

## A Missense Variant in TP53 Could Be a Genetic Biomarker Associated to Bone Tissue Alterations

### Supplementary Materials

**Supplementary Table S1.** Bone morphometry parameters in 72Arg-p53 and 72Pro-p53 mice.

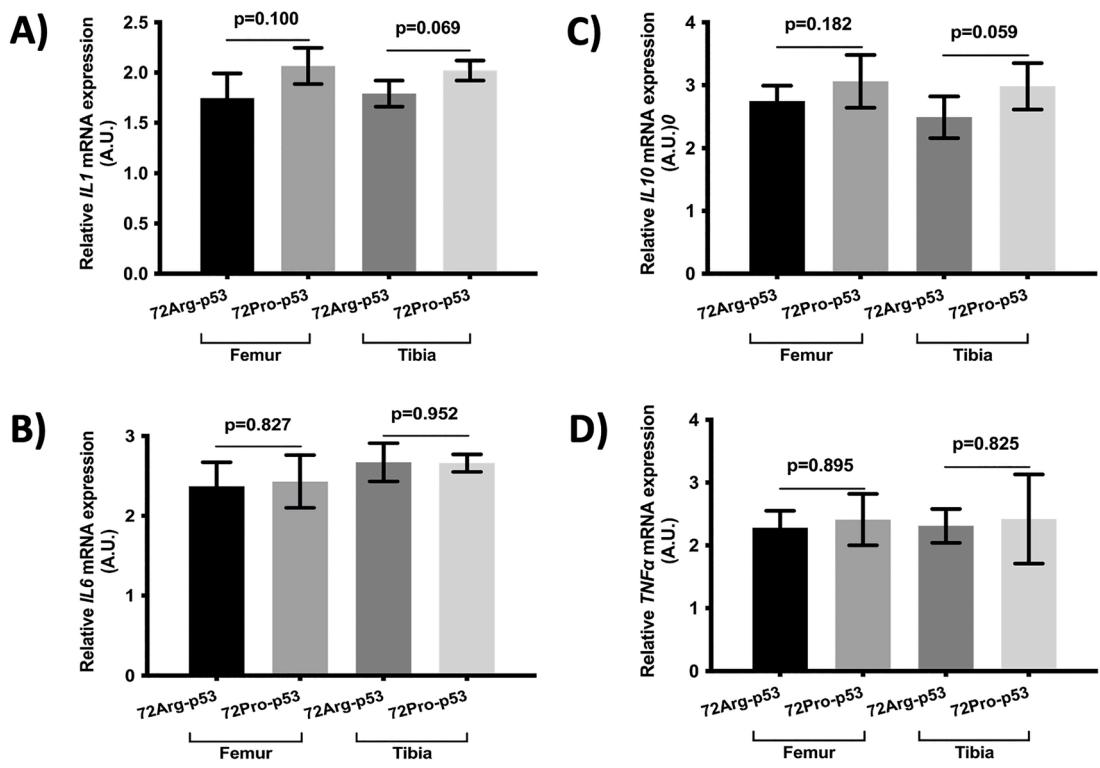
Bone morphometry parameters (mean (SD))	Femur		Tibia			
	72Arg-p53	72Pro-p53	p-value	72Arg-p53	72Pro-p53	p-value
Cortical Thickness	0.5477 (0.039)	0.5561 (0.0481)	0.808	0.4593 (0.041)	0.4329 (0.034)	0.730
Trabecular percent bone volume (BV/TV)	15.1 (1.6)	11.9 (0.7)	0.040	16.4 (0.8)	13.1 (1.1)	0.013
Trabecular number (Tb.N)	11.2 (2.3)	9.1 (0.6)	0.022	8.2 (0.6)	5.9 (0.4)	0.009
Trabecular separation (Tb.S)	0.12 (0.005)	0.15 (0.009)	0.006	0.10 (0.018)	0.14 (0.020)	0.041
Trabecular thickness (Tb.Th)	0.029 (0.004)	0.027 (0.001)	0.449	0.027 (0.002)	0.017 (0.003)	0.015

**Supplementary Table S2.** Scan parameters.

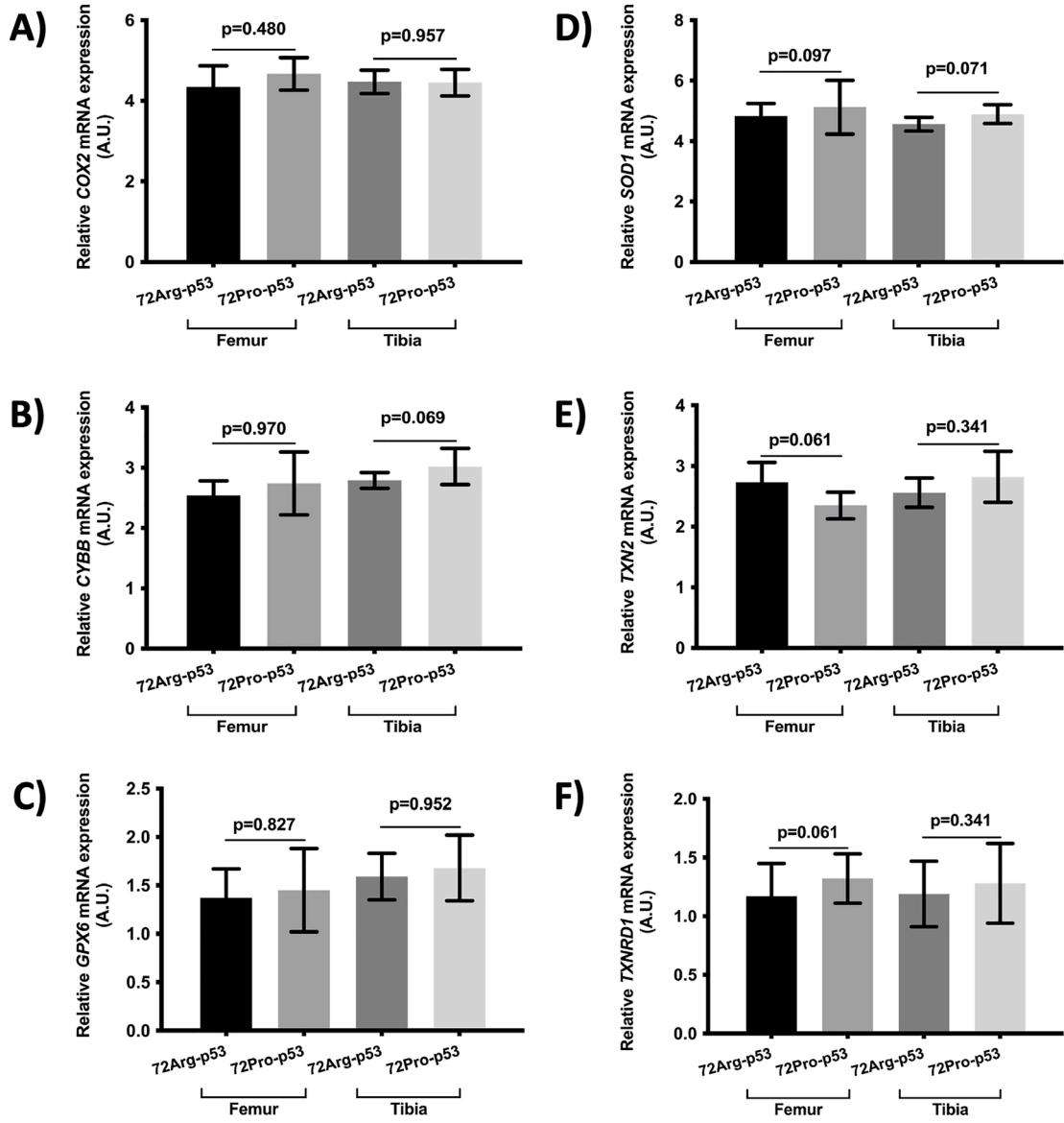
Variable	Standard Unit	Value
Voxel size	µm <sup>3</sup>	300.76
Source Voltage	kV	50
Source Current	µA	100
Exposure time	ms	4920
Frame averaging	N	5
Projections	N	130

**Supplementary Table S3.** Gene-specific primer sequences for real-time quantitative PCR.

Gene	Primer sequence ( 5' to 3')
<i>OPG-Fwd</i>	TACCTGGAGATCGAATTCTGCTT
<i>OPG-Rev</i>	CCATCTGGACATTTTGCAAA
<i>RANKL-Fwd</i>	CCTGAGGCCAGCCATT
<i>RANKL-Rev</i>	CTTGGCCCAGCCTCGAT
<i>BCL2-Fwd</i>	TTCAGGGATGGGTGAAGTG
<i>BCL2-Rev</i>	CACAGGGCGATGTTGT
<i>BAX-Fwd</i>	CCCGAGAGGTCTTCTTCC
<i>BAX-Rev</i>	GCCTTGAGCACCAAGTTG
<i>CASP3-Fwd</i>	GTGGACTCTGGATCTATCT
<i>CASP3-Rev</i>	CCATGAATGTCTCTGAGG
<i>CASP8-Fwd</i>	CGGGAAGACATAACCCAAC
<i>CASP8-Rev</i>	GTGGGATAGGATACAGCAGA
<i>CASP9-Fwd</i>	AGTTCCGGGTGCTGTCTAT
<i>CASP9-Rev</i>	GCCATGGTCTTCTGCTCAC
<i>IL1-Fwd</i>	ACAAACCACCCGTTCACCT
<i>IL1-Rev</i>	ATGGGTGGAGGGTTCACTCT
<i>IL6-Fwd</i>	GAGGATACCACTCCAACAGACC
<i>IL6-Rev</i>	AAGTGCATCATCGTTGTTCATACA
<i>IL10-Fwd</i>	GCTCTTAATGACTGGCATGAG
<i>IL10-Rev</i>	CGCAGCTCTAGGAGCATGTG
<i>TNF<math>\alpha</math>-Fwd</i>	ACCCTCACACTCAGATCATCTTC
<i>TNF<math>\alpha</math>-Rev</i>	TGGTGGTTGCTACGACGT
<i>COX2-Fwd</i>	AACCGAGTCGTTCTGCCAAT
<i>COX2-Rev</i>	GGGACTGCTCATGAGTGGAG
<i>CYBB-Fwd</i>	GACCTCCCAGAGAACACAGC
<i>CYBB-Rev</i>	ACCCTAGCCTGCTTATGGGA
<i>GPX6-Fwd</i>	GTCACGGTTTGGGCTTCC
<i>GPX6-Rev</i>	CCCCCTCTCAAAGAGCTGG
<i>SOD1-Fwd</i>	GGAACCATCCACTCGAGCA
<i>SOD1-Rev</i>	CCCATGCTGGCCTTCAGTTA
<i>TXN2-Fwd</i>	CTGTAGCCTGACCGCACTAG
<i>TXN2-Rev</i>	AGGCAGGAGAGGAAATGTGC
<i>TXNRD1-Fwd</i>	CTCGGAGGAACGTGTGAA
<i>TXNRD1-Rev</i>	AGTTGCGCGAGTCTTCAGA
<i>GAPDH-Fwd</i>	TGCACCACCAACTGCTTAGC
<i>GAPDH-Rev</i>	CACCACTTCTGATGTCATCA



**Supplementary Figure S1.** Relative mRNA expressions of inflammation-related genes in femur and tibia bone tissue. Relative mRNA expressions of IL1 gene (A), IL6 gene (B), IL10 gene (C), and TNFa gene (D). Bars represent mean values and their respective standard deviation. A.U.: arbitrary units



**Supplementary Figure S2.** Relative mRNA expressions of oxidative stress-related genes in femur and tibia bone tissue. Relative mRNA expressions of COX2 gene (A), CYBB gene (B), GPX6 gene (C), SOD1 gene (D), TXN2 gene (E), and TXNRD1 gene (F). Bars represent mean values and their respective standard deviation. A.U.: arbitrary units.