

1 **Supplemental information**

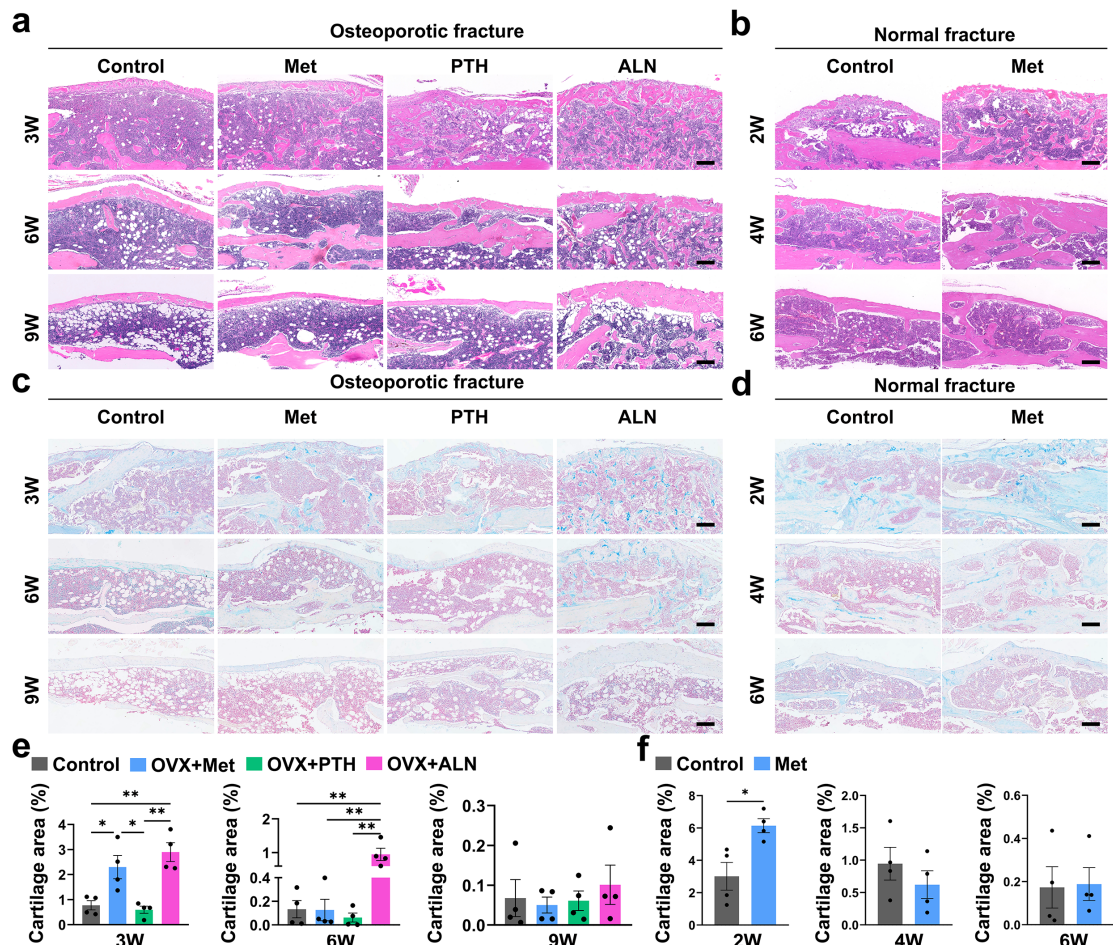
2 **Metformin accelerates bone fracture healing by promoting type H vessels**

3 **formation through inhibited YAP1/TAZ expression**

4 Zhe Ruan<sup>1-2#</sup>, Hao Yin<sup>1-4#</sup>, Teng-Fei Wan<sup>1-4</sup>, Zhi-Rou Lin<sup>6</sup>, Shu-Shan Zhao<sup>1</sup>, Hai-Tao Long<sup>1</sup>, Cheng  
5 Long<sup>1</sup>, Zhao-Hui Li<sup>1</sup>, Yu-Qi Liu<sup>1</sup>, Hao Luo<sup>1</sup>, Liang Cheng<sup>1</sup>, Can Chen<sup>1</sup>, Min Zeng<sup>1</sup>, Zhang-Yuan  
6 Lin<sup>1</sup>, Rui-Bo Zhao<sup>1</sup>, Chun-Yuan Chen<sup>1-5</sup>, Zhen-Xing Wang<sup>1-5</sup>, Zheng-Zhao Liu<sup>1-5</sup>, Jia Cao<sup>1-5</sup>, Yi-Yi  
7 Wang<sup>1-4</sup>, Ling Jin<sup>1-4</sup>, Yi-Wei Liu<sup>1-4</sup>, Guo-Qiang Zhu<sup>1-4</sup>, Jing-Tao Zou<sup>1-4</sup>, Jiang-Shan Gong<sup>1-4</sup>, Yi  
8 Luo<sup>1-4</sup>, Yin Hu<sup>6</sup>, Yong Zhu<sup>1\*</sup>, Hui Xie<sup>1-5\*</sup>.

9 \* Corresponding authors: Hui Xie (huixie@csu.edu.cn); Yong Zhu (doczhu2003@aliyun.com).

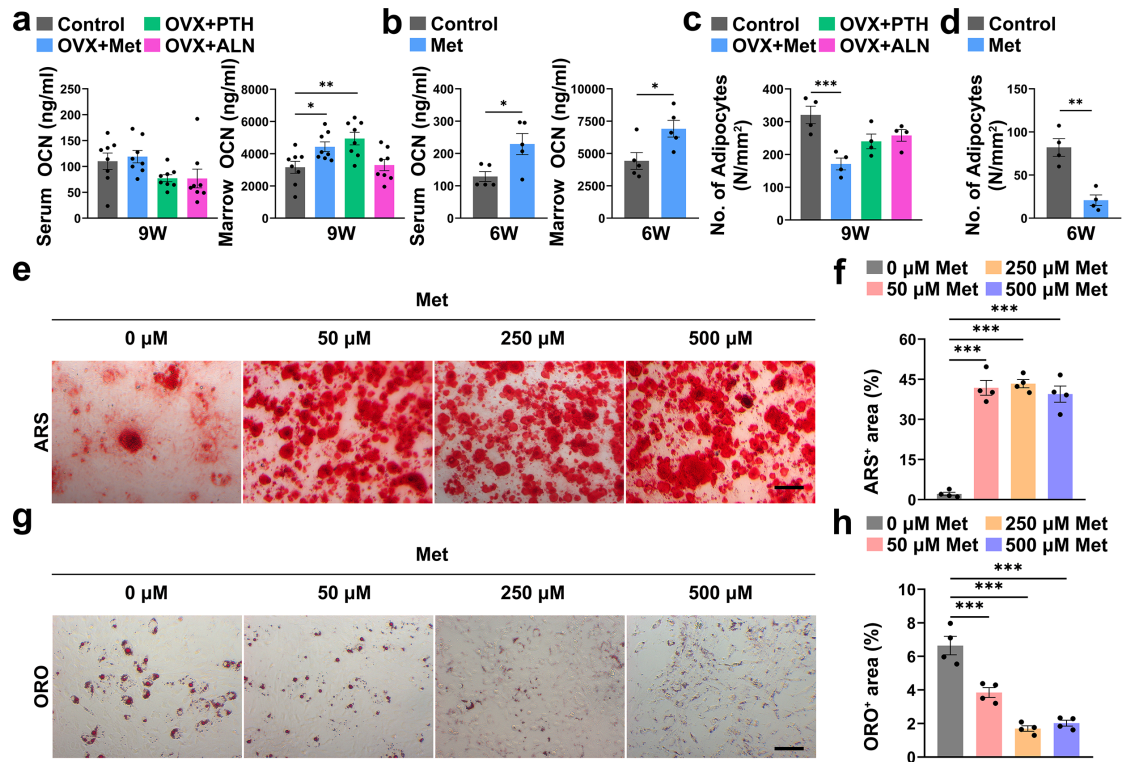
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**Figure. S1 Metformin enhances osteogenesis during osteoporotic and normal fracture healing.**

**(a-b)** Representative images of H&E stained calluses from osteoporotic mice at 3, 6, and 9 weeks post-fracture **(a)** and from normal mice at 2, 4, and 6 weeks post-fracture **(b)**. Scale bar: 200  $\mu$ m; Met: metformin. ALN: alendronate. PTH: parathyroid hormone.

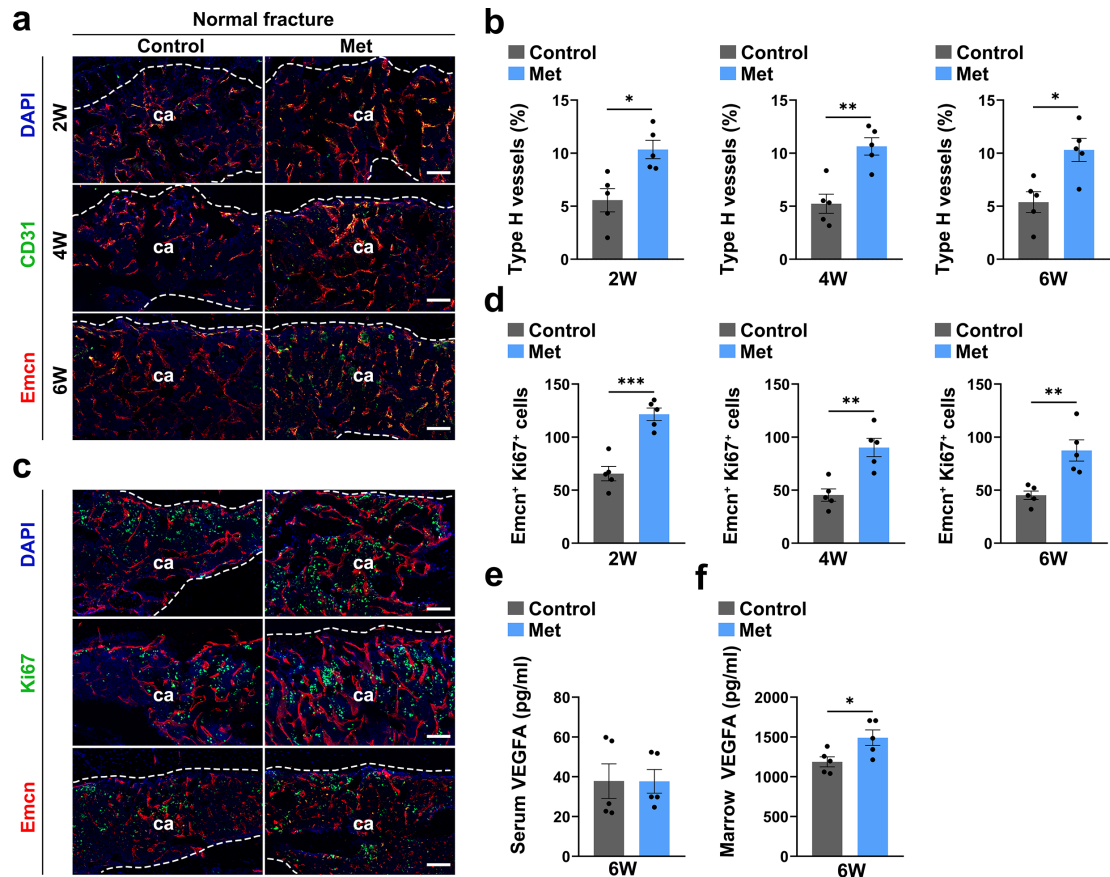
**(c-d)** Representative images of alcian blue stained calluses from osteoporotic mice at 3, 6, and 9 weeks post-fracture **(c)** and from normal mice at 2, 4, and 6 weeks post-fracture **(d)**. Scale bar: 200  $\mu$ m; **(e-f)** Quantification of the cartilage area in calluses from osteoporotic **(e)** and normal **(f)** mice during fracture healing.  $n = 4$  per group. Data were presented as mean  $\pm$  SEM. \* $P < 0.05$ , \*\* $P < 0.01$ , and \*\*\* $P < 0.001$ .



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24 **Figure. S2 Metformin enhances osteogenesis and inhibits adipogenesis *in vivo* and**  
 25 ***in vitro*.**

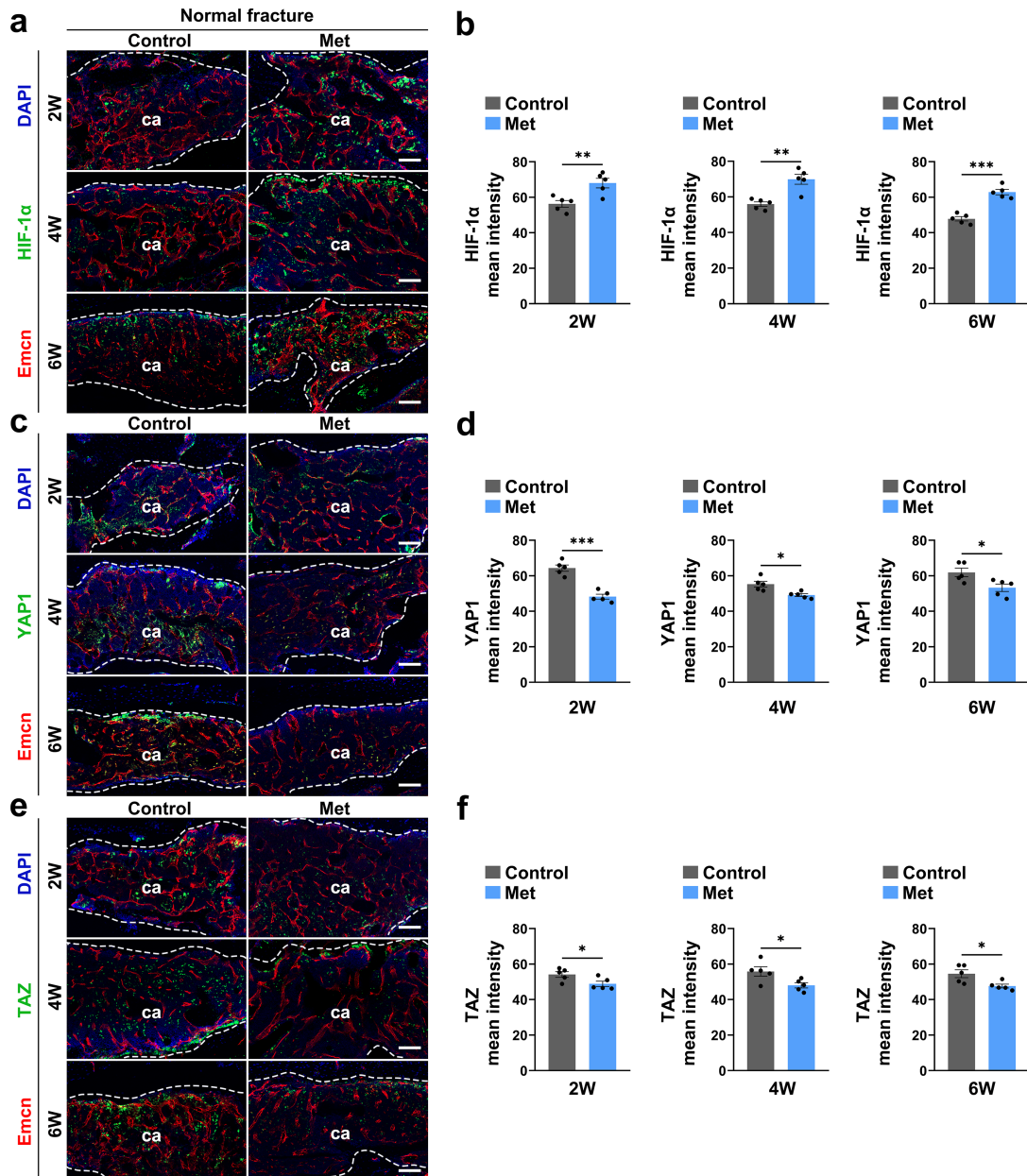
26 **(a-b)** ELISA for the serum and bone marrow OCN concentrations at the endpoint of  
 27 osteoporotic **(a)** (n = 8 per group) and normal **(b)** fracture healing (n = 5 per group). **(c-**  
 28 **d)** Quantification of the number of adipocytes in calluses at the endpoint of osteoporotic  
 29 **(c)** and normal **(d)** fracture healing. n = 4 per group. **(e-f)** Representative Alizarin Red  
 30 S staining images **(e)** of mineralized nodules of BMSCs treated with metformin in  
 31 different concentrations after osteogenic induction for 9 days and quantitation of ARS  
 32 positive areas per field **(f)**. Scale bar: 100 μm. n = 4 per group; **(g-h)** Representative Oil  
 33 Red O staining images **(g)** of lipid droplets of BMSCs treated with metformin in  
 34 different concentrations after adipogenic induction for 15 days and quantitation of ORO  
 35 positive areas per field **(h)**. Scale bar: 100 μm. n = 4 per group; Data were presented as  
 36 mean ± SEM. \*P < 0.05, \*\*P < 0.01, and \*\*\*P < 0.001.



37

38 **Figure. S3 Metformin promotes type H vessel formation in normal fracture mice.**

39 **(a-b)** Representative CD31 and Emcn co-immunostaining images **(a)** with  
 40 quantification of type H vessels ratio in calluses from normal mice treated with PBS or  
 41 metformin at 2, 4, and 6 weeks post-fracture **(b)**. ca: callus. The dotted line represents  
 42 the boundary of calluses. Met: metformin. Scale bar: 100  $\mu$ m. n = 5 per group. **(c-d)**  
 43 Representative Ki67 and Emcn co-immunostaining images **(c)** with quantification of  
 44 Ki67 positive endothelial cells number in calluses from normal mice treated with PBS  
 45 and Met at 2, 4, and 6 weeks post-fracture **(d)**. Scale bar: 100  $\mu$ m. n = 5 per group. **(e-**  
 46 **f)** ELISA for the serum **(e)** and bone marrow **(f)** concentrations of VEGFA at 6 weeks  
 47 post-normal fracture. n = 8 per group; Data were presented as mean  $\pm$  SEM. \* $P$  < 0.05,  
 48 \*\* $P$  < 0.01, and \*\*\* $P$  < 0.001.



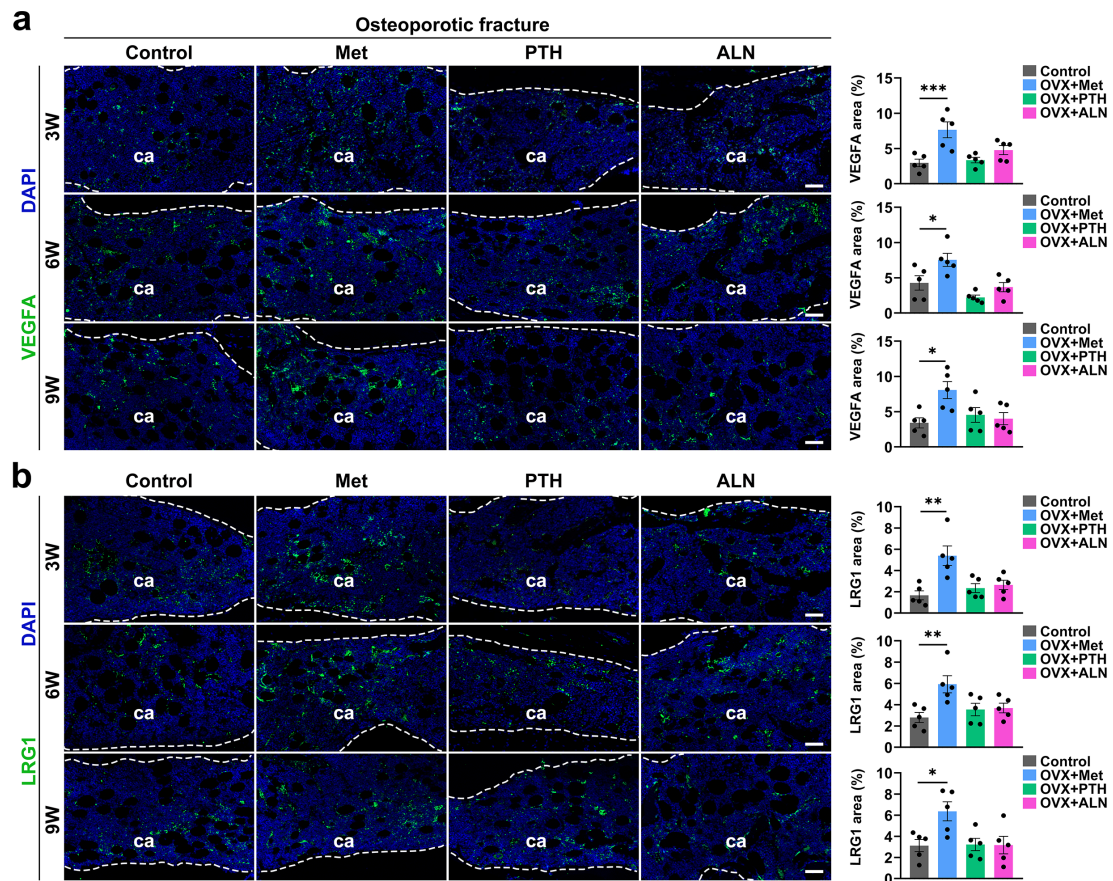
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50 **Figure. S4 Metformin promotes the expression of HIF-1α by inhibiting the**  
 51 **expression of YAP1/TAZ during normal fracture healing**

52 **(a-b)** Representative HIF-1α and Emcn co-immunostaining images **(a)** with  
 53 quantification of the mean intensity of HIF-1α in calluses from normal mice treated  
 54 with PBS or metformin at 2, 4, and 6 weeks post-fracture **(b)**. ca: callus. The dotted line  
 55 represents the boundary of calluses. Met: metformin. Scale bar: 100 μm. n = 5 per group.

56 **(c-d)** Representative YAP1 and Emcn co-immunostaining images **(c)** with

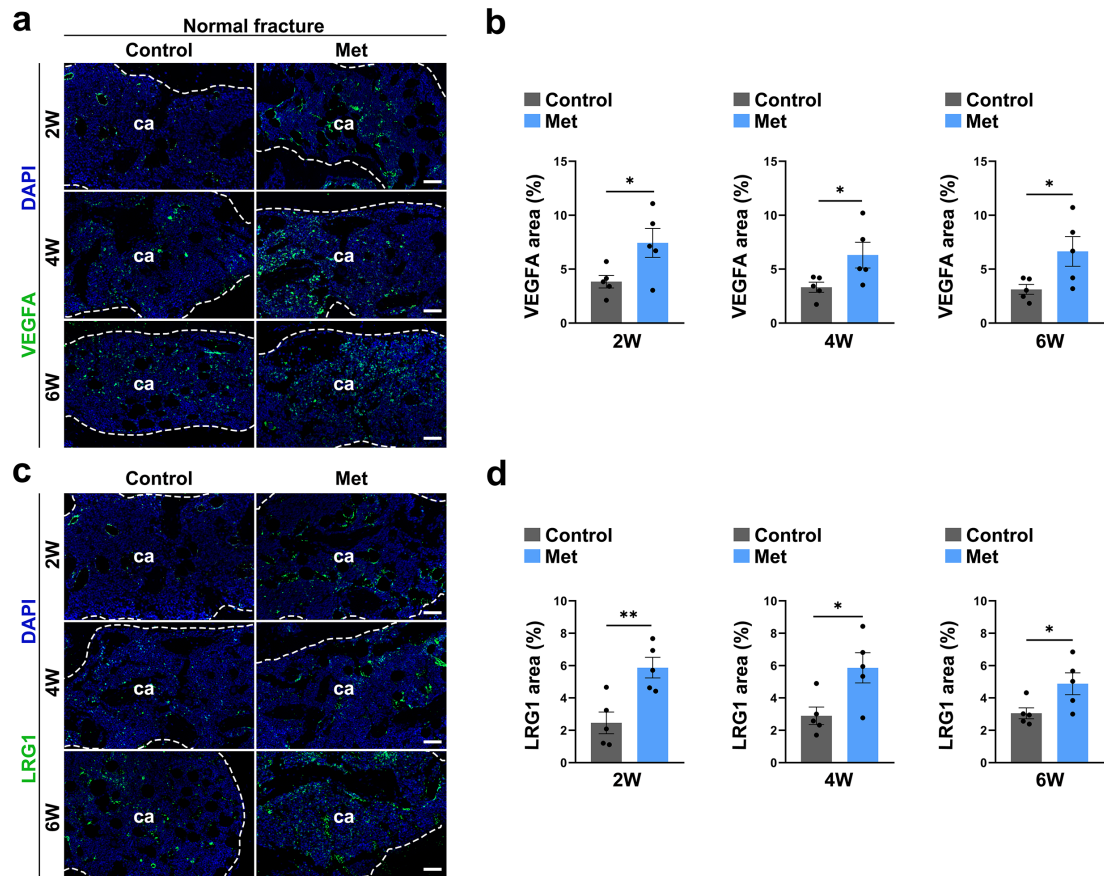
57 quantification of the mean intensity of YAP1 in calluses from normal mice at 2, 4, and  
58 6 weeks post-fracture **(d)**. Scale bar: 100  $\mu\text{m}$ . n = 5 per group. **(e-f)** Representative TAZ  
59 and Emcn co-immunostaining images **(e)** with quantification of the mean intensity of  
60 TAZ in calluses from normal mice at 2, 4, and 6 weeks post-fracture **(f)**. Scale bar: 100  
61  $\mu\text{m}$ . n = 5 per group. Data were presented as mean  $\pm$  SEM. \* $P < 0.05$ , \*\* $P < 0.01$ , and  
62 \*\*\* $P < 0.001$ .



63

64 **Figure. S5 Metformin promotes the expression of VEGFA and LRG1 during**  
 65 **osteoporotic fracture healing.**

66 **(a)** Representative immunostaining images (left) with quantification (right) of VEGFA  
 67 in calluses from osteoporotic mice treated with PBS, Met, PTH, and ALN at 3, 6, and  
 68 9 weeks post-fracture. ca: callus. The dotted line represents the boundary of calluses.  
 69 Met: metformin. ALN: alendronate. PTH: parathyroid hormone. Scale bar: 50  $\mu$ m. n =  
 70 5 per group. **(b)** Representative immunostaining images (left) with quantification (right)  
 71 of LRG1 in calluses from osteoporotic mice treated with PBS, Met, PTH, and ALN at  
 72 3, 6, and 9 weeks post-fracture. Scale bar: 50  $\mu$ m. n = 5 per group. Data were presented  
 73 as mean  $\pm$  SEM. \* $P < 0.05$ , \*\* $P < 0.01$ , and \*\*\* $P < 0.001$ .



74

75 **Figure. S6 Metformin promotes the expression of VEGFA and LRG1 during**  
 76 **normal fracture healing.**

77 **(a)** Representative immunostaining images (left) with quantification (right) of VEGFA  
 78 in calluses from normal mice treated with PBS and Met at 2, 4, and 6 weeks post-  
 79 fracture. ca: callus. The dotted line represents the boundary of calluses. Met: metformin.

80 Scale bar: 50  $\mu$ m. n = 5 per group. **(b)** Representative immunostaining images (left)

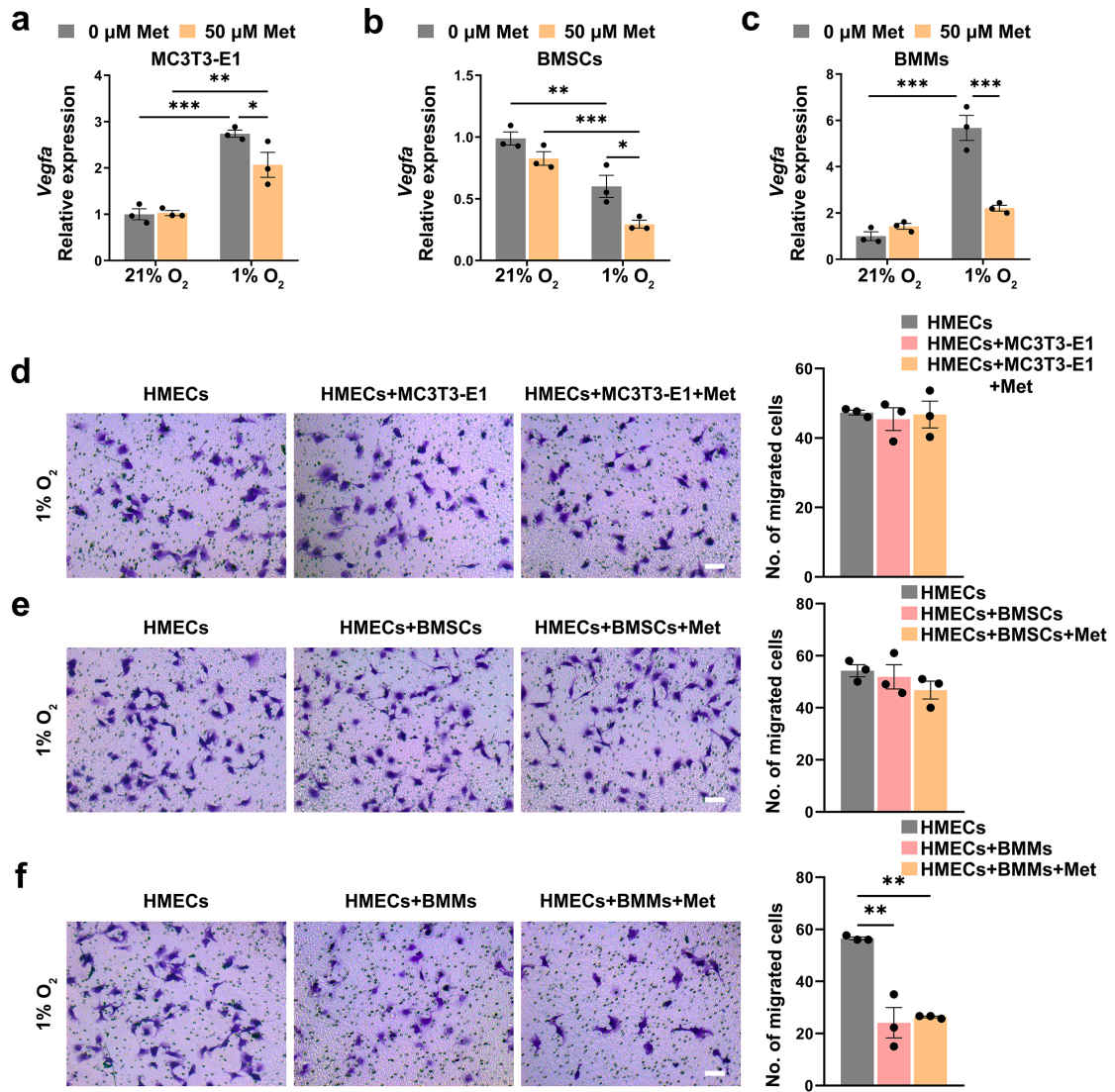
81 with quantification (right) of LRG1 in calluses from normal mice treated with PBS and

82 Met at 2, 4, and 6 weeks post-fracture. ca: callus. The dotted line represents the

83 boundary of calluses. Met: metformin. Scale bar: 50  $\mu$ m. n = 5 per group. Data were

84 presented as mean  $\pm$  SEM. \* $P < 0.05$  and \*\* $P < 0.01$ .

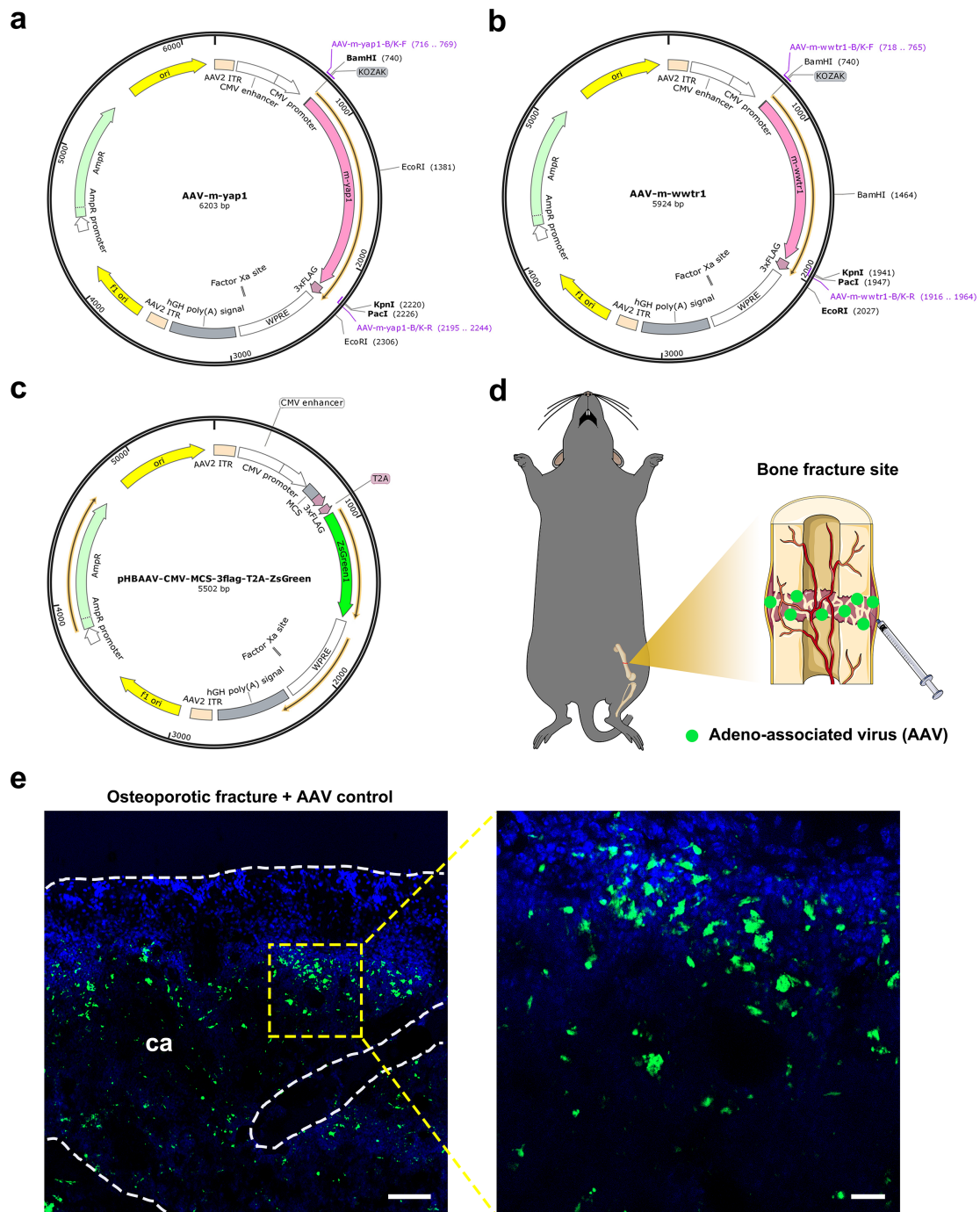




**Figure. S7 Metformin enhances angiogenesis under hypoxic conditions independently of its effects on osteoblast progenitors and bone marrow-derived macrophages.**

**(a-c)** qRT-PCR analysis for *Vegfa* mRNA level in osteoblast progenitors MC3T3-E1 cells **(a)**, BMSCs **(b)**, and BMMs **(c)** with or without metformin treatment under different oxygen concentrations. Met: metformin. n = 3 per group. **(d-f)** Representative images of transwell migration assay (left) with quantification of crystal violet-stained migrated HMECs (right) co-cultured with MC3T3-E1 cells **(d)**, BMSCs **(e)**, and BMMs **(f)** with or without metformin treatment under hypoxic conditions (1% O<sub>2</sub>). Scale bar:

95 100  $\mu\text{m}$ .  $n = 3$  per group. Data were presented as mean  $\pm$  SEM.  $*P < 0.05$ ,  $**P < 0.01$ ,  
96 and  $***P < 0.001$ .



97

98 **Figure. S8 AAV construction and mice model of injection of the AAV into the**

99 **fracture site.**

100 **(a-c) Construction of AAV2 expressing Yap1 (a), Taz (b), and AAV control (c). Note**

101 **that Yap1/Taz-AAV itself does not express fluorescence while AAV control expresses**

102 **green fluorescence (ZsGreen). (d) Schematic of the AAV injection into the bone**

103 fracture area. (e) Immunofluorescence of ZsGreen expression in callus (left) with the  
104 magnified area (right) in the boxed area in the left image of osteoporotic mice that  
105 received AAV control injections at 6 weeks after fracture operation. The AAV control  
106 group expressed ZsGreen as a reporter of AAV2 infection efficiency. ca: callus. The  
107 dotted line represents the boundary of calluses. Scale bar, left 100  $\mu\text{m}$ ; right 20  $\mu\text{m}$ .  
108

109 **Supplementary Table 1. Primer sequences for qRT-PCR.**

<b>Gene</b>	<b>Forward (5'-3')</b>	<b>Reverse (5'-3')</b>
<i>h-HIF-1<math>\alpha</math></i>	AGAGGTTGAGGGACGGAGAT	GACG TTCAGAACTTATCCTACCAT
<i>h-YAP1</i>	GAACTGCTTCGGCAGGTGAG	GCAGGGCTAACTCCTGACATT
<i>h-TAZ</i>	TCACATCCTGGCGACTCTCA	GAGGCCGGATTCATCTTCTGG
<i>h-VEGFA</i>	ACATCACCATGCAGATTATGCG	CTCCAGGGCATTAGACAGCA
<i>h-LRG1</i>	GACAGCGACCAAAAAGCCCA	TGAAGAATTCCACGGCCAGG
<i>h-GAPDH</i>	GGATTTGGTCGTATTGGGCG	TCCCGTTCTCAGCCATGTAGT
<i>m-VEGFA</i>	GCACATAGAGAGAATGAGCTTCC	CTCCGCTCTGAACAAGGCT
<i>m-GAPDH</i>	AGGTCGGTGTGAACGGATTTG	TGTAGACCATGTAGTTGAGGTCA

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111 **Supplementary Table 2. siRNA target Sequences.**

<b>siRNA</b>	<b>Target sequences</b>
<i>si-HIF-1α</i> #1	GGAACATGATGGTTCACTT
<i>si-HIF-1α</i> #2	CTACCCACATACATAAAGA
<i>si-HIF-1α</i> #3	CCAGCAACTTGAGGAAGTA
<i>si-YAP1</i> #1	CCACCAAGCTAGATAAAGA
<i>si-YAP1</i> #2	GAGATGGAATGAACATAGA
<i>si-YAP1</i> #3	GTAGCCAGTTACCAACT
<i>si-TAZ</i> #1	CGATGAATCAGCCTCTGAA
<i>si-TAZ</i> #2	GGACAAACACCCATGAACA
<i>si-TAZ</i> #3	AGAGTCTGCTCTGAACAAA

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