# **Supplementary material**



Transcriptomic comparison of osteoblasts (OB) between ovariectomized mice that undertook exercise (OVX+T) and those that did not (OVX). aa) Hierarchical clustering was employed to grouping gene expression of OB in the OVX+T and OVX mouse. ab) Scatter plot was applied to representing the different expression value of a gene in the OVX+T and OVX group. Red dots indicate genes that have been upregulated in the OVX+T group compared with the OVX group; green dots indicate genes that have been downregulated in the OVX+T group compared with OVX group. ac) The relative percentage of different type genes upregulated or downregulated (>1.5 or <-1.5-fold change compared with OVX group) was presented in a pie chart.

## **Supplementary Methods**

**Mouse strain and training protocol.** Irregular cycling oestrogen level begins at 8- to 12-month-old female C57BL/6 mice. Thereafter, the oestrogen level declines by 45% to 80%, but persists at a detectable level.<sup>1,2</sup> Uterine weight, a physiological indicator of oestrogen, keeps on normal levels up to at least 31 months.<sup>3</sup> So, there is no true menopause in mice. Meanwhile, ageing is associated with elevated levels of inflammatory cytokines. This is caused by innate cells such as macrophages, a process known as inflamm-ageing.<sup>4</sup> Aged macrophages have increased nitric oxide production under the resting condition and higher surface density of TLR4, leading to a

faster and enhanced inflammatory response.<sup>5,6</sup> The ageinduced inflammatory cytokines will be beneficial for OC formation. To minimize these influences, we chose the adult ovariectomized mice for our study.

Chen et al<sup>7</sup> reported that medium-intensity treadmill exercise (speed: 12 m/mime to 18 m/mime; time: 20 mins to 50 mins; frequency: six days/week; duration: nine weeks) was more effective on the increase of BMD and bone strength than a low-intensity exercise in the senile mice. Based on the protocol, we trained ovariectomized mice with modified medium-intensity treadmill (speed: 10 m/mime; time: 60 mins; frequency: five days/ week; duration: eight weeks) in the present study.

### Table i. WikiPathway analysis of differentially expressed genes

Sequence

5'-GCTGAGGTTTTGACCTTGTGG-3'

5'- TTGGGCGACTTTCCAATCCA- 3'

5'- ACAATCCGTGCCACTCACTC -3'

5'- GTGATCACCGCTTTTGGTCC -3'

5'-CAGCCAGTCCTGACAGATCC-3'

5'-TAGCGGAGGATGGCTTTGTT- 3'

5'-CAGCCGACTTTTGTGGTCTTC- 3'

5'- GTACAAGTATGCCTCTGCCA - 3'

5'- ACGATGAACATGGCACTCCA - 3'

5'- AGAGAGGACTCGGAGACGTG - 3'

5'- GGAGTTGCACCTGTATGCCT - 3'

5'-CTTGCTGGTGGAAGGAGGCAGG-3'

5'-CACGTCTTCTCCACCGTGGGTC-3'

5'-CGACTTCAACAGCAACTCCCACTCTTCC-3'

5'- TGGGTGGTCCAGGGTTTCTTACTCCTT-3'

5'-ATCTCCTGGTGCTGATGGAC-3'

5'-ACCTTGTTTGCCAGGTTCAC-3'

5'- TGCAACTATGCTCCAAAGGGT - 3'

5'- CCGGTACTTAAAGACCCCGTT -3'

5'- ACCACCCATGAATCCATCCTG -3'

5'-CATGAGACACAATCATATCACAGAT-3'

5'-CAGCCAAATCACCCGTCCT -3'

Pathway	Downregulated genes	Upregulated genes
IL-1 signalling pathway	ll1b, ll1rn, ll1r1	
IL-6 signalling pathway	ll6, ll6ra, ll6st, Btk, Jak1, Crebbp, Rb1	
IL-7 signalling pathway	Pik3r1, II7r, Jak1, Irs2, Rb1, Cblb, Cbl	
TNF-alpha NF-kB signalling pathway	Rnf216, Casp8ap2, Tnfrsf1b, Nfkbia, Psmd, Papola, Glg1, Birc2, Crebbp, Tnfrsf11a	
Inflammatory response pathway	Col3a1, Lamc1, Tnfrsf1b	
TGF-beta signalling pathway	Tgfbr3, Jak1, Zeb2, Crebbp, Skil, Tgfbr3, Prkar2a, Skil, Anapc1, Ctcf, Map2k3, Crebbp, Kpnb1, Rb1, Cdk6	Serpine1

#### Table ii. Primer sequence

Gene

DMP-1-forward

DMP-1-reverse

SLc13A5-forward

SLc13A5-reverse

**IBSP-forward** 

IBSP-reverse

Acp5-forward

Acp5-reverse

THBS4-forward

THBS4-reverse

MMP9-forward

MMP9-reverse

PI15-forward

PI15-reverse

LPL-forward

LPL-reverse

ALP-forward

ALP-reverse

Col I-forward

Col I-reverse

GAPDH-forward

GAPDH-reverse

# References

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