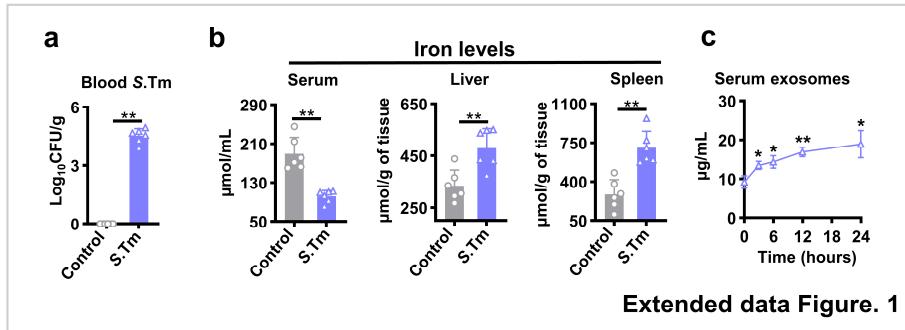


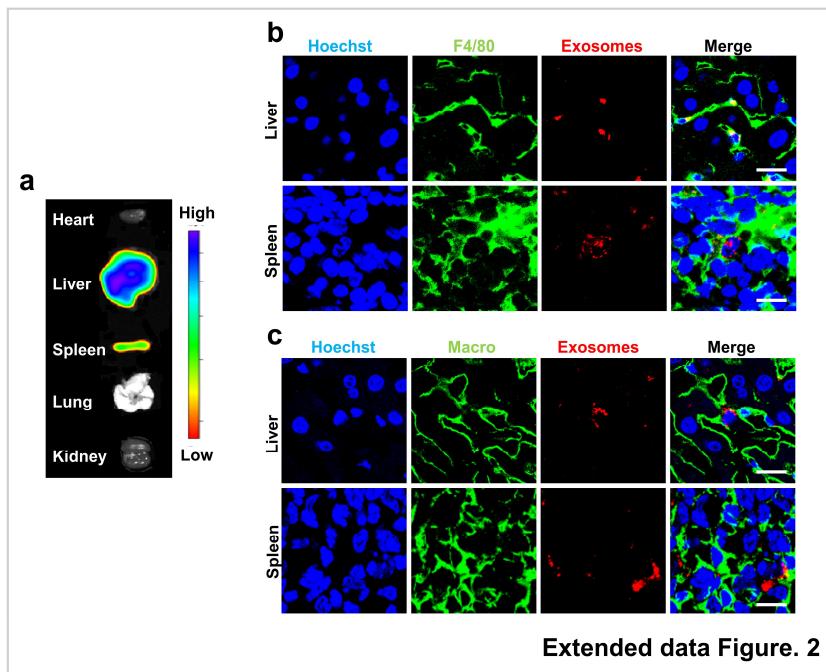
Extended Data



Extended data Figure. 1

Extended Data Fig. 1 The establishment and characterization of S.Tm-infected mice.

(a-c) The C57BL/6J mice were intraperitoneally administrated with *S.Tm*, and blood and tissues samples were collected for further analysis. **a**, The viable counts of *S.Tm* in the blood at 24h after infection. n = 6 mice. **b**, Serum (left), hepatic (middle), and splenic (right) iron levels in mice at 24h after infection. n = 6 mice. **c**, The concentration of exosomes in serum within 24 hours after infection. n = 3 mice per time point. For **a-c**, data are presented as the mean ± s.d. For **a-c**, statistical significance was assessed by unpaired two-tailed Student's t test. *p < 0.05, **p < 0.01.

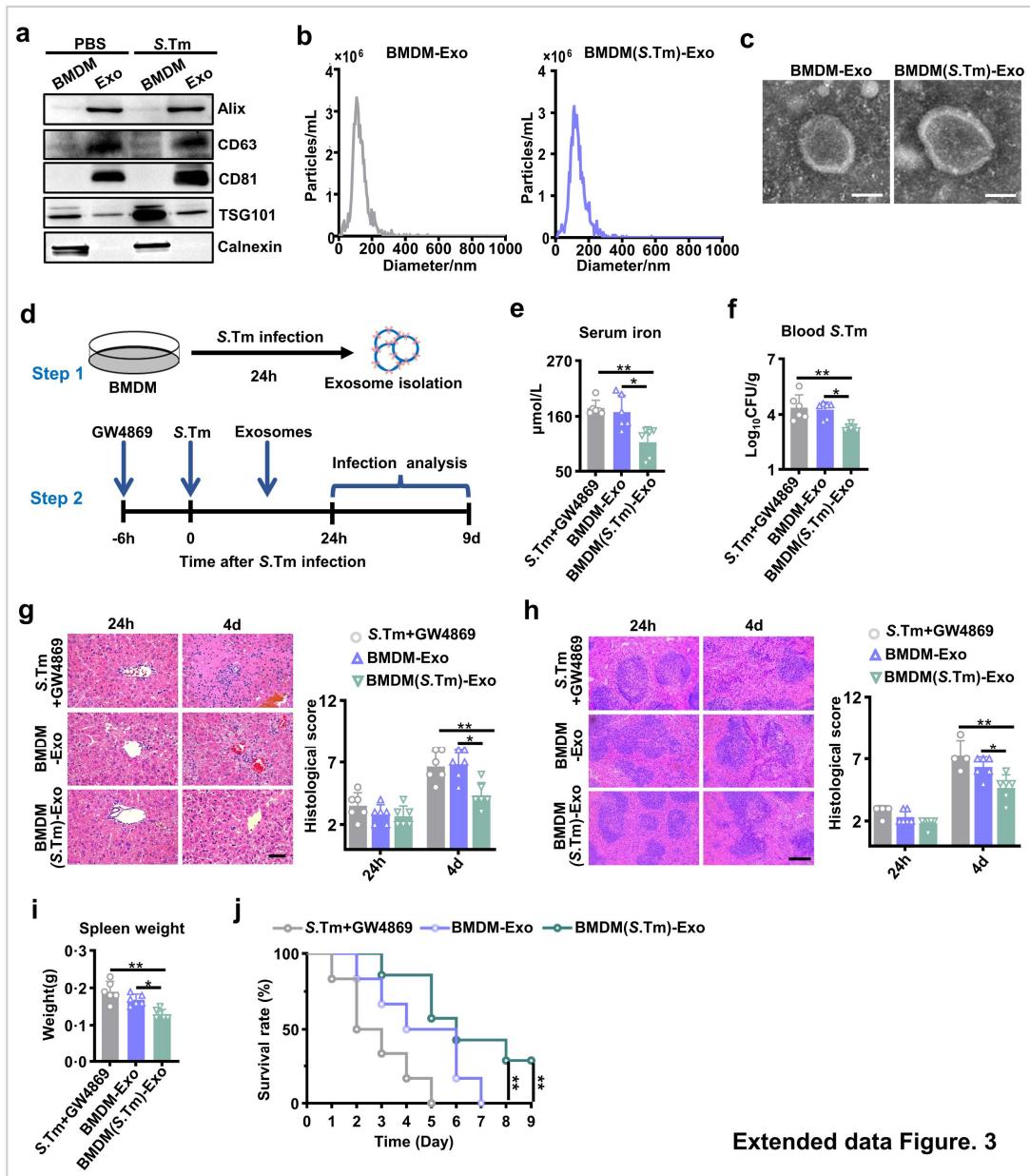


Extended data Figure. 2

Extended Data Fig. 2 Serum exosomes were captured in liver and spleen *in vivo*.

a, *Ex vivo* fluorescence images of various organs in mice systemically injected with DiR-labeled serum exosomes. n = 3 mice. **b, c**, Confocal microscopy images showing the uptake of PKH26-labelled exosomes (red) by F4/80⁺ cells (green) (**b**) or Macro⁺ cells (green) (**c**) in liver or spleen.

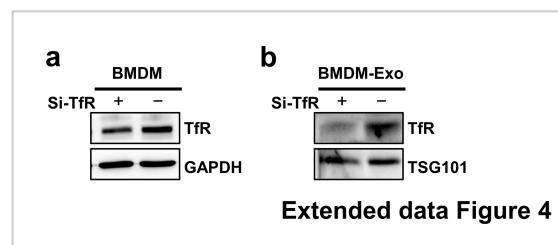
Scale bar, 10 μ m. n = 3 biologically independent samples.



Extended Data Fig. 3 Supplementation with exosomes derived from BMDM decreases infection severity in exosome-deficiency mice.

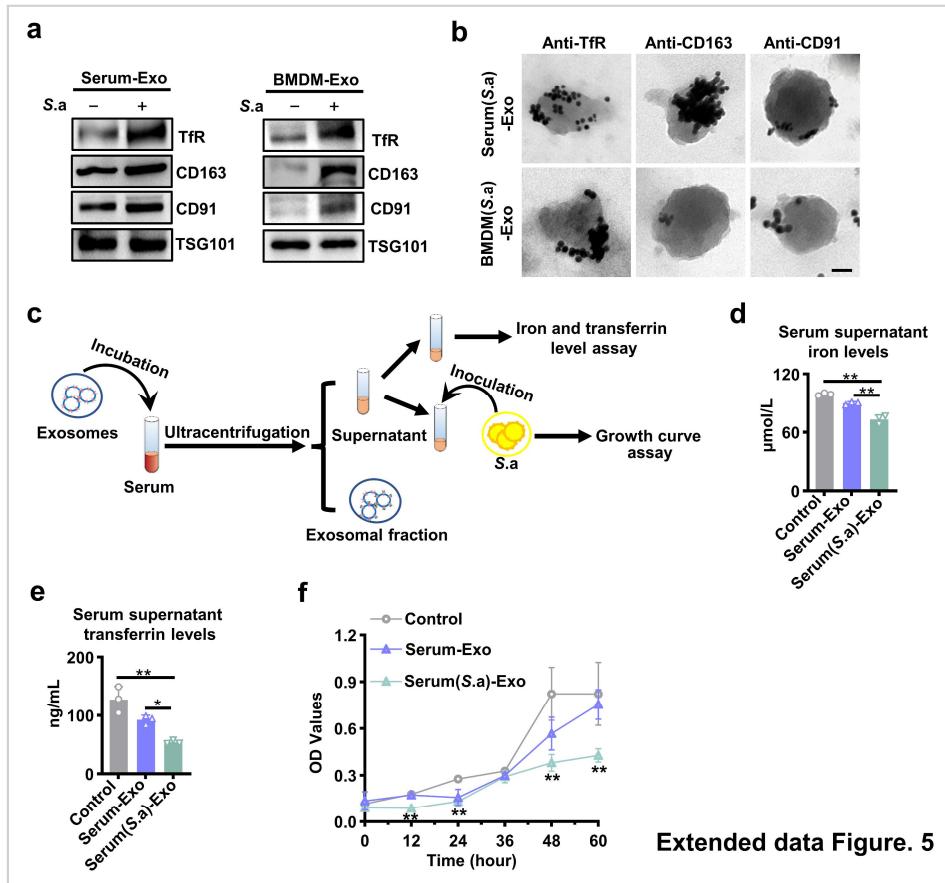
(a-c), BMDM were infected with S.Tm for 24 hours at an MOI of 10. Exosomes were isolated from the uninfected BMDM (BMDM-Exo group) or S.Tm-infected BMDM [BMDM(S.Tm)-Exo group] and characterized. **a**, Western blot analysis of the exosome markers Alix, CD81, CD63 and TSG101 and the negative mitochondrial markers calnexin. **b**, NTA analysis of the concentration and size distribution of exosomes. **c**, TEM images of exosomes, scale bar, 50 nm. **d**, Schematic diagram of the experimental procedure. Exosomes were isolated from uninfected BMDM or S.Tm-infected BMDM (Step 1). To investigate the role of host exosomes in iron metabolism and infection

outcomes, GW4869-pretreated *S.Tm*-infected mice were intravenously injected with exosomes derived from uninfected BMDM (BMDM-Exo group) or *S.Tm*-infected BMDM (BMDM (*S.Tm*)-Exo group), and the mice were euthanized after 24 hours for further analysis (Step 2). **e**, The iron levels in serum. n = 6 mice. **f**, Viable count of *S.Tm* in blood. n = 6 mice. **g, h**, Representative H&E staining of the liver (**g**) and spleen (**h**) at 24 hours or day 4 after *S.Tm* infection and quantitative analysis of histological scores. scale bar, 50 μ m (**g**) and 250 μ m (**h**). n = 6 mice. **i**, Quantitative analysis of the spleen weights at day 4 after infection. n = 6 mice. **j**, Survival rate of mice. n = 6 mice. For **e-i**, data are presented as the mean \pm s.d. For **f, g-i**, statistical significance was assessed by one-way ANOVA with Tukey's post-hoc test. For **e**, statistical significance was assessed by the Kruskal-Wallis test. For **j**, statistical significance was assessed by the log-rank test. *p < 0.05, **p < 0.01, ns, not significant.



Extended Data Fig. 4 Inhibition of the TfR expression in BMDM and BMDM-derived exosomes via siRNA.

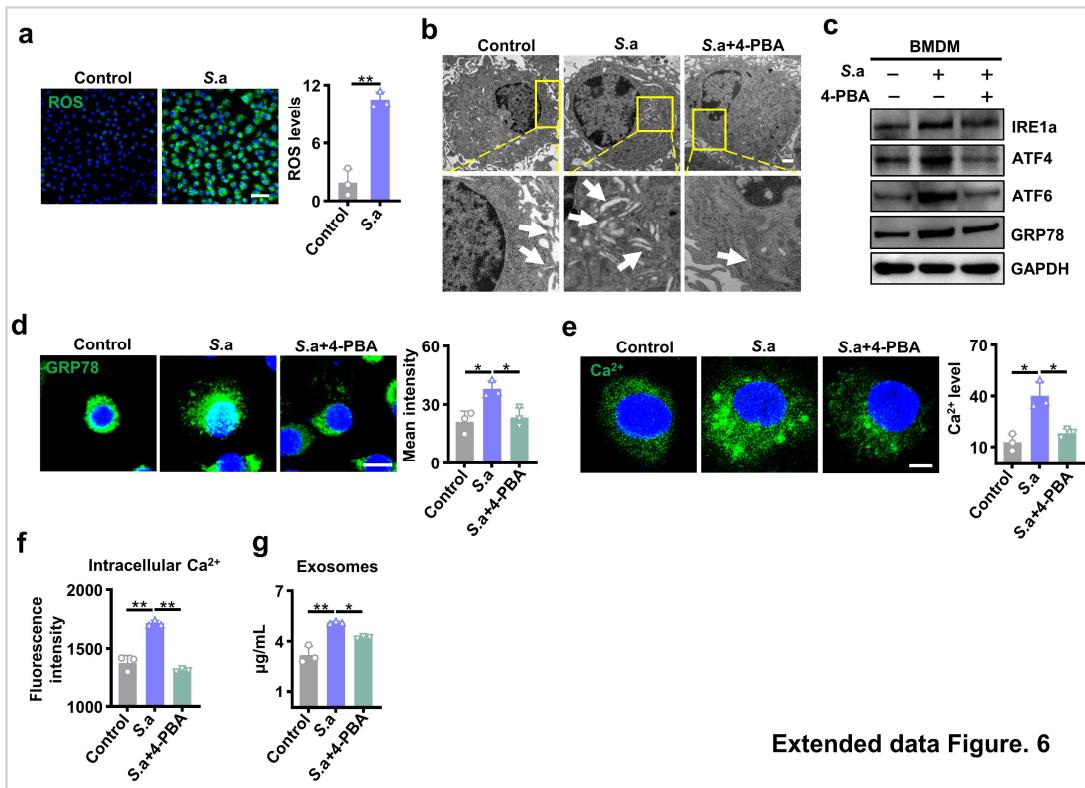
a, Western blot analysis of TfR in BMDM transfected with TfR siRNA. **b**, Western blot analysis of TfR in exosomes derived from BMDM transfected with TfR siRNA.



Extended data Figure. 5

Extended Data Fig. 5 TfR-, CD163-, CD91-bearing exosomes derived from *S.a*-infected mice or BMDM bind iron.

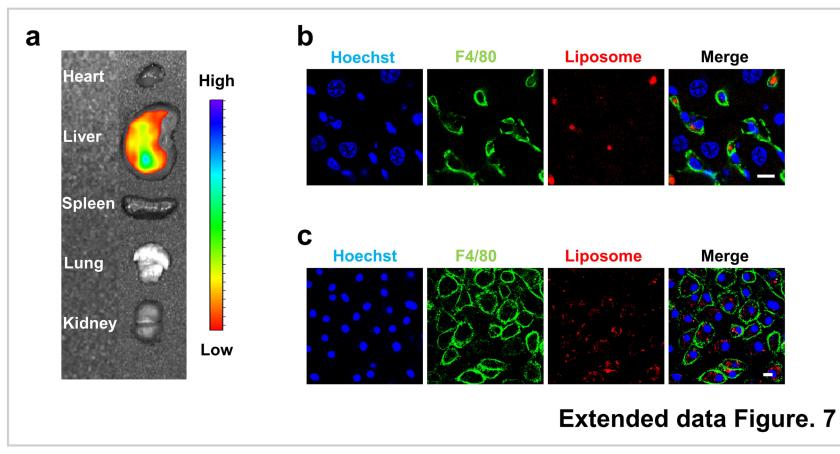
(a-c), Normal mice was intraperitoneally injected with *S.a* and the serum were collected after 24 h. BMDM were infected with *S.a* for 24 hours at an MOI of 25 and supernatant was collected. Exosomes were isolated from the serum or supernatant. **a**, Western blot analysis of Tfr, CD163, CD91 and TSG101 expression in exosomes derived from uninfected and infected mouse serum (left), and in exosomes released from uninfected or infected BMDM (right). **b**, Immunoelectron microscopy detection for Tfr, CD163, and CD91 antibodies in exosomes derived from infected mouse serum (upper) or infected BMDM (bottom). Scale bar, 50 nm. **c**, Schematic diagram of the overall design of the experiments to test the ability of exosomes to bind iron in serum. Exosomes derived from uninfected mouse serum (Serum-Exo group) or *S.a*-infected mouse serum [Serum (*S.a*)-Exo group] were added to the serum respectively and incubated for 12 hours and then removed by ultracentrifugation. The serum supernatant was collected for further analysis. **d,e**, Total iron levels (**d**) and transferrin levels (**e**) in the serum supernatant after incubation with exosomes derived from uninfected or infected mouse serum. n = 3 biologically independent samples. **f**, Growth of *S.a* in serum supernatant. n = 5 biologically independent samples. For **d-f**, data are presented as the mean ± s.d. For **d** and **e**, statistical significance was assessed by one-way ANOVA with Tukey's post-hoc test. For **f**, statistical significance was assessed by one-way ANOVA with Tukey's post hoc test and Kruskal-Wallis test. *p < 0.05, **p < 0.01, ns, not significant.



Extended data Figure. 6

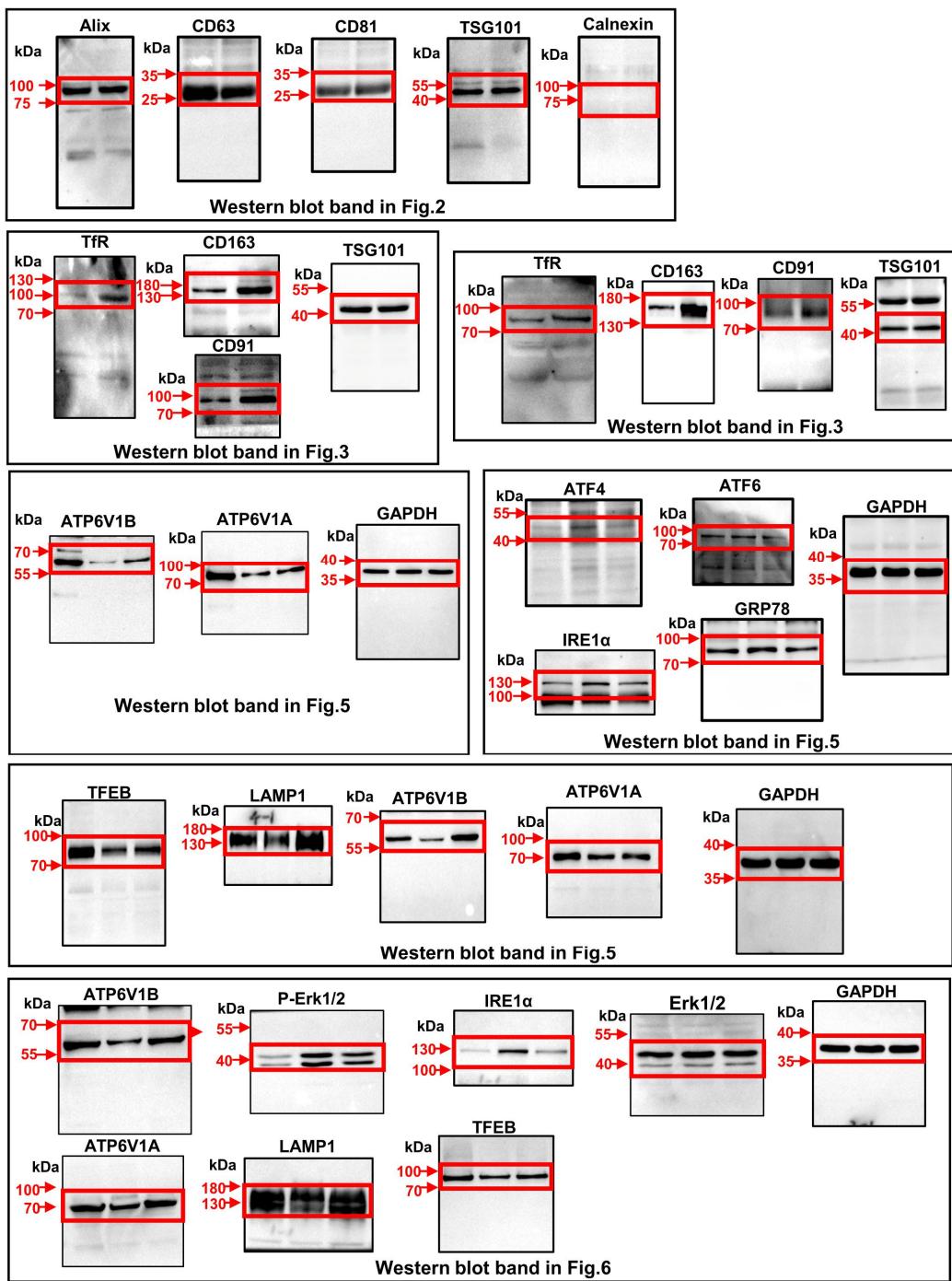
Extended Data Fig. 6 S.a infection induces exosome release via endoplasmic reticulum stress.

a, Representative fluorescence images of ROS in BMDM infected with S.a at MOI of 25, and quantitative analysis of the ROS levels in cells. Scale bar, 50 μ m. n = 3 biologically independent samples. **(b-g)**, BMDM were infected with S.a in the absence or presence of 4-PBA to clarify the association between ERS and exosome release. **b**, TEM images showed the ultrastructural morphology of the endoplasmic reticulum in BMDM. Scale bar, 1 μ m. High-magnification images of the area marked by yellow boxes are arrayed at the lower panel. White arrow indicated endoplasmic reticulum. **c**, Western blot analysis of the expression of IRE1 α , ATF4, ATF6 and GRP78 in BMDM. **d**, Representative fluorescence images of GRP78 in BMDM, and quantitative analysis of the fluorescence intensity Scale bar, 10 μ m. n = 3 biologically independent samples. **e**, Representative fluorescence images of intracellular Ca²⁺ level in cells, and quantitative analysis of the Ca²⁺ levels. Scale bar, 4 μ m. n = 3 biologically independent samples. **f**, Intracellular Ca²⁺ levels measured by fluorescence intensity. n = 3 biologically independent samples. **g**, The concentration of exosomes in supernatant. n = 3 biologically independent samples. For **a** and **d-g**, data are presented as the means \pm s.d. For **a**, statistical significance was analyzed by unpaired two-tailed Student's t test. For **d-g**, statistical significance was analyzed by one-way ANOVA with Tukey's post-hoc test. *p < 0.05, **p < 0.01, ns, not significant.



Extended Data Fig. 7 The biodistribution of 4-PBA-encapsulated liposome.

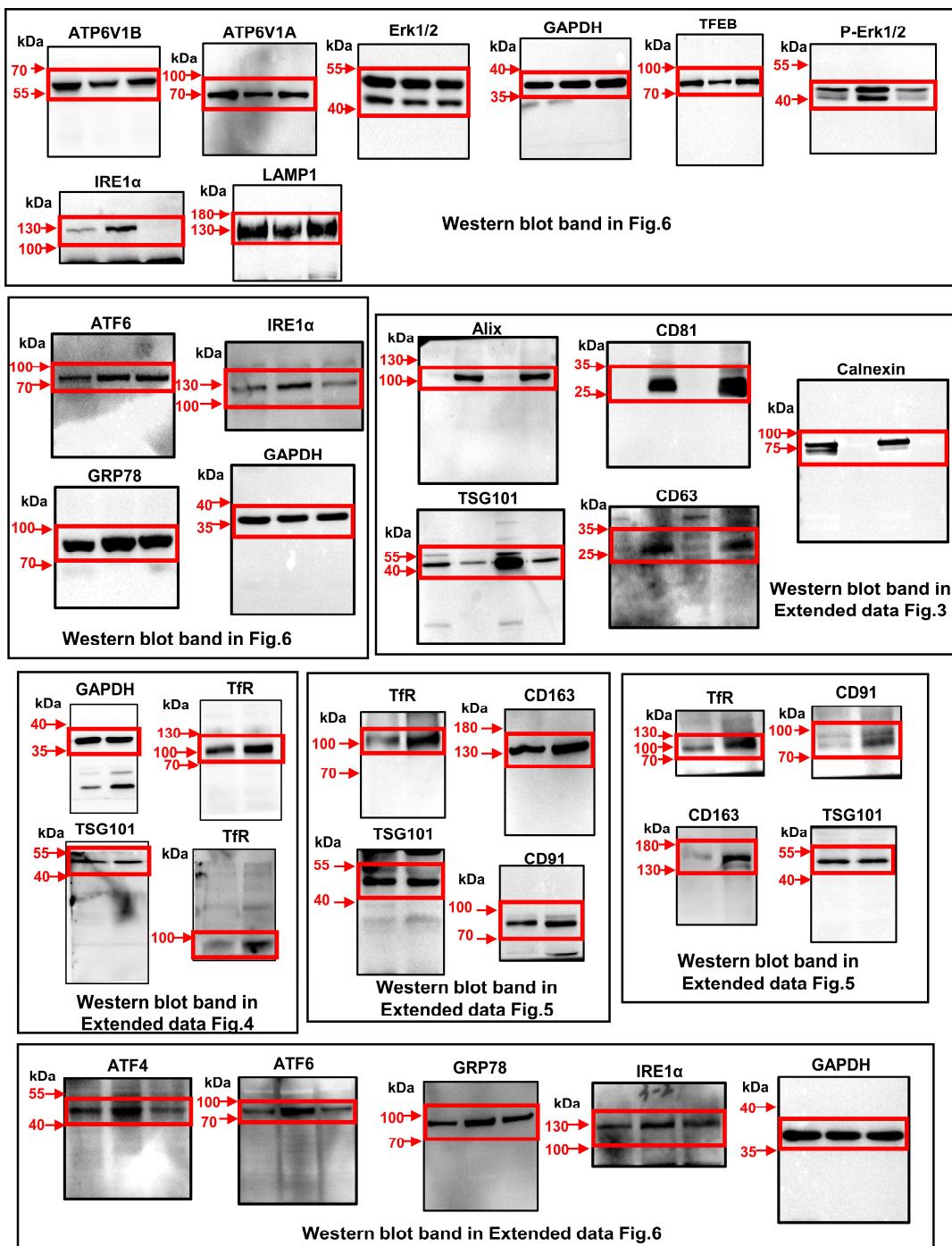
a, *Ex vivo* fluorescent images of various organs in mice injected with RhB-labeled 4-PBA-encapsulated liposome. n=3 mice. **b,c**, The uptake of RhB -labelled liposome (red) by macrophages in liver (**b**) or *in vitro* cultured BMDM (**c**) stained with Hoechst (nucleus; blue) and F4/80 (cell membrane; green). Scale bar, 10 μ m. n = 3 biologically independent sample.



Extended data Figure 8

Extended Data Fig. 8 Uncropped Western blot bands.

Uncropped western blot bands for Figure 2, Figure 3, Figure 5, Figure 6.



Extended data Figure 9

Extended Data Fig. 9 Uncropped Western blot bands.

Uncropped western blot bands for Figure 6, Ext. Figure 3, Ext. Figure 4, Ext. Figure 5, and Ext. Figure 6.