Genome **Medicine**

REVIEW

Genome-wide approaches for identifying genetic risk factors for osteoporosis

Shuyan Wu[1], Yongjun Liu[2], Lei Zhang[1,2], Yingying Han[1], Yong Lin[1] and Hong-Wen Deng[1,2]*

Abstract

Osteoporosis, the most common type of bone disease worldwide, is clinically characterized by low bone mineral density (BMD) and increased susceptibility to fracture. Multiple genetic and environmental factors and gene-environment interactions have been implicated in its pathogenesis. Osteoporosis has strong genetic determination, with the heritability of BMD estimated to be as high as 60%. More than 80 genes or genetic variants have been implicated in risk of osteoporosis by hypothesis-free genome-wide studies. However, these genes or genetic variants can only explain a small portion of BMD variation, suggesting that many other genes or genetic variants underlying osteoporosis risk await discovery. Here, we review recent progress in genome-wide studies of osteoporosis and discuss their implications for medicine and the major challenges in the field.

Osteoporosis and the search for risk factors

Osteoporosis is the most common metabolic bone disease and is estimated to affect more than 200 million people worldwide [1]. About 30% of women and 20% of men over 50 suffer from osteoporosis or osteoporotic fractures [1]. Osteoporotic fractures are not only associated with increased mortality in both sexes, but are also responsible for about 1% of the worldwide disability caused by prevalent noncommunicable diseases [1]. Current pharmacological interventions for osteoporosis focus on hormone replacement therapy and anti-resorptive treatment with bisphosphonates [2]. Anabolic therapy with parathyroid hormone (PTH) peptides has also been used for severe osteoporosis [3]. In addition, prevention strategies such as physical exercise and

*Correspondence: hdeng2@tulane.edu
[2]Center for Bioinformatics and Genomics, Department of Biostatistics and Bioinformatics, School of Public Health and Tropical Medicine, Tulane University, 1440 Canal St, New Orleans, LA 70112, USA
Full list of author information is available at the end of the article

BioMed Central

dietary vitamin D were introduced to reduce lifetime risk of osteoporosis [4]. Despite these efforts, osteoporosis and osteoporotic fractures are still a serious public health issue, with low diagnosis and treatment rates. Deeper understanding of the pathophysiology of osteoporosis and predisposition to fracture is necessary [5].

Bone mineral density (BMD) is a widely used index for diagnosis of osteoporosis and fracture prediction [5]. Other traits, such as bone geometry, bone size, and fracture (the outcome of osteoporosis) have also been used in genetic studies of osteoporosis [6]. Osteoporosis involves an imbalance between the activity of osteoclasts and osteoblasts that determines bone remodeling [7]. Osteoclasts are derived from monocytes; they digest and remove mature bone tissue (a process known as resorption) [8]. Osteoblasts are derived from multipotential mesenchymal stem cells (MSCs); they synthesize bone matrix and form new bone that replaces previously resorbed tissue [8]. Bone remodeling is controlled by complex genetic and environmental factors that act together. Identification of genes that influence variations in bone-related traits will provide insight into the genetic architecture of osteoporosis [9].

In genetic studies of osteoporosis, candidate gene association analysis is a conventional approach for detecting genetic variants associated with disease susceptibility; however, a major limitation of the candidate gene approach is that the 'right' candidate genes are sometimes difficult to identify because of our limited knowledge about the pathophysiology of osteoporosis [10]. With recent advances in molecular genetic technologies, it has become feasible to perform whole-genome studies to search for osteoporosis risk genes [11]. This hypothesis-free approach has an important advantage in identification and assessment of susceptibility genes as it does not require any prior assumptions or knowledge about the genes [12]. Depending on experimental technologies and analytical approaches, genome-wide scans may include linkage, association, gene expression, proteomic, and epigenetic studies [13]. Here, we summarize recent findings of such genome-wide studies of osteoporosis and we discuss their implications for pathogenesis and for the development of targeted interventions.

Genome-wide linkage studies

Genome-wide linkage studies (GWLSs) are conducted to identify genomic regions associated with inherited diseases or traits in generations of families comprising affected and unaffected individuals by examining whether molecular markers (usually microsatellite markers spaced throughout the entire human genome) co-segregate with the diseases or traits under study [14]. GWLSs are designed to identify genomic regions contributing to predisposition to complex human diseases, and they do not require any information on the potential functions of genomic regions [15]. Before the advent of genome-wide association studies (GWAS), GWLSs had been widely used for genetic mapping of human diseases, and have successfully mapped contributing genes for many Mendelian diseases.

Traditional GWLSs have focused on individual diseases or traits (such as BMD) using univariate analytical approaches. For example, Styrkarsdottir *et al.* [16] conducted a GWLS for hip and spine BMD in a large number of extended families with osteoporosis in Iceland and identified bone morphogenetic protein gene *BMP2* on chromosome 20p12.3; they followed up this discovery with association analysis. Kammerer *et al.* [17] performed a GWLS using BMD data at the forearm and hip for 664 individuals from 29 Mexican-American families. They obtained evidence for quantitative trait loci (QTL) on chromosome 4p affecting forearm BMD overall, and on chromosomes 2p and 13q affecting hip BMD in men [17].

Univariate analysis generally ignores the relationship between study traits, and this may result in loss of statistical power in gene identification for osteoporosis [18]. The problem can partially be overcome by bivariate analysis, which can improve the power to detect QTLs, especially when the effects of QTLs are too small to be detected by univariate analysis. Between 2007 and 2009, bivariate GWLSs identified significant loci influencing BMD and other bone-related traits such as bone size, total body lean mass [19], body fat mass [20], and age at menarche [21].

In an effort to improve the power of GWLSs, Ioannidis *et al.* [22] conducted a meta-analysis of GWLSs of bone mass that included 11,842 individuals. This large-scale meta-analysis provided replication evidence for several QTLs identified in previous studies and also identified a new QTL on chromosome 18p11-q12.3 [22]. The limitations of GWLSs are related to limited statistical power, genetic heterogeneity, population stratification, sparse marker density, and phenotypic heterogeneity, which have resulted in difficulty in replicating study findings [18].

Nevertheless, GWLSs have provided valuable information for future fine-mapping studies and have also provided a basis for comparison and cross-validation of study results using different approaches (for example, gene expression and proteomic studies) [23]. So far, more than 60 QTLs for BMD have been reported on all chromosomes except chromosome Y [8], with a few replicated in multiple studies, such as 7p21-22, 11q12-13, 15q13, and Xq27 [8]. Table 1 summarizes the main findings of GWLSs for osteoporosis.

Genome-wide association studies

GWASs provide an unbiased approach by which a large number of participants are genotyped for dense genetic markers (normally single nucleotide polymorphisms, SNPs) covering the whole genome to identify susceptibility genes for human diseases or traits. Compared with GWLSs, GWASs can capitalize on all meiotic recombination events in a population, rather than only those in the families studied, and thus have higher statistical power and mapping resolution. Over the past decade, GWASs have become one of the most popular tools for gene mapping of complex human diseases or traits [24]. Various different strategies have been adopted in GWASs, including individual studies (for example, in single or multiple ethnicities) and meta-analyses.

GWASs for osteoporosis-related traits have primarily been performed for single ethnicities [25]. For example, Hsu *et al.* [26] integrated a GWAS of Caucasians with gene expression profiling of various human tissues and identified three novel genes associated with BMD - *RAP1A* (encoding a Ras oncogene family member), *TBC1D8* (TBC1 domain family member 8), and *OSBPL1A* (oxysterol binding protein-like 1A) - and replicated the identification of *OPG* (osteoprotegerin) [26]. GWASs have also been conducted in populations of different ethnicities [27]. Koller *et al.* [28] found that SNPs (rs1298989 and rs1285635) in *CATSPERB* (encoding the catsper channel auxiliary subunit β) were associated with femoral neck BMD in both premenopausal European-American women and African-American women [28]. Ichikawa *et al.* [29] found that one SNP in the *C6orf97/ESR1* (estrogen receptor 1) region was significantly associated with BMD in premenopausal white women and premenopausal black women.

Besides SNPs, other genetic variants have also been studied. Copy number variants (CNVs; that is, duplication or deletion of a relatively large segment of DNA) have been analyzed in GWASs [27]. For example, Liu *et al.* [30] reported a CNV (*CNP267*) on chromosome 2q12.2 that was significantly associated with hip bone size in both Chinese Han and Caucasian samples. A candidate gene, *FHL2* (four-and-a-half-LIM gene), is located downstream of *CNP267* [30].

A simple and efficient way to improve statistical power over individual GWASs is meta-analysis of multiple GWASs [31-33]. Recently, the Genetic Factors for Osteoporosis (GEFOS) consortium published a large

Table 1. Examples of genome-wide linkage studies of osteoporosis and related traits*

Study participants	No. of markers	Phenotype	Results	Refs
3,730 men and 4,374 women from the Framingham Osteoporosis Study	209,546 SNPs. Genotypic call rates ≥97%, HWE *P* ≥ 0.01; MAF ≥0.2	Hip and spine BMD heel ultrasound, geometric indices of the hip	For BMD, 9p and 11p, LOD ≥3.0; for ultrasound, 4p, LOD = 3.9, 16p, LOD = 3.8, 22p, LOD = 4.0; for femoral neck width, 7p, LOD ≥5.0	[23]
4,498 individuals from 451 pedigrees	410	TBLM and spine BMD in women	15q13, LOD = 4.86	[19]
		TBLM and spine BMD	7p22, LOD >2.2; Xq25, LOD >3.5	[19]
		TBLM and BMD at both spine and hip in women	7q32, LOD = 2.67	[19]
		TBLM and BMD at both spine and hip in men	7q21, LOD = 2.52; 13p11, LOD = 325	[19]
1,323 individuals from 207 extended Icelandic families	1,100	Hip BMD	16q, LOD = 1.99	[16]
		Spine BMD	18p, LOD = 2.12	[16]
664 individuals from 29 Mexican-American families	416	Forearm BMD	4p, LOD = 4.33; 12q, LOD = 2.35	[17]
		Trochanter BMD in both men and women	6p, LOD = 2.27	[17]
		Neck BMD only in men	2p, LOD = 3.98	[17]
		Trochanter BMD only in men	13q, LOD = 3.46	[17]
11,842 individuals from 9 groups	Varied between 270 and 1,008	Lumbar spine BMD only in women; lumbar spine BMD in both women and men; femoral neck BMD	LOD >1.6 for 1p13.3-q23.3, 12q24.31-qter, 3p25.3-p22.1, 11p12-q13.3, 1q32-q42.3, 18p11-q12.3, 9q31.1-q33.3, 17p12-q21.33, 14q13.1-q24.1, 9q21.32-q31.1, and 5q14.3-q23.2	[22]

*HWE *P*, Hardy-Weinberg Equilibrium *P*-value; LOD, logarithm of odds; MAF, minor allele frequency; TBLM, total body lean mass.

meta-analysis of GWASs of lumbar spine and femoral neck BMD [33]. Seventeen GWAS datasets were analyzed, comprising 32,961 individuals of European and East Asian ancestry [33]. A total of 56 loci (32 of which were new) were found to be associated with BMD, and several of these loci clustered within specific pathways, including those involved in mesenchymal stem cell differentiation, endochondral ossification, the RANKL/RANK/OPG pathway (involving receptor activator of nuclear factor (NF)-κB, its ligand, and osteoprotegerin) and the Wnt signaling pathway [33]. It should be noted that homogeneous phenotypes (for example, types of fractures or skeletal sites of BMD) are necessary for meta-analysis to provide dependable results.

In addition to univariate GWASs, multivariate GWASs have been conducted to identify pleiotropic genes underlying diseases with shared genetic susceptibility to reveal the interconnected pathophysiological networks for a spectrum of common human diseases [34]. A bivariate GWAS for femoral neck bone geometry and body lean mass - two major risk factors for musculo-skeletal disease - was conducted in Chinese people and US Caucasians [35], and SNPs in four genes (the hexokinase gene *HK2*, the uromodulin gene *UMOD*, and microRNA genes *MIR873* and *MIR876*) showed strong association with both traits [35].

Although the number of GWASs has grown dramati-cally during the last five years [36,37], GWASs have several limitations, such as small sample size, dependence on minor allele frequency and genetic effects, stringent statistical significance, and the difficulty of replication across studies [38]. Using empirical data, we recently performed theoretical analyses to address the usefulness and limitations of GWASs and meta-analyses (our un-published observations). The results suggested that discordant findings in GWASs and meta-analyses are not unexpected, even for true susceptible genes. We concluded that although meta-analyses can detect many more true and novel loci for complex diseases than individual GWASs, they should not be used as a gold standard to evaluate the results of individual GWASs. In particular, individual GWASs in homogeneous popula-tions can detect true disease genes that meta-analyses might have low power to replicate.

So far, over 30 GWASs have been published on osteo-porosis and related traits [25,26,28-57], and these have identified over 50 genes or genomic loci; examples are shown in Table 2. About 20 genes have also been detected in multiple GWASs (Table 2). Some of the identified genes are involved in well-established pathways, such as the RANKL/RANK/OPG pathway and the Wnt signaling pathway, that are important for bone metabolism [44].

Table 2. Examples of genome-wide-association studies of osteoporosis and related traits[a]

Genotyping	Total markers	Significant markers	Discovery participants	Replication participants	Phenotype	*P*-value	Candidate gene/ related pathway[b]	Refs
Affymetrix 500K array set	342,854 SNPs. HWE $P \geq 0.0001$; MAF ≥5%	rs9630182, rs2036417, rs7125774; rs8057551, rs8061992, rs7199138	495 females and 488 males, unrelated	2,557 phenotyped white individuals from 750 families	Femoral neck BMD	3.98×10^{-7} to 6.74×10^{-3}	*IL21R* and *PTH*/PTH pathway	[52]
Affymetrix 500K array set	281,533 SNPs. Genotypic call rates ≥90%; HWE $P \geq 0.001$; MAF ≥5%	rs13182402	700 elderly Chinese Han	906 Chinese, 4,054 US Midwest Caucasians, 2,953 US Framingham samples	BMD; low-trauma osteoporotic fractures	2.08×10^{-9} to 6.39×10^{-6}	*ALDH7A1*	[40]
Infinium assay Human 610-quad chip	564,214 SNPs. Genotypic call rates ≥95%; HWE $P \geq 0.0001$; MAF ≥1%	rs2273061	800 unrelated Hong Kong Chinese females	720 Hong Kong and 17,378 of European or Asian descent	BMD	5.27×10^{-8} to 3.47×10^{-5}	*JAG1*; Wnt and Notch pathways	[46]
High-density oligonucleotide arrays	224,507 SNPs. Genotypic call rates ≥90%; HWE $P \geq 10^{-6}$	rs7605378	1,747 (190 cases and 1,557 controls) in Japan	5,206 (2,092 cases, 3,114 controls) in Japanese		1.51×10^{-8}	*FONG*	[45]
Affymetrix genome-wide human SNP array 6.0	689,368 SNPs. HWE $P \geq 0.01$; MAF ≥1%	rs17743190, rs3857454, rs3907327, rs17799762, rs17799805, rs1385530, rs17799462, rs3857453, rs3857449, rs10484943, rs196670, rs16890720	1,627 Han adults	1,728 from Midwestern US (Kansas City, MO and Omaha, NE)	Spine bone size	6.2×10^{-5} to 1.8×10^{-6}	*HMGN3*	[50]
Affymetrix GeneChip human mapping SNP 6.0 array	194 CNVs	CNP267	1,627 Chinese Han	2,286 unrelated US Caucasians	Hip bone size	4.73×10^{-3} and 5.66×10^{-3}	*FHL2*	[30]
Meta-analysis	1,200 SNPs	467 SNPs	19,195 Northern Europeans		Femoral neck and lumbar spine BMD	$<5 \times 10^{-8}$	*SPTBN1*, *CTNNB1*, *MEPE*, *STARD3NL*, *FLJ42280*; *ARHGAP1*, *DCDC5*, *SOX6*, *FOXL1*, *HDAC5 ESR1*, *SP7*, and others; Wnt and MAPK pathways	[31]
Meta-analysis		96 SNPs	32,961 of European and East Asian ancestry	Replication in 50,933 individuals	Lumbar spine and femoral neck BMD	$<5 \times 10^{-8}$	*FAM210A*, *SLC25A13*, *LRP5*, *MEPE*, *SPTBN1*, *DKK1*; RANK-RANKL-OPG and Wnt pathways	[33]

[a]About 20 genes have been detected in multiple GWASs, including *ARHGAP1* [31,32], *C6orf97* [29,32], *CLCN7* [25,43], *CTNNB1* [31,53], *DCDC5* [31,53], *ESR1* [29,31,32,48,53,57], *FLJ42280* [31,53,55], *FOXL1* [31,53], *GPR177* [31,53,54], *HDAC5* [31,53], *LRP4* [31,32,56,57], *LRP5* [31,33,53], *MEPE* [31,33,53], *PTH* [43,52], *STARD3NL* [31,53], *SOST* [53,56], *SOX6* [31,41,51,53], *SPTBN1* [31,33,57], *TNFSF11* [55,56], *TNFRSF11A* [31,37,55,56], *TNFSF11B* [31,53,56,57], and *ZBTB40* [31,53]. [b]For gene abbreviations and explanations of pathways, see Table 5.

Overlap between results obtained from GWLSs and GWASs has been limited. *COL1A1* (encoding Collagen type I α1) is among the very few genes detected by both GWLS and GWAS [18,43]. The limited overlap may be due to false positive or false negative results, or because the linkage approach is more likely to find functional rare variants that are enriched in large pedigrees, whereas GWAS mainly aims to identify common variants [46,47].

Gene expression studies

Unlike GWASs and GWLSs, which search for genetic variants at the DNA level, gene expression analysis can

simultaneously detect gene expression (at the RNA level) for tens of thousands of genes. It is a powerful scanning tool to investigate biochemical processes and intermediates of pathways that are linked with pathophysiology of osteoporosis [58]. Gene expression studies of osteoporosis have been conducted both *in vivo* and *in vitro*.

Because of the difficulty in obtaining sufficient amounts of fresh osteoblasts, osteoclasts, and osteocytes, most gene expression studies have been conducted using cell cultures. *In vivo* studies using blood monocytes have also been reported. Monocytes are important sources of cytokines and chemokines, are involved in immune system functions and have been related to bone metabolism. Peripheral blood monocytes (PBMs) are the precursors of osteoclasts [59], and thus represent an important sample for studying the molecular mechanisms of osteoporosis *in vivo*. Chen *et al.* [60] found that *STAT1* (encoding signal transducer and activator of transcription 1) was significantly upregulated in the low versus the high BMD groups in both Chinese and Caucasian people, suggesting its importance in the etiology of osteoporosis. However, this was a pilot study conducted with a relatively small sample size and the findings need to be confirmed in other populations.

In vitro studies of osteoporosis using cell cultures have provided a wealth of information on the pathophysiology of osteoporosis [61]. Trost *et al.* [62] conducted a study on cultures of osteoblasts isolated from osteoporotic and non-osteoporotic human bone tissue samples. They found higher levels of protein synthesis and lower levels of cell proliferation in osteoblasts from osteoporotic tissue than in those from non-osteoporotic tissue [62]. MSCs, the precursors of osteoblasts, have also been investigated in gene expression studies of osteoporosis [63]. Kulterer *et al.* [64] identified the expression of *ID4* (encoding inhibitor of DNA binding dominant negative helix-loop-helix protein), *CRYAB* (alpha-crystallin B chain), and *SORT1* (sortilin) in osteogenic differentiation of MSCs. Furthermore, Tanabe *et al.* [65] identified four genes - *EPHA5* (ephrin type-A receptor 5 gene), *NOV* (nephroblastoma overexpressed), *NDN* (necdin), and *RUNX2* (runt-related transcription factor 2) - as stage-specific markers of osteogenic differentiation of MSCs.

Gene expression studies have also provided useful information about the molecular mechanisms of bone healing [66-68]. Oleanolic acid was reported to have an osteoprotective effect in rats with ovariectomy-induced osteoporosis; its ability to stimulate osteoblastic differentiation might be related to the Notch signaling pathway [69]. Li *et al.* [70] explored the anabolic and catabolic effects of intermittent and continuous treatments with three different PTH peptides in bone metabolism. A large number of genes, including *SLPI* (encoding secretory leukocyte peptidase inhibitor), *TFPI2* (tissue factor pathway inhibitor), *SOCS3* (cytokine signaling suppressor) and *GRO1* (melanoma growth stimulating activity α), were verified to be functional in the regulation of bone remodeling using PTH treatment [70]. These investigations might thus provide insights into mechanisms underlying PTH treatment of osteoporosis.

High-throughput microarrays have been informative in genetic studies of osteoporosis, but studies using PBMs and MSCs are not expected to be as useful as studies of osteoclasts, osteoblasts, and osteocytes. Because of the relatively small sample size and relatively poor signal/ noise ratio for genes with low expression levels, most microarray technology using human blood or monocyte samples has produced results that have not been replicated well. Also, novel transcripts, gene fusion, and alternative splicing may not be detected because of the dependence on commercial chips. To address these issues, transcriptome sequencing (RNA-seq) could be an attractive alternative [71].

Taken together, recent gene expression studies have shown that osteoporosis involves numerous genes and pathways (some of which were also identified in GWLSs or GWASs and some of which were novel) with complex regulatory mechanisms that are controlled by hormones, cytokines, or various receptors [72-74]. Examples of these studies are summarized in Table 3.

Proteomic studies

Proteomics is the large-scale study of proteins, allowing analyses of the entire complement of proteins in a cell or sample simultaneously, and made possible today by technological advances in computing and data processing. These approaches have been used to characterize biochemical interactions and protein signaling in bone remodeling [75,76]. Like gene expression studies, recent proteomic studies of osteoporosis have focused on osteoblasts and osteoclasts and their precursors [77-80].

Saad and Hofstaetter [81] identified 16 proteins that may have a role in osteoblast matrix mineralization. Choi *et al.* [82] investigated differentiation of MSCs and osteoblastogenesis and identified SMOC1 (SPARC-related modular calcium-binding protein) as an important extracellular matrix protein in osteoblast differentiation. By using both gene and protein expression analyses in aged bone, MSC-derived adipocytes were also shown to have potential roles in regulating osteoblast differentiation through transforming growth factor β (TGF-β)-mediated canonical Wnt signaling [83]. A proteomic study conducted using PBMs identified a novel annexin protein, ANXA2, that was upregulated twofold in Caucasians with extremely low BMD compared with those with extremely high BMD [39]. ANXA2 protein significantly promoted monocyte migration across an endothelial barrier *in vitro*; this suggested that elevated ANXA2

Table 3. Examples of gene expression studies of osteoporosis

Subjects and samples	Treatment	Differentially expressed genes	Important regulated genes[a]	Refs
Human osteoblasts isolated from trabecular bone tissue of femoral neck and proximal femur	Comparing the gene expression profiles of osteoblasts from osteoporotic versus non-osteoporotic bone tissues	1,606	Upregulated: *IBSP*, *CXCL2*; downregulated: *PTN*, *COL15A1*	[62]
Human MSCs	Oleanolic acid	256	Genes involved in osteoblastic differentiation	[69]
	Ex vivo long-term cultivation		*ID4*, *CRYAB*, *SORT1*, *TGF-β2*, and BMPs	[64]
	Cell culture		*NDN*, *EPHA5*, *NOV*, *RUNX2*	[65]
Human monocytes of low BMD subjects	Isolation from human blood	13	*STAT1*	[60]
Differentiation and proliferation of mouse osteoblast cells	High cholesterol	992 upregulated, 2,290 downregulated	Upregulated: *TGF-β*, *BMP2*, *CBFA1*, and proteins involved in Wnt signaling pathways; downregulated: *IL-6* and *AGER*	[61]
Bone resorption and formation of male mice in high-fat diet	Antioxidant lipoic acid	17 upregulated, 19 downregulated	Upregulated: *COL1A1*, *ALP1*, *IGF-1*, and *IL12*; downregulated: *MMP9*, *CTSK*, *P53*, *TGFBR1*, and *IL17a*	[66]
Both pairs of femora and tibiae of Sprague-Dawley female rats	Three different PTH peptides, PTH(1-34), (1-31), and (3-34)		*SLPI*, *TFPI2*, *SOCS3*, *GRO1*, *RANKL*, *PHEX*, *GPRC5C*, and *CXCR4*	[70]

[a]For gene abbreviations and explanations of pathways, see Table 5.

protein expression levels in subjects with low BMD may be involved in increased PBM migration to bone resorption surfaces in *vivo*, where higher numbers of osteoclasts might resorb bone at higher rates resulting in decreased BMD [39].

A proteomic approach was used to show that specific antibodies could suppress bone turnover [84]. Kostenuik *et al.* [85] also reported that the human monoclonal antibody denosumab bound to human RANKL but not to murine RANKL, human TRAIL, or other human TNF family members in direct binding assays. Knock-in technology was applied to create 'huRANKL' mice by replacement with a human RANKL fragment encoded primarily by the fifth exon of the *RANKL* gene [85]. In young huRANKL mice, denosumab and OPG-Fc (an osteoprotegerin-immunoglobulin Fc segment complex) each reduced the osteoclast surfaces of trabecular bone (spongy bone or cancellous bone) by 95% and also increased bone density and volume [85]. In adult huRANKL mice, denosumab reduced bone resorption, increased the bone mass of both cortical bone (a dense type of bone tissue) and cancellous bone (the spongy inner layer of bone), and improved trabecular microarchitecture [84]. Subsequently, Kendler *et al.* [84] separated 504 postmenopausal women over 55 with low BMD who had been receiving alendronate therapy (which is used to slow down bone loss and increase bone density) for at least 6 months into two groups of continued weekly alendronate therapy or subcutaneous denosumab therapy. Transition to

denosumab produced greater increases in BMD at all measured skeletal sites and a greater reduction in bone turnover than did continued alendronate, with a similar safety profile in both groups [84].

Like gene expression studies, proteomic studies have also been conducted using relatively small sample sizes, and there have been difficulties in replicating results. Although proteomic approaches are still at an early stage in the bone research field, they represent one of the most promising methods for generating insights for human osteoporosis and have shown promise for the identification of novel proteins and genes [86-90]. Examples of recent proteomic studies of osteoporosis are summarized in Table 4.

Epigenome-wide studies

Epigenetic regulation is important for sustaining normal growth and development of animals [91]. Dysregulation of these mechanisms is involved in many human diseases, such as cancer, intellectual disability, and immunodeficiency, and in aging [91-94]. DNA methylation, histone modifications, and RNA-mediated mechanisms are all known to have key roles in epigenetic regulation, and they are being investigated in bone disease [95].

DNA methylation involves the covalent transfer of a methyl group to the fifth carbon of cytosine in CpG dinucleotides in the genome [96]. The influence of CpG methylation in human bone has been investigated. Hsiao *et al.* [97] found that suppression of the *TRIP10*

Table 4. Examples of proteomic studies of osteoporosis[a]

Participants or cells/treatment	Identified protein expression	Related functions/pathways	Refs
Human bone MSCs	64 secreted proteins upregulated, especially SMOC1	Osteoblast mineralization	[82]
Human PBMs	ANXA2	Osteoclast differentiation	[39]
Human osteocytes	LRP4	A sclerostin interaction partner	[87]
Chinese with low BMD	SOD 2 upregulated	Located in circulating monocytes (potential osteoclast precursors)	[89]
Osteoblast differentiation in mouse osteoprogenitor MC3T3-E1 cells	Upregulation of IQGAP1, gelsolin, moesin, radixin, and CFL1	Cytoskeleton regulation	[79]
	Upregulation of FLNA, LAMA1, LAMA5, COL1A1, COL3A1, COL4A6, COL5A2; downregulation of COL4A1, COL4A2, and COL4A4	Focal adhesion signaling	[79]
Osteoblast differentiation in MC3T3-E1 preosteoblast cells/ leukocyte common antigen-related tyrosine phosphatase	ALP, BSP, DLX5, OCN, and RUNX2	Erk activation	[80]
Osteoblasts and osteoclasts induced from RAW 264.7 macrophage cell line (from murine blood)/Er-Xian Decoction treatment	In osteoblasts: 8 proteins upregulated	Hmgb1, acidic ribosomal phosphoprotein P0, histone H2, carbonyl reductase 1, ATP synthase, aldolase A, and GDIα	[78]
	In osteoblasts: 3 proteins downregulated	Carbonic anhydrase 3, prohibitin, hemiferrin, far upstream element-binding protein	[78]
	In osteoclasts: 3 proteins upregulated	Vimentin, protein disulfide isomerase associated 3 and α-fetoprotein	[78]
	In osteoclasts: 1 protein downregulated	Calnexin	[78]
Rat primary calvarial osteoblast/Kaempferol	9 proteins upregulated, 9 downregulated	Including cytoskeletal proteins, intracellular signaling protein, chaperone, extracellular matrix protein, and proteins involved in glycolysis and cell-matrix interactions	[77]
Ovariectomized rats	SOD1, ATP synthase, and COMT	Protection against bone loss	[90]

[a]For gene abbreviations and explanations of pathways, see Table 5.

(encoding thyroid receptor-interacting protein 10) promoter by DNA methylation resulted in acceleration of MSC-to-osteocyte differentiation [97]. Delgado-Calle *et al*. reported [98] that the *SOST* gene (encoding sclerostin, an inhibitor of bone formation) was dramatically upregulated by demethylating agent AzadC, and that DNA methylation strongly hindered *RANKL* and *OPG* expression [99].

Histone modifications can regulate gene expression by influencing interactions between DNA and histones, for example by acetylation and methylation of conserved lysine residues in the amino-terminal tail domains [100]. Histone modification has been studied in a variety of cancers, such as prostate, breast, lymphoma, and ovarian cancer [54]. However, studies of osteoporosis are scarce, with the limited information suggesting a role in developmental processes that may be related to bone metabolism [101].

RNA interference (RNAi) and noncoding RNAs (such as microRNAs) have drawn much attention in the field [95]. You *et al.* [102] reported that the zinc finger protein

Zfp467 stimulated osteoblast differentiation of cultured adipose-derived stem cells, and that *Zfp467*-targeted RNAi could restore bone function and structure in an ovariectomy-induced osteoporotic mouse model.

In summary, some novel factors and mechanisms have been identified in a limited number of epigenetic studies of bone pathogenesis. However, further epigenome-wide studies will be needed to investigate the role of these epigenetic mechanisms in osteoporosis.

Implications for pathogenesis

Most of the genetic variants or genomic regions that have so far been identified by GWASs of osteoporosis-related traits have been intronic or intergenic [71]. These variants or regions could be transcription factor binding sites that regulate or affect gene expression [71], but precisely how they might influence bone mass awaits further investigation. Ultimately, GWAS is an indirect genetic mapping approach that relies on linkage disequilibrium, so further studies are needed to pinpoint functional variants by deep sequencing and functional molecular studies.

Table 5. Key pathways associated with osteoporosis[a]

Genes	Full names	Refs
RANK/RANKL/OPG pathway		
TNFSF11	TNF (ligand) superfamily, member 11 (RANKL)	[55,56]
TNFRSF11A	TNF receptor 11a, NF-κB activator (RANK)	[26,37,55]
TNFRSF11B	TNF receptor 11b (OPG)	[26,53,56]
TNF-R1/TRAIL signaling pathway[b]		
CFLAR	CASP8 and FADD-like apoptosis regulator	[37]
NFKB1	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1	[37]
TNFSF10	TNF (ligand) superfamily, member 10	[37]
TNFRSF1B, TNFRSF10B	TNF receptors	[37]
TRAF3	TNF receptor-associated factor 3	[37]
Wnt signaling pathway		
CTNNB1	B-catenin	[26,53]
DKK1	Dickkopf-related protein 1	[33,74]
LRP4, LRP5	Lipoprotein receptor related peptides	[32,33,53,56,57]
RSPO3	R-spondin 3	[25]
SOST	Sclerostin	[56,57]
WNT4, WNT15	Wnt proteins	[61]
Autophagy regulation pathway		
ATG5, ATG7, ATG12	Autophagy-related proteins	[36]
IFNA4, IFNA5, IFNA7, IFNA8, IFNA13, IFNA14, IFNA16, IFNA17, IFNA21,	Interferon α proteins	[36]
PIK3C3	Phosphatidylinositol 3-kinase catalytic subunit type 3	[36]
Other pathways		
ALDH7A1	Aldehyde dehydrogenase 7 family, member A1	[33]
ARHGAP1	Rho GTPase activating protein 1	[26,32]
COL1A1	Collagen, type I, α1	[43,66,79]
DCDC5	Doublecortin domain containing 5	[26,53]
ESR1	Estrogen receptor 1	[29,32,48]
FLJ42280	Putative uncharacterized protein FLJ42280	[26,53,55]
FOXL1	Forkhead box L1	[26,53]
GALNT3	UDP-N-acetyl-a-d-galactosamine: polypeptide N-acetylgalactosaminyltransferase 3	[25]
HDAC5	Histone deacetylase 5	[26,53]
JAG1	Jagged 1 (Notch ligand)	[46]
MEF2C	Myocyte enhancer factor 2C	[26]
MEPE	Matrix extracellular phosphoglycoprotein	[26,33,53]
STARD3NL	STARD3 amino-terminal like protein	[26,53]
SOX6	Sex-determining region Y-box 6	[26,41,51]
SP7	Sp7 transcription factor	[26]
SPTBN1	Spectrin, β, non-erythrocytic 1	[26,33,58]
TGFBR1	TGF, β receptor I	[66]

[a]Gene abbreviations: *AGER*, Advanced glycosylation end product-specific receptor; *ALP1*, Actinin-associated LIM protein; *ANXA2*, Annexin A2; *BMP2*, Bone morphogenetic protein; *BSP*, Binder of sperm; *C6orf97*, Chromosome 6 open reading frame 97; *CBFA1*, Core binding factor A1; *CFL1*, Cofilin 1; *CLCN7*, Chloride channel 7; *COL*, Collagen; *COMT*, Catechol-O-methyltransferase; *CRYAB*, α-crystallin B chain; *CTSK*, Cathepsin K; *CXCL2*, Chemokine ligand 2; *CXCR4*, Chemokine receptor 4; *DLX5*, Distal-less homeobox 5; *EPHA5*, Ephrin A receptor 5; *Erk*, Extracellular signal-regulated kinase; *FAM210A*, Family with sequence similarity 210A; *FHL2*, Four-and-a-half LIM domain; *FLNA*, Filamin A α; *FONG*, Formiminotransferase amino-terminal subdomain-containing precursor; *GDIα*, Rho GDP dissociation inhibitor α; *GPR177*, G protein-coupled receptor 177; *GPRC5C*, G protein-coupled receptor; *GRO1*, Melanoma growth stimulating activity α; *Hmgb1*, High mobility group protein; *HMGN3*, High mobility group nucleosomal binding domain 3; *IBSP*, Integrin-binding sialoprotein; *ID4*, Inhibitor of DNA binding dominant negative helix-loop-helix protein; *IGF-1*, Insulin-like growth factor; *IL*, Interleukin; *IL21R*, Interleukin 21 receptor; *IQGAP1*, IQ motif containing GTPase activating protein; *LAMA*, Laminin α; *MMP9*, Matrix metallopeptidase 9; *NDN*, Necdin; *NOV*, Nephroblastoma overexpressed; *OCN*, Osteocalcin; *P53*, P53 oncogene; *PHEX*, phosphate regulating endopeptidase homolog; *PTH*, Parathyroid hormone; *PTN*, pleiotrophin; *RUNX2*, Runt-related transcription factor 2; *SLC25A13*, Aspartate/glutamate carrier; *SLPI*, Secretory leukocyte peptidase inhibitor; *SOCS3*, Cytokine signaling suppressor 3; *SOD1*, Superoxide dismutase 1, soluble; *SOD2*, Superoxide dismutase 2, mitochondrial; *SORT1*, Sortilin 1; *STARD3NL*, STARD3 amino-terminal like gene; *STAT1*, Signal transducer and activator of transcription 1; *TFPI2*, Tissue factor pathway inhibitor; *ZBTB40*, Zinc finger and BTB domain containing 40. [b]This pathway also includes *TNFSF11*, *TNFRSF11A*, and *TNFRSF11B*.

Several genes or proteins have shown remarkable association with osteoporosis-related traits in genome-wide studies, and these have become interesting candidates for further studies. For example, both GWASs and gene expression studies have shown that *DKK1* (encoding a dickkopf-related protein) [31,74], *SOST* [53], *MEPE* (encoding matrix extracellular phosphoglycoprotein) [33], *SOX4* (sex-determining region Y-box 4 gene) [25] and the spectrin gene *SPTBN1* [31,67] were strongly associated with BMD. *COL1A1* [18,43,66,79] is a candidate gene whose association with BMD has been confirmed by four types of genome-wide approaches (GWLS, GWAS, gene expression, and proteomic studies). Also, results from GWAS, gene expression, and proteomic studies have confirmed that *RANK, RANKL, OPG*, and *LRP4* (encoding lipoprotein receptor related peptide 4) have important roles in regulating BMD.

These significant risk factors can be grouped into different pathways, which provide insights into the pathogenesis of osteoporosis. For example, LRP-4, -5, and -6 can bind Wnt ligands to form a receptor complex and initiate the Wnt signaling pathway, which is involved in differentiation and growth of cell types such as osteoblasts or osteoclasts [103]. However, these proteins are also essential oncogenic receptors that may increase the risk of cancers by interacting with components of the Wnt signaling pathway [104]. *RANK, RANKL*, and *OPG* are known to be involved in different biological pathways that are important for bone mass regulation, such as the RANKL pathway, the TNF-R1 signaling pathway and the TRAIL pathway [103]. Table 5 summarizes the key genes, loci, and pathways associated with osteoporosis and related traits.

From genome-wide approaches to targeted interventions

Although a large number of genome-wide linkage and association studies on osteoporosis have been published over the past decade, there have been many unreplicated results [27]. As mentioned earlier, factors that may significantly contribute to inconsistencies in genetic studies of osteoporosis include inadequate statistical power, population stratification, genetic heterogeneity, experimental errors, and limited coverage of genomic regions [27]. The occurrence of gene-gene interactions and gene-environment interactions might also contribute to these challenges.

Significant gene-gene interaction effects have been found to influence osteoporosis risk in different studies [103]. For example, a role for the CD40/CD40L system was revealed in bone metabolism regulation [105]. Pineda *et al.* [105] conducted an association study of BMD with SNPs in *CD40* and *CD40L* genes. The study indicated a strong interaction between polymorphisms in these genes that might have a synergistic role in BMD

regulation [105]. Also, the role of environmental factors and their potential interactions with key genes or loci requires further study. Environmental factors such as dietary intake and medication can trigger gene responses and gene-gene interactions. For example, Sonoda *et al.* [106] found that the SNPs rs2077647 and rs2234693 in the estrogen receptor α gene were significantly associated with osteoporosis risk, and that the osteoporotic haplotype CC at these SNPs was also significantly associated with alcohol drinking [106].

The confounding factors and complicated nature of osteoporosis indicate that appropriate study design and interpretation of results are crucial to ensure reproducibility. Therefore, it is also important to use multidisciplinary approaches, such as gene expression profiling, proteomics, and epigenetics, which may complement each other and provide information for cross-validation. Combinations of different genome-wide analyses have recently been used in bone research. Lei *et al.* [59] performed gene expression profiling using monocytes from 26 Chinese and 20 Caucasian premenopausal women with extremely high or low BMD, and identified a list of differentially expressed genes, some of which were further confirmed by GWAS. By combining information from gene expression and genome-wide association studies, Farber *et al.* [107] identified the *ASXL2* gene as a novel regulator of BMD and osteoclastogenesis. Although integrating data from multidisciplinary studies could be challenging, such approaches may help to identify some of the most interesting susceptibility genes and factors for osteoporosis, and could provide leads for the development of new targeted preventive interventions and treatments.

The estrogen receptor gene *ESR1* has been reported to be involved in bone metabolism in numerous studies [29,31,32,48,53,57]. In current osteoporosis treatments, estrogen or estrogen-like medications known as estrogen receptor modulators have been clinically applied to provide protection against postmenopausal bone loss [106]. Such medications can exclusively target the estrogen receptor and produce estrogen-like effects in the bone, in addition to their effects in decreasing the occurrence of breast cancer [106].

Similarly, the role of the RANK/RANKL/OPG pathway in osteoporosis has been confirmed in many studies and involves several susceptibility genes and factors that influence bone modeling [103]. Denosumab, which is a specific antibody that targets RANKL, may reduce reproduction of osteoclasts and may be useful as an approach for restoring bone metabolism balance. Administration of denosumab has been reported to improve BMD and to reduce fractures in postmenopausal women who suffer from osteoporosis, although some side effects have been reported [108].

In gene expression studies, PTH has shown an ability to stimulate both bone resorption and new bone formation [70]. PTH has been used for the treatment of severe osteoporosis [108]. The effects of intermittent or continuous PTH treatment on bone metabolism are still under investigation to understand the underlying mechanisms and optimize its application to osteoporosis [109].

Concluding remarks and future perspectives

Despite extensive efforts, currently there is not sufficient information to allow effective assessment of osteoporosis risk. The majority of the recently identified risk factors are still pending further investigation, and it is therefore too early to define novel biological factors as preventive or treatment targets for osteoporosis. This does not imply that current genome-wide approaches are futile, but rather indicates that appropriate implementation of these studies might help to reduce potential bias and confounding factors.

Genome-wide approaches individually have specific limitations. Gene expression is a complex process that is regulated simultaneously and interactively at DNA, RNA, protein, epigenomic, and environmental levels. Therefore, a genomic convergence or systems biology approach that integrates the information from studies such as GWLSs, GWASs, DNA sequencing, gene expression, proteomics (including studies of post-translational modifications), epigenomics, and gene-environment studies may help facilitate the identification of key pathways that are globally involved in the pathogenesis of osteoporosis and osteoporotic fractures. Ultimately, the functional relevance of the identified variants then needs to be confirmed by *in vivo* and/or *in vitro* molecular biology studies.

Abbreviations

BMD, bone mineral density; CNV, copy number variation; GWAS, genome-wide association study; GWLS, genome-wide linkage study; MSC, mesenchymal stem cell; PBM, peripheral blood monocyte; PTH, parathyroid hormone; QTL, quantitative trait loci; SNP, single nucleotide polymorphism. For gene abbreviations see Table 5.

Competing interests

The authors declare that they have no competing interests.

Author details

[1]The Center for System Biomedical Research, School of Medical Instrument and Food Engineering, University of Shanghai for Science and Technology, No. 516 Jungong Rd, Yangpu district, Shanghai, 200093, China. [2]Center for Bioinformatics and Genomics, Department of Biostatistics and Bioinformatics, School of Public Health and Tropical Medicine, Tulane University, 1440 Canal St, New Orleans, LA 70112, USA

References

1. Mitchell BD, Yerges-Armstrong LM: **The genetics of bone loss: challenges and prospects.** *J Clin Endocrinol Metab* 2011, **96**:1258-1268.
2. Riancho JA, Hernandez JL: **Pharmacogenomics of osteoporosis: a pathway approach.** *Pharmacogenomics* 2011, **13**:815-829.
3. Daroszewska A: **Prevention and treatment of osteoporosis in women: an update.** *Obst Gyn Reproduct Med* 2012, **22**:162-169.
4. Biino G, Casula L, de Terlizzi F, Adamo M, Vaccargiu S, Francavilla M, Loi D, Casti A, Atzori M, Pirastu M: **Epidemiology of osteoporosis in an isolated Sardinian population by using quantitative ultrasound.** *Am J Epidemiol* 2011, **174**:432-439.
5. Duncan EL, Brown MA: **Clinical review 2: Genetic determinants of bone density and fracture risk--state of the art and future directions.** *J Clin Endocrinol Metab* 2010, **95**:2576-2587.
6. Duncan EL, Brown MA: **Mapping genes for osteoporosis--old dogs and new tricks.** *Bone* 2010, **46**:1219-1225.
7. Cummings SR, Cosman F, Eastell R, Reid IR, Mehta M, Lewiecki EM: **Goal-directed treatment of osteoporosis.** *J Bone Miner Res* 2013, **28**:433-438.
8. Lee JH, Kim BG, Ahn JM, Park HJ, Park SK, Yoo JS, Yates JR 3rd, Cho JY: **Role of PI3K on the regulation of BMP2-induced beta-Catenin activation in human bone marrow stem cells.** *Bone* 2010, **46**:1522-1532.
9. Zhao L, Cui B, Liu JM, Zhang MJ, Zhao HY, Sun LH, Tao B, Zhang LZ, Ning G: **Interactions of osteoporosis candidate genes for age at menarche, age at natural menopause, and maximal height in Han Chinese women.** *Menopause* 2011, **18**:1018-1025.
10. Xu XH, Dong SS, Guo Y, Yang TL, Lei SF, Papasian CJ, Zhao M, Deng HW: **Molecular genetic studies of gene identification for osteoporosis: the 2009 update.** *Endocr Rev* 2010, **31**:447-505.
11. Karasik D, Hsu YH, Zhou Y, Cupples LA, Kiel DP, Demissie S: **Genome-wide pleiotropy of osteoporosis-related phenotypes: the Framingham Study.** *J Bone Miner Res* 2010, **25**:1555-1563.
12. Cheung CL, Xiao SM, Kung AW: **Genetic epidemiology of age-related osteoporosis and its clinical applications.** *Nat Rev Rheumatol* 2010, **6**:507-517.
13. Guan Y, Ackert-Bicknell CL, Kell B, Troyanskaya OG, Hibbs MA: **Functional genomics complements quantitative genetics in identifying disease-gene associations.** *PLoS Comput Biol* 2010, **6**:e1000991.
14. Qiu C, Papasian CJ, Deng HW, Shen H: **Genetics of osteoporotic fracture.** *Orth Res Rev* 2011, **3**:11-21.
15. Ralston SH: **Genetics of osteoporosis.** *Ann N Y Acad Sci* 2010, **1192**:181-189.
16. Styrkarsdottir U, Cazier JB, Kong A, Rolfsson O, Larsen H, Bjarnadottir E, Johannsdottir VD, Sigurdardottir MS, Bagger Y, Christiansen C, Reynisdottir I, Grant SF, Jonasson K, Frigge ML, Gulcher JR, Sigurdsson G, Stefansson K: **Linkage of osteoporosis to chromosome 20p12 and association to BMP2.** *PLoS Biol* 2003, **1**:e69.
17. Kammerer CM, Schneider JL, Cole SA, Hixson JE, Samollow PB, O'Connell JR, Perez R, Dyer TD, Almasy L, Blangero J, Bauer RL, Mitchell BD: **Quantitative trait loci on chromosomes 2p, 4p, and 13q influence bone mineral density of the forearm and hip in Mexican Americans.** *J Bone Miner Res* 2003, **18**:2245-2252.
18. Kuipers AL, Gundberg C, Kammerer CM, Dressen AS, Nestlerode CS, Patrick AL, Wheeler VW, Bunker CH, Newman AB, Zmuda JM: **Genetic analysis of serum osteocalcin and bone mineral in multigenerational Afro-Caribbean families.** *Osteoporos Int* 2012, **23**:1521-1531.
19. Wang XL, Deng FY, Tan LJ, Deng HY, Liu YZ, Papasian CJ, Recker RR, Deng HW: **Bivariate whole genome linkage analyses for total body lean mass and BMD.** *J Bone Miner Res* 2008, **23**:447-452.
20. Lei S, Deng F, Xiao P, Zhong K, Deng H, Recker RR, Deng H: **Bivariate whole-genome linkage scan for bone geometry and total body fat mass.** *J Genet Genomics* 2009, **36**:89-97.
21. Zhang ZX, Lei SF, Deng FY, Zhang F, Liu YJ, Recker RR, Papasian CJ, Deng HW: **Bivariate genome-wide linkage analysis for traits BMD and AAM: effect of menopause on linkage signals.** *Maturitas* 2009, **62**:16-20.
22. Ioannidis JP, Ng MY, Sham PC, Zintzaras E, Lewis CM, Deng HW, Econs MJ, Karasik D, Devoto M, Kammerer CM, Spector T, Andrew T, Cupples LA, Duncan EL, Foroud T, Kiel DP, Koller D, Langdahl B, Mitchell BD, Peacock M, Recker R, Shen H, Sol-Church K, Spotila LD, Uitterlinden AG, Wilson SG, Kung AW, Ralston SH: **Meta-analysis of genome-wide scans provides evidence for sex- and site-specific regulation of bone mass.** *J Bone Miner Res* 2007,

22:173-183.

23. Karasik D, Dupuis J, Cho K, Cupples LA, Zhou Y, Kiel DP, Demissie S: **Refined QTLs of osteoporosis-related traits by linkage analysis with genome-wide SNPs: Framingham SHARe.** *Bone* 2010, **46:**1114-1121.

24. Zheng HF, Spector TD, Richards JB: **Insights into the genetics of osteoporosis from recent genome-wide association studies.** *Expert Rev Mol Med* 2011, **13:**e28.

25. Duncan EL, Danoy P, Kemp JP, Leo PJ, McCloskey E, Nicholson GC, Eastell R, Prince RL, Eisman JA, Jones G, Sambrook PN, Reid IR, Dennison EM, Wark J, Richards JB, Uitterlinden AG, Spector TD, Esapa C, Cox RD, Brown SD, Thakker RV, Addison KA, Bradbury LA, Center JR, Cooper C, Cremin C, Estrada K, Felsenberg D, Glüer CC, Hadler J, *et al.*: **Genome-wide association study using extreme truncate selection identifies novel genes affecting bone mineral density and fracture risk.** *PLoS Genet* 2011, **7:**e1001372.

26. Hsu YH, Zillikens MC, Wilson SG, Farber CR, Demissie S, Soranzo N, Bianchi EN, Grundberg E, Liang L, Richards JB, Estrada K, Zhou Y, van Nas A, Moffatt MF, Zhai G, Hofman A, van Meurs JB, Pols HA, Price RI, Nilsson O, Pastinen T, Cupples LA, Lusis AJ, Schadt EE, Ferrari S, Uitterlinden AG, Rivadeneira F, Spector TD, Karasik D, Kiel DP: **An integration of genome-wide association study and gene expression profiling to prioritize the discovery of novel susceptibility loci for osteoporosis-related traits.** *PLoS Genet* 2010, **6:**e1000977.

27. Li WF, Hou SX, Yu B, Li MM, Ferec C, Chen JM: **Genetics of osteoporosis: accelerating pace in gene identification and validation.** *Hum Genet* 2010, **127:**249-285.

28. Koller DL, Ichikawa S, Lai D, Padgett LR, Doheny KF, Pugh E, Paschall J, Hui SL, Edenberg HJ, Xuei X, Peacock M, Econs MJ, Foroud T: **Genome-wide association study of bone mineral density in premenopausal European-American women and replication in African-American women.** *J Clin Endocrinol Metab* 2010, **95:**1802-1809.

29. Ichikawa S, Koller DL, Padgett LR, Lai D, Hui SL, Peacock M, Foroud T, Econs MJ: **Replication of previous genome-wide association studies of bone mineral density in premenopausal American women.** *J Bone Miner Res* 2010, **25:**1821-1829.

30. Liu SL, Lei SF, Yang F, Li X, Liu R, Nie S, Liu XG, Yang TL, Guo Y, Deng FY, Tian Q, Li J, Liu YZ, Liu YJ, Shen H, Deng HW: **Copy number variation in CNP267 region may be associated with hip bone size.** *PLoS One* 2011, **6:**e22035.

31. Rivadeneira F, Styrkársdottir U, Estrada K, Halldórsson BV, Hsu YH, Richards JB, Zillikens MC, Kavvoura FK, Amin N, Aulchenko YS, Cupples LA, Deloukas P, Demissie S, Grundberg E, Hofman A, Kong A, Karasik D, van Meurs JB, Oostra B, Pastinen T, Pols HA, Sigurdsson G, Soranzo N, Thorleifsson G, Thorsteinsdottir U, Williams FM, Wilson SG, Zhou Y, Ralston SH, van Duijn CM, *et al.*: **Twenty bone-mineral-density loci identified by large-scale meta-analysis of genome-wide association studies.** *Nat Genet* 2009, **41:**1199-1206.

32. Cheung CL, Sham PC, Xiao SM, Bow CH, Kung AW: **Meta-analysis of gene-based genome-wide association studies of bone mineral density in Chinese and European subjects.** *Osteoporos Int* 2012, **23:**131-142.

33. Estrada K, Styrkarsdottir U, Evangelou E, Hsu YH, Duncan EL, Ntzani EE, Oei L, Albagha OM, Amin N, Kemp JP, Koller DL, Li G, Liu CT, Minster RL, Moayyeri A, Vandenput L, Willner D, Xiao SM, Yerges-Armstrong LM, Zheng HF, Alonso N, Eriksson J, Kammerer CM, Kaptoge SK, Leo PJ, Thorleifsson G, Wilson SG, Wilson JF, Aalto V, Alen M, *et al.*: **Genome-wide meta-analysis identifies 56 bone mineral density loci and reveals 14 loci associated with risk of fracture.** *Nat Genet* 2012, **44:**491-501.

34. Saint-Pierre A, Kaufman JM, Ostertag A, Cohen-Solal M, Boland A, Toye K, Zelenika D, Lathrop M, de Vernejoul MC, Martinez M: **Bivariate association analysis in selected samples: application to a GWAS of two bone mineral density phenotypes in males with high or low BMD.** *Eur J Hum Genet* 2011, **19:**710-716.

35. Sun L, Tan LJ, Lei SF, Chen XD, Li X, Pan R, Yin F, Liu QW, Yan XF, Papasian CJ, Deng HW: **Bivariate genome-wide association analyses of femoral neck bone geometry and appendicular lean mass.** *PLoS One* 2011, **6:**e27325.

36. Zhang L, Guo YF, Liu YZ, Liu YJ, Xiong DH, Liu XG, Wang L, Yang TL, Lei SF, Guo Y, Yan H, Pei YF, Zhang F, Papasian CJ, Recker RR, Deng HW: **Pathway-based genome-wide association analysis identified the importance of regulation-of-autophagy pathway for ultradistal radius BMD.** *J Bone Miner Res* 2010, **25:**1572-1580.

37. Zhang YP, Liu YZ, Guo Y, Liu XG, Xu XH, Guo YF, Chen Y, Zhang F, Pan F, Zhu XZ, Deng HW: **Pathway-based association analyses identified TRAIL pathway for osteoporotic fractures.** *PLoS One* 2011, **6:**e21835.

38. Hindorff LA, Sethupathy P, Junkins HA, Ramos EM, Mehta JP, Collins FS, Manolio TA: **Potential etiologic and functional implications of genome-wide association loci for human diseases and traits.** *Proc Natl Acad Sci U S A* 2009, **106:**9362-9367.

39. Deng FY, Lei SF, Zhang Y, Zhang YL, Zheng YP, Zhang LS, Pan R, Wang L, Tian Q, Shen H, Zhao M, Lundberg YW, Liu YZ, Papasian CJ, Deng HW: **Peripheral blood monocyte-expressed ANXA2 gene is involved in pathogenesis of osteoporosis in humans.** *Mol Cell Proteomics* 2011, **10:**M111.011700.

40. Guo Y, Tan LJ, Lei SF, Yang TL, Chen XD, Zhang F, Chen Y, Pan F, Yan H, Liu X, Tian Q, Zhang ZX, Zhou Q, Qiu C, Dong SS, Xu XH, Guo YF, Zhu XZ, Liu SL, Wang XL, Li X, Luo Y, Zhang LS, Li M, Wang JT, Wen T, Drees B, Hamilton J, Papasian CJ, Recker RR, *et al.*: **Genome-wide association study identifies ALDH7A1 as a novel susceptibility gene for osteoporosis.** *PLoS Genet* 2010, **6:**e1000806.

41. Liu YZ, Pei YF, Liu JF, Yang F, Guo Y, Zhang L, Liu XG, Yan H, Wang L, Zhang YP, Levy S, Recker RR, Deng HW: **Powerful bivariate genome-wide association analyses suggest the SOX6 gene influencing both obesity and osteoporosis phenotypes in males.** *PLoS One* 2009, **4:**e6827.

42. Deng FY, Zhao LJ, Pei YF, Sha BY, Liu XG, Yan H, Wang L, Yang TL, Recker RR, Papasian CJ, Deng HW: **Genome-wide copy number variation association study suggested VPS13B gene for osteoporosis in Caucasians.** *Osteoporos Int* 2010, **21:**579-587.

43. Yao S, Sucheston LE, Smiley SL, Davis W, Conroy JM, Nowak NJ, Ambrosone CB, McCarthy PL Jr, Hahn T: **Common genetic variants are associated with accelerated bone mineral density loss after hematopoietic cell transplantation.** *PLoS One* 2011, **6:**e25940.

44. Roshandel D, Holliday KL, Pye SR, Boonen S, Borghs H, Vanderschueren D, Huhtaniemi IT, Adams JE, Ward KA, Bartfai G, Casanueva F, Finn JD, Forti G, Giwercman A, Han TS, Kula K, Lean ME, Pendleton N, Punab M, Silman AJ, Wu FC, Thomson W, O'Neill TW; EMAS Study Group: **Genetic variation in the RANKL/RANK/OPG signaling pathway is associated with bone turnover and bone mineral density in men.** *J Bone Miner Res* 2010, **25:**1830-1838.

45. Kou I, Takahashi A, Urano T, Fukui N, Ito H, Ozaki K, Tanaka T, Hosoi T, Shiraki M, Inoue S, Nakamura Y, Kamatani N, Kubo M, Mori S, Ikegawa S: **Common variants in a novel gene, FONG on chromosome 2q33.1 confer risk of osteoporosis in Japanese.** *PLoS One* 2011, **6:**e19641.

46. Kung AW, Xiao SM, Cherny S, Li GH, Gao Y, Tso G, Lau KS, Luk KD, Liu JM, Cui B, Zhang MJ, Zhang ZL, He JW, Yue H, Xia WB, Luo LM, He SL, Kiel DP, Karasik D, Hsu YH, Cupples LA, Demissie S, Styrkarsdottir U, Halldorsson BV, Sigurdsson G, Thorsteinsdottir U, Stefansson K, Richards JB, Zhai G, Soranzo N, *et al.*: **Association of JAG1 with bone mineral density and osteoporotic fractures: a genome-wide association study and follow-up replication studies.** *Am J Hum Genet* 2010, **86:**229-239.

47. He JW, Yue H, Hu WW, Hu YQ, Zhang ZL: **Contribution of the sclerostin domain-containing protein 1 (SOSTDC1) gene to normal variation of peak bone mineral density in Chinese women and men.** *J Bone Miner Metab* 2011, **29:**571-581.

48. Holliday KL, Pye SR, Thomson W, Boonen S, Borghs H, Vanderschueren D, Gielen E, Huhtaniemi IT, Adams JE, Ward KA, Bartfai G, Casanueva F, Finn JD, Forti G, Giwercman A, Han TS, Kula K, Labrie F, Lean ME, Pendleton N, Punab M, Wu FC, O'Neill TW: **The ESR1 (6q25) locus is associated with calcaneal ultrasound parameters and radial volumetric bone mineral density in European men.** *PLoS One* 2011, **6:**e22037.

49. Yang TL, Guo Y, Liu YJ, Shen H, Liu YZ, Lei SF, Li J, Tian Q, Deng HW: **Genetic variants in the SOX6 gene are associated with bone mineral density in both Caucasian and Chinese populations.** *Osteoporos Int* 2012, **23:**781-787.

50. Lei SF, Shen H, Yang TL, Guo Y, Dong SS, Xu XH, Deng FY, Tian Q, Liu YJ, Liu YZ, Li J, Deng HW: **Genome-wide association study identifies HMGN3 locus for spine bone size variation in Chinese.** *Hum Genet* 2012, **131:**463-469.

51. Tan L, Liu R, Lei S, Pan R, Yang T, Yan H, Pei Y, Yang F, Zhang F, Pan F, Zhang Y, Hu H, Levy S, Deng H: **A genome-wide association analysis implicates SOX6 as a candidate gene for wrist bone mass.** *Sci China Life Sci* 2010, **53:**1065-1072.

52. Guo Y, Zhang LS, Yang TL, Tian Q, Xiong DH, Pei YF, Deng HW: **IL21R and PTH may underlie variation of femoral neck bone mineral density as revealed by a genome-wide association study.** *J Bone Miner Res* 2010, **25:**1042-1048.

53. Styrkarsdottir U, Halldorsson BV, Gudbjartsson DF, Tang NL, Koh JM, Xiao SM, Kwok TC, Kim GS, Chan JC, Cherny S, Lee SH, Kwok A, Ho S, Gretarsdottir S, Kostic JP, Palsson ST, Sigurdsson G, Sham PC, Kim BJ, Kung AW, Kim SY, Woo J, Leung PC, Kong A, Thorsteinsdottir U, Stefansson K: **European bone mineral density loci are also associated with BMD in East-Asian populations.** *PLoS*

One 2010, **5**:e13217.

54. Li WF, Hou SX, Yu B, Li MM, Ferec C, Chen JM: **Genetics of osteoporosis: accelerating pace in gene identification and validation.** *Hum Genet* 2010, **127**:249-285.

55. Guo Y, Wang JT, Liu H, Li M, Yang TL, Zhang XW, Liu YZ, Tian Q, Deng HW: **Are bone mineral density loci associated with hip osteoporotic fractures? A validation study on previously reported genome-wide association loci in a Chinese population.** *Genet Mol Res* 2012, **11**:202-210.

56. Richards JB, Kavvoura FK, Rivadeneira F, Styrkársdóttir U, Estrada K, Halldórsson BV, Hsu YH, Zillikens MC, Wilson SG, Mullin BH, Amin N, Aulchenko YS, Cupples LA, Deloukas P, Demissie S, Hofman A, Kong A, Karasik D, van Meurs JB, Oostra BA, Pols HA, Sigurdsson G, Thorsteinsdottir U, Soranzo N, Williams FM, Zhou Y, Ralston SH, Thorleifsson G, van Duijn CM, Kiel DP, *et al.*: **Collaborative meta-analysis: associations of 150 candidate genes with osteoporosis and osteoporotic fracture.** *Ann Intern Med* 2009, **151**:528-537.

57. Wang C, Zhang Z, Zhang H, He JW, Gu JM, Hu WW, Hu YQ, Li M, Liu YJ, Fu WZ, Yue H, Ke YH, Zhang ZL: **Susceptibility genes for osteoporotic fracture in postmenopausal Chinese women.** *J Bone Miner Res* 2012, **27**:2582-2591.

58. Urano T: **[Genetics of osteoporosis].** *Nihon Rinsho* 2011, **69**:1315-1321.

59. Lei SF, Wu S, Li LM, Deng FY, Xiao SM, Jiang C, Chen Y, Jiang H, Yang F, Tan LJ, Sun X, Zhu XZ, Liu MY, Liu YZ, Chen XD, Deng HW: **An in vivo genome wide gene expression study of circulating monocytes suggested GBP1, STAT1 and CXCL10 as novel risk genes for the differentiation of peak bone mass.** *Bone* 2009, **44**:1010-1014.

60. Chen XD, Xiao P, Lei SF, Liu YZ, Guo YF, Deng FY, Tan LJ, Zhu XZ, Chen FR, Recker RR, Deng HW: **Gene expression profiling in monocytes and SNP association suggest the importance of the STAT1 gene for osteoporosis in both Chinese and Caucasians.** *J Bone Miner Res* 2009, **25**:339-355.

61. You L, Sheng ZY, Tang CL, Chen L, Pan L, Chen JY: **High cholesterol diet increases osteoporosis risk via inhibiting bone formation in rats.** *Acta Pharmacol Sin* 2011, **32**:1498-1504.

62. Trost Z, Trebse R, Prezelj J, Komadina R, Logar DB, Marc J: **A microarray based identification of osteoporosis-related genes in primary culture of human osteoblasts.** *Bone* 2010, **46**:72-80.

63. Kominsky SL, Abdelmagid SM, Doucet M, Brady K, Weber KL: **Macrophage inflammatory protein-1 delta: a novel osteoclast stimulating factor secreted by renal cell carcinoma bone metastasis.** *Cancer Res* 2008, **68**:1261-1266.

64. Kulterer B, Friedl G, Jandrositz A, Sanchez-Cabo F, Prokesch A, Paar C, Scheideler M, Windhager R, Preisegger KH, Trajanoski Z: **Gene expression profiling of human mesenchymal stem cells derived from bone marrow during expansion and osteoblast differentiation.** *BMC Genomics* 2007, **8**:70.

65. Tanabe S, Sato Y, Suzuki T, Suzuki K, Nagao T, Yamaguchi T: **Gene expression profiling of human mesenchymal stem cells for identification of novel markers in early- and late-stage cell culture.** *J Biochem* 2008, **144**:399-408.

66. Xiao Y, Cui J, Shi Y, Le G: **Lipoic acid increases the expression of genes involved in bone formation in mice fed a high-fat diet.** *Nutr Res* 2011, **31**:309-317.

67. Tarroni P, Villa I, Mrak E, Zolezzi F, Mattioli M, Gattuso C, Rubinacci A: **Microarray analysis of 1,25(OH)$_2$D$_3$ regulated gene expression in human primary osteoblasts.** *J Cell Biochem* 2012, **113**:640-649.

68. Grigsby IF, Pham L, Gopalakrishnan R, Mansky LM, Mansky KC: **Downregulation of Gnas, Got2 and Snord32a following tenofovir exposure of primary osteoclasts.** *Biochem Biophys Res Commun* 2011, **391**:1324-1329.

69. Bian Q, Liu SF, Huang JH, Yang Z, Tang DZ, Zhou Q, Ning Y, Zhao YJ, Lu S, Shen ZY, Wang YJ: **Oleanolic acid exerts an osteoprotective effect in ovariectomy-induced osteoporotic rats and stimulates the osteoblastic differentiation of bone mesenchymal stem cells in vitro.** *Menopause* 2012, **19**:225-233.

70. Li X, Liu H, Qin L, Tamasi J, Bergenstock M, Shapses S, Feyen JH, Notterman DA, Partridge NC: **Determination of dual effects of parathyroid hormone on skeletal gene expression in vivo by microarray and network analysis.** *J Biol Chem* 2007, **282**:33086-33097.

71. Farber CR: **Systems genetics: a novel approach to dissect the genetic basis of osteoporosis.** *Curr Osteoporos Rep* 2012, **10**:228-235.

72. Martin A, Liu S, David V, Li H, Karydis A, Feng JQ, Quarles LD: **Bone proteins PHEX and DMP1 regulate fibroblastic growth factor Fgf23 expression in osteocytes through a common pathway involving FGF receptor (FGFR) signaling.** *FASEB J* 2011, **25**:2551-2562.

73. Choi HY, Dieckmann M, Herz J, Niemeier A: **Lrp4, a novel receptor for**

74. Dickkopf 1 and sclerostin, is expressed by osteoblasts and regulates bone growth and turnover in vivo. *PLoS One* 2009, **4**:e7930.

74. Reppe S, Refvem H, Gautvik VT, Olstad OK, Hovring PI, Reinholt FP, Holden M, Frigessi A, Jemtland R, Gautvik KM: **Eight genes are highly associated with BMD variation in postmenopausal Caucasian women.** *Bone* 2010, **46**:604-612.

75. Alves RD, Eijken M, Swagemakers S, Chiba H, Titulaer MK, Burgers PC, Luider TM, van Leeuwen JP: **Proteomic analysis of human osteoblastic cells: relevant proteins and functional categories for differentiation.** *J Proteome Res* 2010, **9**:4688-4700.

76. Taniguchi T, Kido S, Yamauchi E, Abe M, Matsumoto T, Taniguchi H: **Induction of endosomal/lysosomal pathways in differentiating osteoblasts as revealed by combined proteomic and transcriptomic analyses.** *FEBS Lett* 2010, **584**:3969-3974.

77. Kumar A, Singh AK, Gautam AK, Chandra D, Singh D, Changkija B, Singh MP, Trivedi R: **Identification of kaempferol-regulated proteins in rat calvarial osteoblasts during mineralization by proteomics.** *Proteomics* 2010, **10**:1730-1739.

78. Zhu Z, Xue LM, Han T, Jiao L, Qin LP, Li YS, Zheng HC, Zhang QY: **Antiosteoporotic effects and proteomic characterization of the target and mechanism of an Er-Xian Decoction on osteoblastic UMR-106 and osteoclasts induced from RAW264.7.** *Molecules* 2010, **15**:4695-4710.

79. Hong D, Chen HX, Yu HQ, Liang Y, Wang C, Lian QQ, Deng HT, Ge RS: **Morphological and proteomic analysis of early stage of osteoblast differentiation in osteoblastic progenitor cells.** *Exp Cell Res* 2010, **316**:2291-2300.

80. Kim WK, Bae KH, Choi HR, Kim DH, Choi KS, Cho YS, Kim HD, Park SG, Park BC, Ko Y, Lee SC: **Leukocyte common antigen-related (LAR) tyrosine phosphatase positively regulates osteoblast differentiation by modulating extracellular signal-regulated kinase (ERK) activation.** *Mol Cells* 2010, **30**:335-340.

81. Saad FA, Hofstaetter JG: **Proteomic analysis of mineralising osteoblasts identifies novel genes related to bone matrix mineralisation.** *Int Orthop* 2011, **35**:447-451.

82. Choi YA, Lim J, Kim KM, Acharya B, Cho JY, Bae YC, Shin HI, Kim SY, Park EK: **Secretome analysis of human BMSCs and identification of SMOC1 as an important ECM protein in osteoblast differentiation.** *J Proteome Res* 2010, **9**:2946-2956.

83. Zhang H, Lu W, Zhao Y, Rong P, Cao R, Gu W, Xiao J, Miao D, Lappe J, Recker R, Xiao GG: **Adipocytes derived from human bone marrow mesenchymal stem cells exert inhibitory effects on osteoblastogenesis.** *Curr Mol Med* 2011, **11**:489-502.

84. Kendler DL, Roux C, Benhamou CL, Brown JP, Lillestol M, Siddhanti S, Man HS, San Martin J, Bone HG: **Effects of denosumab on bone mineral density and bone turnover in postmenopausal women transitioning from alendronate therapy.** *J Bone Miner Res* 2010, **25**:72-81.

85. Kostenuik PJ, Nguyen HQ, McCabe J, Warmington KS, Kurahara C, Sun N, Chen C, Li L, Cattley RC, Van G, Scully S, Elliott R, Grisanti M, Morony S, Tan HL, Asuncion F, Li X, Ominsky MS, Stolina M, Dwyer D, Dougall WC, Hawkins N, Boyle WJ, Simonet WS, Sullivan JK: **Denosumab, a fully human monoclonal antibody to RANKL, inhibits bone resorption and increases BMD in knock-in mice that express chimeric (murine/human) RANKL.** *J Bone Miner Res* 2009, **24**:182-195.

86. Guo D, Keightley A, Guthrie J, Veno PA, Harris SE, Bonewald LF: **Identification of osteocyte-selective proteins.** *Proteomics* 2010, **10**:3688-3698.

87. Leupin O, Piters E, Halleux C, Hu S, Kramer I, Morvan F, Bouwmeester T, Schirle M, Bueno-Lozano M, Fuentes FJ, Itin PH, Boudin E, de Freitas F, Jennes K, Brannetti B, Charara N, Ebersbach H, Geisse S, Lu CX, Bauer A, Van Hul W, Kneissel M: **Bone overgrowth-associated mutations in the LRP4 gene impair sclerostin facilitator function.** *J Biol Chem* 2011, **286**:19489-19500.

88. Bab I, Smoum R, Bradshaw H, Mechoulam R: **Skeletal lipidomics: regulation of bone metabolism by fatty acid amide family.** *Br J Pharmacol* 2011, **163**:1441-1446.

89. Deng FY, Lei SF, Chen XD, Tan LJ, Zhu XZ, Deng HW: **An integrative study ascertained SOD2 as a susceptibility gene for osteoporosis in Chinese.** *J Bone Miner Res* 2011, **26**:2695-2701.

90. Shao C, Chen L, Lu C, Shen CL, Gao W: **A gel-based proteomic analysis of the effects of green tea polyphenols on ovariectomized rats.** *Nutrition* 2011, **27**:681-686.

91. Hamilton JP: **Epigenetics: principles and practice.** *Dig Dis* 2011, **29**:130-135.

92. Graff J, Mansuy IM: **Epigenetic dysregulation in cognitive disorders.** *Eur J*

Neurosci 2009, **30**:1-8.

93. Brooks WH, Le Dantec C, Pers JO, Youinou P, Renaudineau Y: **Epigenetics and autoimmunity.** *J Autoimmun* 2010, **34**:J207-219.

94. Calvanese V, Lara E, Kahn A, Fraga MF: **The role of epigenetics in aging and age-related diseases.** *Ageing Res Rev* 2009, **8**:268-276.

95. Barter MJ, Bui C, Young DA: **Epigenetic mechanisms in cartilage and osteoarthritis: DNA methylation, histone modifications and microRNAs.** *Osteoarthritis Cartilage* 2012, **20**:339-349.

96. Berdasco M, Esteller M: **DNA methylation in stem cell renewal and multipotency.** *Stem Cell Res Ther* 2011, **2**:42.

97. Hsiao SH, Lee KD, Hsu CC, Tseng MJ, Jin VX, Sun WS, Hung YC, Yeh KT, Yan PS, Lai YY, Sun HS, Lu YJ, Chang YS, Tsai SJ, Huang TH, Leu YW: **DNA methylation of the Trip10 promoter accelerates mesenchymal stem cell lineage determination.** *Biochem Biophys Res Commun* 2010, **400**:305-312.

98. Delgado-Calle J, Sanudo C, Bolado A, Fernandez AF, Arozamena J, Pascual-Carra MA, Rodriguez-Rey JC, Fraga MF, Bonewald L, Riancho JA: **DNA methylation contributes to the regulation of sclerostin expression in human osteocytes.** *J Bone Miner Res* 2011, **27**:926-937.

99. Delgado-Calle J, Sañudo C, Fernández AF, García-Renedo R, Fraga MF, Riancho JA: **Role of DNA methylation in the regulation of the RANKL-OPG system in human bone.** *Epigenetics* 2012, **7**:83-91.

100. Han JW, Yoon YS: **Epigenetic landscape of pluripotent stem cells.** *Antioxid Redox Signal* 2012, **17**:205-223.

101. Holroyd C, Harvey N, Dennison E, Cooper C: **Epigenetic influences in the developmental origins of osteoporosis.** *Osteoporos Int* 2012, **23**:401-410.

102. You L, Pan L, Chen L, Chen JY, Zhang X, Lv Z, Fu D: **Suppression of zinc finger protein 467 alleviates osteoporosis through promoting differentiation of adipose derived stem cells to osteoblasts.** *J Transl Med* 2012, **10**:11.

103. Zupan J, Mencej-Bedrac S, Jurkovic-Mlakar S, Prezelj J, Marc J: **Gene-gene interactions in RANK/RANKL/OPG system influence bone mineral density in postmenopausal women.** *J Steroid Biochem Mol Biol* 2010, **118**:102-106.

104. King TD, Suto MJ, Li Y: **The Wnt/beta-catenin signaling pathway: a potential therapeutic target in the treatment of triple negative breast cancer.** *J Cell Biochem* 2012, **113**:13-18.

105. Pineda B, Tarin JJ, Hermenegildo C, Laporta P, Cano A, Garcia-Perez MA: **Gene-gene interaction between CD40 and CD40L reduces bone mineral density and increases osteoporosis risk in women.** *Osteoporos Int* 2011, **22**:1451-1458.

106. Sonoda T, Takada J, Iba K, Asakura S, Yamashita T, Mori M: **Interaction between ESRalpha polymorphisms and environmental factors in osteoporosis.** *J Orthop Res* 2012, **30**:1529-1534.

107. Farber CR, Bennett BJ, Orozco L, Zou W, Lira A, Kostem E, Kang HM, Furlotte N, Berberyan A, Ghazalpour A, Suwanwela J, Drake TA, Eskin E, Wang QT, Teitelbaum SL, Lusis AJ: **Mouse genome-wide association and systems genetics identify Asxl2 as a regulator of bone mineral density and osteoclastogenesis.** *PLoS Genet* 2011, **7**:e1002038.

108. Rojo Venegas K, Aguilera Gomez M, Eisman JA, Garcia Sanchez A, Faus Dader MJ, Calleja Hernandez MA: **Pharmacogenetics of osteoporosis-related bone fractures: moving towards the harmonization and validation of polymorphism diagnostic tools.** *Pharmacogenomics* 2010, **11**:1287-1303.

109. Shiraki M, Sugimoto T, Nakamura T: **Effects of a single injection of teriparatide on bone turnover markers in postmenopausal women.** *Osteoporos Int* 2013, **24**: 219-226.