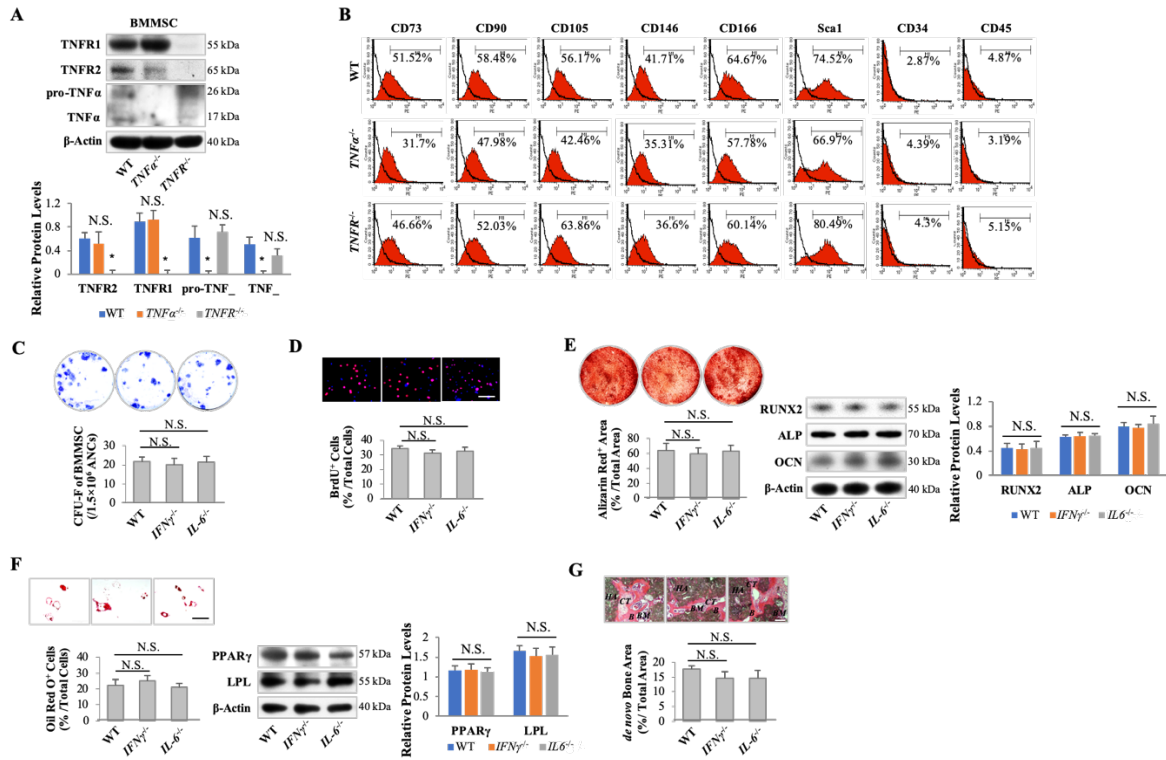


1 Supplemental Figures and Figure Legends



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3 **Fig. S1. Characterization of MSCs derived from the genetic mouse models. (A)** Western blot

4 analyses of *TNFα* and *TNFR* gene knockout efficiency (***N* = 3**). **(B)** Flow cytometric analyses of surface

5 markers of MSCs derived from WT, *TNFα*^{-/-} and *TNFR*^{-/-} mice (***N* = 3**). **(C-G)** Functional analyses of

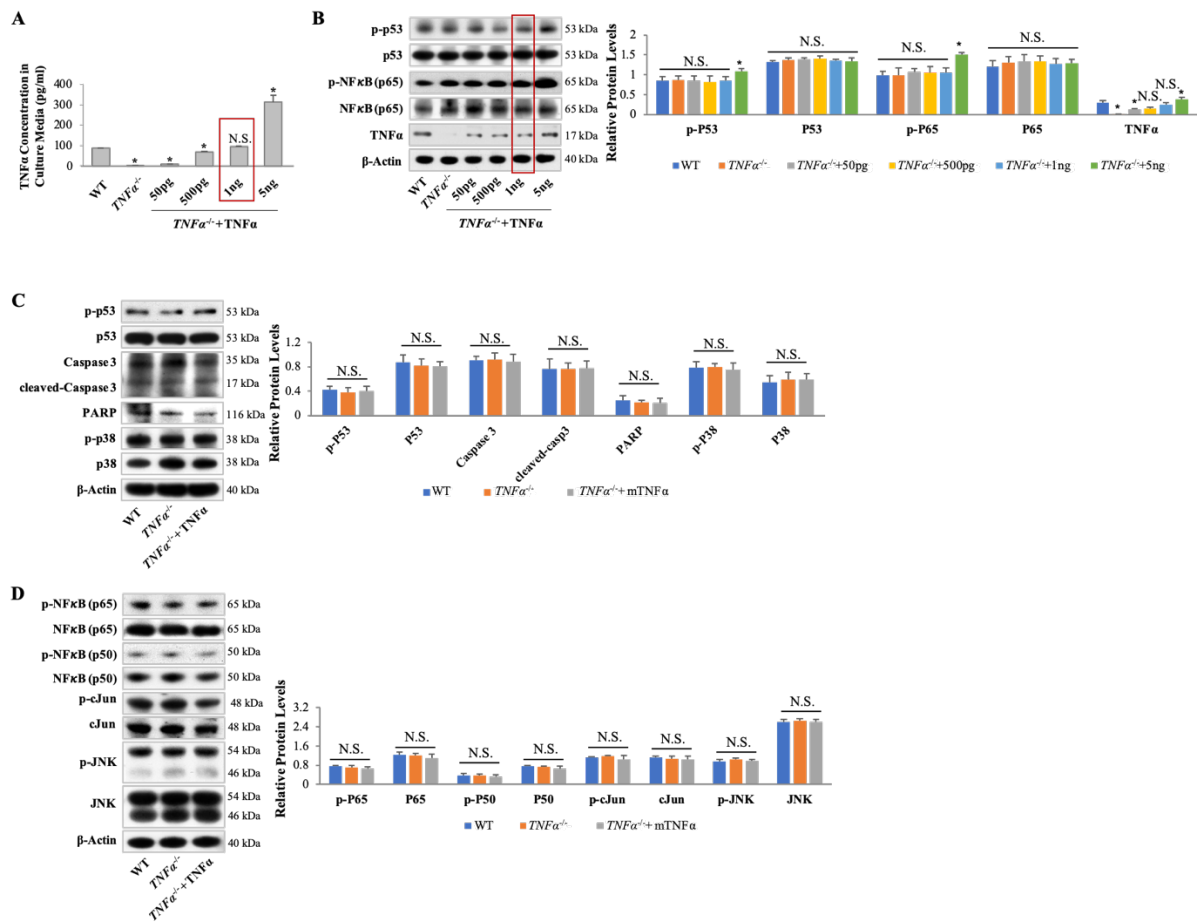
6 MSCs according to CFU, BrdU labeling, osteogenic and adipogenic differentiation, and ectopic tissue

7 formation. MSCs were derived from WT, *IFNγ*^{-/-} or *IL-6*^{-/-} mice (***N* = 3**). B, bone; CT, connective tissue;

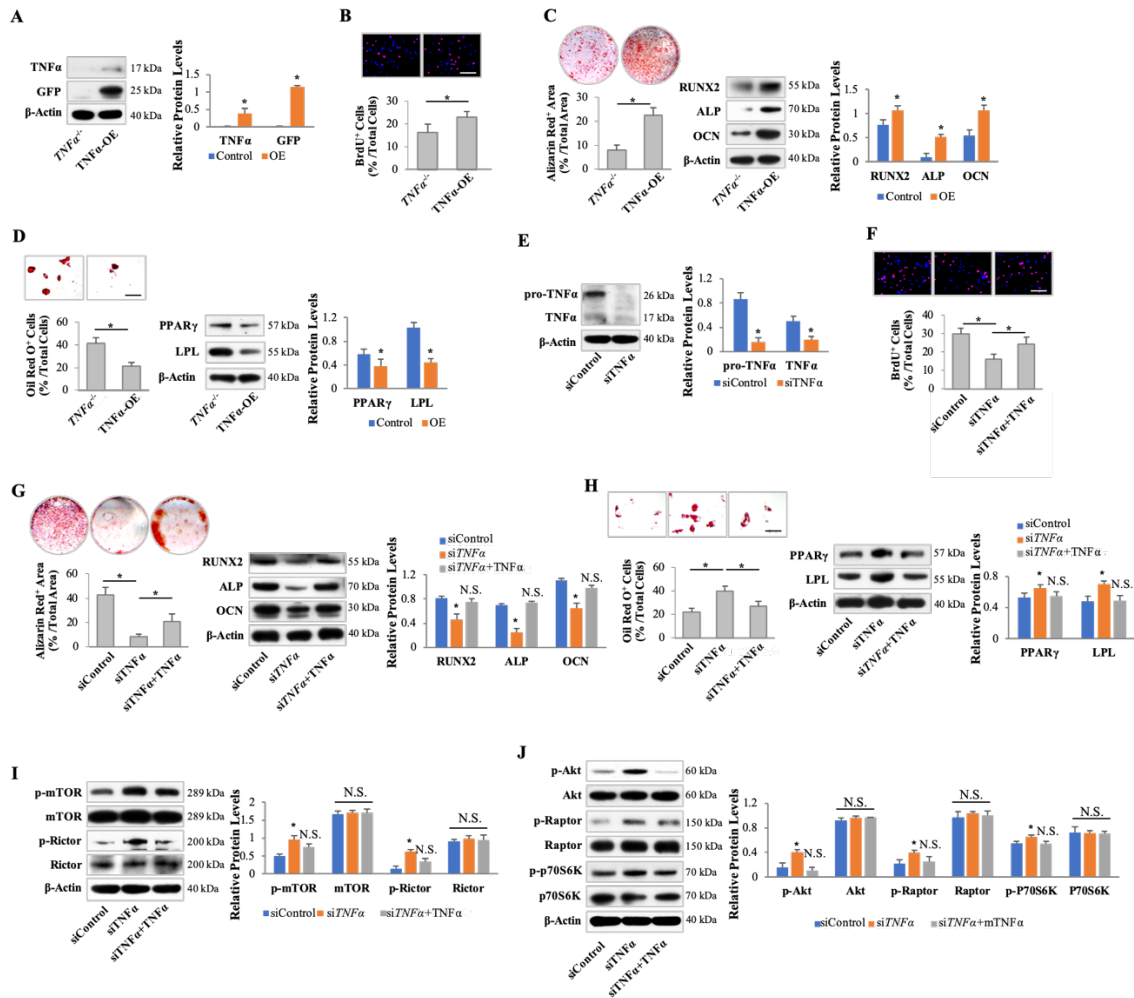
8 BM, bone marrow; HA, implanted scaffolds. Scale bars = 100 μm. **For quantification of Western blotting,**

9 **two-tailed Student t test was used for the comparison between treatment and WT group.** N.S., not

10 significant. Data represent mean ± SD.

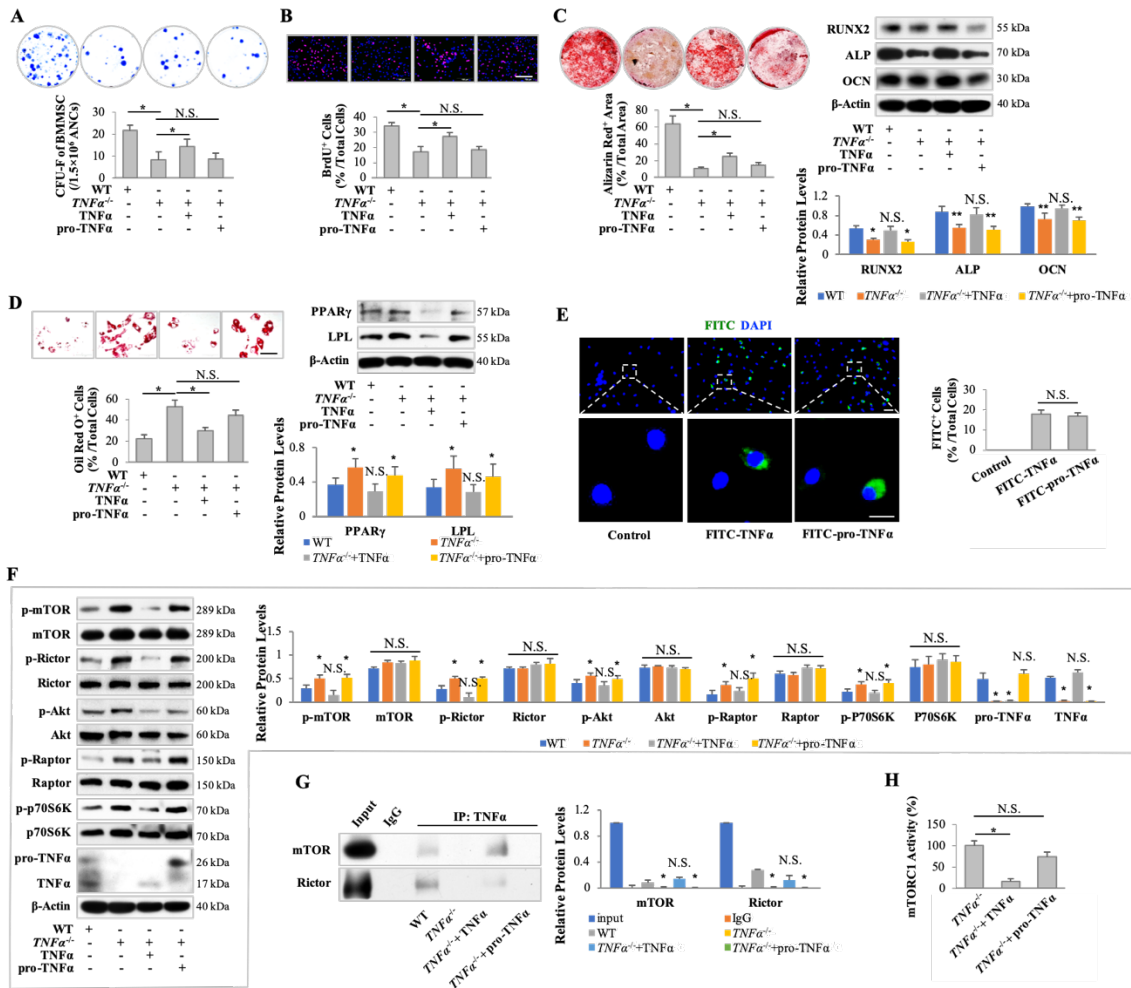


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 2 **Fig. S2. Physiological level of TNFα does not induce receptor-mediated signaling responses. (A)**
 3 **ELISA analysis of secreted TNFα levels by MSCs. *N* = 3. TNFα was added at different doses. (B)**
 4 **Western blot analyses of TNFR downstream signaling. *N* = 3. TNFα was added at different doses. (C,**
 5 **D) Western blot analyses of TNFR downstream signaling. *N* = 3. TNFα was added at 1 ng/ml. For**
 6 **quantification of Western blotting, two-tailed Student t test was used for the comparison between**
 7 **treatment and WT group. *, *P* < 0.05. N.S., not significant. Data represent mean ± SD.**



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Fig. S3. TNFα regulates MSC homeostasis *in vitro*. (A) Western blot analysis of TNFα overexpression (OE) efficiency in *TNFα*^{-/-} MSCs (N = 3). (B-D) Functional analyses of MSCs according to BrdU labeling, osteogenic and adipogenic differentiation (N = 3). (E) Western blot analysis of TNFα knockdown efficiency in WT MSCs (N = 3). (F-H) Functional analyses of MSCs according to BrdU labeling, osteogenic and adipogenic differentiation. N = 3. TNFα was added at 1 ng/ml. (I, J) Western blot analyses of mTOR signaling (N = 3). For quantification of Western blotting, two-tailed Student t test was used for the comparison between treatment and control group. *, P < 0.05. N.S., not significant. Data represent mean ± SD.



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2 **Fig. S4. Pro-TNFα fails to regulate MSC function despite endocytosis. (A-D) Functional analyses**

3 **of MSCs according to CFU, BrdU labeling, osteogenic and adipogenic differentiation. $N = 3$. Scale bars**

4 **$= 100 \mu\text{m}$. (E) Endocytosis analysis of FITC-labeled TNFα or pro-TNFα uptake by MSCs for 24 h *in***

5 ***vitro*. $N = 3$. Scale bars = 20 μm (up) and 7 μm (bottom). (F) Western blot analyses of mTOR signaling**

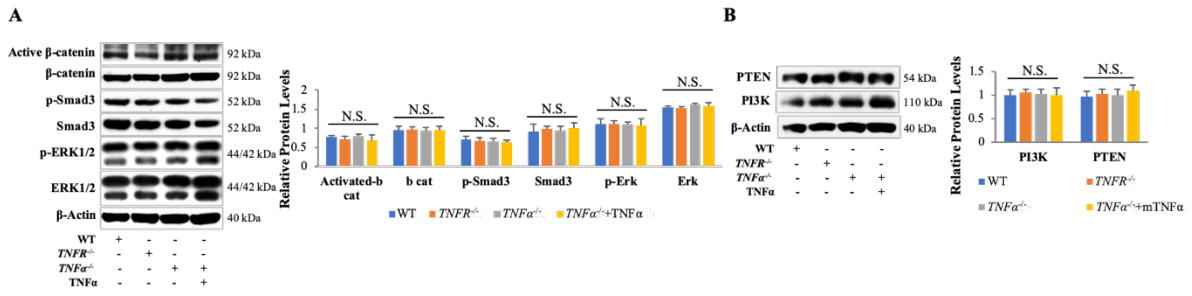
6 **($N = 3$). (G) Co-IP analysis of binding of TNFα and pro-TNFα to mTOR complex components ($N = 3$).**

7 **(H) Analysis of mTORC1 activity using an ELISA-based assay ($N = 3$). TNFα and pro-TNFα were added**

8 **at 1 ng/ml, respectively. For quantification of Western blotting, two-tailed Student t test was used for the**

9 **comparison between treatment and WT group. *, $P < 0.05$. N.S., not significant. Data represent mean \pm**

10 **SD.**



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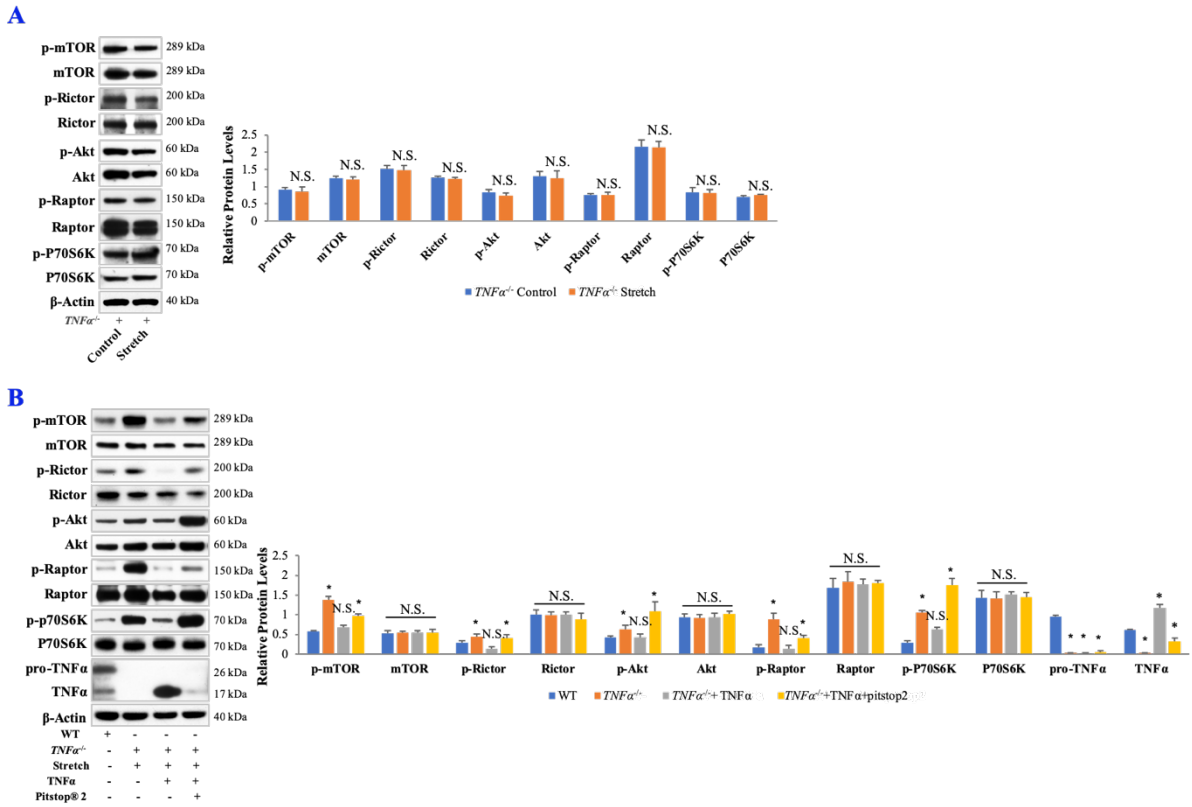
2 **Fig. S5. TNFα exerts limited effects on canonical Wnt, TGF-β or ERK pathways, nor the PI3K**

3 **pathway upstream of Akt. (A, B) Western blot analyses of multiple signaling pathways in MSCs. *N* =**

4 **3. TNFα was added at 1 ng/ml. For quantification of Western blotting, two-tailed Student t test was used**

5 **for the comparison between treatment and WT group. *, *P* < 0.05. N.S., not significant. Data represent**

6 **mean ± SD.**



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Fig. S6. Mechanical stretching restrains mTOR signaling via TNFα endocytosis. (A, B) Western

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blot analysis of mTOR signaling in MSCs. *N* = 3. TNFα and Pitstop® 2 were added at 1 ng/ml and 12

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μM, respectively. For quantification of Western blotting, two-tailed Student t test was used for the

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comparison between treatment and WT/control group. *, *P* < 0.05. N.S., not significant. Data represent

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mean ± SD.