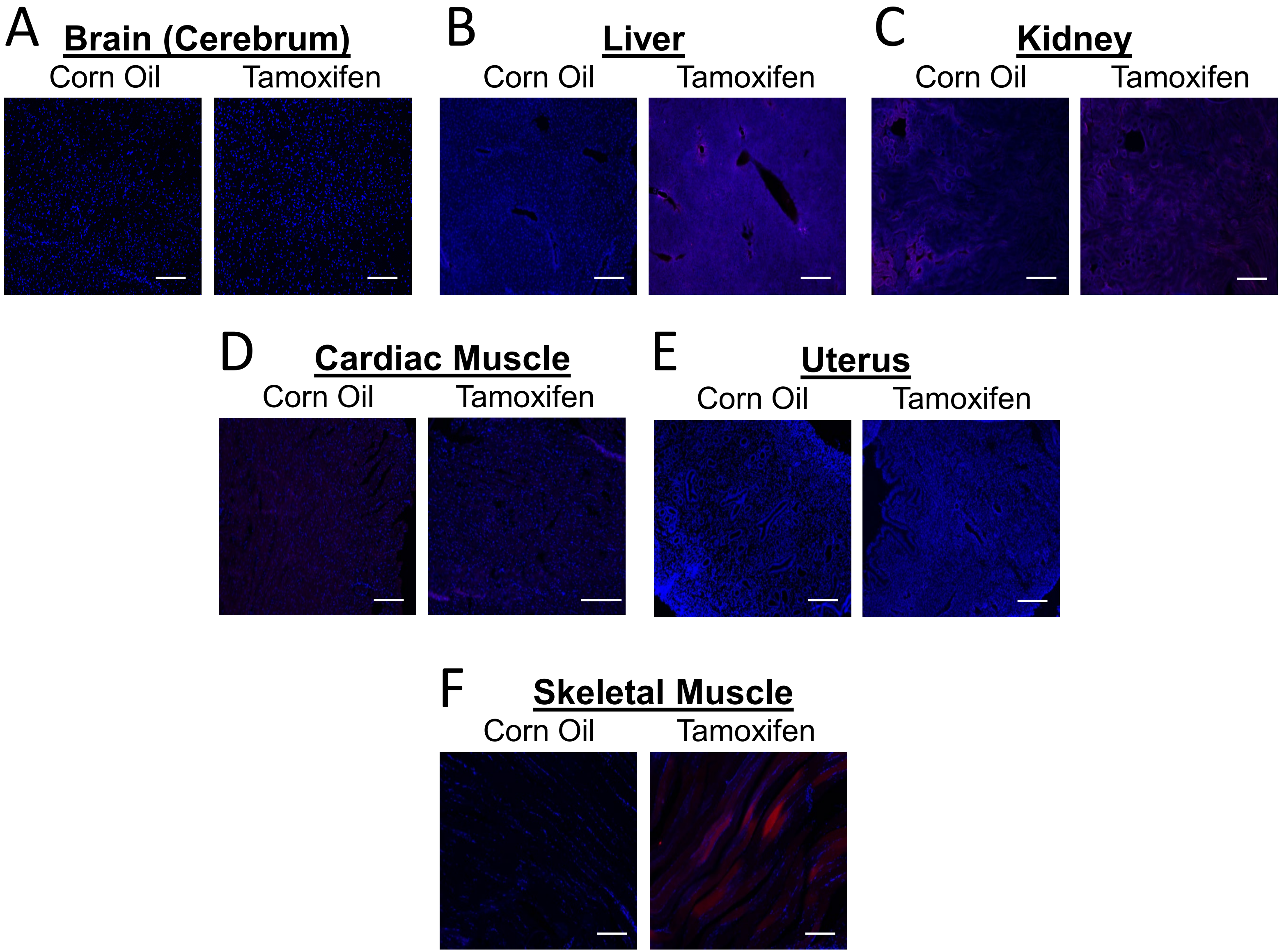
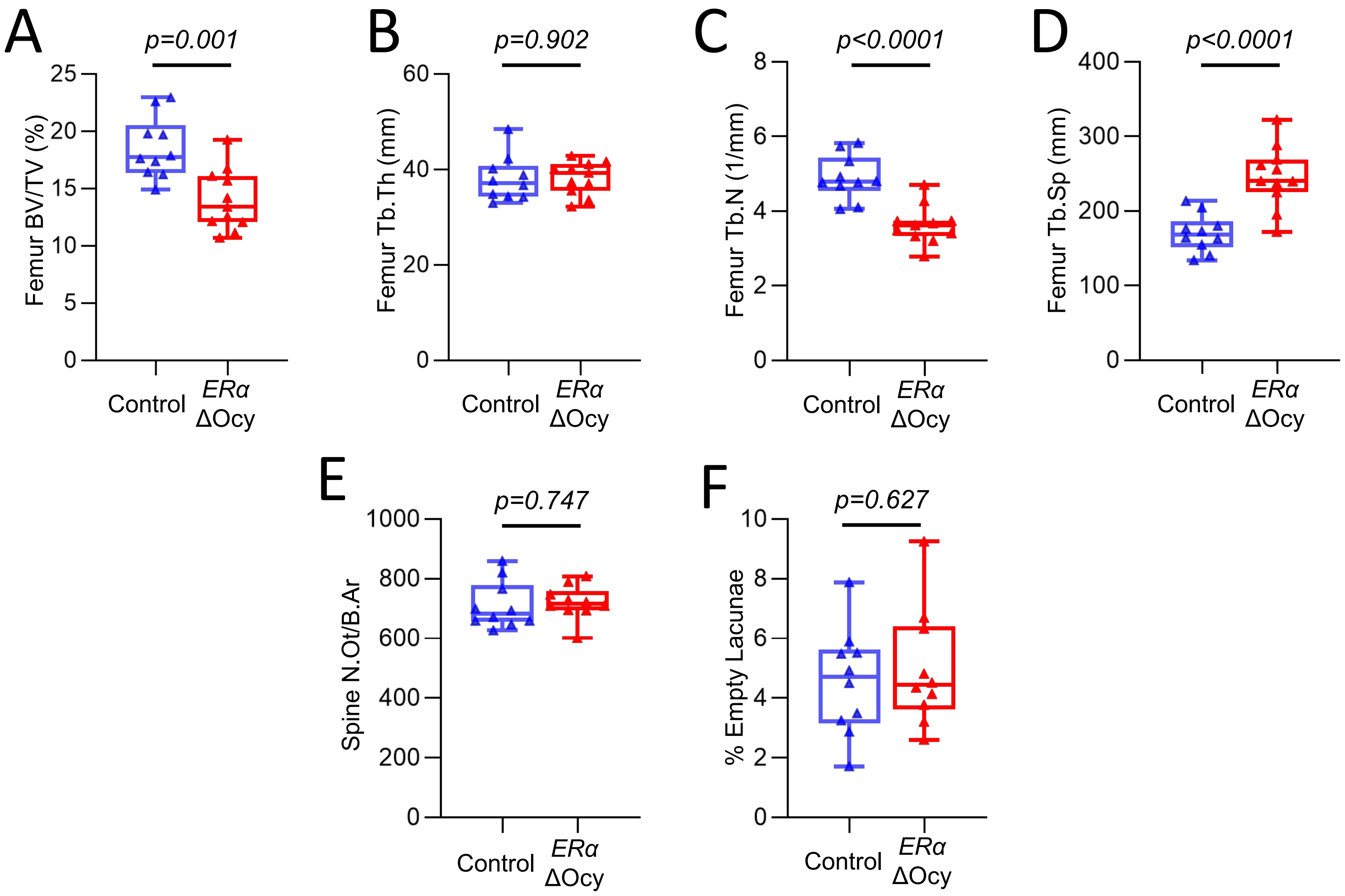
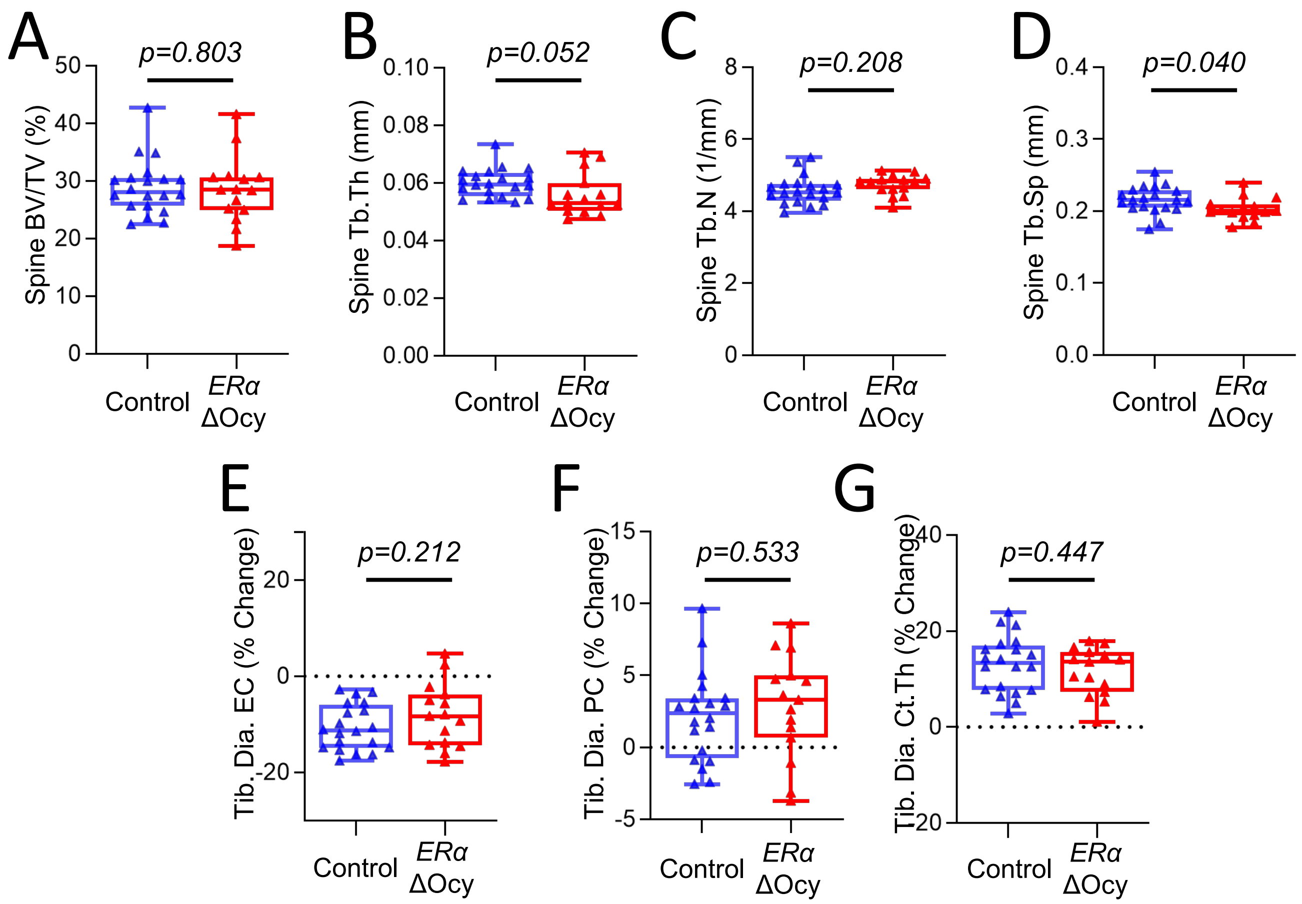
Supplementary Figure 1



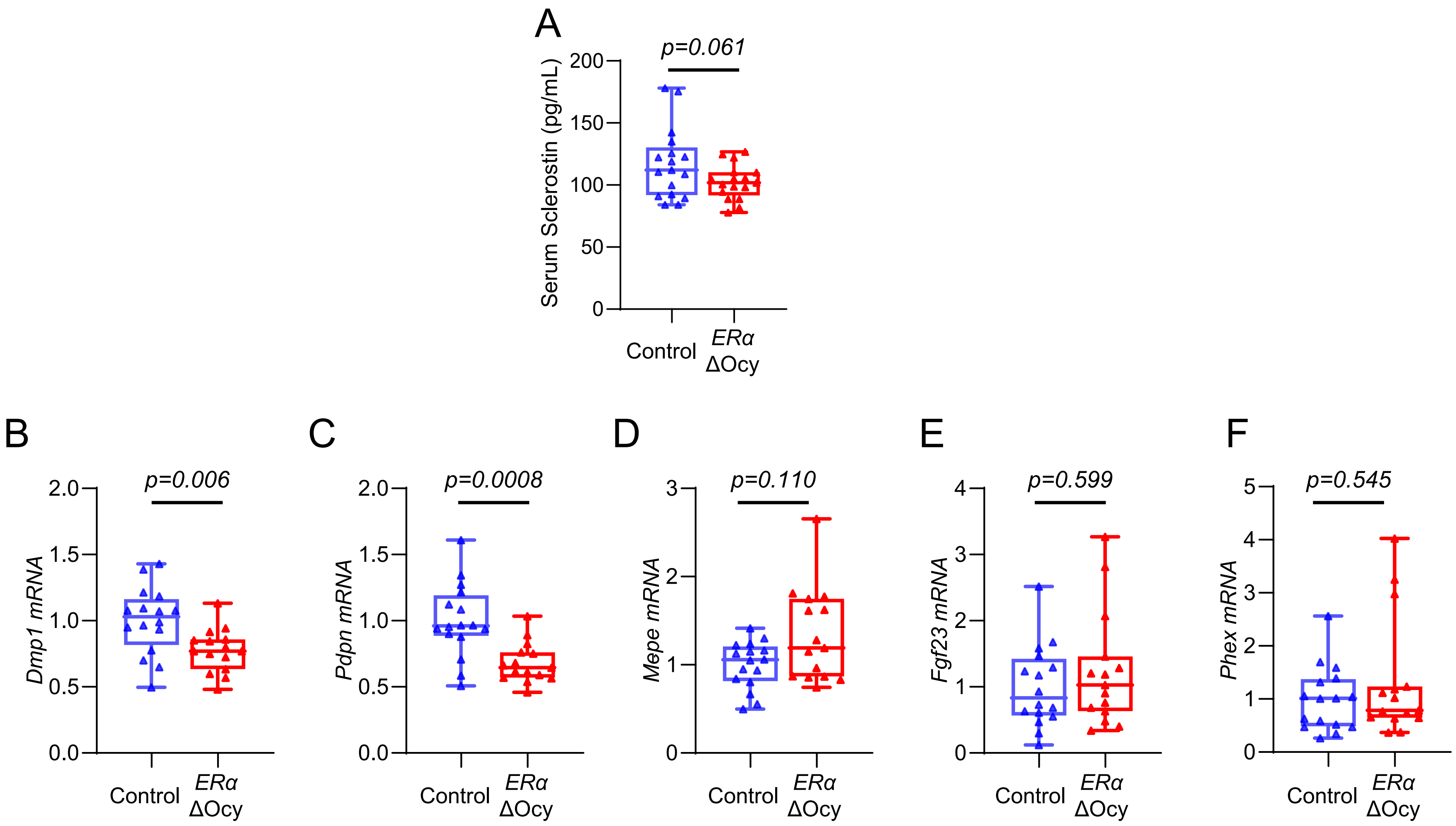
Supplementary Figure 2



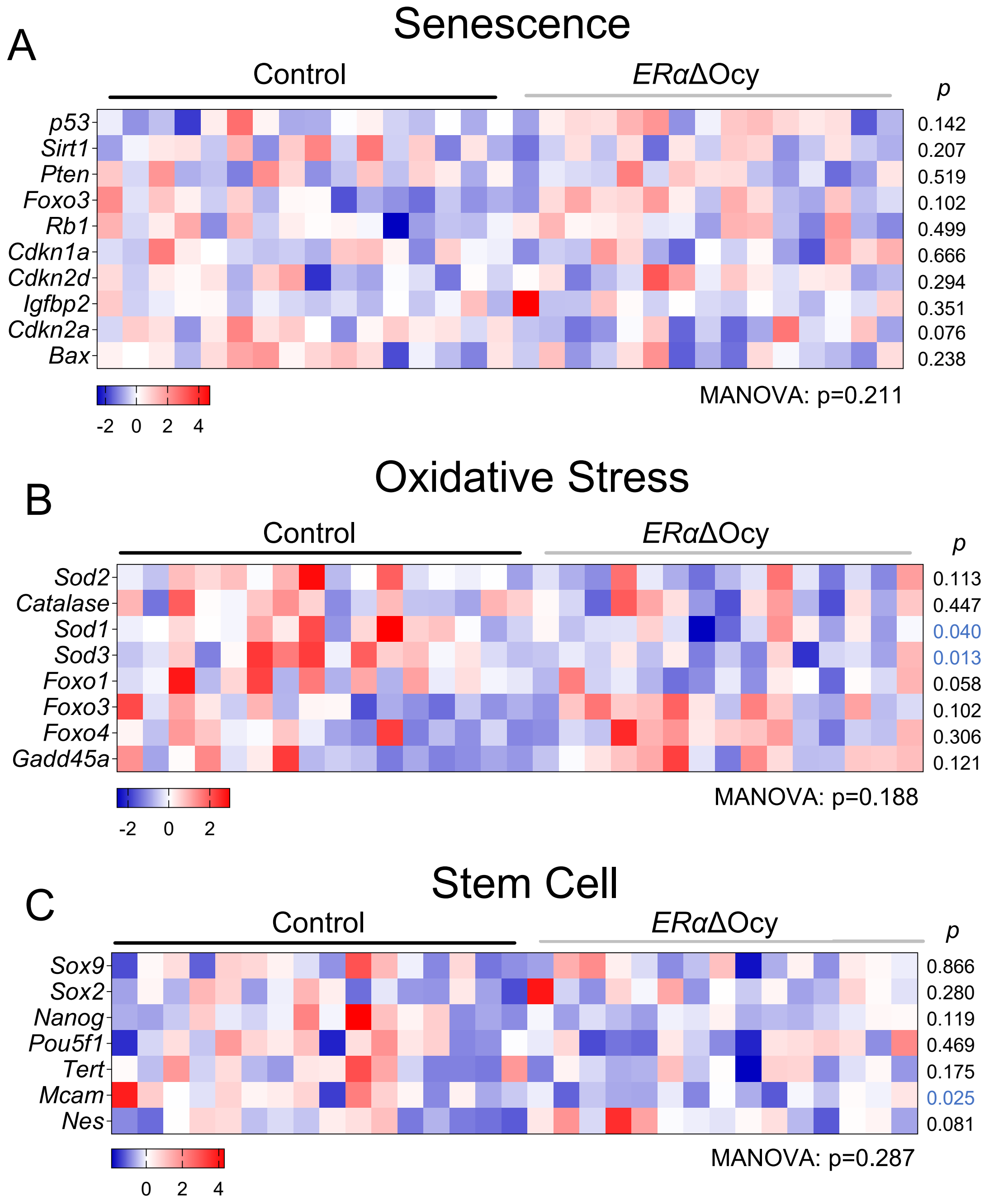
Supplementary Figure 3



Supplementary Figure 4



Supplementary Figure 5



Supplementary Figure Legends

Supplementary Figure 1. Expression of *Dmp1*^{CreERT2} in soft tissues. (A-F) Representative images of induced *TdTomato* expression in various soft tissues of corn oil- versus tamoxifen-treated *Dmp1*^{CreERT2} *x TdTomato* mice. Scale bars = 10μm (10X magnification).

Supplementary Figure 2. ERα deletion in osteocytes reduces femoral trabecular bone mass in female mice, with no significant effect on osteocyte numbers. (A-D) Histological analyses of trabecular bone at the femur metaphysis describing BV/TV, Tb.Th, Tb.N, and Tb.Sp. Osteocyte number per bone area (N.Ot/B.Ar) (E) and % empty lacunae (F) measured histologically at the lumbar spine. n=10-11 mice per group. Boxes represent median and interquartile range and whiskers represent minimum and maximum values. Datasets analyzed by unpaired t-test.

Supplementary Figure 3. ERα deletion in osteocytes does not significantly alter bone mass in adult male mice. (A-D) Micro-CT analyses of trabecular bone at the lumbar spine describing BV/TV, Tb.Th, Tb.N, and Tb.Sp. (E-G) Longitudinal Tib. Dia. micro-CT analyses of cortical bone showing % change between baseline and endpoint describing EC, PC, and Ct.Th. n=15-20 mice per group. Boxes represent median and interquartile range and whiskers represent minimum and maximum values. Datasets analyzed by unpaired t-test.

Supplementary Figure 4. (A) Serum sclerostin levels in the Control and *ERα*ΔOcy mice. (B-F) Osteocyte genes and their expression in Control and *ERα*ΔOcy mice. (B) *Dmp1* is significantly reduced in the *ERα*ΔOcy mice, as is (C) *Pdpn*, while neither *Mepe* (D), *Fgf23* (E) or *Phex* (F) are significantly altered. Boxes represent median and interquartile range and whiskers represent minimum and maximum values. Datasets analyzed by Mann-Whitney test.

Supplemental Figure 5. *ERα*ΔOcy mice do not exhibit disrupted gene expression in stress or stem cell signaling pathways. (A-C) Heatmap of mRNA expression changes in (A) senescence, (B) oxidative stress, and (C) stem cell signaling pathways from spines of tamoxifen-treated Control and *ERα*ΔOcy mice by qRT-PCR. Datasets analyzed by MANOVA, with pathway-level significance-values listed below each heatmap and individual gene p-values beside each row; blue font indicates significantly downregulated gene in the *ERα*ΔOcy mice

Supplementary Table 1. Primers used for qRT-PCR analyses. Each primer shows forward and reverse sequences, along with the assigned pathway for the MANOVA analyses.

Pathway	***Gene***	***Forward Primer Sequence***	***Reverse Primer Sequence***
Osteoblast	*Bglap*	CCTGAGTCTGACAAAGCCTTCA	GCCGGAGTCTGTTCACTACCTT
	Runx2	GGCACAGACAGAAGCTTGATGA	GAATGCGCCCTAAATCACTGA
	Spp1	CCCGGTGAAAGTGACTGATTCT	GATCTGGGTGCAGGCTGTAAA
	Col1α1	GCTTCACCTACAGCACCCTTGT	TGACTGTCTTGCCCCAAGTTC
	Col1α2	TTGCTGCTTGCAGTAACTTCGT	TTTCGTACTGATCCCGATTGC
	Ibsp	CCAAGAAGGCTGGAGATGCA	TTCCTCGTCGCTTTCCTTCA
	Alpl	CACAGATTCCCAAAGCACCT	GGGATGGAGGAGAGAAGGTC
	Sparc	GAGGAGGTGGTGGCTGACAA	CACCTTGCCATGTTTGCAAT
	Sp7	AAGTTCACTTGCCTGCTCTGTT	TGCGCTGATGTTTGCTCAAG
Wnt Signaling	*Ccnd1*	AGAAGGAGATTGTGCCATCCAT	CTCACAGACCTCCAGCATCCA
	Postn	TCCCGACTTCAGGCTGATTAA	ATGACTGGCTCTCCGTGGAT
	Lef1	CTGGCAAGGTCAGCCTGTTTA	GTGTCGCCTGACAGTGAGGAT
	Axin2	CGCCACCAAGACCTACATACG	ACATGACCGAGCCGATCTGT
	Cyr61	CAGCTCACTGAAGAGGCTTCCT	GCGTGCAGAGGGTTGAAAAG
	Ephb4	CCTCGCCACTGCTTTAGAAGAG	ATTTCAGATCCGCCGTTTCC
	Gja1	ACAAGTCCTTCCCCATCTCTCA	GGGCACAGACACGAATATGATC
	Tcf7	CGGTCAAGGGAAAAACATCAA	CGGGTAAGTACCGAATGCATTT
	Vcan	ATGCGCTTCTTGCTGGCTAT	TTCCATCGTTGGGAGTCACA
	Fosl1	CCGAAGAAAGGAGCTGACAGA	CCGATTTCTCATCCTCCAATTT
	Tnfrsf11b (Opg)	CCAAGAGCCCAGTGTTTCTT	CCAAGCCAGCCATTGTTAAT
BMP Signaling	*Hes1*	AACACGACACCGGACAAACC	TTCGCCTCTTCTCCATGATAGG
	Id2	CCCAGAACAAGAAGGTGACCAA	TGCAGGTCCAAGATGTAATCGA
	Klf10	TTCAGACAGTCCCAGCATTTTG	TGGGAGGGTTCGAAGTCAGA
	Id1	AGATCCTGCAGCATGTAATCGA	CCCGACTTCAGACTCCGAGTT
	JunB	AGTGCTGCCGGTCTCCTAAG	CTTGACCCCTAGCAGCAACTG
	Smad6	GCCACTGGATCTGTCCGATT	GAGCAGTGATGAGGGAGTTGGT
	Zeb1	CACAGTGGAGAGAAGCCATACG	GGAGCCAGAATGGGAAAACC
	Sox4	GGGCAGTTTCAGCTCCTCATC	GCCGGGTTCGAAGTTAAAATC
	Lox	ACCTGCTTGATGCCAACACA	CTCCAGACAGAAGCTTGCTTTG
	Smad7	TTTGCCTCGGACAGCTCAAT	GATCTTGCTCCGCACTTTCTG
Notch Signaling	*Jag1*	CTGTGTGGATGAGATCAATGG	TATGTCCTGGAGGGCAGATAC
	Notch1	CGCAAGAGGCTTGAGATGCT	CCACTTCGCACCTACCTCCAT
	Hey1	CACTGCAGGAGGGAAAGGTTAT	CCCCAAACTCCGATAGTCCAT
	Hes1	AACACGACACCGGACAAACC	TTCGCCTCTTCTCCATGATAGG
	Notch2	CAGTCTGAAGCACACCCCAAT	GGCATGGTGCTCTTGGTGTT
	Hey2	GTGCGCCTTGTCTCTCATCTC	GCCATGGAGGATGTCATCACT
	HeyL	CCTGGTCCTTCCTGCATAGC	GATGGCGAGCTGACTGTTCAG
	Jag2	ATCAATGCTGAGCCTGACCAAT	TCGCAGTTCTTGCCCAAGTA
Proliferation	*Ccnd1*	AGAAGGAGATTGTGCCATCCAT	CTCACAGACCTCCAGCATCCA
	E2F1	TGACCACCAAACGCTTCTTG	GCTGCCCAGTTCAGGTCAAC

	Ccne1	CGTCTAAGCCCTCTGACCATTG	CGTTGACATAGGCCACTTGGA
	Ccnb1	CTCCCTGCTTCCTGTTATGCA	GTGCTTTGTGAGGCCACAGTT
	Ccnb2	AAGCCGGAGAGGTGGATGTT	GAGCGTCAGCTCCATCAGGTA
	Ccnc	CCCTTGCATGGAGGATAGTGAA	GAACGGAGGGTACAGCAGACA
	Mki67	AGACTGCCTCCCAGGAGACA	GGCCCCGAGATGTAGATTTCT
	Ccna2	GAAGAGGCAGCCAGACATCAC	CTCAACCAGCCAGTCCACAA
Apoptosis	*Bad*	GCAGGCACTGCAACACAGAT	TCCCACCAGGACTGGATAATG
	Bax	CGGCGAATTGGAGATGAACT	GTCCACGTCAGCAATCATCCT
	Bcl2	CGGGAGATCGTGATGAAGTACA	ATCTCCAGCATCCCACTCGTA
	Bcl2l1	AGGCCCCAGAAGAAACTGAAG	AGGATGGGTTGCCATTGATG
	Birc5	CCGAGAACGAGCCTGATTTG	GTTCCCAGCCTTCCAATTCC
	Casp8	GCCACCTTCAGTTTTGGATGA	CTCTTGGCGAGTCACACAGTTC
	Casp3	TGCACATTCTCACTCGCGTTA	TCCAGGGAGAAGGACTCGAA
	Fasl	CCGCTCTGATCTCTGGAGTGA	CACGAAGTACAACCCAGTTTCG
	Fas	CTGCACCCTGACCCAGAATAC	ACAGCCAGGAGAATCGCAGTA
Senescence	*Trp53 (p53)*	TCTTATCCGGGTGGAAGGAAA	GGCGAAAAGTCTGCCTGTCTT
	Sirt1	GCAGGTTGCAGGAATCCAAA	GGCAAGATGCTGTTGCAAAG
	Pten	CCCAGTCAGAGGCGCTATGTA	GTGCCACGGGTCTGTAATCC
	Foxo3	CAACCGGCTCCTTCAACAGTA	GGTGACTGACGCAAGGAGTTC
	Rb1	AAACAGCTGCAATCCCCATTA	GCGCTCCTGTTCTGACCTCTT
	Cdkn1a (p21)	GAACATCTCAGGGCCGAAAA	TGCGCTTGGAGTGATAGAAATC
	Cdkn2d (p19)	GCGATAAGAGAGGGCCATAGC	CCTGTGGTGGAGATCAGATTCA
	Igfbp2	GCCCCCTGGAACATCTCTACT	GTTGTACCGGCCATGCTTGT
	Cdkn2a-p16ink4a	GAACTCTTTCGGTCGTACCC	AGTTCGAATCTGCACCGTAGT
	Bax	CGGCGAATTGGAGATGAACT	GTCCACGTCAGCAATCATCCT
Oxidative Stress	*Sod2*	CCCAGACCTGCCTTACGACTAT	CTGCATGATCTGCGCGTTAA
	Catalase	GGTGCGGACATTCTACACAAAG	TGTTCTCACACAGGCGTTTCC
	Sod1	GTTGGAGACCTGGGCAATGT	CACACGATCTTCAATGGACACA
	Sod3	CCTTCTTGTTCTACGGCTTGCT	AGCTGGACTCCCCTGGATTT
	Foxo1	TTCTCTCGTCCCCAACATCTTT	AATAGCATGGTGTCTGCTGCAT
	Foxo3	CAACCGGCTCCTTCAACAGTA	GGTGACTGACGCAAGGAGTTC
	Foxo4	CCACGAAGCAGTTCAAATGCT	TTCAGACTCCGGCCTCATTG
	Gadd45a	GGACTCGCACTTGCAATATGAC	GTGTCCATCCTTTCGGTCTTCT
Stemness	*Sox9*	GCGTGCAGCACAAGAAAGAC	TCCGTTCTTCACCGACTTCCT
	Sox2	GCACAACTCGGAGATCAGCAA	CTCGGTCTCGGACAAAAGTTTC
	Nanog	AGTGGAGTATCCCAGCATCCA	TCCAGATGCGTTCACCAGATAG
	Pou5f1	GAGGAGTCCCAGGACATGAAAG	GCTTCAGCAGCTTGGCAAAC
	Tert	GGTCACATTGCAGGTTTCGA	GGCTGGTGTTCAAGGCATCT
	Mcam	TGATTTTCCGTGTGCACCAA	GGCTAAGGCGGTGCTCATATT
	Nes	AGGCGCTGGAACAGAGATTG	TCCACAGCCAGCTGGAACTT
Independently Run	*Cxcl12 (SDF-1)*	GCCAACGTCAAGCATCTGAAA	CAGCCGTGCAACAATCTGAA
	Sost (Sclerostin)	ACTTGTGCACGCTGCCTTCT	TGACCTCTGTGGCATCATTCC
	Sostdc1	CGTGCAAGTGCAAGAGGTACA	GCGACACGCTTTCAAAGTTGT
	Tnfsf11 (Rankl)	GCTGGGACCTGCAAATAAGT	TTGCACAGAAAACATTACACCTG

Housekeeping	*Tbp*	CTTCACCAATGACTCCTATGACCC	CGCAGTTGTCCGTGGCTCTCTTA
	Gapdh	GGGAAGCCCATCACCATCTT	GCCTCACCCCATTTGATGTT
	Actb	AATCGTGCGTGACATCAAAGAG	GCCATCTCCTGCTCGAAGTC
	Hprt	CGTGATTAGCGATGATGAACCA	TCCAAATCCTCGGCATAATGA
	Tuba1a	GGTTCCCAAAGATGTCAATGCT	CAAACTGGATGGTACGCTTGGT