

Table S1. Mendelian ratio.

Gender	Genotype	
	flox/flox +/+	flox/flox cre/+
Female	43 (32%)	29 (22%)
Male	33 (25%)	28 (21%)
Total	76 (57%)	57 (43%)

Mendelian ratio of offspring from $Men1^{flox}$ ($Men1^{flox/flox}; +/+$) \times $Men1^{Runx2Cre}$ ($Men1^{flox/flox}; Tg(Runx2-cre)/+$). Data are shown as mouse numbers with percentage in parentheses.

Table S2. Cancellous parameters measured by micro CT.

Group	n	Age	Gender	Bone		BV/TV (%)	Tb.Th. (μm)	Tb.N. (per μm)	Tb.Sp. (μm)
1	5	12 weeks	Male	Femur	<i>MenI</i> ^{fllox}	7.50 \pm 0.64	51.73 \pm 9.68	0.00185 \pm 0.00055	304.2 \pm 80.15
	5				<i>MenI</i> ^{Runx2Cre}	3.80 \pm 0.43**	52.34 \pm 9.22	0.00084 \pm 0.00019	377.1 \pm 92.48
2	5	12 weeks	Female	Tibia	<i>MenI</i> ^{fllox}	1.95 \pm 0.25	44.94 \pm 2.91	0.00044 \pm 0.00006	681.1 \pm 35.34
	5				<i>MenI</i> ^{Runx2Cre}	0.94 \pm 0.10**	39.98 \pm 1.34	0.00024 \pm 0.00003*	596.4 \pm 75.96
3	6	12 weeks	Female	Vertebra	<i>MenI</i> ^{fllox}	14.02 \pm 0.75	96.58 \pm 3.09	0.00145 \pm 0.00006	481.6 \pm 7.89
	6				<i>MenI</i> ^{Runx2Cre}	11.92 \pm 0.54*	101.7 \pm 2.73	0.00118 \pm 0.00005**	493.4 \pm 21.20
4	6	12 weeks	Female	Femur	<i>MenI</i> ^{fllox}	3.87 \pm 0.62	62.55 \pm 2.42	0.00061 \pm 0.00008	380.7 \pm 11.39
	6				<i>MenI</i> ^{OsxCre}	0.83 \pm 0.14***	54.45 \pm 2.12*	0.00015 \pm 0.00002***	828.7 \pm 68.07***

Parameters are shown as bone volume per tissue volume (BV/TV), trabecular thickness (Tb.Th.), trabecular numbers (Tb.N.), and trabecular separation (Tb.Sp.) (n=3–6; * p < 0.05, ** p < 0.01, *** p < 0.001). Data are represented as mean \pm SEM.

Table S3. Cortical thickness and porosity determined by micro CT.

Age	Gender	Tissue		Cs.Th. (μm)	Porosity (%)
12 weeks	Female	Femur	<i>MenI</i> ^{fllox}	174.9 \pm 8.18	0.21 \pm 0.19
			<i>MenI</i> ^{Runx2Cre}	164.6 \pm 11.61	0.08 \pm 0.05

Parameters are shown as cross-sectional thickness (Cs.Th.) and porosity. (n=4 or 5).

Data are represented as mean \pm SEM.

Table S4. Microarray-revealed differentially expressed genes and their expression levels (log₂ scale).

Upregulated in *Men1*-deficient primary osteocytes

Gene symbol	Expression level (log ₂ scale)		Fold change
	Ctrl	<i>Men1</i> -deficient	
F13a1	7.35618	9.695811	5.06
Saa3	9.465763	11.42916	3.90
Mmp13	10.7719	12.56339	3.46
Hpse	8.150388	9.541623	2.62
Fcgr2b	9.995169	11.24563	2.38
Mcpt8	7.323074	8.41571	2.13
Cp	9.710932	10.76933	2.08
Apoc2	8.689564	9.585059	1.86
Cxcl5	8.230485	9.12476	1.86
Lcn2	8.23552	9.036465	1.74
Npy	8.112924	8.899504	1.72
Wif1	8.13022	8.886517	1.69
Apoe	8.772759	9.513904	1.67
Cd5l	8.948753	9.671456	1.65
Trf	9.717886	10.4178	1.62
Lgals3bp	10.97108	11.66893	1.62
Tinagl1	9.096196	9.777411	1.60
Mmp8	9.338769	9.993589	1.57
Hp	7.629641	8.278437	1.57
Plbd1	7.68419	8.328152	1.56
Acan	7.746571	8.38426	1.56
Ccl3	9.981727	10.60944	1.55
Ngf	9.31053	9.937298	1.54
Siglec1	10.1172	10.74208	1.54
Acpp	7.415874	8.037115	1.54
Ccl6	7.024841	7.617164	1.51
Il4ra	11.12462	11.68265	1.47
Mmp12	9.385585	9.935935	1.46
Cxcl10	7.668655	8.21177	1.46
Pla2g7	10.87439	11.36798	1.41

Downregulated in *Men1*-deficient primary osteocytes

Gene symbol	Expression level (log2 scale)		Fold change
	Ctrl	<i>Men1</i> -deficient	
Matn2	10.25597	9.840894	0.75
Postn	12.43594	12.01974	0.75
Ccdc80	9.717469	9.297493	0.75
Fam180a	9.605881	9.157597	0.73
Col18a1	9.433644	8.980346	0.73
Fam19a1	8.077728	7.61897	0.73
Lamb2	11.61246	11.14792	0.72
Igfbp4	12.73658	12.26349	0.72
Lama1	8.851841	8.361239	0.71
Fst	11.20136	10.67059	0.69
Tgfb2	10.14087	9.604809	0.69
Col6a2	11.66239	11.11617	0.68
Ltbp3	10.5877	10.04005	0.68
Ptn	11.63688	11.08813	0.68
Adamts5	12.0442	11.49463	0.68
Clec3b	8.115891	7.565344	0.68
Matn4	9.640471	9.084593	0.68
Pgf	8.150695	7.594744	0.68
Hhip	7.710243	7.15002	0.68
Fbln5	11.93608	11.37126	0.68
Eda	9.347228	8.777605	0.67
Bmp5	7.846486	7.275277	0.67
Arsi	9.261346	8.687857	0.67
Timp3	12.63602	12.05095	0.67
Vit	8.152734	7.562057	0.66
Nov	12.20697	11.61445	0.66
Svep1	12.08025	11.48415	0.66
Omd	10.42361	9.821304	0.66
Lgi2	8.502823	7.867727	0.64
Ucma	9.251044	8.610236	0.64
Slit3	11.92557	11.28276	0.64
Wisp2	12.93158	12.28748	0.64
Podn	11.33899	10.69049	0.64
Pdgfrl	10.16468	9.51122	0.64
Igfbp5	11.5805	10.92281	0.63
Col11a1	10.43427	9.773326	0.63
Adamts12	9.641748	8.979573	0.63
Nid2	11.1511	10.48538	0.63

Gene symbol	Expression level (log2 scale)		Fold change
	Ctrl	<i>Men1</i> -deficient	
Thsd4	9.364558	8.695619	0.63
Mdk	8.691753	7.993898	0.62
Htra3	9.149244	8.436374	0.61
Ecm2	7.495006	6.777874	0.61
Bmp6	8.430196	7.700482	0.60
Kazald1	9.239113	8.49776	0.60
Nog	9.225143	8.476961	0.60
Igsf10	11.56717	10.78823	0.58
Comp	9.126153	8.345913	0.58
Egfl6	11.31441	10.52462	0.58
C1qtnf7	7.203754	6.413078	0.58
Itih5	7.934453	7.136135	0.58
Ism1	10.0227	9.196692	0.56
Ostn	8.073424	7.223412	0.55
Mfap5	11.6336	10.77945	0.55
Igf2	10.50575	9.61452	0.54
Eln	8.465084	7.563308	0.54
Cdsn	11.28851	10.38523	0.53
Dkk2	10.89053	9.987156	0.53
Lama2	9.887217	8.980033	0.53
Hapln1	10.20322	9.295397	0.53
Clec11a	11.20922	10.30105	0.53
Adamtsl4	9.446327	8.510282	0.52
Igfbp3	10.70945	9.765949	0.52
Npnt	10.83807	9.884694	0.52
Spock3	9.324848	8.341289	0.51
Rspo3	12.32692	11.30021	0.49
Gdf6	9.822467	8.764868	0.48
Cpxm2	8.859323	7.785863	0.48
Pi15	7.955539	6.860623	0.47
Fbn2	10.29051	9.18915	0.47
Sod3	11.21276	10.1035	0.46
Ltbp2	12.15063	11.02642	0.46
Epha3	10.19808	9.068214	0.46
Sfrp1	11.59235	10.4572	0.46
Gdf10	11.17581	10.02972	0.45
Col8a2	9.027334	7.843607	0.44
Col14a1	10.30187	9.062504	0.42
C1qtnf3	10.64427	9.351943	0.41
Smoc1	10.44718	9.012997	0.37
Frem1	9.579592	7.988935	0.33
Prss35	10.08394	8.136783	0.26
Chrdl1	9.84583	7.649113	0.22

Rankl and OPG in microarray

Gene symbol	Expression level (log2 scale)		Fold change
	Ctrl	<i>Men1</i> -deficient	
Tnfsf11	7.937284	8.162434	1.17
Tnfrsf11b	10.60535	11.01384	1.33