

Table S1: List of dysregulated miRNAs (n = 46) in studies comparing fibromyalgia patients to healthy volunteers (miRNAs are presented according to their nomenclature).

Differentially expressed microRNAs in fibromyalgia			
microRNA	No. studies	Regulation	References
Same direction for FM and OP			
miR-1	n = 1	↓	[28]
let-7a-5p	n = 1	↓	[29]
miR-9-5p	n = 1	↑	[30]
miR-29a-3p	n = 1	↓	[31]
miR-128-3p	n = 1	↑	[30]
miR-328-3p	n = 1	↓	[30]
miR-335-5p	n = 1	↑	[32]
Opposite direction for FM and OP			
miR-7-5p	n = 1	↑	[30]
miR-23b-3p	n = 1	↓	[31]
miR-107	n = 2	↓	[29,33]
miR-139-5p	n = 1	↓	[28]
miR-143-3p	n = 1	↓	[34]
miR-151a-5p	n = 1	↓	[29]
miR-186-5p	n = 1	↑	[30]
miR-338-3p	n = 1	↓	[34]
miR-766-3p	n = 1	↓	[30]
Same or opposite direction for FM and OP			
miR-21-5p	n = 1	↓	[31]
miR-23a-3p	n = 1	↓	[28]
miR-133a	n = 1	↓	[28]
miR-145-5p	n = 2	↓	[31,34]
miR-148a-3p	n = 1	↑	[30]
miR-320a	n = 1	↑	[29]
miR-532-3p	n = 1	↓	[30]
Other miRNAs found			
let-7d	n = 1	↓	[35]
miR-27b-3p	n = 1	↑	[30]
miR-30b-5p	n = 1	↓	[29]
miR-101-3p	n = 1	↑	[30]
miR-103a-(3p)	n = 3	↓	[29,33,35]
miR-125a-5p	n = 1	↑	[33]
miR-130a-3p	n = 1	↓	[33]
miR-142-3p	n = 1	↓	[29]

miR-146a	n = 1	↓	[35]
miR-182-5p	n = 1	↑	[30]
miR-183-5p	n = 1	↑	[30]
miR-223-3p	n = 2	↓	[31,34]
miR-320b	n = 1	↓	[28]
miR-346	n = 1	↓	[28]
miR-374a-5p	n = 1	↑	[30]
miR-374b-5p	n = 1	↓	[29]
miR-451a	n = 1	↓	[34]
miR-454-3p	n = 1	↑	[30]
miR-548d-5p	n = 1	↑	[30]
miR-625-5p	n = 1	↓	[30]
miR-671-5p	n = 1	↓	[30]
miR-1275	n = 1	↓	[30]
miR-3609	n = 1	↓	[30]

Table S2: List of dysregulated miRNAs (n = 166) in studies comparing osteoporosis patients to healthy volunteers (miRNAs are presented according to their nomenclature).

microRNA	No. studies	Regulation	References
Same direction for FM and OP			
miR-1-3p	n = 2	↓	[36,37]
let-7a-3p	n = 1	↓	[37]
miR-9-(3p or 5p)	n = 2	↑	[38,39]
miR-29a-3p	n = 1	↓	[23]
miR-128	n = 1	↑	[40]
miR-328-3p	n = 1	↓	[41]
miR-335-5p	n = 2	↑	[42,43]
Opposite direction for FM and OP			
miR-7-5p	n = 1	↓	[42]
miR-23b-(3p)	n = 2	↑	[44,45]

miR-107	n = 1	↑	[46]
miR-139-5p	n = 1	↑	[44]
miR-143	n = 1	↑	[47]
miR-151a-3p	n = 2	↑	[48,49]
miR-186-5p	n = 1	↓	[42]
miR-338-3p	n = 1	↑	[50]
miR-766-5p	n = 1	↑	[51]

Same or opposite direction for FM and OP

miR-21-(5p)	n = 12	↑↓	[23,41,43,52–0]
miR-23a-(3p or 5p)	n = 8	↑↓	[23,41,43,52,53,56,59,61]
miR-133a	n = 5	↑↓	[37,57,62–64]
miR-145-(3p or 5p)	n = 2	↑↓	[65,66]
miR-148a-(3p)	n = 5	↑↓	[56,59,66–68]
miR-320a	n = 4	↑↓	[42,53,69,70]
miR-532-(3p or 5p)	n = 4	↑↓	[42,43,71,72]

Other miRNAs found

let-7b-5p	n = 1	↓	[42]
let-7c	n = 1	↑	[73]
let-7g-5p	n = 2	↓	[41,74]
miR-10a-3p	n = 2	↑	[75,76]
miR-10b-5p	n = 3	↑↓	[37,41,66]
miR-15a-5p	n = 1	↓	[77]
miR-15b-5p	n = 1	↓	[66]
miR-16-5p	n = 1	↓	[42]
miR-17-5p	n = 2	↑	[37,44]
miR-17-92a	n = 1	↓	[78]
miR-18a-3p	n = 2	↑	[79,80]
miR-19a-3p	n = 2	↓	[42,81]
miR-19b-3p	n = 4	↑↓	[42,43,66,82]
miR-22-3p	n = 3	↓	[41,74,83]
miR-24-(3p)	n = 3	↑	[56,59,84]
miR-25-(3p or 5p)	n = 3	↑	[51,59,85]
miR-26a	n = 1	↑	[86]
miR-27a-(3p)	n = 4	↑↓	[87–90]
miR-29b-3p	n = 3	↓	[42,91,92]
miR-30(a-5p)	n = 3	↑↓	[93–95]
miR-30c-5p	n = 1	↓	[42]
miR-31	n = 1	↑	[96]
miR-34c-3p	n = 1	↑	[37]
miR-92b-3p	n = 1	↓	[66]

miR-93-(5p)	n = 4	↑↓	[42,56,59,97]
miR-96	n = 2	↑	[46,94]
miR-99b-5p	n = 1	↓	[75]
miR-100-(5p)	n = 7	↑	[37,41,56,59,84,98,99]
miR-106b-5p	n = 1	↓	[66]
miR-122(a-5p)	n = 5	↑↓	[56,58,59,67,100]
miR-124(a-3p)	n = 3	↑	[23,56,59]
miR-125b-(5p)	n = 9	↑↓	[41,52,56,58,59,84,94,101,102]
miR-127-(3p or 5p)	n = 3	↑↓	[38,41,103]
miR-133b	n = 1	↓	[37]
miR-135a-5p	n = 1	↑	[104]
miR-135b-5p	n = 1	↑	[105]
miR-137-(3p)	n = 2	↑	[38,106]
miR-138-5p	n = 1	↑	[38]
miR-140-(3p or 5p)	n = 3	↑↓	[42,44,107]
miR-144-(3p or 5p)	n = 4	↑↓	[66,84,108,109]
miR-150-(5p)	n = 2	↑↓	[110,111]
miR-152-3p	n = 2	↓	[42,43]
miR-155-(5p)	n = 3	↑↓	[112–114]
miR-181a-2-3p	n = 1	↑	[75]
miR-181c-5p	n = 1	↓	[115]
miR-187	n = 1	↓	[116]
miR-193b-(3p or 5p)	n = 1	↓	[37]
miR-194-5p	n = 1	↑	[117]
miR-195	n = 1	↓	[110]
miR-197-3p	n = 1	↑	[44]
miR-200a-3p	n = 1	↑	[118]
miR-200b-3p	n = 1	↑	[38]
miR-203	n = 2	↓	[119,120]
miR-205-5p	n = 2	↑	[121,122]
miR-206	n = 3	↑↓	[37,38,123]
miR-208a-3p	n = 1	↑	[112]
miR-210-3p	n = 1	↑	[124]
miR-211-5p	n = 1	↓	[125]
miR-214-(3p)	n = 2	↑↓	[37,126]
miR-215-5p	n = 2	↓	[42,127]
miR-217	n = 2	↑	[128,129]
miR-219a-2-3p	n = 1	↑	[38]
miR-221-(5p)	n = 2	↓	[130,131]
miR-222	n = 1	↑	[110]
miR-224-3p	n = 1	↑	[51]
miR-302a-3p	n = 1	↓	[51]
miR-324-3p	n = 1	↓	[42]

miR-340-5p	n = 1	↑	[109]
miR-361-5p	n = 1	↑	[132]
miR-363-3p	n = 1	↑	[133]
miR-365a-3p	n = 3	↑↓	[42,114,134]
miR-373	n = 1	↓	[135]
miR-374c-3p	n = 1	↓	[66]
miR-375	n = 2	↑	[43,136]
miR-378a-5p	n = 1	↓	[42]
miR-378g	n = 1	↓	[137]
miR-410	n = 1	↑	[138]
miR-422a	n = 1	↑	[139]
miR-423-5p	n = 1	↑	[114]
miR-455-3p	n = 1	↓	[140]
miR-483-(3p or 5p)	n = 4	↑↓	[69,141–143]
miR-485-5p	n = 1	↑	[144]
miR-486-3p	n = 1	↓	[145]
miR-495-3p	n = 1	↓	[38]
miR-497-5p	n = 3	↑↓	[114,115,146]
miR-498	n = 1	↑	[147]
miR-499a-5p	n = 1	↓	[37]
miR-500a-5p	n = 1	↓	[38]
miR-503	n = 1	↓	[148]
miR-506-3p	n = 1	↑	[109]
miR-518(f)	n = 2	↑↓	[41,116]
miR-548aa	n = 1	↑	[37]
miR-548t-3p	n = 1	↑	[37]
miR-548x-3p	n = 1	↑	[149]
miR-550a-3p	n = 1	↓	[42]
miR-579-3p	n = 1	↑	[150]
miR-582-3p	n = 1	↑	[151]
miR-627-5p	n = 1	↑	[37]
miR-629-5p	n = 1	↑	[37]
miR-637	n = 1	↑	[112]
miR-642a-3p	n = 1	↑	[51]
miR-655-3p	n = 1	↓	[75]
miR-668-3p	n = 1	↓	[75]
miR-708-(5p)	n = 2	↑↓	[152,153]
miR-758-3p	n = 1	↓	[75]
miR-760	n = 1	↑	[37]
miR-874-3p	n = 1	↓	[154]
miR-885-5p	n = 1	↑	[44]
miR-889-3p	n = 1	↑	[155]
miR-920	n = 1	↓	[156]

miR-1227-3p	n = 1	↑	[44]
miR-1249-5p	n = 1	↓	[157]
miR-1270	n = 1	↑	[158]
miR-1271-5p	n = 2	↑↓	[38,159]
miR-1286	n = 1	↑	[160]
miR-1297	n = 1	↑	[161]
miR-1299	n = 1	↓	[75]
miR-1915-5p	n = 1	↓	[38]
miR-2278	n = 1	↓	[75]
miR-2861	n = 3	↑↓	[23,41,162]
miR-3065-5p	n = 1	↑	[50]
miR-3119	n = 1	↓	[38]
miR-3168	n = 1	↓	[38]
miR-3190-5p	n = 1	↓	[75]
miR-3191-3p	n = 1	↓	[75]
miR-3656	n = 1	↑	[37]
miR-3678-3p	n = 1	↓	[75]
miR-3679	n = 1	↑	[163]
miR-3690	n = 1	↓	[75]
miR-4274	n = 1	↑	[163]
miR-4516	n = 1	↓	[100]
miR-4665-3p	n = 1	↑	[94]
miR-4731-3p	n = 1	↓	[38]
miR-4767	n = 1	↓	[38]
miR-5009-5p	n = 1	↑	[75]
miR-5914	n = 1	↑	[94]
miR-6511a-3p	n = 1	↑	[37]
miR-6741-3p	n = 1	↑	[38]
miR-4746-3p	n = 1	↓	[38]
miR-6803-5p	n = 1	↑	[38]
miR-6851-3p	n = 1	↑	[109]
miR-6886-3p	n = 1	↓	[38]
miR-8068	n = 1	↑	[109]

Table S3: Characteristics of fibromyalgia studies with miRNAs in common with osteoporosis studies (n = 7)

First author, year	Tissue	Extraction Detection	Study design	Sample size	Age (years)	Gender	Primary outcome	Reference
Bjersing et al., 2013	cerebro spinal fluid	Q q	case-control	10 FM 8 HV	48.5 58.5	FM: 100% F HV: NK	To identify cerebrospinal miRNAs with expression specific for FM and to determine their correlation to pain and fatigue.	[31]
Bjersing et al., 2015	serum	Q q	case-control	20 FM 20 HV	52.5	100% F	To identify characteristic miRNAs in FM and relations of specific miRNAs with characteristic symptoms	[29]
Braun et al., 2020	white blood cell	Q q	case-control	31 FM 16 HV	50.7 NK	FM: 100% F HV: NK	To identify miRNA signatures distinguishing patient clusters with FM.	[33]
Cerdá-Olmedo et al., 2015	peripheral blood mononuclear cells	ITF q	case-control	11 FM 10 HV	50.7 47.5	FM: 100% F HV: NK	To identify changes in miRNA expression profiles (miRNome) of FM patients for the development of a quantitative diagnostic method of FM	[34]
Clos-Garcia et al., 2019	serum	NK m	case-control	36 FM 36 HV	52,52 ± 10,3 53,5 ± 12,4	FM: 69,5% F, 30,48% M HV: 48,15% F, 51,85% M	To identify potential molecular biomarkers for FM diagnosis and characterization, with different omics technologies.	[32]
Erbacher et al., 2022	whole blood	TF q	case-control	49 FM 25 HV	53	100% F	To profile microRNA regulators of cholinergic transcripts (CholinomiRs)	[30]
Masotti et al., 2017	serum (& saliva)	Q q	case-control	14 FM 14 HV	NK	100% F	To investigate the c-miRNA profiles in FM, correlating their expression with clinical and clinimetric parameters and to suggest a mathematical model for the diagnosis of FM	[28]

Abbreviations: c-miRNA, circulating miRNA; F, Female; FM, fibromyalgia; HV, Healthy Volunteers; ITF, Invitrogen Thermo Fisher; M, Male; m, multiplex assays; NK, not know; q, Quantitative Reverse Transcription Polymerase Chain Reaction; Q, Qiagen; TF, Thermo Fisher

Table S4: Characteristics of osteoporosis studies with miRNAs in common with fibromyalgia studies (n = 38)

First author, Year	Tissue	Extraction Detection	Study design	Gender	Sample size	Age (years)	Primary outcome	Reference
Al-Rawaf et al., 2021	serum	Q q	cross-sectional	100% F PM	55 OP 45 HV	63.9 ± 3.2 62.6 ± 4.1	Potential diagnostic role of circulating miRNAs, miR-148a and miR-122-5p, in the pathogenesis of OP and its association with bone markers, hypercortisolism, and vitamin D deficiency	[67]
Bedene et al., 2016	plasma	Q q	case-control	100% F PM	17 OP 57 HV	62 61	To identify c-miRNAs which could serve as potential biomarkers.	[68]
Chen et al., 2018	serum	ITF q	cross-sectional	NK	9 OP 9 HV	69.2 ± 2.7 67.1 ± 2.6	To find the early diagnostic marker for OP using c-miRNAs	[41]
Chen et al., 2019	serum	Q q	case-control	100% F PM	46 OP 13 HV	69.6 ± 5.6 68.9 ± 6.5	To examine the difference in bone and muscle specific c-miRNAs in PM women based on their bone and muscle status, and to determine the associations between these specific c-miRNAs and muscle and bone variables	[52]
Ciuffi et al., 2022	serum	Q NGS	case-control	OP: 74% F, 26% M HV: 73.3% F, 36.7% M	50 OP 30 HV	68.0 ± 4.9 67.2 ± 5.0	Measure global miRNA expression in OP vs normal BMD.	[53]
Cong et al., 2020	plasma	ITF q	cross-sectional	42 F, 24 M for OP and HV	66 OP 66 HV	54,1 ± 5,3 54,3 ± 5,2	To investigate the interactions between miR-21 and GAS5	[54]
De-Ugarte et al., 2015	bone	Q q	cross-sectional	100% F PM	6 OP 6 HV	75,16 ± 3,54 72,5 ± 7,42	To identify miRNAs differentially expressed in fractured vs non-fractured bones.	[69]
Fu et al., 2020	whole blood	ITF q	cross-sectional	100% F	11 PM OP 11 HV	NK	To investigate the expression level of miR-151a-3p and asses it effects on bone formation and resorption	[48]
Fu et al., 2021	serum	ITF q	cross-sectional	OP: 73.2% F, 26.8% M HV: 73.4% F, 26.6% M	82 OP 79 HV	50.48 ± 3.5 49.68 ± 4.17	To investigate the effects of ROR and miR-145-5p on the proliferation and apoptosis of osteoblasts.	[65]

Table S4: Continued

First author, Year	Tissue	Extraction Detection	Study design	Gender	Sample size	Age (years)	Primary outcome	Reference
Gao et al., 2018	hBMSCs	ITF q	cross-sectional	2 F, 1 M for OP and HV	3 OP 3 HV	47 - 66 45 - 63	To investigate whether MALAT1 regulates Osterix expression by sponging miR-143 to promote hBMSCs osteogenic differentiation.	[47]
Gu et al., 2020	hBMSCs	ITF s	cross-sectional	100% F	29 PM OP 20 HV	67.5 ± 9.52 65.27 ± 7.63	To identify miRNAs and investigate the role of miR-1-3p in the shift from OP and adipogenesis of hBMSCs in vitro and bone metabolism in vivo.	[36]
Guo et al., 2020	bone	ITF q	cross-sectional	100% F PM	10 OP 10 HV	62.15 ± 3.54 63.44 ± 6.07	To investigate whether miR-532-5p plays a role in the regulation of osteoporosis.	[71]
He et al., 2021	serum	ITF q	cross-sectional	100% F PM	15 OP 15 HV	57 - 80 61 - 76	To explore the biological functions of miRNA-151a-3p in OP	[49]
Jiang et al., 2020	hBMSCs	NK q	cross-sectional	100% F PM	25 OP 25 HV	≥ 65	To determine the role and mechanism of miR-23 with respect to regulating the osteogenic differentiation of hBMSCs.	[61]
Jiang et al., 2018	hBMSCs	ITF q	cross-sectional	NK	NK	NK	To explore whether hBMSCs-derived exosomes extracted from OP patients could inhibit osteogenesis via microRNA-21/SMAD7.	[55]
Kelch et al., 2017	Serum & bone	Q q	case-control	OP: 50% F, 50% M HV: 50% F, 50% M	14 OP 14 HV	80 71.4	To determine the correlation of miRNAs with BMD and gender and study the intracellular expression of these miRNAs in different bone cell populations.	[56]
Kocijan et al., 2016	whole blood	Q q	case-control	OP: 55.6% F, 4.4% M HV: 59% F, 41% M	36 idiopathic OP & low-traumatic fractures 39 HV	46.6 ± 13.0 46.6 ± 9.4	Evaluation of c-miRNA signatures with idiopathic and PMOP low-traumatic fractures	[42]
Kong et al., 2021	plasma	Q s	case-control	100% F PM	5 OP 5 HV	57,6 ± 2,88 55,20 ± 3,27	To explore the role of plasma miRNAs in exosomes in early PM women with various bone mineral densities	[51]

Table S4: Continued

First author, Year	Tissue	Extraction Detection	Study design	Gender	Sample size	Age (years)	Primary outcome	Reference
Li et al., 2014	plasma	Q q	case-control	100% F PM	40 OP 40 HV	57.5 ± 11.3 56.5 ± 10.5	To examine the levels of miR-21, miR-133a and miR-146a in the plasma of PM women and investigate with sensitivity to BMD whether these plasma miRNAs levels correlate	[57]
Li et al., 2018	whole blood	Q q	cross-sectional	100% F PM	10 OP 10 HV	59 - 80 62 - 75	To assess miR-133 expression in serum isolated from PMOP patients	[62]
Li et al., 2021	serum	ITF q	cross-sectional	NK	10 PM OP 10 HV	NK	To explore the function of lncRNA H19 in estrogen-induced osteogenic differentiation of hBMSCs	[72]
Lin et al., 2019	serum	Q q	cross-sectional	100% F PM	15 OP 15 HV	58 - 65 58 - 65	To identify circulating miR-338 associated with PMOP and perform functional validation <i>in vivo</i> and <i>in vitro</i> .	[50]
Liu et al., 2018	serum	ITF q	cross-sectional	NK	5 OP 5 HV	NK	To research whether miR-96 can regulate osteogenic differentiation of BMSCs and be regarded as a biomarker in serum for OP	[46]
Lv et al., 2015	hBMSCs	ITF q	cross-sectional	100% F	5 PM OP 5 HV	51 – 59 41 - 46	To explore how estrogen deficiency affects miR-133 expression and how miR-133 is involved in osteogenic differentiation of hBMSCs	[63]
Panach et al., 2015	serum	Q q	case-control	100% F	8 OP 5 HV	79.6 ± 3.1 63.4 ± 8.1	To identify specific miRNAs in OP bone fracture patients compared to those in osteoarthritic controls	[58]
Ramírez-Salazar et al., 2018	serum	Q q	case-control	100% F PM	20 OP 20 HV	73.75 ± 4.46 71.1 ± 3.72	To analyze the expression of miRNAs in serum of patients with OP and HV.	[44]
Seeliger et al., 2014	serum & bone	Q q	case-control	OP: 70% F, 30% M HV: 100% F	10 OP 10 HV	79.3 78.8	To identify specific miRNAs in patients with OP fractures compared with non-OP fractures	[59]
Shao et al., 2020	serum exosome	ITF s	case-control	100% PM	12 OP 6 HV	NK	To evaluate the role of exosomal miRNAs in the diagnosis and prediction of OP in PM females with OP.	[38]

Table S4: Continued

First author, Year	Tissue	Extraction Detection	Study design	Gender	Sample size	Age (years)	Primary outcome	Reference
Suarjana et al., 2019	serum	ATF q	cross-sectional	100% F	60 PM OP 60 HV	62 58.5	To determine the role of serum miR-21 expression, concentration of RANKL, OPG, TGF- β 1, sclerostin and serum calcium, RANKL/OPG ratio, and physical activity on BMD of spine in hypoestrogenic PMOP compared with no osteoporosis	[60]
Sun et al., 2020	plasma	ITF q	cross-sectional	OP: 91.7% F, 8.3% M HV: 66.7% F, 33.3% M	12 OP 4 HV	68.9 47.8	To investigate miRNAs in the plasma of OP patients \pm VF compared with non-osteoporotic HV subjects and to discover a role for miR-19b in osteogenesis	[66]
Teng et al., 2021	plasma	ITF q	cross-sectional	100% F PM	28 OP 25 HV	60.8 \pm 6.86 50.1 \pm 3.65	To analyze the involvement of TUG1 in OP and to explore the interaction between TUG1 and miR-23b in the osteogenic differentiation of human hBMSCs.	[45]
Wang et al., 2012	circulating monocytes	ATF q	case-control	100% F PM	10 OP 10 HV	61.6 \pm 2.6 63.6 \pm 3.2	To find significant miRNA biomarkers in human circulating monocytes underlying PMOP.	[64]
Wang et al., 2020	hBMSCs	ITF q	cross-sectional	100% F	30 PM PO 20 HV	NK	To determine how lncRNA DANCER, miR-320a, and CTNNB1 interact with each other and regulate osteogenic differentiation in OP.	[70]
Wang et al., 2020	whole blood	ITF, Qs	cross-sectional	100% F	3 PM OP 3 HV	75,16 \pm 3,54 72,5 \pm 7,42	To find the potential differentially expressed miRNAs in PMOP	[37]
Yavropoulou et al., 2017	serum	Q q	case control	100% F PM	70 LBM \pm VF 30 normal BMD	69.5 \pm 7.0 68 \pm 5	To investigate serum levels of specific miRNAs, know regulators of bone metabolism, in PM women with LBM \pm VF.	[23]
Zarecki et al., 2020	serum	Q q	case-control	100% F PM	76 low BMD \pm VF \pm treatment 40 HV	69.03 68.8	To compare the levels of c-miRNAs in older women with OP VF, \pm low BMD and HV, and to correlate miRNAs expression levels with bone turnover markers.	[43]

Table S4: Continued

First author, Year	Tissue	Extraction Detection	Study design	Gender	Sample size	Age (years)	Primary outcome	Reference
Zhang et al., 2019	whole blood	ITF q	cross-sectional	NK	30 OP 30 HV	NK	To explore the role of miRNA-9-5p in regulating OP development and its underlying mechanism.	[39]
Zhao et al., 2019	bone	ITF q	cross-sectional	100% F	40 PM OP with fractures 40 HV with fractures	NK	To explore the potential mechanism of miR-128 in OP	[40]

Abbreviations: ATF, Ambion Thermo Fisher; BMD, Bone Mineral Density; c-miRNAs, circulating miRNAs; CTNNB1, Catenin beta-1's gene; DANCER, Differentiation Antagonizing Non-Protein Coding RNA; F, female; FM, fibromyalgia; GAS5, Growth Arrest Specific 5; hBMSCs, Human Bone Marrow Mesenchymal Stem Cell; HV, Healthy volunteers; ITF, Invitrogen Thermo Fisher; LBM, low bone mass; MALAT1, metastasis associated lung adenocarcinoma transcript 1; M, male; NGS, next-generation sequencing; NK, not know; OP, osteoporosis; OPG, Osteoprotegerin; PM, post menopause; q, Quantitative Reverse Transcription Polymerase Chain Reaction; Q, Qiagen; RANKL, receptor activator of nuclear factor- κ B ligand; ROR, regulator of reprogramming; s, sequencing ; TGF- β 1, Transforming growth factor beta 1; TUG1, taurine up-regulated 1; VF, vertebral fracture

